Matthew F Buas

List of Publications by Year
in descending order

35 papers	1,283 citations	361413 20 h-index	414414 32 g-index
35 all docs	35 docs citations	35 times ranked	2501 citing authors

#	Article	IF	Citations
1	Epidemiology and Risk Factors for Gastroesophageal Junction Tumors: Understanding the Rising Incidence of This Disease. Seminars in Radiation Oncology, 2013, 23, 3-9.	2.2	232
2	Genome-wide association studies in oesophageal adenocarcinoma and Barrett's oesophagus: a large-scale meta-analysis. Lancet Oncology, The, 2016, 17, 1363-1373.	10.7	133
3	Regulation of skeletal myogenesis by Notch. Experimental Cell Research, 2010, 316, 3028-3033.	2.6	99
4	Multitrait genetic association analysis identifies 50 new risk loci for gastro-oesophageal reflux, seven new loci for Barrettâ€™s oesophagus and provides insights into clinical heterogeneity in reflux diagnosis. Gut, 2022, 71, 1053-1061.	12.1	74
5	Inhibition of myogenesis by Notch: Evidence for multiple pathways. Journal of Cellular Physiology, 2009, 218, 84-93.	4.1	73
6	The Notch Effector Hey1 Associates with Myogenic Target Genes to Repress Myogenesis. Journal of Biological Chemistry, 2010, 285, 1249-1258.	3.4	71
7	Determining Risk of Barrettâ€™s Esophagus and Esophageal Adenocarcinoma Based on Epidemiologic Factors and GeneticÂVariants. Gastroenterology, 2018, 154, 1273-1281.e3.	1.3	67
8	Salivary metabolite profiling distinguishes patients with oral cavity squamous cell carcinoma from normal controls. PLoS ONE, 2018, 13, e0204249.	2.5	62
9	Identification of novel candidate plasma metabolite biomarkers for distinguishing serous ovarian carcinoma and benign serous ovarian tumors. Gynecologic Oncology, 2016, 140, 138-144.	1.4	56
10	Targeted plasma metabolome response to variations in dietary glycemic load in a randomized, controlled, crossover feeding trial in healthy adults. Food and Function, 2015, 6, 2949-2956.	4.6	43
11	Germline variation in inflammation-related pathways and risk of Barrett's oesophagus and oesophageal adenocarcinoma. Gut, 2017, 66, 1739-1747.	12.1	38
12	Impact of polymorphisms in microRNA biogenesis genes on colon cancer risk and microRNA expression levels: a population-based, case-control study. BMC Medical Genomics, 2016, 9, 21.	1.5	33
13	Integrative post-genome-wide association analysis of CDKN2A and TP53 SNPs and risk of esophageal adenocarcinoma. Carcinogenesis, 2014, 35, 2740-2747.	2.8	31
14	Candidate serum metabolite biomarkers for differentiating gastroesophageal reflux disease, Barrettâ€™s esophagus, and high-grade dysplasia/esophageal adenocarcinoma. Metabolomics, 2017, 13, 1.	3.0	26
15	SNP Regulation of microRNA Expression and Subsequent Colon Cancer Risk. PLoS ONE, 2015, 10, e0143894.	2.5	25
16	Candidate early detection protein biomarkers for ER+/PR+ invasive ductal breast carcinoma identified using pre-clinical plasma from the WHI observational study. Breast Cancer Research and Treatment, 2015, 153, 445-454.	2.5	25
17	A Newly Identified Susceptibility Locus nearFOXP1Modifies the Association of Gastroesophageal Reflux with Barrett's Esophagus. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1739-1747.	2.5	24
18	FOXA1 hypermethylation: link between parity and ER-negative breast cancer in African American women?. Breast Cancer Research and Treatment, 2017, 166, 559-568.	2.5	24

#	Article	IF	Citations
19	Survival disparities among racial/ethnic groups of women with ovarian cancer: An update on data from the Surveillance, Epidemiology and End Results (SEER) registry. Cancer Epidemiology, 2019, 62, 101580.	1.9	22
20	MiRNA-Related SNPs and Risk of Esophageal Adenocarcinoma and Barrettâ€™s Esophagus: Post Genome-Wide Association Analysis in the BEACON Consortium. PLoS ONE, 2015, 10, e0128617.	2.5	21
21	Differences in microRNA expression in breast cancer between women of African and European ancestry. Carcinogenesis, 2019, 40, 61-69.	2.8	21
22	Interactions Between Genetic Variants and Environmental Factors Affect Risk of Esophageal Adenocarcinoma and Barrettâ€™s Esophagus. Clinical Gastroenterology and Hepatology, 2018, 16, 1598-1606.e4.	4.4	16
23	Germline variation in the insulin-like growth factor pathway and risk of Barrettâ€™s esophagus and esophageal adenocarcinoma. Carcinogenesis, 2021, 42, 369-377.	2.8	11
24	Quantitative global lipidomics analysis of patients with ovarian cancer versus benign adnexal mass. Scientific Reports, 2021, 11, 18156.	3.3	11
25	FOXA1 Protein Expression in ER+ and ERâˆ’ Breast Cancer in Relation to Parity and Breastfeeding in Black and White Women. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 379-385.	2.5	8
26	Constrained Score Statistics Identify Genetic Variants Interacting with Multiple Risk Factors in Barrettâ€™s Esophagus. American Journal of Human Genetics, 2016, 99, 352-365.	6.2	7
27	Whole-genome sequencing of esophageal adenocarcinoma in Chinese patients reveals distinct mutational signatures and genomic alterations. Communications Biology, 2018, 1, 174.	4.4	6
28	Clinical and Lifestyle-Related Prognostic Indicators among Esophageal Adenocarcinoma Patients Receiving Treatment at a Comprehensive Cancer Center. Cancers, 2021, 13, 4653.	3.7	6
29	Recommendation to use exact P-values in biomarker discovery research in place of approximate P-values. Cancer Epidemiology, 2018, 56, 83-89.	1.9	4
30	Circulating CD14 + HLAâ€ÐR lo/âˆ’ monocytic cells as a biomarker for epithelial ovarian cancer progression. American Journal of Reproductive Immunology, 2021, 85, e13343.	1.2	4
31	Genes Relevant to Tissue Response to Cancer Therapy Display Diurnal Variation in mRNA Expression in Human Oral Mucosa. Journal of Circadian Rhythms, 2021, 19, 8.	1.3	4
32	Prioritization and functional analysis of GWAS risk loci for Barrettâ€™s esophagus and esophageal adenocarcinoma. Human Molecular Genetics, 2022, 31, 410-422.	2.9	4
33	eQTL set-based association analysis identifies novel susceptibility loci for Barrett's esophagus and esophageal adenocarcinoma. Cancer Epidemiology Biomarkers and Prevention, 0, , .	2.5	1
34	A risk variant for Barrettâ€™s esophagus and esophageal adenocarcinoma at chr8p23.1 affects enhancer activity and implicates multiple gene targets. Human Molecular Genetics, 2022, 31, 3975-3986.	2.9	1
35	Deletion of in the mouse mammary gland results in abnormal accumulation of luminal progenitor cells: a link between reproductive factors and ER-/TNBC breast cancer?. American Journal of Cancer Research, 2021, 11, 3263-3270.	1.4	0