

David C Wedge

List of Publications by Citations

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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.

136
papers

27,834
citations

56
h-index

166
g-index

172
ext. papers

35,373
ext. citations

20.6
avg, IF

7.3
L-index

#	Paper	IF	Citations
136	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013 , 500, 415-21	50.4	5895
135	Mutational processes molding the genomes of 21 breast cancers. <i>Cell</i> , 2012 , 149, 979-93	56.2	1279
134	The landscape of cancer genes and mutational processes in breast cancer. <i>Nature</i> , 2012 , 486, 400-4	50.4	1264
133	Somatic CALR mutations in myeloproliferative neoplasms with nonmutated JAK2. <i>New England Journal of Medicine</i> , 2013 , 369, 2391-2405	59.2	1262
132	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016 , 534, 47-54	50.4	1193
131	Clinical and biological implications of driver mutations in myelodysplastic syndromes. <i>Blood</i> , 2013 , 122, 3616-27; quiz 3699	2.2	1169
130	Tumor evolution. High burden and pervasive positive selection of somatic mutations in normal human skin. <i>Science</i> , 2015 , 348, 880-6	33.3	983
129	The life history of 21 breast cancers. <i>Cell</i> , 2012 , 149, 994-1007	56.2	979
128	The evolutionary history of lethal metastatic prostate cancer. <i>Nature</i> , 2015 , 520, 353-357	50.4	857
127	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
126	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. <i>Science</i> , 2014 , 346, 251-6	33.3	752
125	Deciphering signatures of mutational processes operative in human cancer. <i>Cell Reports</i> , 2013 , 3, 246-59	10.6	725
124	Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. <i>Science</i> , 2014 , 346, 256-9	33.3	659
123	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. <i>Nature Communications</i> , 2014 , 5, 2997	17.4	564
122	Clock-like mutational processes in human somatic cells. <i>Nature Genetics</i> , 2015 , 47, 1402-7	36.3	531
121	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. <i>Nature Medicine</i> , 2015 , 21, 751-9	50.5	521
120	Distinct H3F3A and H3F3B driver mutations define chondroblastoma and giant cell tumor of bone. <i>Nature Genetics</i> , 2013 , 45, 1479-82	36.3	482

119	Genomic Evolution of Breast Cancer Metastasis and Relapse. <i>Cancer Cell</i> , 2017 , 32, 169-184.e7	24.3	346
118	Effect of mutation order on myeloproliferative neoplasms. <i>New England Journal of Medicine</i> , 2015 , 372, 601-612	59.2	334
117	The evolutionary history of 2,658 cancers. <i>Nature</i> , 2020 , 578, 122-128	50.4	307
116	Analysis of the genetic phylogeny of multifocal prostate cancer identifies multiple independent clonal expansions in neoplastic and morphologically normal prostate tissue. <i>Nature Genetics</i> , 2015 , 47, 367-372	36.3	292
115	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. <i>New England Journal of Medicine</i> , 2018 , 379, 1416-1430	59.2	256
114	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermuted cancers. <i>Nature Genetics</i> , 2015 , 47, 257-62	36.3	253
113	Genome sequencing and analysis of the Tasmanian devil and its transmissible cancer. <i>Cell</i> , 2012 , 148, 780-91	56.2	251
112	Mobile DNA in cancer. Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014 , 345, 1251343	33.3	250
111	Genome sequencing of normal cells reveals developmental lineages and mutational processes. <i>Nature</i> , 2014 , 513, 422-425	50.4	249
110	Tracking the origins and drivers of subclonal metastatic expansion in prostate cancer. <i>Nature Communications</i> , 2015 , 6, 6605	17.4	245
109	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2014 , 46, 116-25	36.3	244
108	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. <i>Cell</i> , 2018 , 173, 611-623.e17	56.2	228
107	Myelodysplastic syndromes are propagated by rare and distinct human cancer stem cells in vivo. <i>Cancer Cell</i> , 2014 , 25, 794-808	24.3	216
106	Association of a germline copy number polymorphism of APOBEC3A and APOBEC3B with burden of putative APOBEC-dependent mutations in breast cancer. <i>Nature Genetics</i> , 2014 , 46, 487-91	36.3	208
105	Recurrent PTPRB and PLCG1 mutations in angiosarcoma. <i>Nature Genetics</i> , 2014 , 46, 376-379	36.3	196
104	Whole exome sequencing of adenoid cystic carcinoma. <i>Journal of Clinical Investigation</i> , 2013 , 123, 2965-85.9		188
103	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. <i>Cell</i> , 2019 , 176, 1282-1294.e20	56.2	165
102	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. <i>Nature</i> , 2017 , 543, 714-718	50.4	157

101	Automated workflows for accurate mass-based putative metabolite identification in LC/MS-derived metabolomic datasets. <i>Bioinformatics</i> , 2011 , 27, 1108-12	7.2	156
100	Mutational signatures of ionizing radiation in second malignancies. <i>Nature Communications</i> , 2016 , 7, 12605	17.4	152
99	Frequent mutation of the major cartilage collagen gene COL2A1 in chondrosarcoma. <i>Nature Genetics</i> , 2013 , 45, 923-6	36.3	138
98	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. <i>Nature Communications</i> , 2017 , 8, 15936	17.4	125
97	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020 , 52, 306-319	36.3	122
96	Transmissible [corrected] dog cancer genome reveals the origin and history of an ancient cell lineage. <i>Science</i> , 2014 , 343, 437-440	33.3	116
95	Organoid cultures recapitulate esophageal adenocarcinoma heterogeneity providing a model for clonality studies and precision therapeutics. <i>Nature Communications</i> , 2018 , 9, 2983	17.4	113
94	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. <i>Nature Genetics</i> , 2018 , 50, 682-692	36.3	112
93	Is serum or plasma more appropriate for intersubject comparisons in metabolomic studies? An assessment in patients with small-cell lung cancer. <i>Analytical Chemistry</i> , 2011 , 83, 6689-97	7.8	106
92	CONSeQuence: prediction of reference peptides for absolute quantitative proteomics using consensus machine learning approaches. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.003384	7.6	101
91	Genomic patterns of progression in smoldering multiple myeloma. <i>Nature Communications</i> , 2018 , 9, 3363	7.4	99
90	Diagnostic value of H3F3A mutations in giant cell tumour of bone compared to osteoclast-rich mimics. <i>Journal of Pathology: Clinical Research</i> , 2015 , 1, 113-23	5.3	98
89	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. <i>Nature Communications</i> , 2019 , 10, 3835	17.4	94
88	Untargeted metabolic profiling identifies altered serum metabolites of type 2 diabetes mellitus in a prospective, nested case control study. <i>Clinical Chemistry</i> , 2015 , 61, 487-97	5.5	94
87	A comparison of Raman and FT-IR spectroscopy for the prediction of meat spoilage. <i>Food Control</i> , 2013 , 29, 461-470	6.2	90
86	Array-based evolution of DNA aptamers allows modelling of an explicit sequence-fitness landscape. <i>Nucleic Acids Research</i> , 2009 , 37, e6	20.1	85
85	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. <i>Journal of Pathology</i> , 2012 , 227, 446-55	9.4	72
84	DNMT3A mutations occur early or late in patients with myeloproliferative neoplasms and mutation order influences phenotype. <i>Haematologica</i> , 2015 , 100, e438-42	6.6	70

83	ascatNgs: Identifying Somatically Acquired Copy-Number Alterations from Whole-Genome Sequencing Data. <i>Current Protocols in Bioinformatics</i> , 2016 , 56, 15.9.1-15.9.17	24.2	60
82	Principles of Reconstructing the Subclonal Architecture of Cancers. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2017 , 7,	5.4	58
81	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021 , 184, 2239-2254.e39	56.2	57
80	The evolutionary landscape of colorectal tumorigenesis. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1661-1672.3	12.3	52
79	A comparison of different chemometrics approaches for the robust classification of electronic nose data. <i>Analytical and Bioanalytical Chemistry</i> , 2014 , 406, 7581-90	4.4	50
78	Analysis of a complete DNA-protein affinity landscape. <i>Journal of the Royal Society Interface</i> , 2010 , 7, 397-408	4.1	49
77	Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. <i>Genome Biology</i> , 2016 , 17, 250	18.3	48
76	Aptamer evolution for array-based diagnostics. <i>Analytical Biochemistry</i> , 2009 , 390, 203-5	3.1	45
75	pK(a) prediction from "Quantum Chemical Topology" descriptors. <i>Journal of Chemical Information and Modeling</i> , 2009 , 49, 1914-24	6.1	43
74	Differential and limited expression of mutant alleles in multiple myeloma. <i>Blood</i> , 2014 , 124, 3110-7	2.2	42
73	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. <i>Nature Communications</i> , 2017 , 8, 1221	17.4	40
72	Embryonal precursors of Wilms tumor. <i>Science</i> , 2019 , 366, 1247-1251	33.3	40
71	Real-time vapour sensing using an OFET-based electronic nose and genetic programming. <i>Sensors and Actuators B: Chemical</i> , 2009 , 143, 365-372	8.5	38
70	Neutral tumor evolution?. <i>Nature Genetics</i> , 2018 , 50, 1630-1633	36.3	38
69	Mitochondrial genetic diversity, selection and recombination in a canine transmissible cancer. <i>ELife</i> , 2016 , 5,	8.9	37
68	A community effort to create standards for evaluating tumor subclonal reconstruction. <i>Nature Biotechnology</i> , 2020 , 38, 97-107	44.5	35
67	The genetic heterogeneity and mutational burden of engineered melanomas in zebrafish models. <i>Genome Biology</i> , 2013 , 14, R113	18.3	33
66	On global-local artificial neural networks for function approximation. <i>IEEE Transactions on Neural Networks</i> , 2006 , 17, 942-52		33

65	Liquid chromatography-mass spectrometry calibration transfer and metabolomics data fusion. <i>Analytical Chemistry</i> , 2012 , 84, 9848-57	7.8	31
64	Genomic copy number predicts esophageal cancer years before transformation. <i>Nature Medicine</i> , 2020 , 26, 1726-1732	50.5	31
63	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. <i>Cell Reports</i> , 2016 , 16, 2032-46.6	46.6	30
62	Genetic and epigenetic intratumor heterogeneity impacts prognosis of lung adenocarcinoma. <i>Nature Communications</i> , 2020 , 11, 2459	17.4	29
61	In silico modelling of directed evolution: Implications for experimental design and stepwise evolution. <i>Journal of Theoretical Biology</i> , 2009 , 257, 131-41	2.3	28
60	The evolutionary history of 2,658 cancers		28
59	Fast randomization of large genomic datasets while preserving alteration counts. <i>Bioinformatics</i> , 2014 , 30, i617-23	7.2	27
58	The Genomic Landscape of Pancreatic and Periampullary Adenocarcinoma. <i>Cancer Research</i> , 2016 , 76, 5092-102	10.1	27
57	How Subclonal Modeling Is Changing the Metastatic Paradigm. <i>Clinical Cancer Research</i> , 2017 , 23, 630-635.9	635.9	26
56	Low cost, portable, fast multiparameter data acquisition system for organic transistor odour sensors. <i>Sensors and Actuators B: Chemical</i> , 2009 , 137, 586-591	8.5	25
55	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes		25
54	A practical guide to cancer subclonal reconstruction from DNA sequencing. <i>Nature Methods</i> , 2021 , 18, 144-155	21.6	25
53	Genomic evidence supports a clonal diaspora model for metastases of esophageal adenocarcinoma. <i>Nature Genetics</i> , 2020 , 52, 74-83	36.3	24
52	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). <i>Oncotarget</i> , 2014 , 5, 8223-34	3.3	21
51	Appraising the relevance of DNA copy number loss and gain in prostate cancer using whole genome DNA sequence data. <i>PLoS Genetics</i> , 2017 , 13, e1007001	6	20
50	Fabrication of planar organic nanotransistors using low temperature thermal nanoimprint lithography for chemical sensor applications. <i>Nanotechnology</i> , 2010 , 21, 75301	3.4	20
49	Concomitant inactivation of the p53- and pRB- functional pathways predicts resistance to DNA damaging drugs in breast cancer <i>in vivo</i> . <i>Molecular Oncology</i> , 2015 , 9, 1553-64	7.9	19
48	Promises and challenges of adoptive T-cell therapies for solid tumours. <i>British Journal of Cancer</i> , 2021 , 124, 1759-1776	8.7	19

47	Prostate cancer evolution from multilineage primary to single lineage metastases with implications for liquid biopsy. <i>Nature Communications</i> , 2020 , 11, 5070	17.4	18
46	Uncovering novel mutational signatures by de novo extraction with SigProfilerExtractor		17
45	Perturbed hematopoietic stem and progenitor cell hierarchy in myelodysplastic syndromes patients with monosomy 7 as the sole cytogenetic abnormality. <i>Oncotarget</i> , 2016 , 7, 72685-72698	3.3	16
44	FDRAnalysis: a tool for the integrated analysis of tandem mass spectrometry identification results from multiple search engines. <i>Journal of Proteome Research</i> , 2011 , 10, 2088-94	5.6	14
43	Genomic and evolutionary classification of lung cancer in never smokers. <i>Nature Genetics</i> , 2021 , 53, 1348-1359	8.6	14
42	Germline determinants of the somatic mutation landscape in 2,642 cancer genomes		13
41	A unified haplotype-based method for accurate and comprehensive variant calling. <i>Nature Biotechnology</i> , 2021 , 39, 885-892	44.5	13
40	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. <i>Nature Communications</i> , 2020 , 11, 4306	17.4	12
39	Convergent evolution to an aptamer observed in small populations on DNA microarrays. <i>Physical Biology</i> , 2010 , 7, 036007	3	11
38	Predictive models for population performance on real biological fitness landscapes. <i>Bioinformatics</i> , 2010 , 26, 2145-52	7.2	11
37	Time series analysis of neoadjuvant chemotherapy and bevacizumab-treated breast carcinomas reveals a systemic shift in genomic aberrations. <i>Genome Medicine</i> , 2018 , 10, 92	14.4	11
36	Profiling molecular regulators of recurrence in chemorefractory triple-negative breast cancers. <i>Breast Cancer Research</i> , 2019 , 21, 87	8.3	10
35	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils. <i>PLoS Biology</i> , 2020 , 18, e3000926	9.7	10
34	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
33	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. <i>Nature Communications</i> , 2020 , 11, 3096	17.4	8
32	Peptide detectability following ESI mass spectrometry 2007 ,		7
31	Neural network architectures and overtopping predictions. <i>Proceedings of the Institution of Civil Engineers: Maritime Engineering</i> , 2005 , 158, 123-133	1.8	7
30	Abstract 3000: Pervasive intra-tumour heterogeneity and subclonal selection across cancer types 2018 ,		6

29	Genomic landscape and chronological reconstruction of driver events in multiple myeloma		6
28	Tumor heterogeneity. <i>Cancer Cell</i> , 2021 , 39, 1015-1017	24.3	6
27	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline.. <i>Nature</i> , 2022 ,	50.4	4
26	DNA copy number motifs are strong and independent predictors of survival in breast cancer. <i>Communications Biology</i> , 2020 , 3, 153	6.7	4
25	A unified haplotype-based method for accurate and comprehensive variant calling		4
24	A Systematic Review of Prostate Cancer Heterogeneity: Understanding the Clonal Ancestry of Multifocal Disease. <i>European Urology Oncology</i> , 2021 , 4, 358-369	6.7	4
23	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. <i>American Journal of Epidemiology</i> , 2021 , 190, 962-976	3.8	4
22	Rapid parallel acquisition of somatic mutations after NPM1 in acute myeloid leukaemia evolution. <i>British Journal of Haematology</i> , 2017 , 176, 825-829	4.5	3
21	Creating Standards for Evaluating Tumour Subclonal Reconstruction		3
20	Malignant transformation and genetic alterations are uncoupled in early colorectal cancer progression. <i>BMC Biology</i> , 2020 , 18, 116	7.3	3
19	Germline loss-of-function variants in the base-excision repair gene MBD4 cause a Mendelian recessive syndrome of adenomatous colorectal polyposis and acute myeloid leukaemia		3
18	Detailed Molecular and Immune Marker Profiling of Archival Prostate Cancer Samples Reveals an Inverse Association between TMPRSS2:ERG Fusion Status and Immune Cell Infiltration. <i>Journal of Molecular Diagnostics</i> , 2020 , 22, 652-669	5.1	2
17	Neutral tumor evolution?		2
16	Multi-site clonality analyses uncovers pervasive subclonal heterogeneity and branching evolution across melanoma metastases		2
15	Multi-omic cross-sectional cohort study of pre-malignant Barrett's esophagus reveals early structural variation and retrotransposon activity.. <i>Nature Communications</i> , 2022 , 13, 1407	17.4	2
14	Clonal diversification and histogenesis of malignant germ cell tumours		1
13	Whole-genome analysis of Nigerian patients with breast cancer reveals ethnic-driven somatic evolution and distinct genomic subtypes. <i>Nature Communications</i> , 2021 , 12, 6946	17.4	1
12	A Global-Local Artificial Neural Network with Application to Wave Overtopping Prediction. <i>Lecture Notes in Computer Science</i> , 2005 , 109-114	0.9	1

11	Genomic copy number predicts oesophageal cancer years before transformation		1
10	Genomic evidence supports a clonal diaspora model for metastases of esophageal adenocarcinoma		1
9	Benchmarking small-variant genotyping in polyploids		1
8	Changes in Clonal Architecture Inform MPN Disease Course in Advance of Phenotypic Manifestations. <i>Blood</i> , 2021 , 138, 3590-3590	2.2	0
7	Localized activation of the metastatic phenotype within the perineural region in prostate cancer.. <i>Journal of Clinical Oncology</i> , 2021 , 39, 253-253	2.2	0
6	Subclone Eradication Analysis Identifies Targets for Enhanced Cancer Therapy and Reveals L1 Retrotransposition as a Dynamic Source of Cancer Heterogeneity. <i>Cancer Research</i> , 2021 , 81, 4901-4909 ^{10.1}		0
5	Reference bias in the Illumina Isaac aligner. <i>Bioinformatics</i> , 2020 , 36, 4671-4672	7.2	
4	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils 2020 , 18, e3000926		
3	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils 2020 , 18, e3000926		
2	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils 2020 , 18, e3000926		
1	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils 2020 , 18, e3000926		