Henry M Wood

List of Publications by Year
in descending order

29 papers	1,741 citations	567281 15 h-index	501196 28 g-index
29 all docs	29 docs citations	29 times ranked	3387 citing authors

#	Article	IF	Citations
1	Sparse modelling of cancer patientsâ€™ survival based on genomic copy number alterations. Journal of Biomedical Informatics, 2022, 128, 104025.	4.3	1
2	Prediction of tumour pathological subtype from genomic profile using sparse logistic regression with random effects. Journal of Applied Statistics, 2021, 48, 605-622.	1.3	0
3	Developing a Raman spectroscopy-based tool to stratify patient response to pre-operative radiotherapy in rectal cancer. Analyst, The, 2021, 146, 581-589.	3.5	9
4	Adaptor Template Oligo-Mediated Sequencing (ATOM-Seq) is a new ultra-sensitive UMI-based NGS library preparation technology for use with cfDNA and cfRNA. Scientific Reports, 2021, 11, 3138.	3.3	1
5	The colorectal cancer-associated faecal microbiome of developing countries resembles that of developed countries. Genome Medicine, 2021, 13, 27.	8.2	25
6	Microbiome Analysis of More Than 2,000 NHS Bowel Cancer Screening Programme Samples Shows the Potential to Improve Screening Accuracy. Clinical Cancer Research, 2021, 27, 2246-2254.	7.0	18
7	EGFR Amplification in Metastatic Colorectal Cancer. Journal of the National Cancer Institute, 2021, 113, 1561-1569.	6.3	12
8	Luminal Bioavailability of Orally Administered Ï‰-3 PUFAs in the Distal Small Intestine, and Associated Changes to the Ileal Microbiome, in Humans with a Temporary Ileostomy. Journal of Nutrition, 2021, 151, 2142-2152.	2.9	4
9	Characterisation of dysplastic liver nodules using lowâ€pass <scp>DNA</scp> sequencing and detection of chromosome armâ€level abnormalities in bloodâ€derived cellâ€free <scp>DNA</scp>. Journal of Pathology, 2021, 255, 30-40.	4.5	4
10	Properties and approximate p-value calculation of the Cramer test. Journal of Statistical Computation and Simulation, 2020, 90, 1965-1981.	1.2	1
11	Mutational signature in colorectal cancer caused by genotoxic pks+ E. coli. Nature, 2020, 580, 269-273.	27.8	587
12	No Significant Association Between the Fecal Microbiome and the Presence of Irritable Bowel Syndrome-type Symptoms in Patients with Quiescent Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2018, 24, 1597-1605.	1.9	20
13	A randomised trial of the effect of omega-3 polyunsaturated fatty acid supplements on the human intestinal microbiota. Gut, 2018, 67, 1974-1983.	12.1	332
14	Examining the potential use and long-term stability of guaiac faecal occult blood test cards for microbial DNA 16S rRNA sequencing. Journal of Clinical Pathology, 2017, 70, 600-606.	2.0	16
15	Survival of Head and Neck Cancer Cells Relies upon LZK Kinase-Mediated Stabilization of Mutant p53. Cancer Research, 2017, 77, 4961-4972.	0.9	22
16	The genomic road to invasionâ€”examining the similarities and differences in the genomes of associated oral pre-cancer and cancer samples. Genome Medicine, 2017, 9, 53.	8.2	32
17	Past and future impact of nextâ€generation sequencing in head and neck cancer. Head and Neck, 2016, 38, E2395-402.	2.0	6
18	<scp>HER2</scp> overexpression and amplification as a potential therapeutic target in colorectal cancer: analysis of 3256 patients enrolled in the <scp>QUASAR</scp>, <scp>FOCUS</scp> and <scp>PICCOLO</scp> colorectal cancer trials. Journal of Pathology, 2016, 238, 562-570.	4.5	185

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19	Polycomb Repressor Complex 1 Member, BMI1 Contributes to Urothelial Tumorigenesis through p16-Independent Mechanisms. Translational Oncology, 2015, 8, 387-399.	3.7	6
20	A novel genomic signature reclassifies an oral cancer subtype. International Journal of Cancer, 2015, 137, 2364-2373.	5.1	12
21	The clonal relationships between preâ€cancer and cancer revealed by ultraâ€deep sequencing. Journal of Pathology, 2015, 237, 296-306.	4.5	31
22	Stratifying tumour subtypes based on copy number alteration profiles using next-generation sequence data. Bioinformatics, 2015, 31, 2713-2720.	4.1	9
23	Clinical and genomic analysis of a randomised phase II study evaluating anastrozole and fulvestrant in postmenopausal patients treated for large operable or locally advanced hormone-receptor-positive breast cancer. British Journal of Cancer, 2015, 113, 585-594.	6.4	23
24	Estimating optimal window size for analysis of low-coverage next-generation sequence data. Bioinformatics, 2014, 30, 1823-1829.	4.1	24
25	MicroRNAs and head and neck cancer: Reviewing the first decade of research. European Journal of Cancer, 2014, 50, 2619-2635.	2.8	67
26	The many generations of sequencing technology. Oral Oncology, 2014, 50, e61.	1.5	2
27	Next-generation sequencing analysis for detecting human papillomavirus in oral verrucous carcinoma. Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology, 2014, 118, 117-125.e1.	0.4	18
28	Correcting for cancer genome size and tumour cell content enables better estimation of copy number alterations from next-generation sequence data. Bioinformatics, 2012, 28, 40-47.	4.1	173
29	Using next-generation sequencing for high resolution multiplex analysis of copy number variation from nanogram quantities of DNA from formalin-fixed paraffin-embedded specimens. Nucleic Acids Research, 2010, 38, e151-e151.	14.5	101