

Alisa M Goldstein

List of Publications by Year in descending order

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131
papers

11,707
citations

44042

48
h-index

29127

104
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. <i>Journal of the American Academy of Dermatology</i> , 2023, 88, 433-434.	0.6	4
2	First international workshop of the ATM and cancer risk group (4-5 December 2019). <i>Familial Cancer</i> , 2022, 21, 211-227.	0.9	10
3	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. <i>Familial Cancer</i> , 2022, 21, 347-355.	0.9	1
4	Novel loss-of-function variant in DENND5A impedes melanosomal cargo transport and predisposes to familial cutaneous melanoma. <i>Genetics in Medicine</i> , 2022, 24, 157-169.	1.1	0
5	Integrated Analysis of Coexpression and Exome Sequencing to Prioritize Susceptibility Genes for Familial Cutaneous Melanoma. <i>Journal of Investigative Dermatology</i> , 2022, 142, 2464-2475.e5.	0.3	4
6	Modified eQTL and Somatic DNA Segment Alterations in Esophageal Squamous Cell Carcinoma for Genes Related to Immunity, DNA Repair, and Inflammation. <i>Cancers</i> , 2022, 14, 1629.	1.7	1
7	A Genome-First Approach to Estimate Prevalence of Germline Pathogenic Variants and Risk of Pancreatic Cancer in Select Cancer Susceptibility Genes. <i>Cancers</i> , 2022, 14, 3257.	1.7	6
8	Rare germline variants in <i>PALB2</i> and <i>BRCA2</i> in familial and sporadic chordoma. <i>Human Mutation</i> , 2022, 43, 1396-1407.	1.1	3
9	Low Epstein-Barr Virus Prevalence in Cardia Gastric Cancer Among a High-Incidence Chinese Population. <i>Digestive Diseases and Sciences</i> , 2021, 66, 1220-1226.	1.1	7
10	Integrative molecular characterisation of gallbladder cancer reveals micro-environment-associated subtypes. <i>Journal of Hepatology</i> , 2021, 74, 1132-1144.	1.8	30
11	Sebaceous Carcinoma Epidemiology and Genetics: Emerging Concepts and Clinical Implications for Screening, Prevention, and Treatment. <i>Clinical Cancer Research</i> , 2021, 27, 389-393.	3.2	19
12	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in the Childhood Cancer Survivor Study. <i>JNCI Cancer Spectrum</i> , 2021, 5, p1ab007.	1.4	11
13	Whole genome sequencing of skull-base chordoma reveals genomic alterations associated with recurrence and chordoma-specific survival. <i>Nature Communications</i> , 2021, 12, 757.	5.8	55
14	The Impact of Longitudinal Surveillance on Tumor Thickness for Melanoma-Prone Families with and without Pathogenic Germline Variants of <i>CDKN2A</i> and <i>CDK4</i> . <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 676-681.	1.1	3
15	Rare Germline Variants in Chordoma-Related Genes and Chordoma Susceptibility. <i>Cancers</i> , 2021, 13, 2704.	1.7	5
16	ABO genotypes and the risk of esophageal and gastric cancers. <i>BMC Cancer</i> , 2021, 21, 589.	1.1	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. <i>Journal of Neurosurgery</i> , 2021, 134, 1399-1408.	0.9	8
18	A systematic review of the prevalence of germline pathogenic variants in patients with pancreatic cancer. <i>Journal of Gastroenterology</i> , 2021, 56, 713-721.	2.3	15

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19	Cancer patterns in nasopharyngeal carcinoma multiplex families over 15 years. <i>Cancer</i> , 2021, 127, 4171-4176.	2.0	2
20	Cell-type-specific meQTLs extend melanoma GWAS annotation beyond eQTLs and inform melanocyte gene-regulatory mechanisms. <i>American Journal of Human Genetics</i> , 2021, 108, 1631-1646.	2.6	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. <i>American Journal of Human Genetics</i> , 2021, 108, 1611-1630.	2.6	7
22	Mutational signatures in esophageal squamous cell carcinoma from eight countries with varying incidence. <i>Nature Genetics</i> , 2021, 53, 1553-1563.	9.4	71
23	Variation in Cutaneous Patterns of Melanomagenesis According to Germline CDKN2A/CDK4 Status in Melanoma-Prone Families. <i>Journal of Investigative Dermatology</i> , 2020, 140, 174-181.e3.	0.3	11
24	Using whole-exome sequencing and protein interaction networks to prioritize candidate genes for germline cutaneous melanoma susceptibility. <i>Scientific Reports</i> , 2020, 10, 17198.	1.6	8
25	Sebaceous Carcinoma Incidence and Survival Among Solid Organ Transplant Recipients in the United States, 1987-2017. <i>JAMA Dermatology</i> , 2020, 156, 1307.	2.0	14
26	Ambient Ultraviolet Radiation and Sebaceous Carcinoma Incidence in the United States, 2000â€“2016. <i>JNCI Cancer Spectrum</i> , 2020, 4, pkaa020.	1.4	14
27	A Systematic Literature Review of Whole Exome and Genome Sequencing Population Studies of Genetic Susceptibility to Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1519-1534.	1.1	10
28	Body mass index and height and risk of cutaneous melanoma: Mendelian randomization analyses. <i>International Journal of Epidemiology</i> , 2020, 49, 1236-1245.	0.9	21
29	Insights into Genetic Susceptibility to Melanoma by Gene Panel Testing: Potential Pathogenic Variants in ACD, ATM, BAP1, and POT1. <i>Cancers</i> , 2020, 12, 1007.	1.7	19
30	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. <i>Nature Genetics</i> , 2020, 52, 494-504.	9.4	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. <i>Journal of the American Academy of Dermatology</i> , 2020, 83, 860-869.	0.6	5
32	Estimating CDKN2A mutation carrier probability among global familial melanoma cases using GenoMELPREDICT. <i>Journal of the American Academy of Dermatology</i> , 2019, 81, 386-394.	0.6	17
33	Whole-Exome Sequencing of Nasopharyngeal Carcinoma Families Reveals Novel Variants Potentially Involved in Nasopharyngeal Carcinoma. <i>Scientific Reports</i> , 2019, 9, 9916.	1.6	32
34	Evaluation of Rare and Common Variants from Suspected Familial or Sporadic Nasopharyngeal Carcinoma (NPC) Susceptibility Genes in Sporadic NPC. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1682-1686.	1.1	5
35	Use of Big Data to Estimate Prevalence of Defective DNA Repair Variants in the US Population. <i>JAMA Dermatology</i> , 2019, 155, 72.	2.0	11
36	Risks of Melanoma and Other Cancers in Melanoma-Prone Families over 4 Decades. <i>Journal of Investigative Dermatology</i> , 2018, 138, 1620-1626.	0.3	19

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37	Germline mutations in <i>Protection of Telomeres 1</i> in two families with Hodgkin lymphoma. <i>British Journal of Haematology</i> , 2018, 181, 372-377.	1.2	48
38	Phenocopies in melanoma-prone families with germ-line CDKN2A mutations. <i>Genetics in Medicine</i> , 2018, 20, 1087-1090.	1.1	11
39	Whole-exome sequencing of nevoid basal cell carcinoma syndrome families and review of Human Gene Mutation Database <i>PTCH1</i> mutation data. <i>Molecular Genetics & Genomic Medicine</i> , 2018, 6, 1168-1180.	0.6	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. <i>Genome Medicine</i> , 2018, 10, 99.	3.6	15
41	Cell-type-specific eQTL of primary melanocytes facilitates identification of melanoma susceptibility genes. <i>Genome Research</i> , 2018, 28, 1621-1635.	2.4	67
42	Pediatric melanoma in melanoma-prone families. <i>Cancer</i> , 2018, 124, 3715-3723.	2.0	16
43	Assessing the Incremental Contribution of Common Genomic Variants to Melanoma Risk Prediction in Two Population-Based Studies. <i>Journal of Investigative Dermatology</i> , 2018, 138, 2617-2624.	0.3	52
44	Elevated antibodies against Epstein-Barr virus among individuals predicted to carry nasopharyngeal carcinoma susceptibility variants. <i>Journal of General Virology</i> , 2018, 99, 1268-1273.	1.3	3
45	Identification of new susceptibility loci for gastric non-cardia adenocarcinoma: pooled results from two Chinese genome-wide association studies. <i>Gut</i> , 2017, 66, 581-587.	6.1	68
46	Gastric microbiota features associated with cancer risk factors and clinical outcomes: A pilot study in gastric cardia cancer patients from Shanxi, China. <i>International Journal of Cancer</i> , 2017, 141, 45-51.	2.3	29
47	Germline Mutations in <i>PALB2</i> , <i>BRCA1</i> , and <i>RAD51C</i> , Which Regulate DNA Recombination Repair, in Patients With Gastric Cancer. <i>Gastroenterology</i> , 2017, 152, 983-986.e6.	0.6	98
48	Rare germline variants in known melanoma susceptibility genes in familial melanoma. <i>Human Molecular Genetics</i> , 2017, 26, 4886-4895.	1.4	37
49	Germline Variation at <i>CDKN2A</i> and Associations with Nevus Phenotypes among Members of Melanoma Families. <i>Journal of Investigative Dermatology</i> , 2017, 137, 2606-2612.	0.3	18
50	GWAS follow-up study of esophageal squamous cell carcinoma identifies potential genetic loci associated with family history of upper gastrointestinal cancer. <i>Scientific Reports</i> , 2017, 7, 4642.	1.6	11
51	Association of high-evidence gastric cancer susceptibility loci and somatic gene expression levels with survival. <i>Carcinogenesis</i> , 2017, 38, 1119-1128.	1.3	13
52	Molecular Characterization of the Human Stomach Microbiota in Gastric Cancer Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 302.	1.8	136
53	Rare Germline Copy Number Variations and Disease Susceptibility in Familial Melanoma. <i>Journal of Investigative Dermatology</i> , 2016, 136, 2436-2443.	0.3	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 <i>CDKN2A</i> mutations. <i>Human Genetics</i> , 2016, 135, 1241-1249.	1.8	24

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55	Whole exome sequencing in families at high risk for Hodgkin lymphoma: identification of a predisposing mutation in the KDR gene. <i>Haematologica</i> , 2016, 101, 853-860.	1.7	40
56	Whole exome sequencing in families with CLL detects a variant in Integrin β 2 associated with disease susceptibility. <i>Blood</i> , 2016, 128, 2261-2263.	0.6	15
57	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843.	5.8	86
58	An interstitial deletion within 9p21.3 and extending beyond <i>CDKN2A</i> predisposes to melanoma, neural system tumours and possible haematological malignancies. <i>Journal of Medical Genetics</i> , 2016, 53, 721-727.	1.5	23
59	Genomic Landscape of Somatic Alterations in Esophageal Squamous Cell Carcinoma and Gastric Cancer. <i>Cancer Research</i> , 2016, 76, 1714-1723.	0.4	68
60	Phenotypic and Histopathological Tumor Characteristics According to <i>CDKN2A</i> Mutation Status among Affected Members of Melanoma Families. <i>Journal of Investigative Dermatology</i> , 2016, 136, 1066-1069.	0.3	13
61	Genome-wide association study of gastric adenocarcinoma in Asia: a comparison of associations between cardia and non-cardia tumours. <i>Gut</i> , 2016, 65, 1611-1618.	6.1	99
62	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv279.	3.0	152
63	Nested PCR Biases in Interpreting Microbial Community Structure in 16S rRNA Gene Sequence Datasets. <i>PLoS ONE</i> , 2015, 10, e0132253.	1.1	60
64	Lung Cancer Prognosis Before and After Recurrence in a Population-Based Setting. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv059.	3.0	86
65	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497.	2.6	101
66	Histologic features of melanoma associated with <i>CDKN2A</i> genotype. <i>Journal of the American Academy of Dermatology</i> , 2015, 72, 496-507.e7.	0.6	19
67	Common genetic variants related to vitamin D status are not associated with esophageal squamous cell carcinoma risk in China. <i>Cancer Epidemiology</i> , 2015, 39, 157-159.	0.8	8
68	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. <i>Nature Genetics</i> , 2015, 47, 987-995.	9.4	218
69	Constitutional promoter methylation and risk of familial melanoma. <i>Epigenetics</i> , 2014, 9, 685-692.	1.3	15
70	Variants Associated with Susceptibility to Pancreatic Cancer and Melanoma Do Not Reciprocally Affect Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 1121-1124.	1.1	14
71	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	3.0	109
72	Rare missense variants in <i>POT1</i> predispose to familial cutaneous malignant melanoma. <i>Nature Genetics</i> , 2014, 46, 482-486.	9.4	283

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73	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. <i>Carcinogenesis</i> , 2014, 35, 2698-2705.	1.3	67
74	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. <i>Nature Genetics</i> , 2014, 46, 1001-1006.	9.4	148
75	Characterization of T gene sequence variants and germline duplications in familial and sporadic chordoma. <i>Human Genetics</i> , 2014, 133, 1289-1297.	1.8	54
76	Oesophageal squamous cell carcinoma in high-risk Chinese populations: Possible role for vascular epithelial growth factor A. <i>European Journal of Cancer</i> , 2014, 50, 2855-2865.	1.3	9
77	PLCE1 mRNA and Protein Expression and Survival of Patients with Esophageal Squamous Cell Carcinoma and Gastric Adenocarcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 1579-1588.	1.1	42
78	The Genetics of Melanoma: Recent Advances. <i>Annual Review of Genomics and Human Genetics</i> , 2013, 14, 257-279.	2.5	66
79	A variant in FTO shows association with melanoma risk not due to BMI. <i>Nature Genetics</i> , 2013, 45, 428-432.	9.4	111
80	Melanoma prone families with <i>CDK4</i> germline mutation: phenotypic profile and associations with <i>MC1R</i> variants. <i>Journal of Medical Genetics</i> , 2013, 50, 264-270.	1.5	112
81	Constitutive Mitochondrial DNA Copy Number in Peripheral Blood of Melanoma Families with and without <i>CDKN2A</i> Mutations. <i>Journal of Carcinogenesis & Mutagenesis</i> , 2012, S4, .	0.3	5
82	Genome-wide association study identifies three new melanoma susceptibility loci. <i>Nature Genetics</i> , 2011, 43, 1108-1113.	9.4	230
83	Risk factors for esophageal and gastric cancers in Shanxi Province, China: A case-control study. <i>Cancer Epidemiology</i> , 2011, 35, e91-e99.	0.8	112
84	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. <i>Nature Genetics</i> , 2011, 43, 1114-1118.	9.4	140
85	Clinical features distinguish childhood chordoma associated with tuberous sclerosis complex (TSC) from chordoma in the general paediatric population. <i>Journal of Medical Genetics</i> , 2011, 48, 444-449.	1.5	51
86	Cancer patterns in nasopharyngeal carcinoma multiplex families in Taiwan. <i>International Journal of Cancer</i> , 2009, 124, 1622-1625.	2.3	25
87	Genome-wide association study identifies three loci associated with melanoma risk. <i>Nature Genetics</i> , 2009, 41, 920-925.	9.4	422
88	T (brachyury) gene duplication confers major susceptibility to familial chordoma. <i>Nature Genetics</i> , 2009, 41, 1176-1178.	9.4	284
89	Common sequence variants on 20q11.22 confer melanoma susceptibility. <i>Nature Genetics</i> , 2008, 40, 838-840.	9.4	209
90	Cutaneous phenotype and <i>MC1R</i> variants as modifying factors for the development of melanoma in <i>CDKN2A</i> G101W mutation carriers from 4 countries. <i>International Journal of Cancer</i> , 2007, 121, 825-831.	2.3	45

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91	High-risk Melanoma Susceptibility Genes and Pancreatic Cancer, Neural System Tumors, and Uveal Melanoma across GenoMEL. <i>Cancer Research</i> , 2006, 66, 9818-9828.	0.4	373
92	Distribution of Epstein-Barr viral load in serum of individuals from nasopharyngeal carcinoma high-risk families in Taiwan. <i>International Journal of Cancer</i> , 2006, 118, 780-784.	2.3	36
93	Recent Tanning Bed Use. <i>Archives of Dermatology</i> , 2006, 142, 485-8.	1.7	28
94	Unconditional analyses can increase efficiency in assessing gene-environment interaction of the case-combined-control design. <i>International Journal of Epidemiology</i> , 2006, 35, 1067-1073.	0.9	8
95	Features associated with germline CDKN2A mutations: a GenoMEL study of melanoma-prone families from three continents. <i>Journal of Medical Genetics</i> , 2006, 44, 99-106.	1.5	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. <i>Human Molecular Genetics</i> , 2006, 15, 2682-2689.	1.4	41
97	The Value of Small Observations in the Era of Big Science. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2005, 14, 2472-2473.	1.1	55
98	Familial melanoma, pancreatic cancer and germline CDKN2A mutations. <i>Human Mutation</i> , 2004, 23, 630-630.	1.1	130
99	Epstein-Barr virus seroreactivity among unaffected individuals within high-risk nasopharyngeal carcinoma families in Taiwan. <i>International Journal of Cancer</i> , 2004, 111, 117-123.	2.3	56
100	Geographical Variation in the Penetrance of CDKN2A Mutations for Melanoma. <i>Journal of the National Cancer Institute</i> , 2002, 94, 894-903.	3.0	435
101	High prevalence of the G101W germline mutation in the CDKN2A (P16ink4a) gene in 62 Italian malignant melanoma families. <i>American Journal of Medical Genetics Part A</i> , 2002, 107, 214-221.	2.4	60
102	Gene-Environment Interaction from Case-Control and Case-Case Approaches. <i>Genetic Epidemiology</i> , 2001, 21, S825-30.	0.6	3
103	Use of Weighted p-Values in Regional Inference Procedures. <i>Genetic Epidemiology</i> , 2001, 21, S484-9.	0.6	3
104	Sporadic multiple primary melanoma cases: CDKN2A germline mutations with a founder effect. <i>Genes Chromosomes and Cancer</i> , 2001, 32, 195-202.	1.5	63
105	Chordoma: incidence and survival patterns in the United States, 1973-1995. <i>Cancer Causes and Control</i> , 2001, 12, 1-11.	0.8	820
106	Genetic Epidemiology of Cutaneous Melanoma. <i>Archives of Dermatology</i> , 2001, 137, 1493-6.	1.7	118
107	Mutation screening of the CDKN2A promoter in melanoma families. , 2000, 28, 45-57.		59
108	Genotype-Phenotype Relationships in U.S. Melanoma-Prone Families With CDKN2A and CDK4 Mutations. <i>Journal of the National Cancer Institute</i> , 2000, 92, 1006-1010.	3.0	172

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109	Mutation screening of the CDKN2A promoter in melanoma families. <i>Genes Chromosomes and Cancer</i> , 2000, 28, 45.	1.5	1
110	Deletion analysis of the adenomatous polyposis coli and PTCH gene loci in patients with sporadic and nevoid basal cell carcinoma syndrome-associated medulloblastoma. <i>Cancer</i> , 1999, 85, 2662-2667.	2.0	46
111	A genome-wide search for loci contributing to smoking and alcoholism. <i>Genetic Epidemiology</i> , 1999, 17, S55-60.	0.6	91
112	Sib-pair linkage analyses of alcoholism: Dichotomous and quantitative measures. <i>Genetic Epidemiology</i> , 1999, 17, S205-10.	0.6	0
113	Deletion analysis of the adenomatous polyposis coli and PTCH gene loci in patients with sporadic and nevoid basal cell carcinoma syndrome-associated medulloblastoma. <i>Cancer</i> , 1999, 85, 2662-2667.	2.0	1
114	Familial eosinophilia: Clinical and laboratory results on a U.S. Kindred. <i>American Journal of Medical Genetics Part A</i> , 1998, 76, 229-237.	2.4	35
115	Haplotype analysis of two recurrent CDKN2A mutations in 10 melanoma families: Evidence for common founders and independent mutations. , 1998, 11, 424-431.		61
116	Allelic imbalance, including deletion of PTEN/MMAC1, at the Cowden disease locus on 10q22-23, in hamartomas from patients with cowden syndrome and germline PTEN mutation. , 1998, 21, 61-69.		85
117	CDKN2A Mutations in Multiple Primary Melanomas. <i>New England Journal of Medicine</i> , 1998, 338, 879-887.	13.9	255
118	Familial eosinophilia: Clinical and laboratory results on a U.S. Kindred. , 1998, 76, 229.		1
119	Second cancers after medulloblastoma: population-based results from the United States and Sweden. <i>Cancer Causes and Control</i> , 1997, 8, 865-871.	0.8	96
120	Nevoid basal cell carcinoma syndrome with medulloblastoma in an African-American boy: A rare case illustrating gene-environment interaction. , 1997, 69, 309-314.		30
121	Detecting gene-environment interactions using a case-control design. <i>Genetic Epidemiology</i> , 1997, 14, 1085-1089.	0.6	25
122	Sib-pair linkage analyses of nuclear family data: Quantitative versus dichotomous disease classification. <i>Genetic Epidemiology</i> , 1997, 14, 827-832.	0.6	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. <i>Nature Genetics</i> , 1996, 12, 97-99.	9.4	756
125	Mutations associated with familial melanoma impair p16INK4 function. <i>Nature Genetics</i> , 1995, 10, 114-116.	9.4	273
126	Increased Risk of Pancreatic Cancer in Melanoma-Prone Kindreds with p16INK4 Mutations. <i>New England Journal of Medicine</i> , 1995, 333, 970-975.	13.9	608

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127	Clinical findings in two African-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.	9.4	1,170
129	Clustering of high density lipoprotein cholesterol levels in premenopausal and postmenopausal female twins. Genetic Epidemiology, 1993, 10, 563-567.	0.6	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.	1.6	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.	13.7	448