Michael Peter Alan Davies

List of Publications by Year
in descending order

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44 papers	2,631 citations	279798 23 h-index	265206 42 g-index
44 all docs	44 docs citations	44 times ranked	5350 citing authors

#	Article	IF	Citations
1	Accounting for EGFR Mutations in Epidemiologic Analyses of Nonâ€“Small Cell Lung Cancers: Examples Based on the International Lung Cancer Consortium Data. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 679-687.	2.5	1
2	Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk. Human Molecular Genetics, 2022, 31, 2831-2843.	2.9	4
3	Geneâ€“gene interaction of AhRwith and within the Wntcascade affects susceptibility to lung cancer. European Journal of Medical Research, 2022, 27, 14.	2.2	1
4	Lung cancer risk in painters: results from the SYNERGY pooled caseâ€“control study consortium. Occupational and Environmental Medicine, 2021, 78, 269-278.	2.8	11
5	The relationship between body-mass index and overall survival in non-small cell lung cancer by sex, smoking status, and race: A pooled analysis of 20,937 International lung Cancer consortium (ILCCO) patients. Lung Cancer, 2021, 152, 58-65.	2.0	22
6	Liverpool Lung Project lung cancer risk stratification model: calibration and prospective validation. Thorax, 2021, 76, 161-168.	5.6	27
7	Rare deleterious germline variants and risk of lung cancer. Npj Precision Oncology, 2021, 5, 12.	5.4	19
8	Lung cancer mortality reduction by LDCT screening: UKLS randomised trial results and international meta-analysis. Lancet Regional Health - Europe, The, 2021, 10, 100179.	5.6	82
9	Protein-altering germline mutations implicate novel genes related to lung cancer development. Nature Communications, 2020, 11, 2220.	12.8	31
10	Long non-coding RNA dysregulation is a frequent event in non-small cell lung carcinoma pathogenesis. British Journal of Cancer, 2020, 122, 1050-1058.	6.4	68
11	Lung Cancer Risk in Never-Smokers of European Descent is Associated With Genetic Variation in the 5p15.33 TERT-CLPTM1Ll Region. Journal of Thoracic Oncology, 2019, 14, 1360-1369.	1.1	27
12	Investigation of Leukocyte Telomere Length and Genetic Variants in Chromosome 5p15.33 as Prognostic Markers in Lung Cancer. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1228-1237.	2.5	11
13	Potential genetic modifiers for somatic EGFR mutation in lung cancer: a meta-analysis and literature review. BMC Cancer, 2019, 19, 1068.	2.6	31
14	Elevated Platelet Count Appears to Be Causally Associated with Increased Risk of Lung Cancer: A Mendelian Randomization Analysis. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 935-942.	2.5	21
15	Heterogeneity of PD-L1 expression in non-small cell lung cancer: Implications for specimen sampling in predicting treatment response. Lung Cancer, 2019, 134, 79-84.	2.0	105
16	Implementation planning for lung cancer screening in China. Precision Clinical Medicine, 2019, 2, 13-44.	3.3	28
17	Systematic analyses of regulatory variants in DNase I hypersensitive sites identified two novel lung cancer susceptibility loci. Carcinogenesis, 2019, 40, 432-440.	2.8	5
18	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	12.8	60

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19	Aurora B expression modulates paclitaxel response in non-small cell lung cancer. British Journal of Cancer, 2017, 116, 592-599.	6.4	38
20	AURKA mRNA expression is an independent predictor of poor prognosis in patients with non-small cell lung cancer. Oncology Letters, 2017, 13, 4463-4468.	1.8	26
21	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nature Genetics, 2017, 49, 1126-1132.	21.4	472
22	Common TDP1 Polymorphisms in Relation to Survival among Small Cell Lung Cancer Patients: A Multicenter Study from the International Lung Cancer Consortium. Clinical Cancer Research, 2017, 23, 7550-7557.	7.0	6
23	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. PLoS ONE, 2017, 12, e0177875.	2.5	79
24	Silicon Nanowire Sensors Enable Diagnosis of Patients via Exhaled Breath. ACS Nano, 2016, 10, 7047-7057.	14.6	179
25	Fine mapping of chromosome 5p15.33 based on a targeted deep sequencing and high density genotyping identifies novel lung cancer susceptibility loci. Carcinogenesis, 2016, 37, 96-105.	2.8	36
26	Identification of lung cancer histology-specific variants applying Bayesian framework variant prioritization approaches within the TRICL and ILCCO consortia. Carcinogenesis, 2015, 36, 1314-1326.	2.8	15
27	Associated Links Among Smoking, Chronic Obstructive Pulmonary Disease, and Small Cell Lung Cancer: A Pooled Analysis in the International Lung Cancer Consortium. EBioMedicine, 2015, 2, 1677-1685.	6.1	49
28	Differentiation between genetic mutations of breast cancer by breath volatolomics. Oncotarget, 2015, 6, 44864-44876.	1.8	71
29	Epigenetic biomarkers in lung cancer. Cancer Letters, 2014, 342, 200-212.	7.2	114
30	Frequent mutations in chromatin-remodelling genes in pulmonary carcinoids. Nature Communications, 2014, 5, 3518.	12.8	239
31	Microarray Analysis of Suppression Subtracted Hybridisation Libraries Identifies Genes Associated with Breast Cancer Progression. Analytical Cellular Pathology, 2010, 32, 87-99.	1.4	0
32	Expression and splicing of the unfolded protein response gene XBPâ€1 are significantly associated with clinical outcome of endocrineâ€treated breast cancer. International Journal of Cancer, 2008, 123, 85-88.	5.1	149
33	Association of oestrogen receptor beta 2 (ERÎ²2/ERÎ²cx) with outcome of adjuvant endocrine treatment for primary breast cancer â€“ a retrospective study. BMC Cancer, 2007, 7, 131.	2.6	43
34	Examination of tumour histopathology and gene expression in a neu/S100A4 transgenic model of metastatic breast cancer. International Journal of Experimental Pathology, 2003, 84, 173-184.	1.3	8
35	Declining Estrogen Receptor-Î² Expression Defines Malignant Progression of Human Breast Neoplasia. American Journal of Surgical Pathology, 2003, 27, 1502-1512.	3.7	165
36	Molecular and genetic abnormalities in radial scar. Human Pathology, 2002, 33, 715-722.	2.0	28

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37	Subgroups of non-atypical hyperplasia of breast defined by proliferation of oestrogen receptor-positive cells. Journal of Pathology, 2001, 193, 333-338.	4.5	17
38	Characterisation of molecular alterations in microdissected archival gliomas. Acta Neuropathologica, 2001, 101, 321-333.	7.7	26
39	Novel Polymerase Chain Reaction Approach for Full-Coding p53 Mutation Detection in Microdissected Archival Tumors. Diagnostic Molecular Pathology, 2000, 9, 110-119.	2.1	10
40	Estrogen Receptor-Positive Proliferating Cells in the Normal and Precancerous Breast. American Journal of Pathology, 1999, 155, 1811-1815.	3.8	247
41	Transcriptional Down-regulation of the Metastasis-inducing S100A4 (p9Ka) in Benign but Not in Malignant Rat Mammary Epithelial Cells by GC-factor. Journal of Biological Chemistry, 1997, 272, 20283-20290.	3.4	17
42	Elevated expression of calcium-binding protein p9Ka is associated with increasing malignant characteristics of rat prostate carcinoma cells. , 1997, 71, 832-837.		26
43	Production of the metastatic phenotype by DNA transfection in a rat mammary model.. Cell Biology International, 1993, 17, 871-880.	3.0	16
44	A role for cytoplasmic calcium in the stimulation of neutrophil adhesion. Biochemical Society Transactions, 1989, 17, 123-123.	3.4	1