Daniele Campa

List of Publications by Year
in descending order

168 papers	7,846 citations	81743 39 h-index	60497 81 g-index
176 all docs	176 docs citations	176 times ranked	11718 citing authors

#	Article	IF	Citations
1	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
2	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	9.4	492
3	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
4	Polymorphisms of DNA repair genes and risk of non-small cell lung cancer. Carcinogenesis, 2006, 27, 560-567.	1.3	365
5	Association of ABCB1/MDR1 and OPRM1 Gene Polymorphisms With Morphine Pain Relief. Clinical Pharmacology and Therapeutics, 2008, 83, 559-566.	2.3	303
6	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	9.4	294
7	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	9.4	265
8	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265
9	Common variation at 2p13.3, 3q29, 7p13 and 17q25.1 associated with susceptibility to pancreatic cancer. Nature Genetics, 2015, 47, 911-916.	9.4	224
10	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556.	5.8	188
11	Association of a common polymorphism in the cyclooxygenase 2 gene with risk of non-small cell lung cancer. Carcinogenesis, 2003, 25, 229-235.	1.3	184
12	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. Human Molecular Genetics, 2012, 21, 5373-5384.	1.4	168
13	Interactions Between Genetic Variants and Breast Cancer Risk Factors in the Breast and Prostate Cancer Cohort Consortium. Journal of the National Cancer Institute, 2011, 103, 1252-1263.	3.0	147
14	A comprehensive analysis of phase I and phase II metabolism gene polymorphisms and risk of non-small cell lung cancer in smokers. Carcinogenesis, 2008, 29, 1164-1169.	1.3	123
15	A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. Human Molecular Genetics, 2013, 22, 408-415.	1.4	118
16	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 2520-2528.	1.4	100
17	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
18	Two susceptibility loci identified for prostate cancer aggressiveness. Nature Communications, 2015, 6, 6889.	5.8	88

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19	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. Oncotarget, 2016, 7, 66328-66343.	0.8	88
20	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
21	Association Between TAS2R38 Gene Polymorphisms and Colorectal Cancer Risk: A Case-Control Study in Two Independent Populations of Caucasian Origin. PLoS ONE, 2011, 6, e20464.	1.1	77
22	Prostate Cancer (PCa) Risk Variants and Risk of Fatal PCa in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. European Urology, 2014, 65, 1069-1075.	0.9	75
23	Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROPosal. Scientific Reports, 2016, 6, 25506.	1.6	69
24	DNA Microarray Based on Arrayed-Primer Extension Technique for Identification of Pathogenic Fungi Responsible for Invasive and Superficial Mycoses. Journal of Clinical Microbiology, 2008, 46, 909-915.	1.8	62
25	A comprehensive study of polymorphisms in ABCB1, ABCC2 and ABCG2 and lung cancer chemotherapy response and prognosis. International Journal of Cancer, 2012, 131, 2920-2928.	2.3	60
26	<scp>TERT</scp> gene harbors multiple variants associated with pancreatic cancer susceptibility. International Journal of Cancer, 2015, 137, 2175-2183.	2.3	57
27	Characterizing Associations and SNP-Environment Interactions for GWAS-Identified Prostate Cancer Risk Markersâ€"Results from BPC3. PLoS ONE, 2011, 6, e17142.	1.1	57
28	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
29	ABO blood groups and pancreatic cancer risk and survival: Results from the PANcreatic Disease ReseArch (PANDoRA) consortium. Oncology Reports, 2013, 29, 1637-1644.	1.2	55
30	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
31	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	5.8	50
32	Pancreatic Cancer Susceptibility Loci and Their Role in Survival. PLoS ONE, 2011, 6, e27921.	1.1	49
33	Bitter Taste Receptor Polymorphisms and Human Aging. PLoS ONE, 2012, 7, e45232.	1.1	48
34	Genetic association of gastric cancer with miRNA clusters including the cancerâ€related genes MIR29, MIR25, MIR93 and MIR106: Results from the EPICâ€EURGAST study. International Journal of Cancer, 2014, 135, 2065-2076.	2.3	47
35	Somatic Mutations in Exocrine Pancreatic Tumors: Association with Patient Survival. PLoS ONE, 2013, 8, e60870.	1.1	47
36	Mitochondrial DNA copy number and future risk of B-cell lymphoma in a nested case-control study in the prospective EPIC cohort. Blood, 2014, 124, 530-535.	0.6	46

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37	Genetic susceptibility to pancreatic cancer and its functional characterisation: The PANcreatic Disease ReseArch (PANDoRA) consortium. Digestive and Liver Disease, 2013, 45, 95-99.	0.4	45
38	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
39	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	3.0	45
40	Lack of Association between Polymorphisms in Inflammatory Genes and Lung Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 538-539.	1.1	44
41	Mitochondrial DNA copy number variation, leukocyte telomere length, and breast cancer risk in the European Prospective Investigation into Cancer and Nutrition (EPIC) study. Breast Cancer Research, 2018, 20, 29.	2.2	44
42	Candida albicans isolates with different genomic backgrounds display a differential response to macrophage infection. Microbes and Infection, 2006, 8, 791-800.	1.0	42
43	A gene-wide investigation on polymorphisms in the ABCG2/BRCP transporter and susceptibility to colorectal cancer. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2008, 645, 56-60.	0.4	41
44	Functional single nucleotide polymorphisms within the cyclin-dependent kinase inhibitor 2A/2B region affect pancreatic cancer risk. Oncotarget, 2016, 7, 57011-57020.	0.8	41
45	Mendelian randomisation study of the effects of known and putative risk factors on pancreatic cancer. Journal of Medical Genetics, 2020, 57, 820-828.	1.5	40
46	The FOXE1 locus is a major genetic determinant for familial nonmedullary thyroid carcinoma. International Journal of Cancer, 2014, 134, 2098-2107.	2.3	39
47	Factors associated with oxidative stress and cancer risk in the Breast and Prostate Cancer Cohort Consortium. Free Radical Research, 2014, 48, 380-386.	1.5	38
48	Genome-wide association study identifies variants at 16p13 associated with survival in multiple myeloma patients. Nature Communications, 2015, 6, 7539.	5.8	38
49	Polymorphisms of dopamine receptor/transporter genes and risk of non-small cell lung cancer. Lung Cancer, 2007, 56, 17-23.	0.9	37
50	Post-GWAS geneâ€“environment interplay in breast cancer: results from the Breast and Prostate Cancer Cohort Consortium and a meta-analysis on 79 000 women. Human Molecular Genetics, 2014, 23, 5260-5270.	1.4	37
51	Genetic Variation in the Vitamin D Pathway in Relation to Risk of Prostate Cancerâ€”Results from the Breast and Prostate Cancer Cohort Consortium. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 688-696.	1.1	36
52	Additive Interactions Between Susceptibility Single-Nucleotide Polymorphisms Identified in Genome-Wide Association Studies and Breast Cancer Risk Factors in the Breast and Prostate Cancer Cohort Consortium. American Journal of Epidemiology, 2014, 180, 1018-1027.	1.6	36
53	Leukocyte Telomere Length in Relation to Pancreatic Cancer Risk: A Prospective Study. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2447-2454.	1.1	36
54	Genetic determinants of telomere length and risk of pancreatic cancer: A PANDoRA study. International Journal of Cancer, 2019, 144, 1275-1283.	2.3	36

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55	Lack of Association between -251 T>A Polymorphism of IL8 and Lung Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 2457-2458.	1.1	35
56	A comprehensive study of polymorphisms in the ABCB1, ABCC2, ABCG2, NR1I2 genes and lymphoma risk. International Journal of Cancer, 2012, 131, 803-812.	2.3	35
57	Coffee and tea consumption, genotype-basedCYP1A2andNAT2activity and colorectal cancer risk-Results from the EPIC cohort study. International Journal of Cancer, 2014, 135, 401-412.	2.3	35
58	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228â€‰951 Women of European Descent. Journal of the National Cancer Institute, 2020, 112, 295-304.	3.0	35
59	Fine-Mapping the HOXB Region Detects Common Variants Tagging a Rare Coding Allele: Evidence for Synthetic Association in Prostate Cancer. PLoS Genetics, 2014, 10, e1004129.	1.5	34
60	Taste receptor polymorphisms and male infertility. Human Reproduction, 2017, 32, 2324-2331.	0.4	34
61	Association of breast cancer risk loci with breast cancer survival. International Journal of Cancer, 2015, 137, 2837-2845.	2.3	33
62	Exome sequencing identifies germline variants in DIS3 in familial multiple myeloma. Leukemia, 2019, 33, 2324-2330.	3.3	33
63	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
64	N-Acetyltransferase 2 Polymorphisms, Tobacco Smoking, and Breast Cancer Risk in the Breast and Prostate Cancer Cohort Consortium. American Journal of Epidemiology, 2011, 174, 1316-1322.	1.6	31
65	Polygenic and multifactorial scores for pancreatic ductal adenocarcinoma risk prediction. Journal of Medical Genetics, 2021, 58, 369-377.	1.5	31
66	Risk of multiple myeloma is associated with polymorphisms within telomerase genes and telomere length. International Journal of Cancer, 2015, 136, E351-8.	2.3	30
67	Germline genetic variability in pancreatic cancer risk and prognosis. Seminars in Cancer Biology, 2022, 79, 105-131.	4.3	30
68	A Comprehensive Investigation on Common Polymorphisms in the MDR1/ABCB1 Transporter Gene and Susceptibility to Colorectal Cancer. PLoS ONE, 2012, 7, e32784.	1.1	30
69	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
70	Differential Expression of Secretory Aspartyl Proteinase Genes (SAP1 - 10) in Oral Candida albicans Isolates with Distinct Karyotypes. Journal of Clinical Microbiology, 2004, 42, 4726-4734.	1.8	26
71	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
72	Association of common polymorphisms in inflammatory genes with risk of developing cancers of the upper aerodigestive tract. Cancer Causes and Control, 2007, 18, 449-455.	0.8	25

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73	Genetic risk variants associated with in situ breast cancer. Breast Cancer Research, 2015, 17, 82.	2.2	25
74	Factors Associated With the Risk of Progression of Low-Risk Branch-Duct Intraductal Papillary Mucinous Neoplasms. JAMA Network Open, 2020, 3, e2022933.	2.8	25
75	Polymorphisms of genes coding for ghrelin and its receptor in relation to colorectal cancer risk: a two-step gene-wide case-control study. BMC Gastroenterology, 2010, 10, 112.	0.8	23
76	A gene-wide investigation on polymorphisms in the taste receptor 2R14 (TAS2R14) and susceptibility to colorectal cancer. BMC Medical Genetics, 2010, 11, 88.	2.1	23
77	Replication of Five Prostate Cancer Loci Identified in an Asian Populationâ€"Results from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 212-216.	1.1	23
78	Genomeâ€wide scan of long noncoding <scp>RNA</scp> single nucleotide polymorphism<scp>s</scp> and pancreatic cancer susceptibility. International Journal of Cancer, 2021, 148, 2779-2788.	2.3	23
79	Association between taste receptor (TAS) genes and the perception of wine characteristics. Scientific Reports, 2017, 7, 9239.	1.6	22
80	A Genome-wide Pleiotropy Scan for Prostate Cancer Risk. European Urology, 2015, 67, 649-657.	0.9	21
81	Association between polymorphisms of TAS2R16 and susceptibility to colorectal cancer. BMC Gastroenterology, 2017, 17, 104.	0.8	21
82	Genetic variation in genes of the fatty acid synthesis pathway and breast cancer risk. Breast Cancer Research and Treatment, 2009, 118, 565-574.	1.1	20
83	Interaction between functional polymorphic variants in cytokine genes, established risk factors and susceptibility to basal cell carcinoma of skin. Carcinogenesis, 2011, 32, 1849-1854.	1.3	20
84	Lack of Replication of Seven Pancreatic Cancer Susceptibility Loci Identified in Two Asian Populations. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 320-323.	1.1	20
85	Germline BRCA2 K3326X and CHEK2 I157T mutations increase risk for sporadic pancreatic ductal adenocarcinoma. International Journal of Cancer, 2019, 145, 686-693.	2.3	20
86	Genetic polymorphisms associated with telomere length and risk of developing myeloproliferative neoplasms. Blood Cancer Journal, 2020, 10, 89.	2.8	20
87	Genomeâ€wide association study identifies an early onset pancreatic cancer risk locus. International Journal of Cancer, 2020, 147, 2065-2074.	2.3	20
88	Impact of polymorphic variation at 7p15.3, 3p22.1 and 2p23.3 loci on risk of multiple myeloma. British Journal of Haematology, 2012, 158, 805-809.	1.2	19
89	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	5.8	19
90	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	1.1	19

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91	Telomere Length and Male Fertility. International Journal of Molecular Sciences, 2021, 22, 3959.	1.8	18
92	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. Blood, 2018, 132, 2040-2052.	0.6	17
93	Single nucleotide polymorphism detection by optical DNA-based sensing coupled with whole genomic amplification. Analytical and Bioanalytical Chemistry, 2013, 405, 985-993.	1.9	16
94	Population-specific association of genes for telomere-associated proteins with longevity in an Italian population. Biogerontology, 2015, 16, 353-364.	2.0	16
95	Common genetic variants associated with pancreatic adenocarcinoma may also modify risk of pancreatic neuroendocrine neoplasms. Carcinogenesis, 2018, 39, 360-367.	1.3	16
96	Mitochondrial DNA Copy-Number Variation and Pancreatic Cancer Risk in the Prospective EPIC Cohort. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 681-686.	1.1	16
97	A common variant within the HNF1B gene is associated with overall survival of multiple myeloma patients: Results from the IMMEnSE consortium and meta-analysis. Oncotarget, 2016, 7, 59029-59048.	0.8	16
98	POMC and TP53 genetic variability and risk of basal cell carcinoma of skin: Interaction between host and genetic factors. Journal of Dermatological Science, 2011, 63, 47-54.	1.0	15
99	Common germline variants within the CDKN2A/2B region affect risk of pancreatic neuroendocrine tumors. Scientific Reports, 2016, 6, 39565.	1.6	15
100	SLC22A3 polymorphisms do not modify pancreatic cancer risk, but may influence overall patient survival. Scientific Reports, 2017, 7, 43812.	1.6	15
101	Genetics and molecular epidemiology of multiple myeloma: The rationale for the IMMEnSE consortium (Review). International Journal of Oncology, 2011, 40, 625-38.	1.4	14
102	Polymorphisms in xenobiotic transporters ABCB1, ABCG2, ABCC2, ABCC1, ABCC3 and multiple myeloma risk: a caseâ€“control study in the context of the International Multiple Myeloma rESEarch (IMMEnSE) consortium. Leukemia, 2012, 26, 1419-1422.	3.3	14
103	Association of genetic polymorphisms with survival of pancreatic ductal adenocarcinoma patients. Carcinogenesis, 2016, 37, 957-964.	1.3	14
104	Do pancreatic cancer and chronic pancreatitis share the same genetic risk factors? A PANcreatic Disease ReseArch (PANDoRA) consortium investigation. International Journal of Cancer, 2018, 142, 290-296.	2.3	14
105	Genetic variants in taste-related genes and risk of pancreatic cancer. Mutagenesis, 2019, 34, 391-394.	1.0	14
106	Associations between pancreatic expression quantitative traits and risk of pancreatic ductal adenocarcinoma. Carcinogenesis, 2021, 42, 1037-1045.	1.3	14
107	Could polymorphisms in ATP-binding cassette C3/multidrug resistance associated protein 3 (ABCC3/MRP3) modify colorectal cancer risk?. European Journal of Cancer, 2008, 44, 854-857.	1.3	13
108	Variation in genes coding for AMP-activated protein kinase (AMPK) and breast cancer risk in the European Prospective Investigation on Cancer (EPIC). Breast Cancer Research and Treatment, 2011, 127, 761-767.	1.1	13

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109	Comprehensive investigation of genetic variation in the 8q24 region and multiple myeloma risk in the <scp>IMME</scp>n<scp>SE</scp> consortium. British Journal of Haematology, 2012, 157, 331-338.	1.2	13
110	Genetic Variants and Multiple Myeloma Risk: IMMEnSE Validation of the Best Reported Associationsâ€"An Extensive Replication of the Associations from the Candidate Gene Era. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 670-674.	1.1	13
111	Association between telomere length and mitochondrial copy number and cancer risk in humans: A meta-analysis on more than 300,000 individuals. Critical Reviews in Oncology/Hematology, 2021, 167, 103510.	2.0	13
112	Genetic Variability of the mTOR Pathway and Prostate Cancer Risk in the European Prospective Investigation on Cancer (EPIC). PLoS ONE, 2011, 6, e16914.	1.1	12
113	Type 2 diabetes-related variants influence the risk of developing multiple myeloma: results from the IMMEnSE consortium. Endocrine-Related Cancer, 2015, 22, 545-559.	1.6	11
114	Inherited variation in the xenobiotic transporter pathway and survival of multiple myeloma patients. British Journal of Haematology, 2018, 183, 375-384.	1.2	11
115	Genetic polymorphisms in genes of class switch recombination and multiple myeloma risk and survival: an IMMEnSE study. Leukemia and Lymphoma, 2019, 60, 1803-1811.	0.6	11
116	The INSIG2 rs7566605 polymorphism is not associated with body mass index and breast cancer risk. BMC Cancer, 2010, 10, 563.	1.1	10
117	Genetically determined telomere length and multiple myeloma risk and outcome. Blood Cancer Journal, 2021, 11, 74.	2.8	10
118	Association of Genetic Variants Affecting microRNAs and Pancreatic Cancer Risk. Frontiers in Genetics, 2021, 12, 693933.	1.1	10
119	Polymorphisms in the Gene Regions of the Adaptor Complex LAMTOR2/LAMTOR3 and Their Association with Breast Cancer Risk. PLoS ONE, 2013, 8, e53768.	1.1	9
120	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
121	MAP3K7 and GSTZ1 are associated with human longevity: a two-stage caseâ€"control study using a multilocus genotyping. Age, 2013, 35, 1357-1366.	3.0	8
122	A Genome-Wide â€œPleiotropy Scanâ€•Does Not Identify New Susceptibility Loci for Estrogen Receptor Negative Breast Cancer. PLoS ONE, 2014, 9, e85955.	1.1	8
123	Genetic variability of the ABCC2 gene and clinical outcomes in pancreatic cancer patients. Carcinogenesis, 2019, 40, 544-550.	1.3	8
124	Genetic polymorphisms in inflammatory genes and pancreatic cancer risk: a two-phase study on more than 14 000 individuals. Mutagenesis, 2019, 34, 395-401.	1.0	8
125	Smoking Modifies Pancreatic Cancer Risk Loci on 2q21.3. Cancer Research, 2021, 81, 3134-3143.	0.4	8
126	Identification of Recessively Inherited Genetic Variants Potentially Linked to Pancreatic Cancer Risk. Frontiers in Oncology, 2021, 11, 771312.	1.3	8

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127	Genetic variability of the fatty acid synthase pathway is not associated with prostate cancer risk in the European Prospective Investigation on Cancer (EPIC). European Journal of Cancer, 2011, 47, 420-427.	1.3	7
128	Genetic variability of the forkhead box O3 and prostate cancer risk in the European Prospective Investigation on Cancer. Oncology Reports, 2011, 26, 979-86.	1.2	7
129	Do myeloproliferative neoplasms and multiple myeloma share the same genetic susceptibility loci?. International Journal of Cancer, 2021, 148, 1616-1624.	2.3	7
130	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	2.2	7
131	Outcome of experimental rat vaginitis by Candida albicans isolates with different karyotypes. Microbial Pathogenesis, 2010, 49, 47-50.	1.3	6
132	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	2.6	6
133	Genetic variability in thePRKCIgene and prostate cancer risk. Cell Cycle, 2012, 11, 209-209.	1.3	5
134	Polymorphisms in regulators of xenobiotic transport and metabolism genes PXR and CAR do not affect multiple myeloma risk: a caseâ€“control study in the context of the IMMEnSE consortium. Journal of Human Genetics, 2013, 58, 155-159.	1.1	5
135	Lack of Association for Reported Endocrine Pancreatic Cancer Risk Loci in the PANDoRA Consortium. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1349-1351.	1.1	5
136	Role of OPRM1, clinical and anthropometric variants in neonatal pain reduction. Scientific Reports, 2020, 10, 7091.	1.6	5
137	Genome-Wide Geneâ€“Diabetes and Geneâ€“Obesity Interaction Scan in 8,255 Cases and 11,900 Controls from PanScan and PanC4 Consortia. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1784-1791.	1.1	5
138	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854.	2.9	5
139	Polymorphisms within the TNFSF4 and MAPKAPK2 Loci Influence the Risk of Developing Invasive Aspergillosis: A Two-Stage Case Control Study in the Context of the aspBIOmics Consortium. Journal of Fungi (Basel, Switzerland), 2021, 7, 4.	1.5	5
140	A polygenic risk score for multiple myeloma risk prediction. European Journal of Human Genetics, 2022, 30, 474-479.	1.4	5
141	A polymorphic variant in telomere maintenance is associated with worrisome features and high-risk stigmata development in IPMNs. Carcinogenesis, 2022, 43, 728-735.	1.3	5
142	Polymorphic variants in Sweet and Umami taste receptor genes and birthweight. Scientific Reports, 2021, 11, 4971.	1.6	4
143	Genetic Polymorphisms Involved in Mitochondrial Metabolism and Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 2342-2345.	1.1	4
144	Cereblon (CRBN) Gene Polymorphisms Predict Clinical Response and Progression-Free Survival in Multiple Myeloma Patients Treated with Lenalidomide: A Pharmacogenetic Study of Immense Consortium. Blood, 2014, 124, 3628-3628.	0.6	4

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145	Cereblon (CRBN) gene polymorphisms predict clinical response and progression-free survival in relapsed/refractory multiple myeloma patients treated with lenalidomide: a pharmacogenetic study from the IMMEnSE consortium. Leukemia and Lymphoma, 2020, 61, 699-706.	0.6	3
146	Common gene variants within 3â€²â€untranslated regions as modulators of multiple myeloma risk and survival. International Journal of Cancer, 2021, 148, 1887-1894.	2.3	3
147	Expression quantitative trait loci of genes predicting outcome are associated with survival of multiple myeloma patients. International Journal of Cancer, 2021, 149, 327-336.	2.3	3
148	Genetically Determined Telomere Length Is Associated with Pancreatic Neuroendocrine Neoplasms Onset. Neuroendocrinology, 2022, 112, 1168-1176.	1.2	3
149	Association of a common polymorphism in the cyclooxygenase 2 gene with risk of non-small cell lung cancer. Carcinogenesis, 2005, 26, 1157-1157.	1.3	2
150	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 4239-4239.	1.4	2
151	Host immune genetic variations influence the risk of developing acute myeloid leukaemia: results from the NuCLEAR consortium. Blood Cancer Journal, 2020, 10, 75.	2.8	2
152	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	1.6	2
153	Lack of association of CD44-rs353630 and CHI3L2-rs684559 with pancreatic ductal adenocarcinoma survival. Scientific Reports, 2021, 11, 7570.	1.6	2
154	CD69, a New Potential Clinical Marker in Multiple Myeloma. Blood, 2014, 124, 2027-2027.	0.6	2
155	A Meta-Analysis Of Genome-Wide Association Studies Of Multiple Myeloma In Cases and Controls Of European Origin Identifies a Risk Locus In 12q23.1. Blood, 2013, 122, 3111-3111.	0.6	2
156	Maternal anthropometric variables and clinical factors shape neonatal microbiome. Scientific Reports, 2022, 12, 2875.	1.6	2
157	TAS2R38 polymorphisms, Helicobacter pylori infection and susceptibility to gastric cancer and premalignant gastric lesions. European Journal of Cancer Prevention, 2022, 31, 401-407.	0.6	1
158	Genome-wide association study of mitochondrial copy number. Human Molecular Genetics, 2022, 31, 1346-1355.	1.4	1
159	Validation and functional characterization of GWAS-identified variants for chronic lymphocytic leukemia: a CRuCIAL study. Blood Cancer Journal, 2022, 12, 79.	2.8	1
160	69 Post-GWAS pancreatic cancer susceptibility loci and their importance in survival. European Journal of Cancer, Supplement, 2010, 8, 18.	2.2	0
161	A comprehensive analysis of polymorphic variants in steroid hormone and insulinâ€like growth factorâ€1 metabolism and risk of in situ breast cancer: Results from the Breast and Prostate Cancer Cohort Consortium. International Journal of Cancer, 2018, 142, 1182-1188.	2.3	0
162	Polymorphisms in Regulators of Xenobiotic Transport and Metabolism Genes NR1I2 and NR1I3 and Multiple Myeloma Risk: A Case-Control Study in the Context of IMMEnSE Consortium. Blood, 2011, 118, 5014-5014.	0.6	0

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163	Abstract 2621: Relative excess risk due to interactions between GWAS-identified susceptibility loci and other breast cancer risk factors. , 2012, , .		0
164	Abstract 5078: Genome wide association study identifies variants at 16p13 associated with survival in multiple myeloma patients. , 2014, , .		0
165	Abstract 5064: Pleiotropy analysis identifies a novel prostate cancer variant at 6p21.33: The PAGE, PRACTICAL, and BPC3 Consortia. , 2014, , .		0
166	Type 2 Diabetes-Related Variants Influence on the Risk of Developing Multiple Myeloma: Results from the Immense Consortium. Blood, 2014, 124, 2044-2044.	0.6	0
167	Impact of Drug Transporters ABCB1 and ABCG2 and Regulators of Xenobiotic Transport and Metabolism Pxr and CAR Gene Polymorphisms on Clinical Efficacy of Imatinib in Chronic Myeloid Leukemia (CML). Blood, 2014, 124, 5222-5222.	0.6	0
168	The International Multiple Myeloma Research (IMMEnSE) Consortium: Genetics of Multiple Myeloma Risk and Prognosis. Blood, 2014, 124, 3421-3421.	0.6	0