

David C Wedge

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6019114/publications.pdf>

Version: 2024-02-01

141
papers

40,032
citations

18482

62
h-index

14208

128
g-index

172
all docs

172
docs citations

172
times ranked

49372
citing authors

#	ARTICLE	IF	CITATIONS
1	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
2	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
3	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
4	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	28.9	1,673
5	Clinical and biological implications of driver mutations in myelodysplastic syndromes. Blood, 2013, 122, 3616-3627.	1.4	1,562
6	Somatic <i>CALR</i> Mutations in Myeloproliferative Neoplasms with Nonmutated <i>JAK2</i> . New England Journal of Medicine, 2013, 369, 2391-2405.	27.0	1,556
7	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	27.8	1,535
8	High burden and pervasive positive selection of somatic mutations in normal human skin. Science, 2015, 348, 880-886.	12.6	1,431
9	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	28.9	1,249
10	The evolutionary history of lethal metastatic prostate cancer. Nature, 2015, 520, 353-357.	27.8	1,185
11	Deciphering Signatures of Mutational Processes Operative in Human Cancer. Cell Reports, 2013, 3, 246-259.	6.4	1,087
12	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. Science, 2014, 346, 251-256.	12.6	962
13	Clock-like mutational processes in human somatic cells. Nature Genetics, 2015, 47, 1402-1407.	21.4	837
14	Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. Science, 2014, 346, 256-259.	12.6	834
15	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. Nature Communications, 2014, 5, 2997.	12.8	741
16	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. Nature Medicine, 2015, 21, 751-759.	30.7	711
17	The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128.	27.8	690
18	Distinct H3F3A and H3F3B driver mutations define chondroblastoma and giant cell tumor of bone. Nature Genetics, 2013, 45, 1479-1482.	21.4	667

#	ARTICLE	IF	CITATIONS
19	Genomic Evolution of Breast Cancer Metastasis and Relapse. <i>Cancer Cell</i> , 2017, 32, 169-184.e7.	16.8	534
20	Effect of Mutation Order on Myeloproliferative Neoplasms. <i>New England Journal of Medicine</i> , 2015, 372, 601-612.	27.0	467
21	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. <i>New England Journal of Medicine</i> , 2018, 379, 1416-1430.	27.0	442
22	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. <i>Cell</i> , 2018, 173, 611-623.e17.	28.9	398
23	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.	21.4	380
24	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251343.	12.6	348
25	Genome sequencing of normal cells reveals developmental lineages and mutational processes. <i>Nature</i> , 2014, 513, 422-425.	27.8	315
26	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2014, 46, 116-125.	21.4	313
27	Tracking the origins and drivers of subclonal metastatic expansion in prostate cancer. <i>Nature Communications</i> , 2015, 6, 6605.	12.8	312
28	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermutated cancers. <i>Nature Genetics</i> , 2015, 47, 257-262.	21.4	306
29	Genome Sequencing and Analysis of the Tasmanian Devil and Its Transmissible Cancer. <i>Cell</i> , 2012, 148, 780-791.	28.9	300
30	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. <i>Cell</i> , 2019, 176, 1282-1294.e20.	28.9	298
31	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020, 52, 306-319.	21.4	275
32	Myelodysplastic Syndromes Are Propagated by Rare and Distinct Human Cancer Stem Cells In Vivo. <i>Cancer Cell</i> , 2014, 25, 794-808.	16.8	272
33	Recurrent PTPRB and PLCG1 mutations in angiosarcoma. <i>Nature Genetics</i> , 2014, 46, 376-379.	21.4	269
34	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021, 184, 2239-2254.e39.	28.9	260
35	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, 487-491.	21.4	254
36	Whole exome sequencing of adenoid cystic carcinoma. <i>Journal of Clinical Investigation</i> , 2013, 123, 2965-2968.	8.2	233

#	ARTICLE	IF	CITATIONS
37	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. <i>Nature</i> , 2017, 543, 714-718.	27.8	229
38	Mutational signatures of ionizing radiation in second malignancies. <i>Nature Communications</i> , 2016, 7, 12605.	12.8	214
39	Organoid cultures recapitulate esophageal adenocarcinoma heterogeneity providing a model for clonality studies and precision therapeutics. <i>Nature Communications</i> , 2018, 9, 2983.	12.8	206
40	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. <i>Nature Communications</i> , 2019, 10, 3835.	12.8	183
41	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. <i>Nature Genetics</i> , 2018, 50, 682-692.	21.4	182
42	Frequent mutation of the major cartilage collagen gene COL2A1 in chondrosarcoma. <i>Nature Genetics</i> , 2013, 45, 923-926.	21.4	180
43	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. <i>Nature Communications</i> , 2017, 8, 15936.	12.8	179
44	Automated workflows for accurate mass-based putative metabolite identification in LC/MS-derived metabolomic datasets. <i>Bioinformatics</i> , 2011, 27, 1108-1112.	4.1	173
45	Genomic patterns of progression in smoldering multiple myeloma. <i>Nature Communications</i> , 2018, 9, 3363.	12.8	163
46	Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. <i>Science</i> , 2014, 343, 437-440.	12.6	144
47	Diagnostic value of H3F3A mutations in giant cell tumour of bone compared to osteoclast mimics. <i>Journal of Pathology: Clinical Research</i> , 2015, 1, 113-123.	3.0	135
48	CONSeQUENCE: Prediction of Reference Peptides for Absolute Quantitative Proteomics Using Consensus Machine Learning Approaches. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003384.	3.8	121
49	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, 6689-6697.	6.5	119
50	A comparison of Raman and FT-IR spectroscopy for the prediction of meat spoilage. <i>Food Control</i> , 2013, 29, 461-470.	5.5	115
51	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, 487-497.	3.2	113
52	Promises and challenges of adoptive T-cell therapies for solid tumours. <i>British Journal of Cancer</i> , 2021, 124, 1759-1776.	6.4	113
53	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.	25.8	111
54	Principles of Reconstructing the Subclonal Architecture of Cancers. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2017, 7, a026625.	6.2	109

#	ARTICLE	IF	CITATIONS
55	DNMT3A mutations occur early or late in patients with myeloproliferative neoplasms and mutation order influences phenotype. <i>Haematologica</i> , 2015, 100, e438-e442.	3.5	105
56	A practical guide to cancer subclonal reconstruction from DNA sequencing. <i>Nature Methods</i> , 2021, 18, 144-155.	19.0	103
57	Embryonal precursors of Wilms tumor. <i>Science</i> , 2019, 366, 1247-1251.	12.6	101
58	The evolutionary landscape of colorectal tumorigenesis. <i>Nature Ecology and Evolution</i> , 2018, 2, 1661-1672.	7.8	99
59	Array-based evolution of DNA aptamers allows modelling of an explicit sequence-fitness landscape. <i>Nucleic Acids Research</i> , 2009, 37, e6-e6.	14.5	96
60	Genomic copy number predicts esophageal cancer years before transformation. <i>Nature Medicine</i> , 2020, 26, 1726-1732.	30.7	86
61	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. <i>Journal of Pathology</i> , 2012, 227, 446-455.	4.5	81
62	Genomic and evolutionary classification of lung cancer in never smokers. <i>Nature Genetics</i> , 2021, 53, 1348-1359.	21.4	81
63	Genetic and epigenetic intratumor heterogeneity impacts prognosis of lung adenocarcinoma. <i>Nature Communications</i> , 2020, 11, 2459.	12.8	77
64	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. <i>Nature Communications</i> , 2017, 8, 1221.	12.8	75
65	Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. <i>Genome Biology</i> , 2016, 17, 250.	8.8	68
66	Tumor heterogeneity. <i>Cancer Cell</i> , 2021, 39, 1015-1017.	16.8	66
67	A comparison of different chemometrics approaches for the robust classification of electronic nose data. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 7581-7590.	3.7	63
68	Neutral tumor evolution?. <i>Nature Genetics</i> , 2018, 50, 1630-1633.	21.4	59
69	Analysis of a complete DNA-protein affinity landscape. <i>Journal of the Royal Society Interface</i> , 2010, 7, 397-408.	3.4	58
70	A community effort to create standards for evaluating tumor subclonal reconstruction. <i>Nature Biotechnology</i> , 2020, 38, 97-107.	17.5	58
71	A unified haplotype-based method for accurate and comprehensive variant calling. <i>Nature Biotechnology</i> , 2021, 39, 885-892.	17.5	56
72	Quantum Chemical Topology Descriptors. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 1914-1924.	5.4	54

#	ARTICLE	IF	CITATIONS
73	Differential and limited expression of mutant alleles in multiple myeloma. <i>Blood</i> , 2014, 124, 3110-3117.	1.4	54
74	Genomic evidence supports a clonal diaspora model for metastases of esophageal adenocarcinoma. <i>Nature Genetics</i> , 2020, 52, 74-83.	21.4	53
75	Aptamer evolution for array-based diagnostics. <i>Analytical Biochemistry</i> , 2009, 390, 203-205.	2.4	50
76	Mitochondrial genetic diversity, selection and recombination in a canine transmissible cancer. <i>ELife</i> , 2016, 5, .	6.0	49
77	Prostate cancer evolution from multilineage primary to single lineage metastases with implications for liquid biopsy. <i>Nature Communications</i> , 2020, 11, 5070.	12.8	44
78	Real-time vapour sensing using an OFET-based electronic nose and genetic programming. <i>Sensors and Actuators B: Chemical</i> , 2009, 143, 365-372.	7.8	43
79	The genetic heterogeneity and mutational burden of engineered melanomas in zebrafish models. <i>Genome Biology</i> , 2013, 14, R113.	9.6	40
80	On Globalâ€“Local Artificial Neural Networks for Function Approximation. <i>IEEE Transactions on Neural Networks</i> , 2006, 17, 942-952.	4.2	38
81	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline. <i>Nature</i> , 2022, 602, 623-631.	27.8	38
82	Fast randomization of large genomic datasets while preserving alteration counts. <i>Bioinformatics</i> , 2014, 30, i617-i623.	4.1	36
83	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. <i>Cell Reports</i> , 2016, 16, 2032-2046.	6.4	36
84	How Subclonal Modeling Is Changing the Metastatic Paradigm. <i>Clinical Cancer Research</i> , 2017, 23, 630-635.	7.0	34
85	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.	3.5	34
86	Liquid Chromatographyâ€“Mass Spectrometry Calibration Transfer and Metabolomics Data Fusion. <i>Analytical Chemistry</i> , 2012, 84, 9848-9857.	6.5	33
87	The Genomic Landscape of Pancreatic and Periampullary Adenocarcinoma. <i>Cancer Research</i> , 2016, 76, 5092-5102.	0.9	33
88	In silico modelling of directed evolution: Implications for experimental design and stepwise evolution. <i>Journal of Theoretical Biology</i> , 2009, 257, 131-141.	1.7	30
89	Low cost, portable, fast multiparameter data acquisition system for organic transistor odour sensors. <i>Sensors and Actuators B: Chemical</i> , 2009, 137, 586-591.	7.8	27
90	Profiling molecular regulators of recurrence in chemorefractory triple-negative breast cancers. <i>Breast Cancer Research</i> , 2019, 21, 87.	5.0	26

#	ARTICLE	IF	CITATIONS
91	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. Nature Communications, 2020, 11, 4306.	12.8	26
92	In utero origin of myelofibrosis presenting in adult monozygotic twins. Nature Medicine, 2022, 28, 1207-1211.	30.7	26
93	Fabrication of planar organic nanotransistors using low temperature thermal nanoimprint lithography for chemical sensor applications. Nanotechnology, 2010, 21, 075301.	2.6	24
94	Concomitant inactivation of the p53 and pRB functional pathways predicts resistance to DNA damaging drugs in breast cancer in vivo. Molecular Oncology, 2015, 9, 1553-1564.	4.6	23
95	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils. PLoS Biology, 2020, 18, e3000926.	5.6	23
96	Germline MBD4 deficiency causes a multi-tumor predisposition syndrome. American Journal of Human Genetics, 2022, 109, 953-960.	6.2	23
97	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). Oncotarget, 2014, 5, 8223-8234.	1.8	22
98	Whole-genome analysis of Nigerian patients with breast cancer reveals ethnic-driven somatic evolution and distinct genomic subtypes. Nature Communications, 2021, 12, 6946.	12.8	22
99	Perturbed hematopoietic stem and progenitor cell hierarchy in myelodysplastic syndromes patients with monosomy 7 as the sole cytogenetic abnormality. Oncotarget, 2016, 7, 72685-72698.	1.8	21
100	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. Nature Communications, 2020, 11, 3096.	12.8	19
101	FDRAnalysis: A Tool for the Integrated Analysis of Tandem Mass Spectrometry Identification Results from Multiple Search Engines. Journal of Proteome Research, 2011, 10, 2088-2094.	3.7	18
102	Time series analysis of neoadjuvant chemotherapy and bevacizumab-treated breast carcinomas reveals a systemic shift in genomic aberrations. Genome Medicine, 2018, 10, 92.	8.2	17
103	Malignant transformation and genetic alterations are uncoupled in early colorectal cancer progression. BMC Biology, 2020, 18, 116.	3.8	16
104	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. American Journal of Epidemiology, 2021, 190, 962-976.	3.4	16
105	A Systematic Review of Prostate Cancer Heterogeneity: Understanding the Clonal Ancestry of Multifocal Disease. European Urology Oncology, 2021, 4, 358-369.	5.4	16
106	Multi-omic cross-sectional cohort study of pre-malignant Barrett's esophagus reveals early structural variation and retrotransposon activity. Nature Communications, 2022, 13, 1407.	12.8	15
107	Convergent evolution to an aptamer observed in small populations on DNA microarrays. Physical Biology, 2010, 7, 036007.	1.8	12
108	APOBEC3 mutational signatures are associated with extensive and diverse genomic instability across multiple tumour types. BMC Biology, 2022, 20, .	3.8	12

#	ARTICLE	IF	CITATIONS
109	Predictive models for population performance on real biological fitness landscapes. <i>Bioinformatics</i> , 2010, 26, 2145-2152.	4.1	11
110	Re-evaluating experimental validation in the Big Data Era: a conceptual argument. <i>Genome Biology</i> , 2021, 22, 71.	8.8	10
111	DNA copy number motifs are strong and independent predictors of survival in breast cancer. <i>Communications Biology</i> , 2020, 3, 153.	4.4	9
112	Peptide detectability following ESI mass spectrometry. , 2007, , .		8
113	Abstract 3000: Pervasive intra-tumour heterogeneity and subclonal selection across cancer types. , 2018, , .		8
114	Neural network architectures and overtopping predictions. <i>Proceedings of the Institution of Civil Engineers: Maritime Engineering</i> , 2005, 158, 123-133.	0.2	7
115	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.	2.8	6
116	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.	0.9	6
117	Reference bias in the Illumina Isaac aligner. <i>Bioinformatics</i> , 2020, 36, 4671-4672.	4.1	5
118	A Global-Local Artificial Neural Network with Application to Wave Overtopping Prediction. <i>Lecture Notes in Computer Science</i> , 2005, , 109-114.	1.3	4
119	Benchmarking small-variant genotyping in polyploids. <i>Genome Research</i> , 2022, 32, 403-408.	5.5	4
120	Rapid parallel acquisition of somatic mutations after $\langle i \rangle \langle scp \rangle NPM \langle /scp \rangle 1 \langle /i \rangle$ in acute myeloid leukaemia evolution. <i>British Journal of Haematology</i> , 2017, 176, 825-829.	2.5	3
121	Automated workflows for accurate mass-based putative metabolite identification in LC/MS-derived metabolomic datasets. <i>Bioinformatics</i> , 2012, 28, 149-149.	4.1	2
122	Rare Germline Variants Are Associated with Rapid Biochemical Recurrence After Radical Prostate Cancer Treatment: A Pan Prostate Cancer Group Study. <i>European Urology</i> , 2022, 82, 201-211.	1.9	2
123	Localized activation of the metastatic phenotype within the perineural region in prostate cancer.. <i>Journal of Clinical Oncology</i> , 2021, 39, 253-253.	1.6	1
124	Changes in Clonal Architecture Inform MPN Disease Course in Advance of Phenotypic Manifestations. <i>Blood</i> , 2021, 138, 3590-3590.	1.4	1
125	Shallow Whole Genome Sequencing can Detect Copy Number Changes in FFPE Material in the Progression of Barrett's Esophagus. <i>Gastroenterology</i> , 2017, 152, S106.	1.3	0
126	PO-322 Multi-region deep sequencing of colorectal carcinoma in-situ defines oncogenic transformation as a gradual and adaptive process. <i>ESMO Open</i> , 2018, 3, A147.	4.5	0

#	ARTICLE	IF	CITATIONS
127	464 MULTI-OMIC CHARACTERIZATION OF BARRETT'S ESOPHAGUS REVEALS A MOLECULAR CONTINUUM IN THE PROGRESSION TO ESOPHAGEAL ADENOCARCINOMA. Gastroenterology, 2020, 158, S-88-S-89.	1.3	0
128	Abstract 865: Genomic and evolutionary classification of lung cancer in never smokers from the Sherlock-Lungstudy. , 2021, , .		0
129	Abstract 3049: Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. , 2017, , .		0
130	Clonal Diaspora in Metastatic Esophageal Adenocarcinoma Describes a New Model of Cancer Progression. SSRN Electronic Journal, 0, , .	0.4	0
131	Abstract 218: The evolutionary history of 2,658 cancers. , 2018, , .		0
132	Abstract LB-300: The life history of breast cancer in Nigerian women: Evidence for ethnic differences in tumor evolution based on whole-genome sequencing. , 2019, , .		0
133	Characterizing Genetic Intra-Tumor Heterogeneity Across 2,658 Human Cancer Genomes. SSRN Electronic Journal, 0, , .	0.4	0
134	P-061: Single-cell whole-exome DNA sequencing traces clonal trajectory in paired evolution of MGUS to multiple myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, S72.	0.4	0
135	P-OGC44â€fMulti-omic cohort study of Barrettâ€™s oesophagus reveals structural variation and retrotransposon activity to occur early in cancer evolution. British Journal of Surgery, 2021, 108, .	0.3	0
136	Abstract LB-300: The life history of breast cancer in Nigerian women: Evidence for ethnic differences in tumor evolution based on whole-genome sequencing. , 2019, , .		0
137	Abstract SY26-02:<i>Sherlock-Lung</i>: Tracing lung cancer mutational processes in never smokers. , 2019, , .		0
138	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils. , 2020, 18, e3000926.		0
139	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils. , 2020, 18, e3000926.		0
140	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils. , 2020, 18, e3000926.		0
141	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils. , 2020, 18, e3000926.		0