# Alisa M Goldstein

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | Germline p16 mutations in familial melanoma. Nature Genetics, 1994, 8, 15-21. | 21.4 | 1,170 |
| 2 | Chordoma: incidence and survival patterns in the United States, 1973-1995. Cancer Causes and Control, 2001, 12, 1-11. | 1.8 | 820 |
| 3 | Germline mutations in the p16INK4a binding domain of CDK4 in familial melanoma. Nature Genetics, 1996, 12, 97-99. | 21.4 | 756 |
| 4 | Increased Risk of Pancreatic Cancer in Melanoma-Prone Kindreds withp16<sup>INK4</sup>Mutations. New England Journal of Medicine, 1995, 333, 970-975. | 27.0 | 608 |
| 5 | 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 |
| 6 | Geographical Variation in the Penetrance of CDKN2A Mutations for Melanoma. Journal of the National Cancer Institute, 2002, 94, 894-903. | 6.3 | 435 |
| 7 | Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925. | 21.4 | 422 |
| 8 | 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 |
| 9 | 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 |
| 10 | T (brachyury) gene duplication confers major susceptibility to familial chordoma. Nature Genetics, 2009, 41, 1176-1178. | 21.4 | 284 |
| 11 | Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nature Genetics, 2014, 46, 482-486. | 21.4 | 283 |
| 12 | Mutations associated with familial melanoma impair p16INK4 function. Nature Genetics, 1995, 10, 114-116. | 21.4 | 273 |
| 13 | CDKN2AMutations in Multiple Primary Melanomas. New England Journal of Medicine, 1998, 338, 879-887. | 27.0 | 255 |
| 14 | Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113. | 21.4 | 230 |
| 15 | Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995. | 21.4 | 218 |
| 16 | Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840. | 21.4 | 209 |
| 17 | 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 |
| 18 | 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | 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 |
| 20 | Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118. | 21.4 | 140 |
| 21 | 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 |
| 22 | Molecular Characterization of the Human Stomach Microbiota in Gastric Cancer Patients. Frontiers in Cellular and Infection Microbiology, 2017, 7, 302. | 3.9 | 136 |
| 23 | Familial melanoma, pancreatic cancer and germline CDKN2A mutations. Human Mutation, 2004, 23, 630-630. | 2.5 | 130 |
| 24 | Genetic Epidemiology of Cutaneous Melanoma. Archives of Dermatology, 2001, 137, 1493-6. | 1.4 | 118 |
| 25 | Risk factors for esophageal and gastric cancers in Shanxi Province, China: A caseâ€“control study. Cancer Epidemiology, 2011, 35, e91-e99. | 1.9 | 112 |
| 26 | Melanoma prone families withCDK4germline mutation: phenotypic profile and associations withMC1Rvariants. Journal of Medical Genetics, 2013, 50, 264-270. | 3.2 | 112 |
| 27 | A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432. | 21.4 | 111 |
| 28 | The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, . | 6.3 | 109 |
| 29 | Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497. | 6.2 | 101 |
| 30 | 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 |
| 31 | 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 |
| 32 | Second cancers after medulloblastoma: population-based results from the United States and Sweden. Cancer Causes and Control, 1997, 8, 865-871. | 1.8 | 96 |
| 33 | A genomeâ€wide search for loci contributing to smoking and alcoholism. Genetic Epidemiology, 1999, 17, S55-60. | 1.3 | 91 |
| 34 | Lung Cancer Prognosis Before and After Recurrence in a Population-Based Setting. Journal of the National Cancer Institute, 2015, 107, djv059. | 6.3 | 86 |
| 35 | Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843. | 12.8 | 86 |
| 36 | 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 |

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|---|---|---|---|
| 37 | Mutational signatures in esophageal squamous cell carcinoma from eight countries with varying incidence. Nature Genetics, 2021, 53, 1553-1563. | 21.4 | 71 |
| 38 | Genomic Landscape of Somatic Alterations in Esophageal Squamous Cell Carcinoma and Gastric Cancer. Cancer Research, 2016, 76, 1714-1723. | 0.9 | 68 |
| 39 | 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 |
| 40 | Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. Carcinogenesis, 2014, 35, 2698-2705. | 2.8 | 67 |
| 41 | Cell-typeâ€“specific eQTL of primary melanocytes facilitates identification of melanoma susceptibility genes. Genome Research, 2018, 28, 1621-1635. | 5.5 | 67 |
| 42 | The Genetics of Melanoma: Recent Advances. Annual Review of Genomics and Human Genetics, 2013, 14, 257-279. | 6.2 | 66 |
| 43 | 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 |
| 44 | Sporadic multiple primary melanoma cases:CDKN2Agermline mutations with a founder effect. Genes Chromosomes and Cancer, 2001, 32, 195-202. | 2.8 | 63 |
| 45 | Haplotype analysis of two recurrentCDKN2A mutations in 10 melanoma families: Evidence for common founders and independent mutations. , 1998, 11, 424-431. | | 61 |
| 46 | 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 |
| 47 | Nested PCR Biases in Interpreting Microbial Community Structure in 16S rRNA Gene Sequence Datasets. PLoS ONE, 2015, 10, e0132253. | 2.5 | 60 |
| 48 | Mutation screening of theCDKN2A promoter in melanoma families. , 2000, 28, 45-57. | | 59 |
| 49 | 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 |
| 50 | The Value of Small Observations in the Era of Big Science. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 2472-2473. | 2.5 | 55 |
| 51 | 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 |
| 52 | Characterization of T gene sequence variants and germline duplications in familial and sporadic chordoma. Human Genetics, 2014, 133, 1289-1297. | 3.8 | 54 |
| 53 | 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 |
| 54 | 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 |

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|---|---|---|---|
| 55 | Germline mutations in Protection of Telomeres 1 in two families with Hodgkin lymphoma. British Journal of Haematology, 2018, 181, 372-377. | 2.5 | 48 |
| 56 | 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 |
| 57 | 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 |
| 58 | 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 |
| 59 | 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 |
| 60 | 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 |
| 61 | Rare germline variants in known melanoma susceptibility genes in familial melanoma. Human Molecular Genetics, 2017, 26, 4886-4895. | 2.9 | 37 |
| 62 | 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 |
| 63 | 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 |
| 64 | Whole-Exome Sequencing of Nasopharyngeal Carcinoma Families Reveals Novel Variants Potentially Involved in Nasopharyngeal Carcinoma. Scientific Reports, 2019, 9, 9916. | 3.3 | 32 |
| 65 | 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 |
| 66 | Integrative molecular characterisation of gallbladder cancer reveals micro-environment-associated subtypes. Journal of Hepatology, 2021, 74, 1132-1144. | 3.7 | 30 |
| 67 | 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 |
| 68 | Recent Tanning Bed Use. Archives of Dermatology, 2006, 142, 485-8. | 1.4 | 28 |
| 69 | Detecting gene-environment interactions using a case-control design. Genetic Epidemiology, 1997, 14, 1085-1089. | 1.3 | 25 |
| 70 | Cancer patterns in nasopharyngeal carcinoma multiplex families in Taiwan. International Journal of Cancer, 2009, 124, 1622-1625. | 5.1 | 25 |
| 71 | 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 |
| 72 | 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 |

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|---|---|---|---|
| 73 | Body mass index and height and risk of cutaneous melanoma: Mendelian randomization analyses. International Journal of Epidemiology, 2020, 49, 1236-1245. | 1.9 | 21 |
| 74 | Histologic features of melanoma associated with CDKN2A genotype. Journal of the American Academy of Dermatology, 2015, 72, 496-507.e7. | 1.2 | 19 |
| 75 | Risks of Melanoma and Other Cancers in Melanoma-Prone Families over 4 Decades. Journal of Investigative Dermatology, 2018, 138, 1620-1626. | 0.7 | 19 |
| 76 | 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 |
| 77 | 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 |
| 78 | Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612. | 0.7 | 18 |
| 79 | 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 |
| 80 | Lack of phospholipase A2 mutations in neuroblastoma, melanoma and colon-cancer cell lines. , 1997, 72, 337-339. | | 16 |
| 81 | 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 |
| 82 | Pediatric melanoma in melanomaâ€prone families. Cancer, 2018, 124, 3715-3723. | 4.1 | 16 |
| 83 | Constitutional promoter methylation and risk of familial melanoma. Epigenetics, 2014, 9, 685-692. | 2.7 | 15 |
| 84 | 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 |
| 85 | 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 |
| 86 | 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 |
| 87 | 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 |
| 88 | Sebaceous Carcinoma Incidence and Survival Among Solid Organ Transplant Recipients in the United States, 1987-2017. JAMA Dermatology, 2020, 156, 1307. | 4.1 | 14 |
| 89 | Ambient Ultraviolet Radiation and Sebaceous Carcinoma Incidence in the United States, 2000â€“2016. JNCI Cancer Spectrum, 2020, 4, pkaa020. | 2.9 | 14 |
| 90 | Rare Germline Copy Number Variations and Disease Susceptibility in Familial Melanoma. Journal of Investigative Dermatology, 2016, 136, 2436-2443. | 0.7 | 13 |

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|---|---|---|---|
| 91 | 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 |
| 92 | Association of high-evidence gastric cancer susceptibility loci and somatic gene expression levels with survival. Carcinogenesis, 2017, 38, 1119-1128. | 2.8 | 13 |
| 93 | 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 |
| 94 | 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 |
| 95 | Phenocopies in melanoma-prone families with germ-line CDKN2A mutations. Genetics in Medicine, 2018, 20, 1087-1090. | 2.4 | 11 |
| 96 | Use of Big Data to Estimate Prevalence of Defective DNA Repair Variants in the US Population. JAMA Dermatology, 2019, 155, 72. | 4.1 | 11 |
| 97 | 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 |
| 98 | Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in the Childhood Cancer Survivor Study. JNCI Cancer Spectrum, 2021, 5, pkab007. | 2.9 | 11 |
| 99 | 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 |
| 100 | First international workshop of the ATM and cancer risk group (4-5 December 2019). Familial Cancer, 2022, 21, 211-227. | 1.9 | 10 |
| 101 | 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 |
| 102 | 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 |
| 103 | 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 |
| 104 | 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 |
| 105 | ABO genotypes and the risk of esophageal and gastric cancers. BMC Cancer, 2021, 21, 589. | 2.6 | 8 |
| 106 | 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 |
| 107 | Sib-pair linkage analyses of nuclear family data: Quantitative versus dichotomous disease classification. Genetic Epidemiology, 1997, 14, 827-832. | 1.3 | 7 |
| 108 | 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 |

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|---|---|---|---|
| 109 | 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 |
| 110 | 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 |
| 111 | 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 |
| 112 | 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 |
| 113 | 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 |
| 114 | Rare Germline Variants in Chordoma-Related Genes and Chordoma Susceptibility. Cancers, 2021, 13, 2704. | 3.7 | 5 |
| 115 | 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 |
| 116 | Variation in second cancer risk by melanoma subtype among survivors. Journal of the American Academy of Dermatology, 2023, 88, 433-434. | 1.2 | 4 |
| 117 | Clustering of high density lipoprotein cholesterol levels in premenopausal and postmenopausal female twins. Genetic Epidemiology, 1993, 10, 563-567. | 1.3 | 3 |
| 118 | GeneÃ—Environment Interaction from Caseâ€Control and Caseâ€Case Approaches. Genetic Epidemiology, 2001, 21, S825-30. | 1.3 | 3 |
| 119 | Use of Weighted pâ€Values in Regional Inference Procedures. Genetic Epidemiology, 2001, 21, S484-9. | 1.3 | 3 |
| 120 | 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 |
| 121 | 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 |
| 122 | Rare germline variants in PALB2 and BRCA2 in familial and sporadic chordoma. Human Mutation, 2022, 43, 1396-1407. | 2.5 | 3 |
| 123 | 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 |
| 124 | Cancer patterns in nasopharyngeal carcinoma multiplex families over 15 years. Cancer, 2021, 127, 4171-4176. | 4.1 | 2 |
| 125 | Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. Familial Cancer, 2022, 21, 347-355. | 1.9 | 1 |
| 126 | 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 |

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| 127 | 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 |
| 128 | Mutation screening of the CDKN2A promoter in melanoma families. Genes Chromosomes and Cancer, 2000, 28, 45. | 2.8 | 1 |
| 129 | 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 |
| 130 | Sibâ€pair linkage analyses of alcoholism: Dichotomous and quantitative measures. Genetic Epidemiology, 1999, 17, S205-10. | 1.3 | 0 |
| 131 | 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 |