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	Clonal myelopoiesis promotes adverse outcomes in chronic kidney disease. Leukemia, 2022, 36, 507-515.	7.2	49
2	Long-Term Cognitive Outcome following Aneurysmal Subarachnoid Haemorrhage. Journal of Stroke and Cerebrovascular Diseases, 2022, 31, 106184.	1.6	8
3	Genome-Wide Association Study of Clinical Outcome After Aneurysmal Subarachnoid Haemorrhage: Protocol. Translational Stroke Research, 2022, 13, 565-576.	4.2	5
4	Integration of Genomic Risk Scores to Improve the Prediction of Childhood Asthma Diagnosis. Journal of Personalized Medicine, 2022, 12, 75.	2.5	8
5	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
6	Nonlinear effects of environment on childhood asthma susceptibility. Pediatric Allergy and Immunology, 2022, 33, e13777.	2.6	0
7	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
8	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
9	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
10	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
11	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9
12	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
13	Development of childhood asthma prediction models using machine learning approaches. Clinical and Translational Allergy, 2021, 11, e12076.	3.2	17
14	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
15	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
16	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
17	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
18	Clonal myelopoiesis in the UK Biobank cohort: ASXL1 mutations are strongly associated with smoking. Leukemia, 2020, 34, 2660-2672.	7.2	96

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19	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	3.3	2
20	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
21	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
22	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
23	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
24	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
25	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
26	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
27	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	5.0	24
28	Recurrent activating STAT5B N642H mutation in myeloid neoplasms with eosinophilia. Leukemia, 2019, 33, 415-425.	7.2	65
29	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
30	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
31	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
32	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
33	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
34	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
35	Germline variation in ADAMTSL1 is associated with prognosis following breast cancer treatment in young women. Nature Communications, 2017, 8, 1632.	12.8	18
36	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

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37	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
38	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
39	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
40	Quantifying the cumulative effect of lowâ€penetrance genetic variants on breast cancer risk. Molecular Genetics & Genomic Medicine, 2015, 3, 182-188.	1.2	1
41	Whole genome sequences are required to fully resolve the linkage disequilibrium structure of human populations. BMC Genomics, 2015, 16, 666.	2.8	14
42	Polymorphism at 19q13.41 Predicts Breast Cancer Survival Specifically after Endocrine Therapy. Clinical Cancer Research, 2015, 21, 4086-4096.	7.0	12
43	Genetic variation at MECOM, TERT, JAK2 and HBS1L-MYB predisposes to myeloproliferative neoplasms. Nature Communications, 2015, 6, 6691.	12.8	145
44	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
45	A Genome Wide Meta-Analysis Study for Identification of Common Variation Associated with Breast Cancer Prognosis. PLoS ONE, 2014, 9, e101488.	2.5	42
46	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	12.8	16
47	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
48	Megalencephaly Syndromes: Exome Pipeline Strategies for Detecting Low-Level Mosaic Mutations. PLoS ONE, 2014, 9, e86940.	2.5	20
49	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
50	A Comparison of Methods to Detect Recombination Hotspots. Human Heredity, 2008, 66, 157-169.	0.8	7
51	Mapping a gene for rheumatoid arthritis on chromosome 18q21. BMC Proceedings, 2007, 1, S18.	1.6	6