David C Wedge

List of Publications by Year in Descending Order

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 TOP1 transcription-associated mutagenesis in cancer and germline.. *Nature*, **2022**,	50.4	4
135	Multi-omic cross-sectional cohort study of pre-malignant Barrett's esophagus reveals early structural variation and retrotransposon activity.. *Nature Communications*, **2022**, 13, 1407	17.4	2
134	Whole-genome analysis of Nigerian patients with breast cancer reveals ethnic-driven somatic evolution and distinct genomic subtypes. *Nature Communications*, **2021**, 12, 6946	17.4	1
133	Changes in Clonal Architecture Inform MPN Disease Course in Advance of Phenotypic Manifestations. *Blood*, **2021**, 138, 3590-3590	2.2	0
132	A unified haplotype-based method for accurate and comprehensive variant calling. *Nature Biotechnology*, **2021**, 39, 885-892	44.5	13
131	Promises and challenges of adoptive T-cell therapies for solid tumours. *British Journal of Cancer*, **2021**, 124, 1759-1776	8.7	19
130	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. *Cell*, **2021**, 184, 2239-2254.e39	56.2	57
129	A Systematic Review of Prostate Cancer Heterogeneity: Understanding the Clonal Ancestry of Multifocal Disease. *European Urology Oncology*, **2021**, 4, 358-369	6.7	4
128	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. *American Journal of Epidemiology*, **2021**, 190, 962-976	3.8	4
127	A practical guide to cancer subclonal reconstruction from DNA sequencing. *Nature Methods*, **2021**, 18, 144-155	21.6	25
126	Localized activation of the metastatic phenotype within the perineural region in prostate cancer.. *Journal of Clinical Oncology*, **2021**, 39, 253-253	2.2	0
125	Tumor heterogeneity. *Cancer Cell*, **2021**, 39, 1015-1017	24.3	6
124	Subclone Eradication Analysis Identifies Targets for Enhanced Cancer Therapy and Reveals L1 Retrotransposition as a Dynamic Source of Cancer Heterogeneity. *Cancer Research*, **2021**, 81, 4901-4909	10.1	0
123	Genomic and evolutionary classification of lung cancer in never smokers. *Nature Genetics*, **2021**, 53, 1348-1359	36.3	14
122	Genetic and epigenetic intratumor heterogeneity impacts prognosis of lung adenocarcinoma. *Nature Communications*, **2020**, 11, 2459	17.4	29
121	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. *Nature Communications*, **2020**, 11, 3096	17.4	8
120	Reference bias in the Illumina Isaac aligner. *Bioinformatics*, **2020**, 36, 4671-4672	7.2	

119	The evolutionary history of 2,658 cancers. *Nature*, **2020**, 578, 122-128	50.4	307
118	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
117	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
116	Detailed Molecular and Immune Marker Profiling of Archival Prostate Cancer Samples Reveals an Inverse Association between TMPRSS2:ERG Fusion Status and Immune Cell Infiltration. *Journal of Molecular Diagnostics*, **2020**, 22, 652-669	5.1	2
115	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils. *PLoS Biology*, **2020**, 18, e3000926	9.7	10
114	DNA copy number motifs are strong and independent predictors of survival in breast cancer. *Communications Biology*, **2020**, 3, 153	6.7	4
113	A community effort to create standards for evaluating tumor subclonal reconstruction. *Nature Biotechnology*, **2020**, 38, 97-107	44.5	35
112	Genomic evidence supports a clonal diaspora model for metastases of esophageal adenocarcinoma. *Nature Genetics*, **2020**, 52, 74-83	36.3	24
111	Prostate cancer evolution from multilineage primary to single lineage metastases with implications for liquid biopsy. *Nature Communications*, **2020**, 11, 5070	17.4	18
110	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. *Nature Communications*, **2020**, 11, 4306	17.4	12
109	Genomic copy number predicts esophageal cancer years before transformation. *Nature Medicine*, **2020**, 26, 1726-1732	50.5	31
108	Malignant transformation and genetic alterations are uncoupled in early colorectal cancer progression. *BMC Biology*, **2020**, 18, 116	7.3	3
107	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils **2020**, 18, e3000926		
106	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils **2020**, 18, e3000926		
105	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils **2020**, 18, e3000926		
104	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils **2020**, 18, e3000926		
103	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. *Nature Communications*, **2019**, 10, 3835	17.4	94
102	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. *Cell*, **2019**, 176, 1282-1294.e20	56.2	165

101	Profiling molecular regulators of recurrence in chemorefractory triple-negative breast cancers. *Breast Cancer Research*, **2019**, 21, 87	8.3	10
100	Embryonal precursors of Wilms tumor. *Science*, **2019**, 366, 1247-1251	33.3	40
99	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. *Nature Genetics*, **2018**, 50, 682-692	36.3	112
98	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. *Cell*, **2018**, 173, 611-623.e17	56.2	228
97	Organoid cultures recapitulate esophageal adenocarcinoma heterogeneity providing a model for clonality studies and precision therapeutics. *Nature Communications*, **2018**, 9, 2983	17.4	113
96	Genomic patterns of progression in smoldering multiple myeloma. *Nature Communications*, **2018**, 9, 3363	17.4	99
95	Abstract 3000: Pervasive intra-tumour heterogeneity and subclonal selection across cancer types **2018**,		6
94	Time series analysis of neoadjuvant chemotherapy and bevacizumab-treated breast carcinomas reveals a systemic shift in genomic aberrations. *Genome Medicine*, **2018**, 10, 92	14.4	11
93	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. *New England Journal of Medicine*, **2018**, 379, 1416-1430	59.2	256
92	Neutral tumor evolution?. *Nature Genetics*, **2018**, 50, 1630-1633	36.3	38
91	The evolutionary landscape of colorectal tumorigenesis. *Nature Ecology and Evolution*, **2018**, 2, 1661-1672	12.3	52
90	Principles of Reconstructing the Subclonal Architecture of Cancers. *Cold Spring Harbor Perspectives in Medicine*, **2017**, 7,	5.4	58
89	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. *Nature Communications*, **2017**, 8, 15936	17.4	125
88	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. *Nature*, **2017**, 543, 714-718	50.4	157
87	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. *Nature Communications*, **2017**, 8, 1221	17.4	40
86	Appraising the relevance of DNA copy number loss and gain in prostate cancer using whole genome DNA sequence data. *PLoS Genetics*, **2017**, 13, e1007001	6	20
85	Genomic Evolution of Breast Cancer Metastasis and Relapse. *Cancer Cell*, **2017**, 32, 169-184.e7	24.3	346
84	How Subclonal Modeling Is Changing the Metastatic Paradigm. *Clinical Cancer Research*, **2017**, 23, 630-635	12.9	26

83	Rapid parallel acquisition of somatic mutations after NPM1 in acute myeloid leukaemia evolution. *British Journal of Haematology*, **2017**, 176, 825-829	4.5	3
82	Mutational signatures of ionizing radiation in second malignancies. *Nature Communications*, **2016**, 7, 12605	17.4	152
81	Perturbed hematopoietic stem and progenitor cell hierarchy in myelodysplastic syndromes patients with monosomy 7 as the sole cytogenetic abnormality. *Oncotarget*, **2016**, 7, 72685-72698	3.3	16
80	Mitochondrial genetic diversity, selection and recombination in a canine transmissible cancer. *ELife*, **2016**, 5,	8.9	37
79	Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. *Genome Biology*, **2016**, 17, 250	18.3	48
78	ascatNgs: Identifying Somatically Acquired Copy-Number Alterations from Whole-Genome Sequencing Data. *Current Protocols in Bioinformatics*, **2016**, 56, 15.9.1-15.9.17	24.2	60
77	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. *Nature*, **2016**, 534, 47-54	50.4	1193
76	The Genomic Landscape of Pancreatic and Periampullary Adenocarcinoma. *Cancer Research*, **2016**, 76, 5092-102	10.1	27
75	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. *Cell Reports*, **2016**, 16, 2032-46	8.6	30
74	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. *Nature Medicine*, **2015**, 21, 751-9	50.5	521
73	Concomitant inactivation of the p53- and pRB- functional pathways predicts resistance to DNA damaging drugs in breast cancer in vivo. *Molecular Oncology*, **2015**, 9, 1553-64	7.9	19
72	Analysis of the genetic phylogeny of multifocal prostate cancer identifies multiple independent clonal expansions in neoplastic and morphologically normal prostate tissue. *Nature Genetics*, **2015**, 47, 367-372	36.3	292
71	The evolutionary history of lethal metastatic prostate cancer. *Nature*, **2015**, 520, 353-357	50.4	857
70	Clock-like mutational processes in human somatic cells. *Nature Genetics*, **2015**, 47, 1402-7	36.3	531
69	Untargeted metabolic profiling identifies altered serum metabolites of type 2 diabetes mellitus in a prospective, nested case control study. *Clinical Chemistry*, **2015**, 61, 487-97	5.5	94
68	Diagnostic value of H3F3A mutations in giant cell tumour of bone compared to osteoclast-rich mimics. *Journal of Pathology: Clinical Research*, **2015**, 1, 113-23	5.3	98
67	DNMT3A mutations occur early or late in patients with myeloproliferative neoplasms and mutation order influences phenotype. *Haematologica*, **2015**, 100, e438-42	6.6	70
66	Tumor evolution. High burden and pervasive positive selection of somatic mutations in normal human skin. *Science*, **2015**, 348, 880-6	33.3	983

65	Tracking the origins and drivers of subclonal metastatic expansion in prostate cancer. *Nature Communications*, **2015**, 6, 6605	17.4	245
64	Effect of mutation order on myeloproliferative neoplasms. *New England Journal of Medicine*, **2015**, 372, 601-612	59.2	334
63	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermutated cancers. *Nature Genetics*, **2015**, 47, 257-62	36.3	253
62	Recurrent PTPRB and PLCG1 mutations in angiosarcoma. *Nature Genetics*, **2014**, 46, 376-379	36.3	196
61	Myelodysplastic syndromes are propagated by rare and distinct human cancer stem cells in vivo. *Cancer Cell*, **2014**, 25, 794-808	24.3	216
60	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. *Nature Communications*, **2014**, 5, 2997	17.4	564
59	Transmissible [corrected] dog cancer genome reveals the origin and history of an ancient cell lineage. *Science*, **2014**, 343, 437-440	33.3	116
58	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. *Nature Genetics*, **2014**, 46, 116-25	36.3	244
57	A comparison of different chemometrics approaches for the robust classification of electronic nose data. *Analytical and Bioanalytical Chemistry*, **2014**, 406, 7581-90	4.4	50
56	Mobile DNA in cancer. Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. *Science*, **2014**, 345, 1251343	33.3	250
55	Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. *Science*, **2014**, 346, 256-9	33.3	659
54	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. *Science*, **2014**, 346, 251-6	33.3	752
53	Association of a germline copy number polymorphism of APOBEC3A and APOBEC3B with burden of putative APOBEC-dependent mutations in breast cancer. *Nature Genetics*, **2014**, 46, 487-91	36.3	208
52	Genome sequencing of normal cells reveals developmental lineages and mutational processes. *Nature*, **2014**, 513, 422-425	50.4	249
51	Differential and limited expression of mutant alleles in multiple myeloma. *Blood*, **2014**, 124, 3110-7	2.2	42
50	Fast randomization of large genomic datasets while preserving alteration counts. *Bioinformatics*, **2014**, 30, i617-23	7.2	27
49	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). *Oncotarget*, **2014**, 5, 8223-34	3.3	21
48	Frequent mutation of the major cartilage collagen gene COL2A1 in chondrosarcoma. *Nature Genetics*, **2013**, 45, 923-6	36.3	138

47	Signatures of mutational processes in human cancer. *Nature*, **2013**, 500, 415-21	50.4	5895
46	Deciphering signatures of mutational processes operative in human cancer. *Cell Reports*, **2013**, 3, 246-59	10.6	725
45	Somatic CALR mutations in myeloproliferative neoplasms with nonmutated JAK2. *New England Journal of Medicine*, **2013**, 369, 2391-2405	59.2	1262
44	Clinical and biological implications of driver mutations in myelodysplastic syndromes. *Blood*, **2013**, 122, 3616-27; quiz 3699	2.2	1169
43	A comparison of Raman and FT-IR spectroscopy for the prediction of meat spoilage. *Food Control*, **2013**, 29, 461-470	6.2	90
42	Distinct H3F3A and H3F3B driver mutations define chondroblastoma and giant cell tumor of bone. *Nature Genetics*, **2013**, 45, 1479-82	36.3	482
41	The genetic heterogeneity and mutational burden of engineered melanomas in zebrafish models. *Genome Biology*, **2013**, 14, R113	18.3	33
40	Whole exome sequencing of adenoid cystic carcinoma. *Journal of Clinical Investigation*, **2013**, 123, 2965-8	15.9	188
39	Genome sequencing and analysis of the Tasmanian devil and its transmissible cancer. *Cell*, **2012**, 148, 780-91	56.2	251
38	Liquid chromatography-mass spectrometry calibration transfer and metabolomics data fusion. *Analytical Chemistry*, **2012**, 84, 9848-57	7.8	31
37	The landscape of cancer genes and mutational processes in breast cancer. *Nature*, **2012**, 486, 400-4	50.4	1264
36	Mutational processes molding the genomes of 21 breast cancers. *Cell*, **2012**, 149, 979-93	56.2	1279
35	The life history of 21 breast cancers. *Cell*, **2012**, 149, 994-1007	56.2	979
34	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. *Journal of Pathology*, **2012**, 227, 446-55	9.4	72
33	FDRAnalysis: a tool for the integrated analysis of tandem mass spectrometry identification results from multiple search engines. *Journal of Proteome Research*, **2011**, 10, 2088-94	5.6	14
32	Is serum or plasma more appropriate for intersubject comparisons in metabolomic studies? An assessment in patients with small-cell lung cancer. *Analytical Chemistry*, **2011**, 83, 6689-97	7.8	106
31	Automated workflows for accurate mass-based putative metabolite identification in LC/MS-derived metabolomic datasets. *Bioinformatics*, **2011**, 27, 1108-12	7.2	156
30	CONSeQuence: prediction of reference peptides for absolute quantitative proteomics using consensus machine learning approaches. *Molecular and Cellular Proteomics*, **2011**, 10, M110.003384	7.6	101

29	Analysis of a complete DNA-protein affinity landscape. *Journal of the Royal Society Interface*, **2010**, 7, 397-408	4.1	49
28	Convergent evolution to an aptamer observed in small populations on DNA microarrays. *Physical Biology*, **2010**, 7, 036007	3	11
27	Predictive models for population performance on real biological fitness landscapes. *Bioinformatics*, **2010**, 26, 2145-52	7.2	11
26	Fabrication of planar organic nanotransistors using low temperature thermal nanoimprint lithography for chemical sensor applications. *Nanotechnology*, **2010**, 21, 75301	3.4	20
25	Array-based evolution of DNA aptamers allows modelling of an explicit sequence-fitness landscape. *Nucleic Acids Research*, **2009**, 37, e6	20.1	85
24	Low cost, portable, fast multiparameter data acquisition system for organic transistor odour sensors. *Sensors and Actuators B: Chemical*, **2009**, 137, 586-591	8.5	25
23	Real-time vapour sensing using an OFET-based electronic nose and genetic programming. *Sensors and Actuators B: Chemical*, **2009**, 143, 365-372	8.5	38
22	In silico modelling of directed evolution: Implications for experimental design and stepwise evolution. *Journal of Theoretical Biology*, **2009**, 257, 131-41	2.3	28
21	Aptamer evolution for array-based diagnostics. *Analytical Biochemistry*, **2009**, 390, 203-5	3.1	45
20	pK(a) prediction from "Quantum Chemical Topology" descriptors. *Journal of Chemical Information and Modeling*, **2009**, 49, 1914-24	6.1	43
19	Peptide detectability following ESI mass spectrometry **2007**,		7
18	On global-local artificial neural networks for function approximation. *IEEE Transactions on Neural Networks*, **2006**, 17, 942-52		33
17	Neural network architectures and overtopping predictions. *Proceedings of the Institution of Civil Engineers: Maritime Engineering*, **2005**, 158, 123-133	1.8	7
16	A Global-Local Artificial Neural Network with Application to Wave Overtopping Prediction. *Lecture Notes in Computer Science*, **2005**, 109-114	0.9	1
15	Clonal diversification and histogenesis of malignant germ cell tumours		1
14	Neutral tumor evolution?		2
13	The evolutionary history of 2,658 cancers		28
12	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10

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