

# James D Mckay

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3251254/publications.pdf>

Version: 2024-02-01

40  
papers

2,600  
citations

279798

23  
h-index

289244

40  
g-index

42  
all docs

42  
docs citations

42  
times ranked

6329  
citing authors

#	ARTICLE	IF	CITATIONS
1	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. <i>Nature Genetics</i> , 2017, 49, 1126-1132.	21.4	472
2	Integrative genomic profiling of large-cell neuroendocrine carcinomas reveals distinct subtypes of high-grade neuroendocrine lung tumors. <i>Nature Communications</i> , 2018, 9, 1048.	12.8	254
3	Genome-wide association study of renal cell carcinoma identifies two susceptibility loci on 2p21 and 11q13.3. <i>Nature Genetics</i> , 2011, 43, 60-65.	21.4	220
4	Influence of common genetic variation on lung cancer risk: meta-analysis of 14 900 cases and 29 485 controls. <i>Human Molecular Genetics</i> , 2012, 21, 4980-4995.	2.9	196
5	Identification of Circulating Tumor DNA for the Early Detection of Small-cell Lung Cancer. <i>EBioMedicine</i> , 2016, 10, 117-123.	6.1	153
6	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. <i>Nature Genetics</i> , 2014, 46, 1233-1238.	21.4	147
7	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. <i>Nature Communications</i> , 2017, 8, 15724.	12.8	106
8	Obesity and cancer: Mendelian randomization approach utilizing the FTO genotype. <i>International Journal of Epidemiology</i> , 2009, 38, 971-975.	1.9	96
9	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. <i>American Journal of Human Genetics</i> , 2014, 95, 462-471.	6.2	96
10	A genome-wide association study identifies a novel susceptibility locus for renal cell carcinoma on 12p11.23. <i>Human Molecular Genetics</i> , 2012, 21, 456-462.	2.9	81
11	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. <i>PLoS ONE</i> , 2017, 12, e0177875.	2.5	79
12	<i>KRAS</i> mutations in blood circulating cell-free DNA: a pancreatic cancer case-control. <i>Oncotarget</i> , 2016, 7, 78827-78840.	1.8	70
13	The influence of obesity-related factors in the etiology of renal cell carcinoma—A mendelian randomization study. <i>PLoS Medicine</i> , 2019, 16, e1002724.	8.4	59
14	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. <i>Nature Communications</i> , 2015, 6, 5751.	12.8	58
15	Redefining malignant pleural mesothelioma types as a continuum uncovers immune-vascular interactions. <i>EBioMedicine</i> , 2019, 48, 191-202.	6.1	55
16	Common variation at 2q22.3 (ZEB2) influences the risk of renal cancer. <i>Human Molecular Genetics</i> , 2013, 22, 825-831.	2.9	54
17	Urinary TERT promoter mutations are detectable up to 10 years prior to clinical diagnosis of bladder cancer: Evidence from the Golestan Cohort Study. <i>EBioMedicine</i> , 2020, 53, 102643.	6.1	51
18	The chromosome 2p21 region harbors a complex genetic architecture for association with risk for renal cell carcinoma. <i>Human Molecular Genetics</i> , 2012, 21, 1190-1200.	2.9	37

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19	A Rare Truncating BRCA2 Variant and Genetic Susceptibility to Upper Aerodigestive Tract Cancer. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	33
20	Exome sequencing identifies germline variants in DIS3 in familial multiple myeloma. <i>Leukemia</i> , 2019, 33, 2324-2330.	7.2	33
21	Mendelian Randomization and mediation analysis of leukocyte telomere length and risk of lung and head and neck cancers. <i>International Journal of Epidemiology</i> , 2019, 48, 751-766.	1.9	32
22	Novel pedigree analysis implicates DNA repair and chromatin remodeling in multiple myeloma risk. <i>PLoS Genetics</i> , 2018, 14, e1007111.	3.5	30
23	The causal relevance of body mass index in different histological types of lung cancer: A Mendelian randomization study. <i>Scientific Reports</i> , 2016, 6, 31121.	3.3	27
24	Genome-wide association meta-analysis identifies pleiotropic risk loci for aerodigestive squamous cell cancers. <i>PLoS Genetics</i> , 2021, 17, e1009254.	3.5	19
25	Common Variation at 1q24.1 (ALDH9A1) Is a Potential Risk Factor for Renal Cancer. <i>PLoS ONE</i> , 2015, 10, e0122589.	2.5	19
26	A molecular map of lung neuroendocrine neoplasms. <i>GigaScience</i> , 2020, 9, .	6.4	17
27	Identification of lung cancer histology-specific variants applying Bayesian framework variant prioritization approaches within the TRICL and ILCCO consortia. <i>Carcinogenesis</i> , 2015, 36, 1314-1326.	2.8	15
28	Sexual dimorphism in cancer: insights from transcriptional signatures in kidney tissue and renal cell carcinoma. <i>Human Molecular Genetics</i> , 2021, 30, 343-355.	2.9	14
29	The Shared Genetic Architectures Between Lung Cancer and Multiple Polygenic Phenotypes in Genome-Wide Association Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1156-1164.	2.5	13
30	The shared genetic architecture between epidemiological and behavioral traits with lung cancer. <i>Scientific Reports</i> , 2021, 11, 17559.	3.3	10
31	Germline determinants of humoral immune response to HPV-16 protect against oropharyngeal cancer. <i>Nature Communications</i> , 2021, 12, 5945.	12.8	10
32	Association between anthropometry and lifestyle factors and risk of Bâ€cell lymphoma: An exposomeâ€wide analysis. <i>International Journal of Cancer</i> , 2021, 148, 2115-2128.	5.1	9
33	Genetic Analysis of Lung Cancer and the Germline Impact on Somatic Mutation Burden. <i>Journal of the National Cancer Institute</i> , 2022, 114, 1159-1166.	6.3	8
34	Needlestack: an ultra-sensitive variant caller for multi-sample next generation sequencing data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa021.	3.2	5
35	Mediating effect of soluble B-cell activation immune markers on the association between anthropometric and lifestyle factors and lymphoma development. <i>Scientific Reports</i> , 2020, 10, 13814.	3.3	4
36	Development of a custom next-generation sequencing panel for the determination of bladder cancer risk in a Tunisian cohort. <i>Molecular Biology Reports</i> , 2022, 49, 1233-1258.	2.3	4

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37	Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk. <i>Human Molecular Genetics</i> , 2022, 31, 2831-2843.	2.9	4
38	Circulating Isovalerylcarnitine and Lung Cancer Risk: Evidence from Mendelian Randomization and Prediagnostic Blood Measurements. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 1966-1974.	2.5	4
39	Sequencing at lymphoid neoplasm susceptibility loci maps six myeloma risk genes. <i>Human Molecular Genetics</i> , 2021, 30, 1142-1153.	2.9	2
40	The PI3K/mTOR Pathway Is Targeted by Rare Germline Variants in Patients with Both Melanoma and Renal Cell Carcinoma. <i>Cancers</i> , 2021, 13, 2243.	3.7	2