Alisa M Goldstein

List of Publications by Year
in descending order

131 papers	11,707 citations	44069 48 h-index	28297 105 g-index
135 all docs	135 docs citations	135 times ranked	12154 citing authors

#	Article	IF	Citations
1	Variation in second cancer risk by melanoma subtype among survivors. Journal of the American Academy of Dermatology, 2023, 88, 433-434.	1.2	4
2	First international workshop of the ATM and cancer risk group (4-5 December 2019). Familial Cancer, 2022, 21, 211-227.	1.9	10
3	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. Familial Cancer, 2022, 21, 347-355.	1.9	1
4	Novel loss-of-function variant in DENND5A impedes melanosomal cargo transport and predisposes to familial cutaneous melanoma. Genetics in Medicine, 2022, 24, 157-169.	2.4	0
5	Integrated Analysis of Coexpression and Exome Sequencing to Prioritize Susceptibility Genes for Familial Cutaneous Melanoma. Journal of Investigative Dermatology, 2022, 142, 2464-2475.e5.	0.7	4
6	Modified eQTL and Somatic DNA Segment Alterations in Esophageal Squamous Cell Carcinoma for Genes Related to Immunity, DNA Repair, and Inflammation. Cancers, 2022, 14, 1629.	3.7	1
7	A Genome-First Approach to Estimate Prevalence of Germline Pathogenic Variants and Risk of Pancreatic Cancer in Select Cancer Susceptibility Genes. Cancers, 2022, 14, 3257.	3.7	6
8	Rare germline variants in PALB2 and BRCA2 in familial and sporadic chordoma. Human Mutation, 2022, 43, 1396-1407.	2.5	3
9	Low Epsteinâ€“Barr Virus Prevalence in Cardia Gastric Cancer Among a High-Incidence Chinese Population. Digestive Diseases and Sciences, 2021, 66, 1220-1226.	2.3	7
10	Integrative molecular characterisation of gallbladder cancer reveals micro-environment-associated subtypes. Journal of Hepatology, 2021, 74, 1132-1144.	3.7	30
11	Sebaceous Carcinoma Epidemiology and Genetics: Emerging Concepts and Clinical Implications for Screening, Prevention, and Treatment. Clinical Cancer Research, 2021, 27, 389-393.	7.0	19
12	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in the Childhood Cancer Survivor Study. JNCI Cancer Spectrum, 2021, 5, pkab007.	2.9	11
13	Whole genome sequencing of skull-base chordoma reveals genomic alterations associated with recurrence and chordoma-specific survival. Nature Communications, 2021, 12, 757.	12.8	55
14	The Impact of Longitudinal Surveillance on Tumor Thickness for Melanoma-Prone Families with and without Pathogenic Germline Variants of CDKN2A and CDK4. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 676-681.	2.5	3
15	Rare Germline Variants in Chordoma-Related Genes and Chordoma Susceptibility. Cancers, 2021, 13, 2704.	3.7	5
16	ABO genotypes and the risk of esophageal and gastric cancers. BMC Cancer, 2021, 21, 589.	2.6	8
17	Clinical findings in families with chordoma with and without T gene duplications and in patients with sporadic chordoma reported to the Surveillance, Epidemiology, and End Results program. Journal of Neurosurgery, 2021, 134, 1399-1408.	1.6	8
18	A systematic review of the prevalence of germline pathogenic variants in patients with pancreatic cancer. Journal of Gastroenterology, 2021, 56, 713-721.	5.1	15

#	Article	IF	Citations
19	Cancer patterns in nasopharyngeal carcinoma multiplex families over 15 years. Cancer, 2021, 127, 4171-4176.	4.1	2
20	Cell-type-specific meQTLs extend melanoma GWAS annotation beyond eQTLs and inform melanocyte gene-regulatory mechanisms. American Journal of Human Genetics, 2021, 108, 1631-1646.	6.2	12
21	A UVB-responsive common variant at chromosome band 7p21.1 confers tanning response and melanoma risk via regulation of the aryl hydrocarbon receptor, AHR. American Journal of Human Genetics, 2021, 108, 1611-1630.	6.2	7
22	Mutational signatures in esophageal squamous cell carcinoma from eight countries with varying incidence. Nature Genetics, 2021, 53, 1553-1563.	21.4	71
23	Variation in Cutaneous Patterns of Melanomagenesis According to Germline CDKN2A/CDK4 Status in Melanoma-Prone Families. Journal of Investigative Dermatology, 2020, 140, 174-181.e3.	0.7	11
24	Using whole-exome sequencing and protein interaction networks to prioritize candidate genes for germline cutaneous melanoma susceptibility. Scientific Reports, 2020, 10, 17198.	3.3	8
25	Sebaceous Carcinoma Incidence and Survival Among Solid Organ Transplant Recipients in the United States, 1987-2017. JAMA Dermatology, 2020, 156, 1307.	4.1	14
26	Ambient Ultraviolet Radiation and Sebaceous Carcinoma Incidence in the United States, 2000â€“2016. JNCI Cancer Spectrum, 2020, 4, pkaa020.	2.9	14
27	A Systematic Literature Review of Whole Exome and Genome Sequencing Population Studies of Genetic Susceptibility to Cancer. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1519-1534.	2.5	10
28	Body mass index and height and risk of cutaneous melanoma: Mendelian randomization analyses. International Journal of Epidemiology, 2020, 49, 1236-1245.	1.9	21
29	Insights into Genetic Susceptibility to Melanoma by Gene Panel Testing: Potential Pathogenic Variants in ACD, ATM, BAP1, and POT1. Cancers, 2020, 12, 1007.	3.7	19
30	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	21.4	138
31	Histologic features of melanoma associated with germline mutations of CDKN2A, CDK4, and POT1 in melanoma-prone families from the United States, Italy, and Spain. Journal of the American Academy of Dermatology, 2020, 83, 860-869.	1.2	5
32	Estimating CDKN2A mutation carrier probability among global familial melanoma cases using GenoMELPREDICT. Journal of the American Academy of Dermatology, 2019, 81, 386-394.	1.2	17
33	Whole-Exome Sequencing of Nasopharyngeal Carcinoma Families Reveals Novel Variants Potentially Involved in Nasopharyngeal Carcinoma. Scientific Reports, 2019, 9, 9916.	3.3	32
34	Evaluation of Rare and Common Variants from Suspected Familial or Sporadic Nasopharyngeal Carcinoma (NPC) Susceptibility Genes in Sporadic NPC. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1682-1686.	2.5	5
35	Use of Big Data to Estimate Prevalence of Defective DNA Repair Variants in the US Population. JAMA Dermatology, 2019, 155, 72.	4.1	11
36	Risks of Melanoma and Other Cancers in Melanoma-Prone Families over 4 Decades. Journal of Investigative Dermatology, 2018, 138, 1620-1626.	0.7	19

#	Article	IF	Citations
37	Germline mutations in Protection of Telomeres 1 in two families with Hodgkin lymphoma. British Journal of Haematology, 2018, 181, 372-377.	2.5	48
38	Phenocopies in melanoma-prone families with germ-line CDKN2A mutations. Genetics in Medicine, 2018, 20, 1087-1090.	2.4	11
39	Wholeâ€exome sequencing of nevoid basal cell carcinoma syndrome families and review of Human Gene Mutation Database PTCH1 mutation data. Molecular Genetics & Genomic Medicine, 2018, 6, 1168-1180.	1.2	16
40	Prevalence of pathogenic/likely pathogenic variants in the 24 cancer genes of the ACMG Secondary Findings v2.0 list in a large cancer cohort and ethnicity-matched controls. Genome Medicine, 2018, 10, 99.	8.2	15
41	Cell-typeâ€“specific eQTL of primary melanocytes facilitates identification of melanoma susceptibility genes. Genome Research, 2018, 28, 1621-1635.	5.5	67
42	Pediatric melanoma in melanomaâ€prone families. Cancer, 2018, 124, 3715-3723.	4.1	16
43	Assessing the Incremental Contribution of Common Genomic Variants to Melanoma Risk Prediction in Two Population-Based Studies. Journal of Investigative Dermatology, 2018, 138, 2617-2624.	0.7	52
44	Elevated antibodies against Epsteinâ€“Barr virus among individuals predicted to carry nasopharyngeal carcinoma susceptibility variants. Journal of General Virology, 2018, 99, 1268-1273.	2.9	3
45	Identification of new susceptibility loci for gastric non-cardia adenocarcinoma: pooled results from two Chinese genome-wide association studies. Gut, 2017, 66, 581-587.	12.1	68
46	Gastric microbiota features associated with cancer risk factors and clinical outcomes: A pilot study in gastric cardia cancer patients from Shanxi, China. International Journal of Cancer, 2017, 141, 45-51.	5.1	29
47	Germline Mutations in PALB2, BRCA1, and RAD51C, Which Regulate DNA Recombination Repair, in Patients With Gastric Cancer. Gastroenterology, 2017, 152, 983-986.e6.	1.3	98
48	Rare germline variants in known melanoma susceptibility genes in familial melanoma. Human Molecular Genetics, 2017, 26, 4886-4895.	2.9	37
49	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.7	18
50	GWAS follow-up study of esophageal squamous cell carcinoma identifies potential genetic loci associated with family history of upper gastrointestinal cancer. Scientific Reports, 2017, 7, 4642.	3.3	11
51	Association of high-evidence gastric cancer susceptibility loci and somatic gene expression levels with survival. Carcinogenesis, 2017, 38, 1119-1128.	2.8	13
52	Molecular Characterization of the Human Stomach Microbiota in Gastric Cancer Patients. Frontiers in Cellular and Infection Microbiology, 2017, 7, 302.	3.9	136
53	Rare Germline Copy Number Variations and Disease Susceptibility in Familial Melanoma. Journal of Investigative Dermatology, 2016, 136, 2436-2443.	0.7	13
54	Multiple rare variants in high-risk pancreatic cancer-related genes may increase risk for pancreatic cancer in a subset of patients with and without germline CDKN2A mutations. Human Genetics, 2016, 135, 1241-1249.	3.8	24

#	Article	IF	Citations
55	Whole exome sequencing in families at high risk for Hodgkin lymphoma: identification of a predisposing mutation in the KDR gene. Haematologica, 2016, 101, 853-860.	3.5	40
56	Whole exome sequencing in families with CLL detects a variant in Integrin Î² 2 associated with disease susceptibility. Blood, 2016, 128, 2261-2263.	1.4	15
57	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86
58	An interstitial deletion within 9p21.3 and extending beyondCDKN2Apredisposes to melanoma, neural system tumours and possible haematological malignancies. Journal of Medical Genetics, 2016, 53, 721-727.	3.2	23
59	Genomic Landscape of Somatic Alterations in Esophageal Squamous Cell Carcinoma and Gastric Cancer. Cancer Research, 2016, 76, 1714-1723.	0.9	68
60	Phenotypic and Histopathological Tumor Characteristics According to CDKN2A Mutation Status among Affected Members ofÂMelanoma Families. Journal of Investigative Dermatology, 2016, 136, 1066-1069.	0.7	13
61	Genome-wide association study of gastric adenocarcinoma in Asia: a comparison of associations between cardia and non-cardia tumours. Gut, 2016, 65, 1611-1618.	12.1	99
62	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. Journal of the National Cancer Institute, 2015, 107, djv279.	6.3	152
63	Nested PCR Biases in Interpreting Microbial Community Structure in 16S rRNA Gene Sequence Datasets. PLoS ONE, 2015, 10, e0132253.	2.5	60
64	Lung Cancer Prognosis Before and After Recurrence in a Population-Based Setting. Journal of the National Cancer Institute, 2015, 107, djv059.	6.3	86
65	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
66	Histologic features of melanoma associated with CDKN2A genotype. Journal of the American Academy of Dermatology, 2015, 72, 496-507.e7.	1.2	19
67	Common genetic variants related to vitamin D status are not associated with esophageal squamous cell carcinoma risk in China. Cancer Epidemiology, 2015, 39, 157-159.	1.9	8
68	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	21.4	218
69	Constitutional promoter methylation and risk of familial melanoma. Epigenetics, 2014, 9, 685-692.	2.7	15
70	Variants Associated with Susceptibility to Pancreatic Cancer and Melanoma Do Not Reciprocally Affect Risk. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1121-1124.	2.5	14
71	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	6.3	109
72	Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nature Genetics, 2014, 46, 482-486.	21.4	283

#	Article	IF	Citations
73	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. Carcinogenesis, 2014, 35, 2698-2705.	2.8	67
74	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. Nature Genetics, 2014, 46, 1001-1006.	21.4	148
75	Characterization of T gene sequence variants and germline duplications in familial and sporadic chordoma. Human Genetics, 2014, 133, 1289-1297.	3.8	54
76	Oesophageal squamous cell carcinoma in high-risk Chinese populations: Possible role for vascular epithelial growth factor A. European Journal of Cancer, 2014, 50, 2855-2865.	2.8	9
77	PLCE1 mRNA and Protein Expression and Survival of Patients with Esophageal Squamous Cell Carcinoma and Gastric Adenocarcinoma. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1579-1588.	2.5	42
78	The Genetics of Melanoma: Recent Advances. Annual Review of Genomics and Human Genetics, 2013, 14, 257-279.	6.2	66
79	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	21.4	111
80	Melanoma prone families withCDK4germline mutation: phenotypic profile and associations withMC1Rvariants. Journal of Medical Genetics, 2013, 50, 264-270.	3.2	112
81	Constitutive Mitochondrial DNA Copy Number in Peripheral Blood of Melanoma Families with and without CDKN2A Mutations. Journal of Carcinogenesis & Mutagenesis, 2012, S4`, .	0.3	5
82	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	21.4	230
83	Risk factors for esophageal and gastric cancers in Shanxi Province, China: A caseâ€“control study. Cancer Epidemiology, 2011, 35, e91-e99.	1.9	112
84	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	21.4	140
85	Clinical features distinguish childhood chordoma associated with tuberous sclerosis complex (TSC) from chordoma in the general paediatric population. Journal of Medical Genetics, 2011, 48, 444-449.	3.2	51
86	Cancer patterns in nasopharyngeal carcinoma multiplex families in Taiwan. International Journal of Cancer, 2009, 124, 1622-1625.	5.1	25
87	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	21.4	422
88	T (brachyury) gene duplication confers major susceptibility to familial chordoma. Nature Genetics, 2009, 41, 1176-1178.	21.4	284
89	Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840.	21.4	209
90	Cutaneous phenotype andMC1R variants as modifying factors for the development of melanoma inCDKN2A G101W mutation carriers from 4 countries. International Journal of Cancer, 2007, 121, 825-831.	5.1	45

#	Article	IF	Citations
91	High-risk Melanoma Susceptibility Genes and Pancreatic Cancer, Neural System Tumors, and Uveal Melanoma across GenoMEL. Cancer Research, 2006, 66, 9818-9828.	0.9	373
92	Distribution of Epstein-Barr viral load in serum of individuals from nasopharyngeal carcinoma high-risk families in Taiwan. International Journal of Cancer, 2006, 118, 780-784.	5.1	36
93	Recent Tanning Bed Use. Archives of Dermatology, 2006, 142, 485-8.	1.4	28
94	Unconditional analyses can increase efficiencyin assessing geneâ€“environment interaction of the case-combined-control design. International Journal of Epidemiology, 2006, 35, 1067-1073.	1.9	8
95	Features associated with germline CDKN2A mutations: a GenoMEL study of melanoma-prone families from three continents. Journal of Medical Genetics, 2006, 44, 99-106.	3.2	350
96	Impact of E27X, a novel CDKN2A germ line mutation, on p16 and p14ARF expression in Italian melanoma families displaying pancreatic cancer and neuroblastoma. Human Molecular Genetics, 2006, 15, 2682-2689.	2.9	41
97	The Value of Small Observations in the Era of Big Science. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 2472-2473.	2.5	55
98	Familial melanoma, pancreatic cancer and germline CDKN2A mutations. Human Mutation, 2004, 23, 630-630.	2.5	130
99	Epstein-Barr virus seroreactivity among unaffected individuals within high-risk nasopharyngeal carcinoma families in Taiwan. International Journal of Cancer, 2004, 111, 117-123.	5.1	56
100	Geographical Variation in the Penetrance of CDKN2A Mutations for Melanoma. Journal of the National Cancer Institute, 2002, 94, 894-903.	6.3	435
101	High prevalence of the G101W germline mutation in theCDKN2A(P16ink4a) gene in 62 Italian malignant melanoma families. American Journal of Medical Genetics Part A, 2002, 107, 214-221.	2.4	60
102	GeneÃ—Environment Interaction from Caseâ€Control and Caseâ€Case Approaches. Genetic Epidemiology, 2001, 21, S825-30.	1.3	3
103	Use of Weighted pâ€Values in Regional Inference Procedures. Genetic Epidemiology, 2001, 21, S484-9.	1.3	3
104	Sporadic multiple primary melanoma cases:CDKN2Agermline mutations with a founder effect. Genes Chromosomes and Cancer, 2001, 32, 195-202.	2.8	63
105	Chordoma: incidence and survival patterns in the United States, 1973-1995. Cancer Causes and Control, 2001, 12, 1-11.	1.8	820
106	Genetic Epidemiology of Cutaneous Melanoma. Archives of Dermatology, 2001, 137, 1493-6.	1.4	118
107	Mutation screening of theCDKN2A promoter in melanoma families. , 2000, 28, 45-57.		59
108	Genotype-Phenotype Relationships in U.S. Melanoma-Prone Families With CDKN2A and CDK4 Mutations. Journal of the National Cancer Institute, 2000, 92, 1006-1010.	6.3	172

#	Article	IF	Citations
109	Mutation screening of the CDKN2A promoter in melanoma families. Genes Chromosomes and Cancer, 2000, 28, 45.	2.8	1
110	Deletion analysis of the adenomatous polyposis coli andPTCH gene loci in patients with sporadic and nevoid basal cell carcinoma syndrome-associated medulloblastoma. Cancer, 1999, 85, 2662-2667.	4.1	46
111	A genomeâ€wide search for loci contributing to smoking and alcoholism. Genetic Epidemiology, 1999, 17, S55-60.	1.3	91
112	Sibâ€pair linkage analyses of alcoholism: Dichotomous and quantitative measures. Genetic Epidemiology, 1999, 17, S205-10.	1.3	0
113	Deletion analysis of the adenomatous polyposis coli and PTCH gene loci in patients with sporadic and nevoid basal cell carcinoma syndromeâ€associated medulloblastoma. Cancer, 1999, 85, 2662-2667.	4.1	1
114	Familial eosinophilia: Clinical and laboratory results on a U.S. Kindred. American Journal of Medical Genetics Part A, 1998, 76, 229-237.	2.4	35
115	Haplotype analysis of two recurrentCDKN2A mutations in 10 melanoma families: Evidence for common founders and independent mutations. , 1998, 11, 424-431.		61
116	Allelic imbalance, including deletion ofPTEN/MMAC1, at the Cowden disease locus on 10q22-23, in hamartomas from patients with cowden syndrome and germlinePTEN mutation. , 1998, 21, 61-69.		85
117	CDKN2AMutations in Multiple Primary Melanomas. New England Journal of Medicine, 1998, 338, 879-887.	27.0	255
118	Familial eosinophilia: Clinical and laboratory results on a U.S. Kindred. American Journal of Medical Genetics Part A, 1998, 76, 229-237.	2.4	1
119	Second cancers after medulloblastoma: population-based results from the United States and Sweden. Cancer Causes and Control, 1997, 8, 865-871.	1.8	96
120	Nevoid basal cell carcinoma syndrome with medulloblastoma in an African-American boy: A rare case illustrating gene-environment interaction. American Journal of Medical Genetics Part A, 1997, 69, 309-314.	2.4	30
121	Detecting gene-environment interactions using a case-control design. Genetic Epidemiology, 1997, 14, 1085-1089.	1.3	25
122	Sib-pair linkage analyses of nuclear family data: Quantitative versus dichotomous disease classification. Genetic Epidemiology, 1997, 14, 827-832.	1.3	7
123	Lack of phospholipase A2 mutations in neuroblastoma, melanoma and colon-cancer cell lines. , 1997, 72, 337-339.		16
124	Germline mutations in the p16INK4a binding domain of CDK4 in familial melanoma. Nature Genetics, 1996, 12, 97-99.	21.4	756
125	Mutations associated with familial melanoma impair p16INK4 function. Nature Genetics, 1995, 10, 114-116.	21.4	273
126	Increased Risk of Pancreatic Cancer in Melanoma-Prone Kindreds withp16^{INK4}Mutations. New England Journal of Medicine, 1995, 333, 970-975.	27.0	608

#	Article	IF	Citations
127	Clinical findings in two Africanâ€American families with the nevoid basal cell carcinoma syndrome (NBCC). American Journal of Medical Genetics Part A, 1994, 50, 272-281.	2.4	64
128	Germline p16 mutations in familial melanoma. Nature Genetics, 1994, 8, 15-21.	21.4	1,170
129	Clustering of high density lipoprotein cholesterol levels in premenopausal and postmenopausal female twins. Genetic Epidemiology, 1993, 10, 563-567.	1.3	3
130	A PROBLEM IN IDENTIFYiNG RISK FACTORS FOR DISEASE USING SURROGATE EXPOSURE VARIABLES THAT ARE UNDER GENETIC CONTROL. American Journal of Epidemiology, 1990, 132, 1171-1175.	3.4	2
131	Re-evaluation of the linkage relationship between chromosome 11p loci and the gene for bipolar affective disorder in the Old Order Amish. Nature, 1989, 342, 238-243.	27.8	448