William J Tapper

List of Publications by Year
in descending order

51 papers	2,621 citations	394421 19 h-index	214800 47 g-index
52 all docs	52 docs citations	52 times ranked	5375 citing authors

#	Article	IF	Citations
1	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
2	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
3	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
4	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
5	Genetic variation at MECOM, TERT, JAK2 and HBS1L-MYB predisposes to myeloproliferative neoplasms. Nature Communications, 2015, 6, 6691.	12.8	145
6	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
7	Clonal myelopoiesis in the UK Biobank cohort: ASXL1 mutations are strongly associated with smoking. Leukemia, 2020, 34, 2660-2672.	7.2	96
8	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
9	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
10	Recurrent activating STAT5B N642H mutation in myeloid neoplasms with eosinophilia. Leukemia, 2019, 33, 415-425.	7.2	65
11	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
12	The influence of genetic variation in 30 selected genes on the clinical characteristics of early onset breast cancer. Breast Cancer Research, 2008, 10, R108.	5.0	49
13	Clonal myelopoiesis promotes adverse outcomes in chronic kidney disease. Leukemia, 2022, 36, 507-515.	7.2	49
14	A Genome Wide Meta-Analysis Study for Identification of Common Variation Associated with Breast Cancer Prognosis. PLoS ONE, 2014, 9, e101488.	2.5	42
15	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
16	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
17	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
18	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28

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19	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	5.0	24
20	Megalencephaly Syndromes: Exome Pipeline Strategies for Detecting Low-Level Mosaic Mutations. PLoS ONE, 2014, 9, e86940.	2.5	20
21	Analysis of Mutation and Loss of Heterozygosity by Whole-Exome Sequencing Yields Insights into Pseudomyxoma Peritonei. Journal of Molecular Diagnostics, 2018, 20, 635-642.	2.8	19
22	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	2.5	19
23	Germline variation in ADAMTSL1 is associated with prognosis following breast cancer treatment in young women. Nature Communications, 2017, 8, 1632.	12.8	18
24	Exome Sequencing in Classic Hairy Cell Leukaemia Reveals Widespread Variation in Acquired Somatic Mutations between Individual Tumours Apart from the Signature BRAF V(600)E Lesion. PLoS ONE, 2016, 11, e0149162.	2.5	17
25	Development of childhood asthma prediction models using machine learning approaches. Clinical and Translational Allergy, 2021, 11, e12076.	3.2	17
26	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	12.8	16
27	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407.	1.8	15
28	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
29	Whole genome sequences are required to fully resolve the linkage disequilibrium structure of human populations. BMC Genomics, 2015, 16, 666.	2.8	14
30	Pathogenic Variants in CHEK2 Are Associated With an Adverse Prognosis in Symptomatic Early-Onset Breast Cancer. JCO Precision Oncology, 2020, 4, 472-485.	3.0	14
31	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. Breast Cancer Research and Treatment, 2020, 181, 423-434.	2.5	14
32	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
33	Polymorphism at 19q13.41 Predicts Breast Cancer Survival Specifically after Endocrine Therapy. Clinical Cancer Research, 2015, 21, 4086-4096.	7.0	12
34	Genome-wide association study identifies novel susceptibility loci for KIT D816V positive mastocytosis. American Journal of Human Genetics, 2021, 108, 284-294.	6.2	12
35	PRR14L mutations are associated with chromosome 22 acquired uniparental disomy, age-related clonal hematopoiesis and myeloid neoplasia. Leukemia, 2019, 33, 1184-1194.	7.2	11
36	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9

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37	Meta-analysis of three genome-wide association studies identifies two loci that predict survival and treatment outcome in breast cancer. Oncotarget, 2018, 9, 4249-4257.	1.8	8
38	Long-Term Cognitive Outcome following Aneurysmal Subarachnoid Haemorrhage. Journal of Stroke and Cerebrovascular Diseases, 2022, 31, 106184.	1.6	8
39	Integration of Genomic Risk Scores to Improve the Prediction of Childhood Asthma Diagnosis. Journal of Personalized Medicine, 2022, 12, 75.	2.5	8
40	A Comparison of Methods to Detect Recombination Hotspots. Human Heredity, 2008, 66, 157-169.	0.8	7
41	Type C <scp>TP</scp>53â€<scp>CDKN</scp>1A pathway dysfunction occurs independently of <scp>CDKN</scp>1A gene polymorphisms in chronic lymphocytic leukaemia and is associated with <scp>TP</scp>53 abnormalities. British Journal of Haematology, 2017, 178, 824-826.	2.5	7
42	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	5.0	7
43	Mapping a gene for rheumatoid arthritis on chromosome 18q21. BMC Proceedings, 2007, 1, S18.	1.6	6
44	A CRISPR and high-content imaging assay compliant with ACMG/AMP guidelines for clinical variant interpretation in ciliopathies. Human Genetics, 2021, 140, 593-607.	3.8	6
45	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	6.2	6
46	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
47	Genome-Wide Association Study of Clinical Outcome After Aneurysmal Subarachnoid Haemorrhage: Protocol. Translational Stroke Research, 2022, 13, 565-576.	4.2	5
48	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	3.3	2
49	Quantifying the cumulative effect of lowâ€penetrance genetic variants on breast cancer risk. Molecular Genetics & Genomic Medicine, 2015, 3, 182-188.	1.2	1
50	Single-cell exomes in an index case of amp1q21 multiple myeloma reveal more diverse mutanomes than the whole population. Blood, 2018, 132, 232-235.	1.4	1
51	Nonlinear effects of environment on childhood asthma susceptibility. Pediatric Allergy and Immunology, 2022, 33, e13777.	2.6	0