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	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
2	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
3	Functional dissection of inherited non-coding variation influencing multiple myeloma risk. Nature Communications, 2022, 13, 151.	12.8	10
4	Germline Variants of CYBA and TRPM4 Predispose to Familial Colorectal Cancer. Cancers, 2022, 14, 670.	3.7	11
5	Incidence and survival in oral and pharyngeal cancers in Finland and Sweden through half century. BMC Cancer, 2022, 22, 227.	2.6	6
6	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
7	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
8	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
9	Recurrent Germline Variant in RAD21 Predisposes Children to Lymphoblastic Leukemia or Lymphoma. International Journal of Molecular Sciences, 2022, 23, 5174.	4.1	2
10	Incidence and survival in laryngeal and lung cancers in Finland and Sweden through a half century. PLoS ONE, 2022, 17, e0268922.	2.5	8
11	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
12	Characterization of rare germline variants in familial multiple myeloma. Blood Cancer Journal, 2021, 11, 33.	6.2	7
13	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
14	Second Primary Cancers After Kidney Cancers, and Kidney Cancers as Second Primary Cancers. European Urology Open Science, 2021, 24, 52-59.	0.4	0
15	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
16	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
17	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
18	DNA repair gene polymorphisms and chromosomal aberrations in healthy, nonsmoking population. DNA Repair, 2021, 101, 103079.	2.8	3

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19	Progress in survival in renal cell carcinoma through 50 years evaluated in Finland and Sweden. PLoS ONE, 2021, 16, e0253236.	2.5	13
20	Bladder and upper urinary tract cancers as first and second primary cancers. Cancer Reports, 2021, 4, e1406.	1.4	7
21	DNA Repair Gene Polymorphisms and Chromosomal Aberrations in Exposed Populations. Frontiers in Genetics, 2021, 12, 691947.	2.3	3
22	Search for AL amyloidosis risk factors using Mendelian randomization. Blood Advances, 2021, 5, 2725-2731.	5.2	5
23	Second Primary Cancers After Gastric Cancer, and Gastric Cancer as Second Primary Cancer. Clinical Epidemiology, 2021, Volume 13, 515-525.	3.0	9
24	Combinations of Low-Frequency Genetic Variants Might Predispose to Familial Pancreatic Cancer. Journal of Personalized Medicine, 2021, 11, 631.	2.5	9
25	Epidemiology of Amyloidosis and Genetic Pathways to Diagnosis and Typing. Hemato, 2021, 2, 429-440.	0.6	0
26	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
27	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
28	Epidemiology, genetics and treatment of multiple myeloma and precursor diseases. International Journal of Cancer, 2021, 149, 1980-1996.	5.1	25
29	Familial Risks and Proportions Describing Population Landscape of Familial Cancer. Cancers, 2021, 13, 4385.	3.7	20
30	Family History of Head and Neck Cancers. Cancers, 2021, 13, 4115.	3.7	2
31	A rare large duplication of MLH1 identified in Lynch syndrome. Hereditary Cancer in Clinical Practice, 2021, 19, 10.	1.5	2
32	Types of second primary cancer influence overall survival in cutaneous melanoma. BMC Cancer, 2021, 21, 1123.	2.6	3
33	Diagnostic, Predictive, and Prognostic Biomarkers in Non-Small Cell Lung Cancer (NSCLC) Management. Journal of Personalized Medicine, 2021, 11, 1102.	2.5	40
34	Second primary cancers in nonâ€Hodgkin lymphoma: Family history and survival. International Journal of Cancer, 2020, 146, 970-976.	5.1	15
35	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
36	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

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37	Genetic Variants Associated with Chronic Kidney Disease in a Spanish Population. Scientific Reports, 2020, 10, 144.	3.3	29
38	Epistatic effect of TLR3 and cGASâ€STINGâ€IKKÎµâ€TBK1â€IFN signaling variants on colorectal cancer risk. Cancer Medicine, 2020, 9, 1473-1484.	2.8	10
39	Familial associations for rheumatoid autoimmune diseases. Rheumatology Advances in Practice, 2020, 4, rkaa048.	0.7	7
40	Cancer Predisposition Genes in Cancer-Free Families. Cancers, 2020, 12, 2770.	3.7	2
41	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
42	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
43	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
44	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
45	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
46	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
47	Search for multiple myeloma risk factors using Mendelian randomization. Blood Advances, 2020, 4, 2172-2179.	5.2	27
48	A Germline Mutation in the POT1 Gene Is a Candidate for Familial Non-Medullary Thyroid Cancer. Cancers, 2020, 12, 1441.	3.7	24
49	Identification of Familial Hodgkin Lymphoma Predisposing Genes Using Whole Genome Sequencing. Frontiers in Bioengineering and Biotechnology, 2020, 8, 179.	4.1	12
50	Second Primary Cancers in Melanoma Patients Critically Shorten Survival . Clinical Epidemiology, 2020, Volume 12, 105-112.	3.0	3
51	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
52	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
53	Familial associations between autoimmune hepatitis and primary biliary cholangitis and other autoimmune diseases. PLoS ONE, 2020, 15, e0240794.	2.5	3
54	Familial associations for Addison's disease and between Addison's disease and other autoimmune diseases. Endocrine Connections, 2020, 9, 1114-1120.	1.9	0

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55	Familial associations for Addisonâ€™s disease and between Addisonâ€™s disease and other autoimmune diseases. Endocrine Connections, 2020, 9, 1114-1120.	1.9	2
56	Characterization of Rare Germline Variants in Familial Multiple Myeloma. Blood, 2020, 136, 45-46.	1.4	0
57	Familial Clustering, Second Primary Cancers and Causes of Death in Penile, Vulvar and Vaginal Cancers. Scientific Reports, 2019, 9, 11804.	3.3	9
58	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
59	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
60	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
61	Comparison of Familial Clustering of Anogenital and Skin Cancers Between In Situ and Invasive Types. Scientific Reports, 2019, 9, 16151.	3.3	2
62	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
63	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
64	Types of second primary cancers influence survival in chronic lymphocytic and hairy cell leukemia patients. Blood Cancer Journal, 2019, 9, 40.	6.2	7
65	Single nucleotide polymorphisms within MUC4 are associated with colorectal cancer survival. PLoS ONE, 2019, 14, e0216666.	2.5	15
66	Prognosis Prediction of Colorectal Cancer Using Gene Expression Profiles. Frontiers in Oncology, 2019, 9, 252.	2.8	14
67	Update on genetic predisposition to colorectal cancer and polyposis. Molecular Aspects of Medicine, 2019, 69, 10-26.	6.4	113
68	Genome-wide interaction and pathway-based identification of key regulators in multiple myeloma. Communications Biology, 2019, 2, 89.	4.4	14
69	Second cancers and causes of death in patients with testicular cancer in Sweden. PLoS ONE, 2019, 14, e0214410.	2.5	15
70	Genome-wide association study of monoclonal gammopathy of unknown significance (MGUS): comparison with multiple myeloma. Leukemia, 2019, 33, 1817-1821.	7.2	14
71	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
72	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711

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73	Second primary cancer after female breast cancer: Familial risks and cause of death. Cancer Medicine, 2019, 8, 400-407.	2.8	13
74	Genetic variation associated with chromosomal aberration frequency: A genomeâ€wide association study. Environmental and Molecular Mutagenesis, 2019, 60, 17-28.	2.2	9
75	Familial Risks Between Urolithiasis and Cancer. Scientific Reports, 2018, 8, 3083.	3.3	1
76	Cytogenetic aberrations in multiple myeloma are associated with shifts in serum immunoglobulin isotypes distribution and levels. Haematologica, 2018, 103, e162-e164.	3.5	5
77	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
78	Bortezomibâ€induced peripheral neuropathy: A genomeâ€wide association study on multiple myeloma patients. Hematological Oncology, 2018, 36, 232-237.	1.7	20
79	Familial risks in urolithiasis in the population of Sweden. BJU International, 2018, 121, 479-485.	2.5	18
80	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
81	Familial Risks and Mortality in Second Primary Cancers in Melanoma. JNCI Cancer Spectrum, 2018, 2, pky068.	2.9	12
82	Familial risks of ovarian cancer by age at diagnosis, proband type and histology. PLoS ONE, 2018, 13, e0205000.	2.5	22
83	Prostate cancer survivors: Risk and mortality in second primary cancers. Cancer Medicine, 2018, 7, 5752-5759.	2.8	17
84	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
85	Familial risks of second primary cancers and mortality in ovarian cancer patients. Clinical Epidemiology, 2018, Volume 10, 1457-1466.	3.0	10
86	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	12.8	86
87	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. Blood, 2018, 132, 2040-2052.	1.4	17
88	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
89	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
90	Genetic variation of acquired structural chromosomal aberrations. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2018, 836, 13-21.	1.7	19

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91	Familial Urinary Bladder Cancer with Other Cancers. European Urology Oncology, 2018, 1, 461-466.	5.4	4
92	Coding variants in NOD-like receptors: An association study on risk and survival of colorectal cancer. PLoS ONE, 2018, 13, e0199350.	2.5	6
93	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
94	Familial risks in and between stone diseases: sialolithiasis, urolithiasis and cholelithiasis in the population of Sweden. BMC Nephrology, 2018, 19, 158.	1.8	5
95	Borderline Ovarian Tumors Share Familial Risks with Themselves and Invasive Cancers. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1358-1363.	2.5	2
96	Familial Associations in Testicular Cancer with Other Cancers. Scientific Reports, 2018, 8, 10880.	3.3	12
97	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
98	SNPs related to vitamin D and breast cancer risk: a case-control study. Breast Cancer Research, 2018, 20, 1.	5.0	61
99	Chemotherapy-induced peripheral neuropathy: evidence from genome-wide association studies and replication within multiple myeloma patients. BMC Cancer, 2018, 18, 820.	2.6	18
100	Familial Ovarian Cancer ClustersÂwith Other Cancers. Scientific Reports, 2018, 8, 11561.	3.3	6
101	Multiple myeloma: family history and mortality in second primary cancers. Blood Cancer Journal, 2018, 8, 75.	6.2	5
102	Familial Cancer Variant Prioritization Pipeline version 2 (FCVPPv2) applied to a papillary thyroid cancer family. Scientific Reports, 2018, 8, 11635.	3.3	30
103	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
104	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
105	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
106	Functional germline variants in driver genes of breast cancer. Cancer Causes and Control, 2017, 28, 259-271.	1.8	12
107	Genetics of gallbladder cancer. Lancet Oncology, The, 2017, 18, e296.	10.7	9
108	Genomewide association study on monoclonal gammopathy of unknown significance (MGUS). European Journal of Haematology, 2017, 99, 70-79.	2.2	16

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109	Familial associations of male breast cancer with other cancers. Breast Cancer Research and Treatment, 2017, 166, 897-902.	2.5	7
110	Genetic Predisposition to Multiple Myeloma at 5q15 Is Mediated by an ELL2 Enhancer Polymorphism. Cell Reports, 2017, 20, 2556-2564.	6.4	17
111	Surveillance Bias in Cancer Risk After Unrelated Medical Conditions: Example Urolithiasis. Scientific Reports, 2017, 7, 8073.	3.3	21
112	Familial associations of female breast cancer with other cancers. International Journal of Cancer, 2017, 141, 2253-2259.	5.1	19
113	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	12.8	40
114	Genome-wide association study of clinical parameters in immunoglobulin light chain amyloidosis in three patient cohorts. Haematologica, 2017, 102, e411-e414.	3.5	7
115	Identification of miRSNPs associated with the risk of multiple myeloma. International Journal of Cancer, 2017, 140, 526-534.	5.1	8
116	Genetic Susceptibility to Bortezomib-Induced Peripheral Neuroropathy: Replication of the Reported Candidate Susceptibility Loci. Neurochemical Research, 2017, 42, 925-931.	3.3	15
117	Familial risks for gallstones in the population of Sweden. BMJ Open Gastroenterology, 2017, 4, e000188.	2.7	9
118	Direct evidence for a polygenic etiology in familial multiple myeloma. Blood Advances, 2017, 1, 619-623.	5.2	15
119	Association between polymorphisms of TAS2R16 and susceptibility to colorectal cancer. BMC Gastroenterology, 2017, 17, 104.	2.0	21
120	Inherited variants in genes somatically mutated in thyroid cancer. PLoS ONE, 2017, 12, e0174995.	2.5	5
121	Origin of B-Cell Neoplasms in Autoimmune Disease. PLoS ONE, 2016, 11, e0158360.	2.5	17
122	A review of the infection-associated cancers in North African countries. Infectious Agents and Cancer, 2016, 11, 35.	2.6	17
123	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
124	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
125	Polymorphisms within base and nucleotide excision repair pathways and risk of differentiated thyroid carcinoma. DNA Repair, 2016, 41, 27-31.	2.8	5
126	Runs of homozygosity and inbreeding in thyroid cancer. BMC Cancer, 2016, 16, 227.	2.6	17

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127	Genetic variation in the major mitotic checkpoint genes associated with chromosomal aberrations in healthy humans. Cancer Letters, 2016, 380, 442-446.	7.2	12
128	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050.	12.8	146
129	Pedigree based DNA sequencing pipeline for germline genomes of cancer families. Hereditary Cancer in Clinical Practice, 2016, 14, 16.	1.5	7
130	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
131	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
132	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
133	Genome-wide association study identifies variation at 6q25.1 associated with survival in multiple myeloma. Nature Communications, 2016, 7, 10290.	12.8	31
134	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
135	Evidence of Inbreeding in Hodgkin Lymphoma. PLoS ONE, 2016, 11, e0154259.	2.5	8
136	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
137	Germline genetics of cancer of unknown primary (CUP) and its specific subtypes. Oncotarget, 2016, 7, 22140-22149.	1.8	12
138	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. Scientific Reports, 2015, 5, 16286.	3.3	24
139	Inbreeding and homozygosity in breast cancer survival. Scientific Reports, 2015, 5, 16467.	3.3	4
140	Subsequent Type 2 Diabetes in Patients with Autoimmune Disease. Scientific Reports, 2015, 5, 13871.	3.3	26
141	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
142	Thalassemia and sickle cell anemia in Swedish immigrants: Genetic diseases have become global. SAGE Open Medicine, 2015, 3, 205031211561309.	1.8	13
143	Novel genetic variants in differentiated thyroid cancer and assessment of the cumulative risk. Scientific Reports, 2015, 5, 8922.	3.3	23
144	Cancer risk in patients with type 2 diabetes mellitus and their relatives. International Journal of Cancer, 2015, 137, 903-910.	5.1	57

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145	Risk of Next Melanoma in Patients With Familial and Sporadic Melanoma by Number of Previous Melanomas. JAMA Dermatology, 2015, 151, 607.	4.1	26
146	Heritability estimates on Hodgkinâ€™s lymphoma: a genomic- versus population-based approach. European Journal of Human Genetics, 2015, 23, 824-830.	2.8	9
147	Interactions of DNA repair gene variants modulate chromosomal aberrations in healthy subjects. Carcinogenesis, 2015, 36, 1299-1306.	2.8	24
148	Single Nucleotide Polymorphisms within Interferon Signaling Pathway Genes Are Associated with Colorectal Cancer Susceptibility and Survival. PLoS ONE, 2014, 9, e111061.	2.5	29
149	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
150	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
151	Cancer in immigrants as a pointer to the causes of cancer. European Journal of Public Health, 2014, 24, 64-71.	0.3	20
152	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
153	Toll-like receptor genetic variants and colorectal cancer. OncoImmunology, 2014, 3, e27763.	4.6	10
154	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
155	Increased Risk of Hepatobiliary Cancers After Hospitalization for Autoimmune Disease. Clinical Gastroenterology and Hepatology, 2014, 12, 1038-1045.e7.	4.4	51
156	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
157	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
158	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
159	Incidence of hereditary amyloidosis and autoinflammatory diseases in Sweden: endemic and imported diseases. BMC Medical Genetics, 2013, 14, 88.	2.1	17
160	Non-Hodgkin lymphoma in familial amyloid polyneuropathy patients in Sweden. Blood, 2013, 122, 458-459.	1.4	4
161	Expression Quantitative Trait Loci Reveal Regulatory Regions Important In The Pathogenesis of Multiple Myeloma. Blood, 2013, 122, 1847-1847.	1.4	1
162	Common variation at 3p22.1 and 7p15.3 influences multiple myeloma risk. Nature Genetics, 2012, 44, 58-61.	21.4	137

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163	Incidence and survival in non-hereditary amyloidosis in Sweden. BMC Public Health, 2012, 12, 974.	2.9	84
164	Breast Cancer Genomics Based on Biobanks. Methods in Molecular Biology, 2011, 675, 375-385.	0.9	5
165	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
166	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
167	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
168	Etiologic impact of known cancer susceptibility genes. Mutation Research - Reviews in Mutation Research, 2008, 658, 42-54.	5.5	20
169	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
170	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
171	Single nucleotide polymorphisms in breast cancer. Oncology Reports, 2004, 11, 917-22.	2.6	114
172	Does a Multiple Myeloma Polygenic Risk Score Predict Overall Survival of Myeloma Patients?. Cancer Epidemiology Biomarkers and Prevention, 0, , .	2.5	2