Asta FÃ¶rsti

List of Publications by Year
in descending order

Version: 2024-02-01

172 papers	4,430 citations	236925 25 h-index	149698 56 g-index
177 all docs	177 docs citations	177 times ranked	8173 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.	6.2	711
2	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
3	A genome-wide association study of Hodgkin's lymphoma identifies new susceptibility loci at 2p16.1 (REL), 8q24.21 and 10p14 (GATA3). Nature Genetics, 2010, 42, 1126-1130.	21.4	177
4	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050.	12.8	146
5	Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. Nature Genetics, 2013, 45, 1221-1225.	21.4	143
6	Common variation at 3p22.1 and 7p15.3 influences multiple myeloma risk. Nature Genetics, 2012, 44, 58-61.	21.4	137
7	Single nucleotide polymorphisms in breast cancer. Oncology Reports, 2004, 11, 917-22.	2.6	114
8	Update on genetic predisposition to colorectal cancer and polyposis. Molecular Aspects of Medicine, 2019, 69, 10-26.	6.4	113
9	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
10	The CCND1 c.870G>A polymorphism is a risk factor for t(11;14)(q13;q32) multiple myeloma. Nature Genetics, 2013, 45, 522-525.	21.4	91
11	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	12.8	86
12	Incidence and survival in non-hereditary amyloidosis in Sweden. BMC Public Health, 2012, 12, 974.	2.9	84
13	SNPs related to vitamin D and breast cancer risk: a case-control study. Breast Cancer Research, 2018, 20, 1.	5.0	61
14	Cancer risk in patients with type 2 diabetes mellitus and their relatives. International Journal of Cancer, 2015, 137, 903-910.	5.1	57
15	Polymorphisms in the KDR and POSTN Genes: Association with Breast Cancer Susceptibility and Prognosis. Breast Cancer Research and Treatment, 2007, 101, 83-93.	2.5	56
16	Increased Risk of Hepatobiliary Cancers After Hospitalization for Autoimmune Disease. Clinical Gastroenterology and Hepatology, 2014, 12, 1038-1045.e7.	4.4	51
17	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	12.8	40
18	Diagnostic, Predictive, and Prognostic Biomarkers in Non-Small Cell Lung Cancer (NSCLC) Management. Journal of Personalized Medicine, 2021, 11, 1102.	2.5	40

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19	Single nucleotide polymorphisms in chromosomal instability genes and risk and clinical outcome of breast cancer: A Swedish prospective case-control study. European Journal of Cancer, 2009, 45, 435-442.	2.8	39
20	Second primary cancers in patients with acute lymphoblastic, chronic lymphocytic and hairy cell leukaemia. British Journal of Haematology, 2019, 185, 232-239.	2.5	34
21	Genome-wide association study identifies variation at 6q25.1 associated with survival in multiple myeloma. Nature Communications, 2016, 7, 10290.	12.8	31
22	Genome-wide association analysis of chronic lymphocytic leukaemia, Hodgkin lymphoma and multiple myeloma identifies pleiotropic risk loci. Scientific Reports, 2017, 7, 41071.	3.3	31
23	Familial Cancer Variant Prioritization Pipeline version 2 (FCVPPv2) applied to a papillary thyroid cancer family. Scientific Reports, 2018, 8, 11635.	3.3	30
24	Single Nucleotide Polymorphisms within Interferon Signaling Pathway Genes Are Associated with Colorectal Cancer Susceptibility and Survival. PLoS ONE, 2014, 9, e111061.	2.5	29
25	Genetic Variants Associated with Chronic Kidney Disease in a Spanish Population. Scientific Reports, 2020, 10, 144.	3.3	29
26	The 7p15.3 (rs4487645) association for multiple myeloma shows strong allele-specific regulation of the MYC-interacting gene CDCA7L in malignant plasma cells. Haematologica, 2015, 100, e110-e113.	3.5	27
27	Whole Genome Sequencing of Familial Non-Medullary Thyroid Cancer Identifies Germline Alterations in MAPK/ERK and PI3K/AKT Signaling Pathways. Biomolecules, 2019, 9, 605.	4.0	27
28	Search for multiple myeloma risk factors using Mendelian randomization. Blood Advances, 2020, 4, 2172-2179.	5.2	27
29	Subsequent Type 2 Diabetes in Patients with Autoimmune Disease. Scientific Reports, 2015, 5, 13871.	3.3	26
30	Risk of Next Melanoma in Patients With Familial and Sporadic Melanoma by Number of Previous Melanomas. JAMA Dermatology, 2015, 151, 607.	4.1	26
31	Impact of functional germline variants and a deletion polymorphism in APOBEC3A and APOBEC3B on breast cancer risk and survival in a Swedish study population. Journal of Cancer Research and Clinical Oncology, 2016, 142, 273-276.	2.5	26
32	Epidemiology, genetics and treatment of multiple myeloma and precursor diseases. International Journal of Cancer, 2021, 149, 1980-1996.	5.1	25
33	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. Scientific Reports, 2015, 5, 16286.	3.3	24
34	Interactions of DNA repair gene variants modulate chromosomal aberrations in healthy subjects. Carcinogenesis, 2015, 36, 1299-1306.	2.8	24
35	A Germline Mutation in the POT1 Gene Is a Candidate for Familial Non-Medullary Thyroid Cancer. Cancers, 2020, 12, 1441.	3.7	24
36	Polymorphisms in the transforming growth factor beta 1 pathway in relation to colorectal cancer progression. Genes Chromosomes and Cancer, 2010, 49, 270-281.	2.8	23

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37	Novel genetic variants in differentiated thyroid cancer and assessment of the cumulative risk. Scientific Reports, 2015, 5, 8922.	3.3	23
38	A Comprehensive Meta-analysis of Caseâ€“Control Association Studies to Evaluate Polymorphisms Associated with the Risk of Differentiated Thyroid Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 700-713.	2.5	22
39	Familial risks of ovarian cancer by age at diagnosis, proband type and histology. PLoS ONE, 2018, 13, e0205000.	2.5	22
40	Second primary cancers in nonâ€Hodgkin lymphoma: Bidirectional analyses suggesting role for immune dysfunction. International Journal of Cancer, 2018, 143, 2449-2457.	5.1	22
41	Surveillance Bias in Cancer Risk After Unrelated Medical Conditions: Example Urolithiasis. Scientific Reports, 2017, 7, 8073.	3.3	21
42	Association between polymorphisms of TAS2R16 and susceptibility to colorectal cancer. BMC Gastroenterology, 2017, 17, 104.	2.0	21
43	Etiologic impact of known cancer susceptibility genes. Mutation Research - Reviews in Mutation Research, 2008, 658, 42-54.	5.5	20
44	Cancer in immigrants as a pointer to the causes of cancer. European Journal of Public Health, 2014, 24, 64-71.	0.3	20
45	Analysis of functional germline variants in APOBEC3 and driver genes on breast cancer risk in Moroccan study population. BMC Cancer, 2016, 16, 165.	2.6	20
46	Bortezomibâ€induced peripheral neuropathy: A genomeâ€wide association study on multiple myeloma patients. Hematological Oncology, 2018, 36, 232-237.	1.7	20
47	Investigation of single and synergic effects of NLRC5 and PD-L1 variants on the risk of colorectal cancer. PLoS ONE, 2018, 13, e0192385.	2.5	20
48	Association of NLRP1 Coding Polymorphism with Lung Function and Serum IL-1Î² Concentration in Patients Diagnosed with Chronic Obstructive Pulmonary Disease (COPD). Genes, 2019, 10, 783.	2.4	20
49	Familial risks between Graves disease and Hashimoto thyroiditis and other autoimmune diseases in the population of Sweden. Journal of Translational Autoimmunity, 2020, 3, 100058.	4.0	20
50	Familial Risks and Proportions Describing Population Landscape of Familial Cancer. Cancers, 2021, 13, 4385.	3.7	20
51	Familial associations of female breast cancer with other cancers. International Journal of Cancer, 2017, 141, 2253-2259.	5.1	19
52	Whole genome sequencing reveals DICER1 as a candidate predisposing gene in familial Hodgkin lymphoma. International Journal of Cancer, 2018, 143, 2076-2078.	5.1	19
53	Genetic variation of acquired structural chromosomal aberrations. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2018, 836, 13-21.	1.7	19
54	A Coding IRAK2 Protein Variant Compromises Toll-like receptor (TLR) Signaling and Is Associated with Colorectal Cancer Survival. Journal of Biological Chemistry, 2014, 289, 23123-23131.	3.4	18

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55	Familial risks in urolithiasis in the population of Sweden. BJU International, 2018, 121, 479-485.	2.5	18
56	Chemotherapy-induced peripheral neuropathy: evidence from genome-wide association studies and replication within multiple myeloma patients. BMC Cancer, 2018, 18, 820.	2.6	18
57	Incidence of hereditary amyloidosis and autoinflammatory diseases in Sweden: endemic and imported diseases. BMC Medical Genetics, 2013, 14, 88.	2.1	17
58	Origin of B-Cell Neoplasms in Autoimmune Disease. PLoS ONE, 2016, 11, e0158360.	2.5	17
59	A review of the infection-associated cancers in North African countries. Infectious Agents and Cancer, 2016, 11, 35.	2.6	17
60	Runs of homozygosity and inbreeding in thyroid cancer. BMC Cancer, 2016, 16, 227.	2.6	17
61	Genetic Predisposition to Multiple Myeloma at 5q15 Is Mediated by an ELL2 Enhancer Polymorphism. Cell Reports, 2017, 20, 2556-2564.	6.4	17
62	Prostate cancer survivors: Risk and mortality in second primary cancers. Cancer Medicine, 2018, 7, 5752-5759.	2.8	17
63	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. Blood, 2018, 132, 2040-2052.	1.4	17
64	Systematic Pathway Enrichment Analysis of a Genome-Wide Association Study on Breast Cancer Survival Reveals an Influence of Genes Involved in Cell Adhesion and Calcium Signaling on the Patientsâ€™ Clinical Outcome. PLoS ONE, 2014, 9, e98229.	2.5	16
65	Genomewide association study on monoclonal gammopathy of unknown significance (MGUS). European Journal of Haematology, 2017, 99, 70-79.	2.2	16
66	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.	1.8	16
67	Genetic variation in the major mitotic checkpoint genes does not affect familial breast cancer risk. Breast Cancer Research and Treatment, 2007, 106, 205-213.	2.5	15
68	Genetic Susceptibility to Bortezomib-Induced Peripheral Neuroropathy: Replication of the Reported Candidate Susceptibility Loci. Neurochemical Research, 2017, 42, 925-931.	3.3	15
69	Direct evidence for a polygenic etiology in familial multiple myeloma. Blood Advances, 2017, 1, 619-623.	5.2	15
70	Single nucleotide polymorphisms within MUC4 are associated with colorectal cancer survival. PLoS ONE, 2019, 14, e0216666.	2.5	15
71	Second cancers and causes of death in patients with testicular cancer in Sweden. PLoS ONE, 2019, 14, e0214410.	2.5	15
72	Second primary cancers in nonâ€Hodgkin lymphoma: Family history and survival. International Journal of Cancer, 2020, 146, 970-976.	5.1	15

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73	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	5.0	14
74	The Incidence of Senile Cataract and Glaucoma is Increased in Patients with Plasma Cell Dyscrasias: Etiologic Implications. Scientific Reports, 2016, 6, 28500.	3.3	14
75	Survival in familial and non-familial breast cancer by age and stage at diagnosis. European Journal of Cancer, 2016, 52, 10-18.	2.8	14
76	Risk of second primary cancer following myeloid neoplasia and risk of myeloid neoplasia as second primary cancer: a nationwide, observational follow up study in Sweden. Lancet Haematology,the, 2018, 5, e368-e377.	4.6	14
77	Prognosis Prediction of Colorectal Cancer Using Gene Expression Profiles. Frontiers in Oncology, 2019, 9, 252.	2.8	14
78	Genome-wide interaction and pathway-based identification of key regulators in multiple myeloma. Communications Biology, 2019, 2, 89.	4.4	14
79	Genome-wide association study of monoclonal gammopathy of unknown significance (MGUS): comparison with multiple myeloma. Leukemia, 2019, 33, 1817-1821.	7.2	14
80	Thalassemia and sickle cell anemia in Swedish immigrants: Genetic diseases have become global. SAGE Open Medicine, 2015, 3, 205031211561309.	1.8	13
81	Second primary cancer after female breast cancer: Familial risks and cause of death. Cancer Medicine, 2019, 8, 400-407.	2.8	13
82	Eight novel loci implicate shared genetic etiology in multiple myeloma, AL amyloidosis, and monoclonal gammopathy of unknown significance. Leukemia, 2020, 34, 1187-1191.	7.2	13
83	Whole Genome Sequencing Prioritizes CHEK2, EWSR1, and TIAM1 as Possible Predisposition Genes for Familial Non-Medullary Thyroid Cancer. Frontiers in Endocrinology, 2021, 12, 600682.	3.5	13
84	Progress in survival in renal cell carcinoma through 50 years evaluated in Finland and Sweden. PLoS ONE, 2021, 16, e0253236.	2.5	13
85	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
86	Genetic variation in the major mitotic checkpoint genes associated with chromosomal aberrations in healthy humans. Cancer Letters, 2016, 380, 442-446.	7.2	12
87	Functional germline variants in driver genes of breast cancer. Cancer Causes and Control, 2017, 28, 259-271.	1.8	12
88	Familial Risks and Mortality in Second Primary Cancers in Melanoma. JNCI Cancer Spectrum, 2018, 2, pky068.	2.9	12
89	Familial Associations in Testicular Cancer with Other Cancers. Scientific Reports, 2018, 8, 10880.	3.3	12
90	Impact of family history of cancer on risk and mortality of second cancers in patients with prostate cancer. Prostate Cancer and Prostatic Diseases, 2019, 22, 143-149.	3.9	12

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91	Identification of Familial Hodgkin Lymphoma Predisposing Genes Using Whole Genome Sequencing. Frontiers in Bioengineering and Biotechnology, 2020, 8, 179.	4.1	12
92	Germline genetics of cancer of unknown primary (CUP) and its specific subtypes. Oncotarget, 2016, 7, 22140-22149.	1.8	12
93	Genomic imprinting analyses identify maternal effects as a cause of phenotypic variability in type 1 diabetes and rheumatoid arthritis. Scientific Reports, 2020, 10, 11562.	3.3	11
94	Multiethnic genomeâ€wide association study of differentiated thyroid cancer in the <scp>EPITHYR</scp> consortium. International Journal of Cancer, 2021, 148, 2935-2946.	5.1	11
95	Germline Variants of CYBA and TRPM4 Predispose to Familial Colorectal Cancer. Cancers, 2022, 14, 670.	3.7	11
96	Toll-like receptor genetic variants and colorectal cancer. OncoImmunology, 2014, 3, e27763.	4.6	10
97	Thyroidâ€associated genetic polymorphisms in relation to breast cancer risk in the MalmÃ¶ Diet and Cancer Study. International Journal of Cancer, 2018, 142, 1309-1321.	5.1	10
98	Familial risks of second primary cancers and mortality in ovarian cancer patients. Clinical Epidemiology, 2018, Volume 10, 1457-1466.	3.0	10
99	Epistatic effect of TLR3 and cGASâ€STINGâ€KKÎµâ€TBK1â€IFN signaling variants on colorectal cancer risk. Cancer Medicine, 2020, 9, 1473-1484.	2.8	10
100	Loci associated with genomic damage levels in chronic kidney disease patients and controls. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2020, 852, 503167.	1.7	10
101	Functional dissection of inherited non-coding variation influencing multiple myeloma risk. Nature Communications, 2022, 13, 151.	12.8	10
102	Heritability estimates on Hodgkinâ€™s lymphoma: a genomic- versus population-based approach. European Journal of Human Genetics, 2015, 23, 824-830.	2.8	9
103	Genetics of gallbladder cancer. Lancet Oncology, The, 2017, 18, e296.	10.7	9
104	Familial risks for gallstones in the population of Sweden. BMJ Open Gastroenterology, 2017, 4, e000188.	2.7	9
105	Enrichment of B cell receptor signaling and epidermal growth factor receptor pathways in monoclonal gammopathy of undetermined significance: a genome-wide genetic interaction study. Molecular Medicine, 2018, 24, 30.	4.4	9
106	Familial Clustering, Second Primary Cancers and Causes of Death in Penile, Vulvar and Vaginal Cancers. Scientific Reports, 2019, 9, 11804.	3.3	9
107	Genetic variation associated with chromosomal aberration frequency: A genomeâ€wide association study. Environmental and Molecular Mutagenesis, 2019, 60, 17-28.	2.2	9
108	Rate differences between first and second primary cancers may outline immune dysfunction as a key risk factor. Cancer Medicine, 2020, 9, 8258-8265.	2.8	9

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109	Incidence trends in lung and bladder cancers in the Nordic Countries before and after the smoking epidemic. European Journal of Cancer Prevention, 2022, 31, 228-234.	1.3	9
110	Second Primary Cancers After Gastric Cancer, and Gastric Cancer as Second Primary Cancer. Clinical Epidemiology, 2021, Volume 13, 515-525.	3.0	9
111	Combinations of Low-Frequency Genetic Variants Might Predispose to Familial Pancreatic Cancer. Journal of Personalized Medicine, 2021, 11, 631.	2.5	9
112	Cervical, vaginal and vulvar cancer incidence and survival trends in Denmark, Finland, Norway and Sweden with implications to treatment. BMC Cancer, 2022, 22, 456.	2.6	9
113	Identification of miRSNPs associated with the risk of multiple myeloma. International Journal of Cancer, 2017, 140, 526-534.	5.1	8
114	Evidence of Inbreeding in Hodgkin Lymphoma. PLoS ONE, 2016, 11, e0154259.	2.5	8
115	Incidence and survival in laryngeal and lung cancers in Finland and Sweden through a half century. PLoS ONE, 2022, 17, e0268922.	2.5	8
116	Pedigree based DNA sequencing pipeline for germline genomes of cancer families. Hereditary Cancer in Clinical Practice, 2016, 14, 16.	1.5	7
117	Familial associations of male breast cancer with other cancers. Breast Cancer Research and Treatment, 2017, 166, 897-902.	2.5	7
118	Genome-wide association study of clinical parameters in immunoglobulin light chain amyloidosis in three patient cohorts. Haematologica, 2017, 102, e411-e414.	3.5	7
119	Types of second primary cancers influence survival in chronic lymphocytic and hairy cell leukemia patients. Blood Cancer Journal, 2019, 9, 40.	6.2	7
120	Second Primary Cancers in Patients with Invasive and In Situ Squamous Cell Skin Carcinoma, Kaposi Sarcoma, and Merkel Cell Carcinoma: Role for Immune Mechanisms?. Journal of Investigative Dermatology, 2020, 140, 48-55.e1.	0.7	7
121	Familial associations for rheumatoid autoimmune diseases. Rheumatology Advances in Practice, 2020, 4, rkaa048.	0.7	7
122	Characterization of rare germline variants in familial multiple myeloma. Blood Cancer Journal, 2021, 11, 33.	6.2	7
123	Bladder and upper urinary tract cancers as first and second primary cancers. Cancer Reports, 2021, 4, e1406.	1.4	7
124	Short article: Influence of regulatory NLRC5 variants on colorectal cancer survival and 5-fluorouracil-based chemotherapy. European Journal of Gastroenterology and Hepatology, 2018, 30, 838-842.	1.6	6
125	Coding variants in NOD-like receptors: An association study on risk and survival of colorectal cancer. PLoS ONE, 2018, 13, e0199350.	2.5	6
126	Levels of DNA damage (Micronuclei) in patients suffering from chronic kidney disease. Role of GST polymorphisms. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2018, 836, 41-46.	1.7	6

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127	Familial Ovarian Cancer ClustersÂwith Other Cancers. Scientific Reports, 2018, 8, 11561.	3.3	6
128	Distinct pathways associated with chromosomal aberration frequency in a cohort exposed to genotoxic compounds compared to general population. Mutagenesis, 2019, 34, 323-330.	2.6	6
129	Whole Exome Sequencing Identifies APCDD1 and HDAC5 Genes as Potentially Cancer Predisposing in Familial Colorectal Cancer. International Journal of Molecular Sciences, 2021, 22, 1837.	4.1	6
130	Second Primary Cancers After Liver, Gallbladder and Bile Duct Cancers, and These Cancers as Second Primary Cancers. Clinical Epidemiology, 2021, Volume 13, 683-691.	3.0	6
131	Incidence and survival in oral and pharyngeal cancers in Finland and Sweden through half century. BMC Cancer, 2022, 22, 227.	2.6	6
132	Breast Cancer Genomics Based on Biobanks. Methods in Molecular Biology, 2011, 675, 375-385.	0.9	5
133	Polymorphisms within base and nucleotide excision repair pathways and risk of differentiated thyroid carcinoma. DNA Repair, 2016, 41, 27-31.	2.8	5
134	Cytogenetic aberrations in multiple myeloma are associated with shifts in serum immunoglobulin isotypes distribution and levels. Haematologica, 2018, 103, e162-e164.	3.5	5
135	Familial risks in and between stone diseases: sialolithiasis, urolithiasis and cholelithiasis in the population of Sweden. BMC Nephrology, 2018, 19, 158.	1.8	5
136	Multiple myeloma: family history and mortality in second primary cancers. Blood Cancer Journal, 2018, 8, 75.	6.2	5
137	Search for AL amyloidosis risk factors using Mendelian randomization. Blood Advances, 2021, 5, 2725-2731.	5.2	5
138	Inherited variants in genes somatically mutated in thyroid cancer. PLoS ONE, 2017, 12, e0174995.	2.5	5
139	Familial Risks for Liver, Gallbladder and Bile Duct Cancers and for Their Risk Factors in Sweden, a Low-Incidence Country. Cancers, 2022, 14, 1938.	3.7	5
140	Non-Hodgkin lymphoma in familial amyloid polyneuropathy patients in Sweden. Blood, 2013, 122, 458-459.	1.4	4
141	Inbreeding and homozygosity in breast cancer survival. Scientific Reports, 2015, 5, 16467.	3.3	4
142	Familial Urinary Bladder Cancer with Other Cancers. European Urology Oncology, 2018, 1, 461-466.	5.4	4
143	Familial Cancer: How to Successfully Recruit Families for Germline Mutations Studies? Multiple Myeloma as an Example. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, 635-644.e2.	0.4	4
144	Incidence Differences Between First Primary Cancers and Second Primary Cancers Following Skin Squamous Cell Carcinoma as Etiological Clues . Clinical Epidemiology, 2020, Volume 12, 857-864.	3.0	4

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145	GWAS-Identified Common Variants for Obesity Are Not Associated with the Risk of Developing Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1125-1128.	2.5	3
146	Second Primary Cancers in Melanoma Patients Critically Shorten Survival . Clinical Epidemiology, 2020, Volume 12, 105-112.	3.0	3
147	Association between tumor characteristics and second primary cancers with cutaneous melanoma survival: A nationwide cohort study. Pigment Cell and Melanoma Research, 2020, 33, 625-632.	3.3	3
148	Polymorphisms within Autophagy-Related Genes Influence the Risk of Developing Colorectal Cancer: A Meta-Analysis of Four Large Cohorts. Cancers, 2021, 13, 1258.	3.7	3
149	DNA repair gene polymorphisms and chromosomal aberrations in healthy, nonsmoking population. DNA Repair, 2021, 101, 103079.	2.8	3
150	DNA Repair Gene Polymorphisms and Chromosomal Aberrations in Exposed Populations. Frontiers in Genetics, 2021, 12, 691947.	2.3	3
151	Increased HSP70 and TLR2 Gene Expression and Association of HSP70 rs6457452 Single Nucleotide Polymorphism with the Risk of Chronic Obstructive Pulmonary Disease in the Croatian Population. Diagnostics, 2021, 11, 1412.	2.6	3
152	Familial associations between autoimmune hepatitis and primary biliary cholangitis and other autoimmune diseases. PLoS ONE, 2020, 15, e0240794.	2.5	3
153	Types of second primary cancer influence overall survival in cutaneous melanoma. BMC Cancer, 2021, 21, 1123.	2.6	3
154	Borderline Ovarian Tumors Share Familial Risks with Themselves and Invasive Cancers. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1358-1363.	2.5	2
155	Comparison of Familial Clustering of Anogenital and Skin Cancers Between In Situ and Invasive Types. Scientific Reports, 2019, 9, 16151.	3.3	2
156	Cancer Predisposition Genes in Cancer-Free Families. Cancers, 2020, 12, 2770.	3.7	2
157	Familial risks between giant cell arteritis and Takayasu arteritis and other autoimmune diseases in the population of Sweden. Scientific Reports, 2020, 10, 20887.	3.3	2
158	Impact of genetic polymorphisms in kinetochore and spindle assembly genes on chromosomal aberration frequency in healthy humans. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2020, 858-860, 503253.	1.7	2
159	Family History of Head and Neck Cancers. Cancers, 2021, 13, 4115.	3.7	2
160	A rare large duplication of MLH1 identified in Lynch syndrome. Hereditary Cancer in Clinical Practice, 2021, 19, 10.	1.5	2
161	Familial associations for Addisonâ€™s disease and between Addisonâ€™s disease and other autoimmune diseases. Endocrine Connections, 2020, 9, 1114-1120.	1.9	2
162	Whole-Exome Sequencing Identifies a Novel Germline Variant in PTK7 Gene in Familial Colorectal Cancer. International Journal of Molecular Sciences, 2022, 23, 1295.	4.1	2

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163	Recurrent Germline Variant in RAD21 Predisposes Children to Lymphoblastic Leukemia or Lymphoma. International Journal of Molecular Sciences, 2022, 23, 5174.	4.1	2
164	Does a Multiple Myeloma Polygenic Risk Score Predict Overall Survival of Myeloma Patients?. Cancer Epidemiology Biomarkers and Prevention, 0, , .	2.5	2
165	Familial Risks Between Urolithiasis and Cancer. Scientific Reports, 2018, 8, 3083.	3.3	1
166	Expression Quantitative Trait Loci Reveal Regulatory Regions Important In The Pathogenesis of Multiple Myeloma. Blood, 2013, 122, 1847-1847.	1.4	1
167	Whole exome sequencing identifies novel germline variants of SLC15A4 gene as potentially cancer predisposing in familial colorectal cancer. Molecular Genetics and Genomics, 2022, , 1.	2.1	1
168	Second Primary Cancers After Kidney Cancers, and Kidney Cancers as Second Primary Cancers. European Urology Open Science, 2021, 24, 52-59.	0.4	0
169	A Novel Low-Risk Germline Variant in the SH2 Domain of the SRC Gene Affects Multiple Pathways in Familial Colorectal Cancer. Journal of Personalized Medicine, 2021, 11, 262.	2.5	0
170	Epidemiology of Amyloidosis and Genetic Pathways to Diagnosis and Typing. Hemato, 2021, 2, 429-440.	0.6	0
171	Familial associations for Addison's disease and between Addison's disease and other autoimmune diseases. Endocrine Connections, 2020, 9, 1114-1120.	1.9	0
172	Characterization of Rare Germline Variants in Familial Multiple Myeloma. Blood, 2020, 136, 45-46.	1.4	0