

David C Wedge

List of Publications by Year in descending order

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Version: 2024-02-01

141
papers

40,032
citations

18436

62
h-index

14156

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. <i>Nature</i> , 2013, 500, 415-421.	13.7	8,060
2	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
3	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	13.7	1,760
4	Mutational Processes Molding the Genomes of 21 Breast Cancers. <i>Cell</i> , 2012, 149, 979-993.	13.5	1,673
5	Clinical and biological implications of driver mutations in myelodysplastic syndromes. <i>Blood</i> , 2013, 122, 3616-3627.	0.6	1,562
6	Somatic <i>CALR</i> Mutations in Myeloproliferative Neoplasms with Nonmutated <i>JAK2</i> . <i>New England Journal of Medicine</i> , 2013, 369, 2391-2405.	13.9	1,556
7	The landscape of cancer genes and mutational processes in breast cancer. <i>Nature</i> , 2012, 486, 400-404.	13.7	1,535
8	High burden and pervasive positive selection of somatic mutations in normal human skin. <i>Science</i> , 2015, 348, 880-886.	6.0	1,431
9	The Life History of 21 Breast Cancers. <i>Cell</i> , 2012, 149, 994-1007.	13.5	1,249
10	The evolutionary history of lethal metastatic prostate cancer. <i>Nature</i> , 2015, 520, 353-357.	13.7	1,185
11	Deciphering Signatures of Mutational Processes Operative in Human Cancer. <i>Cell Reports</i> , 2013, 3, 246-259.	2.9	1,087
12	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. <i>Science</i> , 2014, 346, 251-256.	6.0	962
13	Clock-like mutational processes in human somatic cells. <i>Nature Genetics</i> , 2015, 47, 1402-1407.	9.4	837
14	Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. <i>Science</i> , 2014, 346, 256-259.	6.0	834
15	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. <i>Nature Communications</i> , 2014, 5, 2997.	5.8	741
16	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. <i>Nature Medicine</i> , 2015, 21, 751-759.	15.2	711
17	The evolutionary history of 2,658 cancers. <i>Nature</i> , 2020, 578, 122-128.	13.7	690
18	Distinct H3F3A and H3F3B driver mutations define chondroblastoma and giant cell tumor of bone. <i>Nature Genetics</i> , 2013, 45, 1479-1482.	9.4	667

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19	Genomic Evolution of Breast Cancer Metastasis and Relapse. <i>Cancer Cell</i> , 2017, 32, 169-184.e7.	7.7	534
20	Effect of Mutation Order on Myeloproliferative Neoplasms. <i>New England Journal of Medicine</i> , 2015, 372, 601-612.	13.9	467
21	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. <i>New England Journal of Medicine</i> , 2018, 379, 1416-1430.	13.9	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.	13.5	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.	9.4	380
24	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251343.	6.0	348
25	Genome sequencing of normal cells reveals developmental lineages and mutational processes. <i>Nature</i> , 2014, 513, 422-425.	13.7	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.	9.4	313
27	Tracking the origins and drivers of subclonal metastatic expansion in prostate cancer. <i>Nature Communications</i> , 2015, 6, 6605.	5.8	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.	9.4	306
29	Genome Sequencing and Analysis of the Tasmanian Devil and Its Transmissible Cancer. <i>Cell</i> , 2012, 148, 780-791.	13.5	300
30	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. <i>Cell</i> , 2019, 176, 1282-1294.e20.	13.5	298
31	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020, 52, 306-319.	9.4	275
32	Myelodysplastic Syndromes Are Propagated by Rare and Distinct Human Cancer Stem Cells In Vivo. <i>Cancer Cell</i> , 2014, 25, 794-808.	7.7	272
33	Recurrent PTPRB and PLCG1 mutations in angiosarcoma. <i>Nature Genetics</i> , 2014, 46, 376-379.	9.4	269
34	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021, 184, 2239-2254.e39.	13.5	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.	9.4	254
36	Whole exome sequencing of adenoid cystic carcinoma. <i>Journal of Clinical Investigation</i> , 2013, 123, 2965-2968.	3.9	233

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37	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. <i>Nature</i> , 2017, 543, 714-718.	13.7	229
38	Mutational signatures of ionizing radiation in second malignancies. <i>Nature Communications</i> , 2016, 7, 12605.	5.8	214
39	Organoid cultures recapitulate esophageal adenocarcinoma heterogeneity providing a model for clonality studies and precision therapeutics. <i>Nature Communications</i> , 2018, 9, 2983.	5.8	206
40	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. <i>Nature Communications</i> , 2019, 10, 3835.	5.8	183
41	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. <i>Nature Genetics</i> , 2018, 50, 682-692.	9.4	182
42	Frequent mutation of the major cartilage collagen gene COL2A1 in chondrosarcoma. <i>Nature Genetics</i> , 2013, 45, 923-926.	9.4	180
43	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. <i>Nature Communications</i> , 2017, 8, 15936.	5.8	179
44	Automated workflows for accurate mass-based putative metabolite identification in LC/MS-derived metabolomic datasets. <i>Bioinformatics</i> , 2011, 27, 1108-1112.	1.8	173
45	Genomic patterns of progression in smoldering multiple myeloma. <i>Nature Communications</i> , 2018, 9, 3363.	5.8	163
46	Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. <i>Science</i> , 2014, 343, 437-440.	6.0	144
47	Diagnostic value of <i>H3F3A</i> mutations in giant cell tumour of bone compared to osteoclast-rich mimics. <i>Journal of Pathology: Clinical Research</i> , 2015, 1, 113-123.	1.3	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.	2.5	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.	3.2	119
50	A comparison of Raman and FT-IR spectroscopy for the prediction of meat spoilage. <i>Food Control</i> , 2013, 29, 461-470.	2.8	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.	1.5	113
52	Promises and challenges of adoptive T-cell therapies for solid tumours. <i>British Journal of Cancer</i> , 2021, 124, 1759-1776.	2.9	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.	2.9	109

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55	DNMT3A mutations occur early or late in patients with myeloproliferative neoplasms and mutation order influences phenotype. <i>Haematologica</i> , 2015, 100, e438-e442.	1.7	105
56	A practical guide to cancer subclonal reconstruction from DNA sequencing. <i>Nature Methods</i> , 2021, 18, 144-155.	9.0	103
57	Embryonal precursors of Wilms tumor. <i>Science</i> , 2019, 366, 1247-1251.	6.0	101
58	The evolutionary landscape of colorectal tumorigenesis. <i>Nature Ecology and Evolution</i> , 2018, 2, 1661-1672.	3.4	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.	6.5	96
60	Genomic copy number predicts esophageal cancer years before transformation. <i>Nature Medicine</i> , 2020, 26, 1726-1732.	15.2	86
61	Tandem duplication of chromosomal segments is common in ovarian and breast cancer genomes. <i>Journal of Pathology</i> , 2012, 227, 446-455.	2.1	81
62	Genomic and evolutionary classification of lung cancer in never smokers. <i>Nature Genetics</i> , 2021, 53, 1348-1359.	9.4	81
63	Genetic and epigenetic intratumor heterogeneity impacts prognosis of lung adenocarcinoma. <i>Nature Communications</i> , 2020, 11, 2459.	5.8	77
64	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. <i>Nature Communications</i> , 2017, 8, 1221.	5.8	75
65	Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. <i>Genome Biology</i> , 2016, 17, 250.	3.8	68
66	Tumor heterogeneity. <i>Cancer Cell</i> , 2021, 39, 1015-1017.	7.7	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.	1.9	63
68	Neutral tumor evolution?. <i>Nature Genetics</i> , 2018, 50, 1630-1633.	9.4	59
69	Analysis of a complete DNA-protein affinity landscape. <i>Journal of the Royal Society Interface</i> , 2010, 7, 397-408.	1.5	58
70	A community effort to create standards for evaluating tumor subclonal reconstruction. <i>Nature Biotechnology</i> , 2020, 38, 97-107.	9.4	58
71	A unified haplotype-based method for accurate and comprehensive variant calling. <i>Nature Biotechnology</i> , 2021, 39, 885-892.	9.4	56
72	Prediction from Quantum Chemical Topology Descriptors. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 1914-1924.	2.5	54

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73	Differential and limited expression of mutant alleles in multiple myeloma. <i>Blood</i> , 2014, 124, 3110-3117.	0.6	54
74	Genomic evidence supports a clonal diaspora model for metastases of esophageal adenocarcinoma. <i>Nature Genetics</i> , 2020, 52, 74-83.	9.4	53
75	Aptamer evolution for array-based diagnostics. <i>Analytical Biochemistry</i> , 2009, 390, 203-205.	1.1	50
76	Mitochondrial genetic diversity, selection and recombination in a canine transmissible cancer. <i>ELife</i> , 2016, 5, .	2.8	49
77	Prostate cancer evolution from multilineage primary to single lineage metastases with implications for liquid biopsy. <i>Nature Communications</i> , 2020, 11, 5070.	5.8	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.	4.0	43
79	The genetic heterogeneity and mutational burden of engineered melanomas in zebrafish models. <i>Genome Biology</i> , 2013, 14, R113.	13.9	40
80	On Globalâ€“Local Artificial Neural Networks for Function Approximation. <i>IEEE Transactions on Neural Networks</i> , 2006, 17, 942-952.	4.8	38
81	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline. <i>Nature</i> , 2022, 602, 623-631.	13.7	38
82	Fast randomization of large genomic datasets while preserving alteration counts. <i>Bioinformatics</i> , 2014, 30, i617-i623.	1.8	36
83	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. <i>Cell Reports</i> , 2016, 16, 2032-2046.	2.9	36
84	How Subclonal Modeling Is Changing the Metastatic Paradigm. <i>Clinical Cancer Research</i> , 2017, 23, 630-635.	3.2	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.	1.5	34
86	Liquid Chromatographyâ€“Mass Spectrometry Calibration Transfer and Metabolomics Data Fusion. <i>Analytical Chemistry</i> , 2012, 84, 9848-9857.	3.2	33
87	The Genomic Landscape of Pancreatic and Periampullary Adenocarcinoma. <i>Cancer Research</i> , 2016, 76, 5092-5102.	0.4	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.	0.8	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.	4.0	27
90	Profiling molecular regulators of recurrence in chemorefractory triple-negative breast cancers. <i>Breast Cancer Research</i> , 2019, 21, 87.	2.2	26

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91	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. <i>Nature Communications</i> , 2020, 11, 4306.	5.8	26
92	In utero origin of myelofibrosis presenting in adult monozygotic twins. <i>Nature Medicine</i> , 2022, 28, 1207-1211.	15.2	26
93	Fabrication of planar organic nanotransistors using low temperature thermal nanoimprint lithography for chemical sensor applications. <i>Nanotechnology</i> , 2010, 21, 075301.	1.3	24
94	Concomitant inactivation of the p53 and pRB functional pathways predicts resistance to DNA damaging drugs in breast cancer in vivo. <i>Molecular Oncology</i> , 2015, 9, 1553-1564.	2.1	23
95	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils. <i>PLoS Biology</i> , 2020, 18, e3000926.	2.6	23
96	Germline MBD4 deficiency causes a multi-tumor predisposition syndrome. <i>American Journal of Human Genetics</i> , 2022, 109, 953-960.	2.6	23
97	Population distribution and ancestry of the cancer protective MDM2 SNP285 (rs117039649). <i>Oncotarget</i> , 2014, 5, 8223-8234.	0.8	22
98	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.	5.8	22
99	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.	0.8	21
100	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. <i>Nature Communications</i> , 2020, 11, 3096.	5.8	19
101	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, 2088-2094.	1.8	18
102	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.	3.6	17
103	Malignant transformation and genetic alterations are uncoupled in early colorectal cancer progression. <i>BMC Biology</i> , 2020, 18, 116.	1.7	16
104	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. <i>American Journal of Epidemiology</i> , 2021, 190, 962-976.	1.6	16
105	A Systematic Review of Prostate Cancer Heterogeneity: Understanding the Clonal Ancestry of Multifocal Disease. <i>European Urology Oncology</i> , 2021, 4, 358-369.	2.6	16
106	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.	5.8	15
107	Convergent evolution to an aptamer observed in small populations on DNA microarrays. <i>Physical Biology</i> , 2010, 7, 036007.	0.8	12
108	APOBEC3 mutational signatures are associated with extensive and diverse genomic instability across multiple tumour types. <i>BMC Biology</i> , 2022, 20, .	1.7	12

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109	Predictive models for population performance on real biological fitness landscapes. <i>Bioinformatics</i> , 2010, 26, 2145-2152.	1.8	11
110	Re-evaluating experimental validation in the Big Data Era: a conceptual argument. <i>Genome Biology</i> , 2021, 22, 71.	3.8	10
111	DNA copy number motifs are strong and independent predictors of survival in breast cancer. <i>Communications Biology</i> , 2020, 3, 153.	2.0	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.	1.4	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.	1.2	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.	0.4	6
117	Reference bias in the Illumina Isaac aligner. <i>Bioinformatics</i> , 2020, 36, 4671-4672.	1.8	5
118	A Global-Local Artificial Neural Network with Application to Wave Overtopping Prediction. <i>Lecture Notes in Computer Science</i> , 2005, , 109-114.	1.0	4
119	Benchmarking small-variant genotyping in polyploids. <i>Genome Research</i> , 2022, 32, 403-408.	2.4	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.	1.2	3
121	Automated workflows for accurate mass-based putative metabolite identification in LC/MS-derived metabolomic datasets. <i>Bioinformatics</i> , 2012, 28, 149-149.	1.8	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.	0.9	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.	0.8	1
124	Changes in Clonal Architecture Inform MPN Disease Course in Advance of Phenotypic Manifestations. <i>Blood</i> , 2021, 138, 3590-3590.	0.6	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.	0.6	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.	2.0	0

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127	464 MULTI-OMIC CHARACTERIZATION OF BARRETT'S ESOPHAGUS REVEALS A MOLECULAR CONTINUUM IN THE PROGRESSION TO ESOPHAGEAL ADENOCARCINOMA. <i>Gastroenterology</i> , 2020, 158, S-88-S-89.	0.6	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. <i>SSRN Electronic Journal</i> , 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. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
134	P-061: Single-cell whole-exome DNA sequencing traces clonal trajectory in paired evolution of MGUS to multiple myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2021, 21, S72.	0.2	0
135	P-OGC44 Multi-omic cohort study of Barrett's oesophagus reveals structural variation and retrotransposon activity to occur early in cancer evolution. <i>British Journal of Surgery</i> , 2021, 108, .	0.1	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