Thomas J Hudson

List of Publications by Year in Descending Order

112 papers	24,774 citations	62 h-index	118 g-index
118 ext. papers	27,853 ext. citations	14 avg, IF	5.52 L-index

#	Paper	IF	Citations
112	Molecular and Pathology Features of Colorectal Tumors and Patient Outcomes Are Associated with and Its Subspecies. *Cancer Epidemiology Biomarkers and Prevention*, **2021**,	4	1
111	Genetic architectures of proximal and distal colorectal cancer are partly distinct. *Gut*, **2021**, 70, 1325-1334	19.2	7
110	Cumulative Burden of Colorectal Cancer-Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. *Gastroenterology*, **2020**, 158, 1274-1286.e12	13.3	47
109	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. *Nature Communications*, **2020**, 11, 3644	17.4	16
108	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. *American Journal of Human Genetics*, **2020**, 107, 432-444	11	31
107	Activation of hedgehog signaling associates with early disease progression in chronic lymphocytic leukemia. *Blood*, **2019**, 133, 2651-2663	2.2	10
106	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. *Journal of the National Cancer Institute*, **2019**, 111, 146-157	9.7	67
105	Discovery of common and rare genetic risk variants for colorectal cancer. *Nature Genetics*, **2019**, 51, 76-87	36.3	177
104	Simulating thermal effects of MR-guided focused ultrasound in cortical bone and its surrounding tissue. *Medical Physics*, **2018**, 45, 506-519	4.4	9
103	Disease variants alter transcription factor levels and methylation of their binding sites. *Nature Genetics*, **2017**, 49, 131-138	36.3	252
102	Genome-Wide DNA Methylation Analysis Reveals Epigenetic Dysregulation of MicroRNA-34A in TP53-Associated Cancer Susceptibility. *Journal of Clinical Oncology*, **2016**, 34, 3697-3704	2.2	25
101	Common variants in the obesity-associated genes FTO and MC4R are not associated with risk of colorectal cancer. *Cancer Epidemiology*, **2016**, 44, 1-4	2.8	9
100	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. *Gastroenterology*, **2016**, 150, 1633-1645	13.3	64
99	Genome-Wide Interaction Analyses between Genetic Variants and Alcohol Consumption and Smoking for Risk of Colorectal Cancer. *PLoS Genetics*, **2016**, 12, e1006296	6	30
98	Transcriptome-wide characterization of the endogenous miR-34A-p53 tumor suppressor network. *Oncotarget*, **2016**, 7, 49611-49622	3.3	8
97	Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. *Nature Biotechnology*, **2016**, 34, 531-8	44.5	196
96	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. *Nature Communications*, **2015**, 6, 7138	17.4	106

95	Long-range epigenetic regulation is conferred by genetic variation located at thousands of independent loci. *Nature Communications*, **2015**, 6, 6326	17.4	90
94	Association of aspirin and NSAID use with risk of colorectal cancer according to genetic variants. *JAMA - Journal of the American Medical Association*, **2015**, 313, 1133-42	27.4	135
93	A genome-wide association study for colorectal cancer identifies a risk locus in 14q23.1. *Human Genetics*, **2015**, 134, 1249-1262	6.3	25
92	Identification of a common variant with potential pleiotropic effect on risk of inflammatory bowel disease and colorectal cancer. *Carcinogenesis*, **2015**, 36, 999-1007	4.6	21
91	GLI2 inhibition abrogates human leukemia stem cell dormancy. *Journal of Translational Medicine*, **2015**, 13, 98	8.5	66
90	Spatial genomic heterogeneity within localized, multifocal prostate cancer. *Nature Genetics*, **2015**, 47, 736-45	36.3	306
89	Meta-analysis identifies seven susceptibility loci involved in the atopic march. *Nature Communications*, **2015**, 6, 8804	17.4	105
88	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. *Nature Communications*, **2015**, 6, 10001	17.4	199
87	The effect of 5-fluorouracil/leucovorin chemotherapy on CpG methylation, or the confounding role of leukocyte heterogeneity: An illustration. *Genomics*, **2015**, 106, 340-7	4.3	4
86	Identification of pre-leukaemic haematopoietic stem cells in acute leukaemia. *Nature*, **2014**, 506, 328-33	50.4	1011
85	No evidence of gene-calcium interactions from genome-wide analysis of colorectal cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2014**, 23, 2971-6	4	9
84	A Pan-BCL2 inhibitor renders bone-marrow-resident human leukemia stem cells sensitive to tyrosine kinase inhibition. *Cell Stem Cell*, **2013**, 12, 316-28	18	140
83	Discovery of cross-reactive probes and polymorphic CpGs in the Illumina Infinium HumanMethylation450 microarray. *Epigenetics*, **2013**, 8, 203-9	5.7	953
82	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. *Gastroenterology*, **2013**, 144, 799-807.e24	13.3	250
81	Meta-analysis of new genome-wide association studies of colorectal cancer risk. *Human Genetics*, **2012**, 131, 217-34	6.3	173
80	Analysis of early C2C12 myogenesis identifies stably and differentially expressed transcriptional regulators whose knock-down inhibits myoblast differentiation. *Physiological Genomics*, **2012**, 44, 183-97	3.6	25
79	MLH1 region polymorphisms show a significant association with CpG island shore methylation in a large cohort of healthy individuals. *PLoS ONE*, **2012**, 7, e51531	3.7	17
78	Genetic variants and susceptibility to neurological complications following West Nile virus infection. *Journal of Infectious Diseases*, **2011**, 204, 1031-7	7	28

77	Cancer genome variation in children, adolescents, and young adults. *Cancer*, **2011**, 117, 2262-7	6.4	4
76	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
75	A cis-acting regulatory variant in the IL2RA locus. *Journal of Immunology*, **2009**, 183, 5158-62	5.3	19
74	Identification of susceptibility genes for complex diseases using pooling-based genome-wide association scans. *Human Genetics*, **2009**, 125, 305-18	6.3	66
73	Analyses of associations with asthma in four asthma population samples from Canada and Australia. *Human Genetics*, **2009**, 125, 445-59	6.3	91
72	CAG expansion in the Huntington disease gene is associated with a specific and targetable predisposing haplogroup. *American Journal of Human Genetics*, **2009**, 84, 351-66	11	163
71	Asthma and genes encoding components of the vitamin D pathway. *Respiratory Research*, **2009**, 10, 98	7.3	110
70	Personalized medicine: a transformative approach is needed. *Cmaj*, **2009**, 180, 911-3	3.5	6
69	Genome-wide association scan identifies a colorectal cancer susceptibility locus on 11q23 and replicates risk loci at 8q24 and 18q21. *Nature Genetics*, **2008**, 40, 631-7	36.3	486
68	Meta-analysis of genome-wide association data identifies four new susceptibility loci for colorectal cancer. *Nature Genetics*, **2008**, 40, 1426-35	36.3	457
67	Identification of a chromosome 8p locus for early-onset coronary heart disease in a French Canadian population. *European Journal of Human Genetics*, **2008**, 16, 105-14	5.3	15
66	Genetic variation in immune signaling genes differentially expressed in asthmatic lung tissues. *Journal of Allergy and Clinical Immunology*, **2008**, 122, 529-36.e17	11.5	13
65	Allele-specific expression in the germline of patients with familial pancreatic cancer: an unbiased approach to cancer gene discovery. *Cancer Biology and Therapy*, **2008**, 7, 135-44	4.6	37
64	Disruption of AP1S1, causing a novel neurocutaneous syndrome, perturbs development of the skin and spinal cord. *PLoS Genetics*, **2008**, 4, e1000296	6	102
63	Differential allelic expression in the human genome: a robust approach to identify genetic and epigenetic cis-acting mechanisms regulating gene expression. *PLoS Genetics*, **2008**, 4, e1000006	6	190
62	Sex-stratified linkage analysis identifies a female-specific locus for IgE to cockroach in Costa Ricans. *American Journal of Respiratory and Critical Care Medicine*, **2008**, 177, 830-6	10.2	63
61	A genome-wide approach to identifying novel-imprinted genes. *Human Genetics*, **2008**, 122, 625-34	6.3	56
60	Replication of an association between 17q21 SNPs and asthma in a French-Canadian familial collection. *Human Genetics*, **2008**, 123, 93-5	6.3	59

59	Correction of population stratification in large multi-ethnic association studies. *PLoS ONE*, **2008**, 3, e1382	3.7	53
58	Genes to diseases (G2D) computational method to identify asthma candidate genes. *PLoS ONE*, **2008**, 3, e2907	3.7	30
57	Patterns of variation in DNA segments upstream of transcription start sites. *Human Mutation*, **2007**, 28, 441-50	4.7	4
56	Genome-wide association scan identifies a colorectal cancer susceptibility locus on chromosome 8q24. *Nature Genetics*, **2007**, 39, 989-94	36.3	609
55	A genome-wide association study identifies novel risk loci for type 2 diabetes. *Nature*, **2007**, 445, 881-5	50.4	2327
54	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
53	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
52	A genetic linkage map of the vervet monkey (Chlorocebus aethiops sabaeus). *Mammalian Genome*, **2007**, 18, 347-60	3.2	46
51	Toward further mapping of the association between the IL2RA locus and type 1 diabetes. *Diabetes*, **2007**, 56, 1174-6	0.9	76
50	1alpha,25-dihydroxy-vitamin D3 stimulation of bronchial smooth muscle cells induces autocrine, contractility, and remodeling processes. *Physiological Genomics*, **2007**, 29, 161-8	3.6	102
49	Association of urokinase-type plasminogen activator with asthma and atopy. *American Journal of Respiratory and Critical Care Medicine*, **2007**, 175, 1109-16	10.2	41
48	Influence of human genome polymorphism on gene expression. *Human Molecular Genetics*, **2006**, 15 Spec No 1, R9-16	5.6	106
47	An evaluation of the performance of tag SNPs derived from HapMap in a Caucasian population. *PLoS Genetics*, **2006**, 2, e27	6	81
46	PRKCA and multiple sclerosis: association in two independent populations. *PLoS Genetics*, **2006**, 2, e42	6	37
45	Resources for genetic variation studies. *Annual Review of Genomics and Human Genetics*, **2006**, 7, 443-57	9.7	13
44	Detection and characterization of DNA variants in the promoter regions of hundreds of human disease candidate genes. *Genomics*, **2006**, 87, 704-10	4.3	25
43	Mapping cis-acting regulatory variation in recombinant congenic strains. *Physiological Genomics*, **2006**, 25, 294-302	3.6	19
42	Mapping common regulatory variants to human haplotypes. *Human Molecular Genetics*, **2005**, 14, 3963-71	5.6	82

41	Functional promoter SNPs in cell cycle checkpoint genes. *Human Molecular Genetics*, **2005**, 14, 2641-8	5.6	26
40	A predominantly clonal multi-institutional outbreak of Clostridium difficile-associated diarrhea with high morbidity and mortality. *New England Journal of Medicine*, **2005**, 353, 2442-9	59.2	1589
39	A predominant role for the HLA class II region in the association of the MHC region with multiple sclerosis. *Nature Genetics*, **2005**, 37, 1108-12	36.3	252
38	An atypical form of erythrokeratodermia variabilis maps to chromosome 7q22. *Human Genetics*, **2005**, 116, 167-71	6.3	30
37	Anatomy of a founder effect: myotonic dystrophy in Northeastern Quebec. *Human Genetics*, **2005**, 117, 177-87	6.3	42
36	Survey of allelic expression using EST mining. *Genome Research*, **2005**, 15, 1584-91	9.7	99
35	Characterization of a common susceptibility locus for asthma-related traits. *Science*, **2004**, 304, 300-4	33.3	382
34	Functional classes of bronchial mucosa genes that are differentially expressed in asthma. *BMC Genomics*, **2004**, 5, 21	4.5	93
33	Cis-acting regulatory variation in the human genome. *Science*, **2004**, 306, 647-50	33.3	218
32	Association of vitamin D receptor genetic variants with susceptibility to asthma and atopy. *American Journal of Respiratory and Critical Care Medicine*, **2004**, 170, 967-73	10.2	192
31	A survey of genetic and epigenetic variation affecting human gene expression. *Physiological Genomics*, **2004**, 16, 184-93	3.6	201
30	Identification of a gene causing human cytochrome c oxidase deficiency by integrative genomics. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 605-10	11.5	472
29	5Tflanking variants of resistin are associated with obesity. *Diabetes*, **2002**, 51, 1629-34	0.9	129
28	Polymorphisms in toll-like receptor 4 are not associated with asthma or atopy-related phenotypes. *American Journal of Respiratory and Critical Care Medicine*, **2002**, 166, 1449-56	10.2	138
27	Characterization of variability in large-scale gene expression data: implications for study design. *Genomics*, **2002**, 79, 104-13	4.3	165
26	A missense mutation (R565W) in cirhin (FLJ14728) in North American Indian childhood cirrhosis. *American Journal of Human Genetics*, **2002**, 71, 1443-9	11	88
25	A susceptibility locus for asthma-related traits on chromosome 7 revealed by genome-wide scan in a founder population. *Nature Genetics*, **2001**, 28, 87-91	36.3	148
24	A radiation hybrid map of mouse genes. *Nature Genetics*, **2001**, 29, 201-5	36.3	61

23	. *Nature Genetics*, **2001**, 28, 87-91	36.3	58
22	A second-generation association study of the 5q31 cytokine gene cluster and the interleukin-4 receptor in asthma. *Genomics*, **2001**, 77, 35-42	4.3	44
21	A sequence variation in the mitochondrial glycerol-3-phosphate dehydrogenase gene is associated with increased plasma glycerol and free fatty acid concentrations among French Canadians. *Molecular Genetics and Metabolism*, **2001**, 72, 209-17	3.7	8
20	A novel syndrome affecting multiple mitochondrial functions, located by microcell-mediated transfer to chromosome 2p14-2p13. *American Journal of Human Genetics*, **2001**, 68, 386-96	11	62
19	A genomewide linkage-disequilibrium scan localizes the Saguenay-Lac-Saint-Jean cytochrome oxidase deficiency to 2p16. *American Journal of Human Genetics*, **2001**, 68, 397-409	11	37
18	A progressive autosomal recessive cataract locus maps to chromosome 9q13-q22. *American Journal of Human Genetics*, **2001**, 68, 772-7	11	44
17	Manganese superoxide dismutase induction by iron is impaired in Friedreich ataxia cells. *FEBS Letters*, **2001**, 509, 101-5	3.8	63
16	ARSACS, a spastic ataxia common in northeastern QuÞec, is caused by mutations in a new gene encoding an 11.5-kb ORF. *Nature Genetics*, **2000**, 24, 120-5	36.3	332
15	Large-scale discovery and genotyping of single-nucleotide polymorphisms in the mouse. *Nature Genetics*, **2000**, 24, 381-6	36.3	371
14	The common PPARgamma Pro12Ala polymorphism is associated with decreased risk of type 2 diabetes. *Nature Genetics*, **2000**, 26, 76-80	36.3	1486
13	Complete nucleotide sequence and genomic structure of the human NRAMP1 gene region on chromosome region 2q35. *Mammalian Genome*, **2000**, 11, 755-62	3.2	25
12	Localization of a recessive gene for North American Indian childhood cirrhosis to chromosome region 16q22-and identification of a shared haplotype. *American Journal of Human Genetics*, **2000**, 67, 222-8	11	34
11	An optimized set of human telomere clones for studying telomere integrity and architecture. *American Journal of Human Genetics*, **2000**, 67, 320-32	11	270
10	Radiation hybrid map of the mouse genome. *Nature Genetics*, **1999**, 22, 384-7	36.3	103
9	A YAC-based physical map of the mouse genome. *Nature Genetics*, **1999**, 22, 388-93	36.3	68
8	Location score and haplotype analyses of the locus for autosomal recessive spastic ataxia of Charlevoix-Saguenay, in chromosome region 13q11. *American Journal of Human Genetics*, **1999**, 64, 768-75	11	63
7	Autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS): high-resolution physical and transcript map of the candidate region in chromosome region 13q11. *Genomics*, **1999**, 62, 156-64	4.3	20
6	Autosomal recessive spastic ataxia of Charlevoix-Saguenay. *Neuromuscular Disorders*, **1998**, 8, 474-9	2.9	89

5	Genomewide scan of multiple sclerosis in Finnish multiplex families. *American Journal of Human Genetics*, **1997**, 61, 1379-87	11	267
4	Characterization of short tandem repeats from thirty-one human telomeres. *Genome Research*, **1997**, 7, 917-23	9.7	34
3	A PCR-based linkage map of human chromosome 1. *Genomics*, **1993**, 15, 251-8	4.3	36
2	Functional normalization of 450k methylation array data improves replication in large cancer studies		5
1	Large-Scale Uniform Analysis of Cancer Whole Genomes in Multiple Computing Environments		14