

# Brian H Shirts

## List of Publications by Year in descending order

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Version: 2024-02-01

102  
papers

3,984  
citations

186265

28  
h-index

133252

59  
g-index

109  
all docs

109  
docs citations

109  
times ranked

8541  
citing authors

#	ARTICLE	IF	CITATIONS
1	Prevalence and Spectrum of Germline Cancer Susceptibility Gene Mutations Among Patients With Early-Onset Colorectal Cancer. <i>JAMA Oncology</i> , 2017, 3, 464.	7.1	510
2	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. <i>Cancer Discovery</i> , 2018, 8, 730-749.	9.4	367
3	Actionable, Pathogenic Incidental Findings in 1,000 Participants's Exomes. <i>American Journal of Human Genetics</i> , 2013, 93, 631-640.	6.2	342
4	Actionable exomic incidental findings in 6503 participants: challenges of variant classification. <i>Genome Research</i> , 2015, 25, 305-315.	5.5	313
5	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. <i>American Journal of Human Genetics</i> , 2016, 98, 1051-1066.	6.2	137
6	Assessment of Tumor Sequencing as a Replacement for Lynch Syndrome Screening and Current Molecular Tests for Patients With Colorectal Cancer. <i>JAMA Oncology</i> , 2018, 4, 806.	7.1	136
7	A network of dopaminergic gene variations implicated as risk factors for schizophrenia. <i>Human Molecular Genetics</i> , 2008, 17, 747-758.	2.9	124
8	Next-Generation Sequencing Panels for the Diagnosis of Colorectal Cancer and Polyposis Syndromes: A Cost-Effectiveness Analysis. <i>Journal of Clinical Oncology</i> , 2015, 33, 2084-2091.	1.6	118
9	Comparison of <i>CDH1</i> Penetrance Estimates in Clinically Ascertained Families vs Families Ascertained for Multiple Gastric Cancers. <i>JAMA Oncology</i> , 2019, 5, 1325.	7.1	109
10	Antibodies to cytomegalovirus and Herpes Simplex Virus 1 associated with cognitive function in schizophrenia. <i>Schizophrenia Research</i> , 2008, 106, 268-274.	2.0	84
11	Improving performance of multigene panels for genomic analysis of cancer predisposition. <i>Genetics in Medicine</i> , 2016, 18, 974-981.	2.4	80
12	CSER and eMERGE: current and potential state of the display of genetic information in the electronic health record. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1231-1242.	4.4	73
13	Do We Now Know What Inappropriate Laboratory Utilization Is?. <i>American Journal of Clinical Pathology</i> , 2014, 141, 774-783.	0.7	71
14	A survey of current practices for genomic sequencing test interpretation and reporting processes in US laboratories. <i>Genetics in Medicine</i> , 2017, 19, 575-582.	2.4	68
15	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. <i>Nature Communications</i> , 2020, 11, 3644.	12.8	55
16	Association study of IL10, IL1 $\beta$ , and IL1RN and schizophrenia using tag SNPs from a comprehensive database: Suggestive association with rs16944 at IL1 $\beta$ . <i>Schizophrenia Research</i> , 2006, 88, 235-244.	2.0	52
17	Scaling resolution of variant classification differences in ClinVar between 41 clinical laboratories through an outlier approach. <i>Human Mutation</i> , 2018, 39, 1641-1649.	2.5	50
18	Knowledge for Precision Medicine. <i>JAMA - Journal of the American Medical Association</i> , 2017, 318, 1649.	7.4	47

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19	Patients' perspectives of variants of uncertain significance and strategies for uncertainty management. <i>Journal of Genetic Counseling</i> , 2019, 28, 313-325.	1.6	46
20	CADD score has limited clinical validity for the identification of pathogenic variants in noncoding regions in a hereditary cancer panel. <i>Genetics in Medicine</i> , 2016, 18, 1269-1275.	2.4	45
21	Closing the gap: Systematic integration of multiplexed functional data resolves variants of uncertain significance in BRCA1, TP53, and PTEN. <i>American Journal of Human Genetics</i> , 2021, 108, 2248-2258.	6.2	42
22	Polymorphisms in MICB are associated with human herpes virus seropositivity and schizophrenia risk. <i>Schizophrenia Research</i> , 2007, 94, 342-353.	2.0	40
23	One in seven pathogenic variants can be challenging to detect by NGS: an analysis of 450,000 patients with implications for clinical sensitivity and genetic test implementation. <i>Genetics in Medicine</i> , 2021, 23, 1673-1680.	2.4	40
24	Inherited TP53 Variants and Risk of Prostate Cancer. <i>European Urology</i> , 2022, 81, 243-250.	1.9	40
25	Using Somatic Mutations from Tumors to Classify Variants in Mismatch Repair Genes. <i>American Journal of Human Genetics</i> , 2018, 103, 19-29.	6.2	36
26	Changing interpretations, stable genes: responsibilities of patients, professionals, and policy makers in the clinical interpretation of complex genetic information. <i>Genetics in Medicine</i> , 2008, 10, 778-783.	2.4	35
27	Features of Patients With Hereditary Mixed Polyposis Syndrome Caused by Duplication of GREM1 and Implications for Screening and Surveillance. <i>Gastroenterology</i> , 2017, 152, 1876-1880.e1.	1.3	34
28	Characterization of splice-altering mutations in inherited predisposition to cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26798-26807.	7.1	34
29	Outcomes of 92 patient-driven family studies for reclassification of variants of uncertain significance. <i>Genetics in Medicine</i> , 2019, 21, 1435-1442.	2.4	34
30	Cell culture analysis of the regulatory frameshift event required for the expression of mammalian antizymes. <i>Genes To Cells</i> , 2001, 6, 931-941.	1.2	32
31	Systematic misclassification of missense variants in BRCA1 and BRCA2. <i>Genetics in Medicine</i> , 2020, 22, 825-830.	2.4	32
32	Evaluation of the gene-age interactions in HDL cholesterol, LDL cholesterol, and triglyceride levels: The impact of the SORT1 polymorphism on LDL cholesterol levels is age dependent. <i>Atherosclerosis</i> , 2011, 217, 139-141.	0.8	31
33	Prospective Statewide Study of Universal Screening for Hereditary Colorectal Cancer: The Ohio Colorectal Cancer Prevention Initiative. <i>JCO Precision Oncology</i> , 2021, 5, 779-791.	3.0	31
34	Family-Specific Variants and the Limits of Human Genetics. <i>Trends in Molecular Medicine</i> , 2016, 22, 925-934.	6.7	30
35	Are exposure to cytomegalovirus and genetic variation on chromosome 6p joint risk factors for schizophrenia?. <i>Annals of Medicine</i> , 2007, 39, 145-153.	3.8	28
36	Cervical Ribs Are More Prevalent in Stillborn Fetuses than in Live-Born Infants and Are Strongly Associated with Fetal Aneuploidy. <i>Pediatric and Developmental Pathology</i> , 2011, 14, 431-437.	1.0	28

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37	Simultaneous Genotyping of rs12979860 and rs8099917 Variants Near the IL28B Locus Associated with HCV Clearance and Treatment Response. <i>Journal of Molecular Diagnostics</i> , 2011, 13, 446-451.	2.8	26
38	Family Studies for Classification of Variants of Uncertain Classification: Current Laboratory Clinical Practice and a New Web-Based Educational Tool. <i>Journal of Genetic Counseling</i> , 2016, 25, 1146-1156.	1.6	26
39	Development of clinical decision support alerts for pharmacogenomic incidental findings from exome sequencing. <i>Genetics in Medicine</i> , 2015, 17, 939-942.	2.4	25
40	Experiences of patients seeking to participate in variant of uncertain significance reclassification research. <i>Journal of Community Genetics</i> , 2019, 10, 189-196.	1.2	23
41	Molecular diagnosis of childhood immune dysregulation, polyendocrinopathy, and enteropathy, and implications for clinical management. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 327-339.	2.9	22
42	A comprehensive genetic association and functional study of TNF in schizophrenia risk. <i>Schizophrenia Research</i> , 2006, 83, 7-13.	2.0	21
43	Large numbers of individuals are required to classify and define risk for rare variants in known cancer risk genes. <i>Genetics in Medicine</i> , 2014, 16, 529-534.	2.4	21
44	Practical considerations for implementing genomic information resources. <i>Applied Clinical Informatics</i> , 2016, 07, 870-882.	1.7	21
45	Vitamin D dependent effects of APOA5 polymorphisms on HDL cholesterol. <i>Atherosclerosis</i> , 2012, 222, 167-174.	0.8	20
46	A Population-Based Description of Familial Clustering of Pancreatic Cancer. <i>Clinical Gastroenterology and Hepatology</i> , 2010, 8, 812-816.	4.4	19
47	A comparison of cosegregation analysis methods for the clinical setting. <i>Familial Cancer</i> , 2018, 17, 295-302.	1.9	19
48	Grey matter changes associated with host genetic variation and exposure to Herpes Simplex Virus 1 (HSV1) in first episode schizophrenia. <i>Schizophrenia Research</i> , 2010, 118, 232-239.	2.0	18
49	Provider Management of and Satisfaction With Laboratory Testing in the Nursing Home Setting: Results of a National Internet-Based Survey. <i>Journal of the American Medical Directors Association</i> , 2009, 10, 161-166.e3.	2.5	17
50	Physician perspectives of CYP2C19 and clopidogrel drug-gene interaction active clinical decision support alerts. <i>International Journal of Medical Informatics</i> , 2016, 86, 117-125.	3.3	16
51	Clinical laboratory analytics: Challenges and promise for an emerging discipline. <i>Journal of Pathology Informatics</i> , 2015, 6, 9.	1.7	15
52	The 2013 symposium on pathology data integration and clinical decision support and the current state of field. <i>Journal of Pathology Informatics</i> , 2014, 5, 2.	1.7	14
53	Insurance coverage does not predict outcomes of genetic testing: The search for meaning in payer decisions for germline cancer tests. <i>Journal of Genetic Counseling</i> , 2019, 28, 1208-1213.	1.6	14
54	Partitioning Reference Intervals by Use of Genetic Information. <i>Clinical Chemistry</i> , 2011, 57, 475-481.	3.2	13

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55	Deep sequencing with intronic capture enables identification of an APC exon 10 inversion in a patient with polyposis. <i>Genetics in Medicine</i> , 2014, 16, 783-786.	2.4	13
56	Effects of germline and somatic events in candidate BRCA-like genes on breast-tumor signatures. <i>PLoS ONE</i> , 2020, 15, e0239197.	2.5	13
57	Hereditary cancer gene panel test reports: wide heterogeneity suggests need for standardization. <i>Genetics in Medicine</i> , 2018, 20, 1438-1445.	2.4	12
58	Exploring the effect of ascertainment bias on genetic studies that use clinical pedigrees. <i>European Journal of Human Genetics</i> , 2019, 27, 1800-1807.	2.8	12
59	Multiplexing mutation rate assessment: determining pathogenicity of Msh2 variants in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2021, 218, .	2.9	12
60	Seropositivity Rates for Measles, Mumps, and Rubella IgG and Costs Associated with Testing and Revaccination. <i>Vaccine Journal</i> , 2013, 20, 443-445.	3.1	11
61	What improves the likelihood of people receiving genetic test results communicating to their families about genetic risk?. <i>Patient Education and Counseling</i> , 2021, 104, 726-731.	2.2	11
62	Pragmatic and Ethical Challenges of Incorporating the Genome into the Electronic Health Record. <i>Current Genetic Medicine Reports</i> , 2014, 2, 201-211.	1.9	10
63	Rare loss of function variants in candidate genes and risk of colorectal cancer. <i>Human Genetics</i> , 2018, 137, 795-806.	3.8	10
64	Applying Ancestry and Sex Computation as a Quality Control Tool in Targeted Next-Generation Sequencing. <i>American Journal of Clinical Pathology</i> , 2016, 145, 308-315.	0.7	9
65	Pilot Study of Linking Web-Based Supplemental Interpretive Information to Laboratory Test Reports. <i>American Journal of Clinical Pathology</i> , 2009, 132, 818-823.	0.7	8
66	Using Patients Like My Patient for Clinical Decision Support: Institution-Specific Probability of Celiac Disease Diagnosis Using Simplified Near-Neighbor Classification. <i>Journal of General Internal Medicine</i> , 2013, 28, 1565-1572.	2.6	8
67	A bayesian approach to laboratory utilization management. <i>Journal of Pathology Informatics</i> , 2015, 6, 10.	1.7	7
68	Power of pedigree likelihood analysis in extended pedigrees to classify rare variants of uncertain significance in cancer risk genes. <i>Familial Cancer</i> , 2017, 16, 611-620.	1.9	7
69	Efficient Detection of Copy Number Mutations in PMS2 Exons with a Close Homolog. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 512-521.	2.8	7
70	Modified capture-recapture estimates of the number of families with Lynch syndrome in Central Ohio. <i>Familial Cancer</i> , 2019, 18, 67-73.	1.9	7
71	Harmonizing variant classification for return of results in the All of Us Research Program. <i>Human Mutation</i> , 2022, 43, 1114-1121.	2.5	7
72	Socioeconomic Status and Interest in Genetic Testing in a US-Based Sample. <i>Healthcare (Switzerland)</i> , 2022, 10, 880.	2.0	7

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73	Clinical exome sequencing vs. usual care for hereditary colorectal cancer diagnosis: A pilot comparative effectiveness study. <i>Contemporary Clinical Trials</i> , 2019, 84, 105820.	1.8	6
74	Utilization and utility of clinical laboratory reports with graphical elements. <i>Journal of Pathology Informatics</i> , 2012, 3, 26.	1.7	6
75	Informatics methods for laboratory evaluation of HPV ordering patterns with an example from a nationwide sample in the United States, 2003-2009. <i>Journal of Pathology Informatics</i> , 2010, 1, 26.	1.7	6
76	Laboratory-related outcomes from integrating an accessible delivery model for hereditary cancer risk assessment and genetic testing in populations with barriers to access. <i>Genetics in Medicine</i> , 2022, 24, 1196-1205.	2.4	6
77	Next Generation Sequencing in the Clinic: a Patterns of Care Study in a Retrospective Cohort of Subjects Referred to a Genetic Medicine Clinic for Suspected Lynch Syndrome. <i>Journal of Genetic Counseling</i> , 2016, 25, 515-519.	1.6	5
78	Patient goals, motivations, and attitudes in a patient-driven variant reclassification study. <i>Journal of Genetic Counseling</i> , 2019, 28, 558-569.	1.6	5
79	Design of a study to implement population-based risk assessment for hereditary cancer genetic testing in primary care. <i>Contemporary Clinical Trials</i> , 2021, 101, 106257.	1.8	5
80	Complexities of Next-Generation Sequencing in Solid Tumors: Case Studies. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2020, 18, 1150-1155.	4.9	5
81	Modeling the costs of clinical decision support for genomic precision medicine. <i>AMIA Summits on Translational Science Proceedings</i> , 2016, 2016, 60-4.	0.4	5
82	The genomic CDS sandbox: An assessment among domain experts. <i>Journal of Biomedical Informatics</i> , 2016, 60, 84-94.	4.3	4
83	Exploring relatives'™ perceptions of participation, ethics, and communication in a patient-driven study for hereditary cancer variant reclassification. <i>Journal of Genetic Counseling</i> , 2020, 29, 857-866.	1.6	4
84	Implementation of pharmacogenomic clinical decision support for health systems: a cost-utility analysis. <i>Pharmacogenomics Journal</i> , 2022, 22, 188-197.	2.0	4
85	Laboratory informatics based evaluation of methylene tetrahydrofolate reductase C677T genetic test overutilization. <i>Journal of Pathology Informatics</i> , 2013, 4, 33.	1.7	3
86	Technical, Biological, and Systems Barriers for Molecular Clinical Decision Support. <i>Clinics in Laboratory Medicine</i> , 2019, 39, 281-294.	1.4	3
87	Infobuttons for Genomic Medicine: Requirements and Barriers. <i>Applied Clinical Informatics</i> , 2021, 12, 383-390.	1.7	3
88	Proffered Papers and Posters Presented at the Seventh International Symposium on Hereditary Breast and Ovarian Cancer—BrcA: From the Personal to the Population. <i>Current Oncology</i> , 2018, 25, 224-262.	2.2	2
89	The FamilyTalk randomized controlled trial: patient-reported outcomes in clinical genetic sequencing for colorectal cancer. <i>Cancer Causes and Control</i> , 2021, 32, 483-492.	1.8	2
90	An algorithm for optimal testing in co-segregation analysis. <i>Human Mutation</i> , 2022, 43, 547-556.	2.5	2

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91	Postmortem Somatic Sequencing of Tumors From Patients With Suspected Lynch Syndrome Has Clinical Utility for Surviving Relatives. <i>JCO Precision Oncology</i> , 2018, 2, 1-7.	3.0	1
92	Relationship between genetic knowledge and familial communication of CRC risk and intent to communicate CRCP genetic information: insights from FamilyTalk eMERGE III. <i>Translational Behavioral Medicine</i> , 2021, 11, 563-572.	2.4	1
93	eP097: The utility of CSF-derived cell free DNA in molecular diagnostics for the Megalencephaly-capillary Malformation (MCAP) syndrome: A case report. <i>Genetics in Medicine</i> , 2022, 24, S63-S64.	2.4	1
94	Prothrombin time, activated partial thromboplastin time and dilute Russell's Viper Venom times are not shorter in patients with the prothrombin G20210A mutation, and dilute Russell's Viper Venom time may be longer. <i>Thrombosis Research</i> , 2012, 130, e134-e138.	1.7	0
95	Incorporating user feedback in the design of a genetics analysis tool: A two-part approach. <i>Journal of Biomedical Informatics</i> , 2019, 95, 103204.	4.3	0
96	Family-specific genetic variants: Principles, detection, and clinical interpretation. , 2020, , 73-104.		0
97	eP493: Population genetic screening study participants intend to share test results with family members. <i>Genetics in Medicine</i> , 2022, 24, S313-S314.	2.4	0
98	eP514: Extending cascade screening using genealogy, DTC genetics and social media – the ConnectMyVariant exploratory pilot study. <i>Genetics in Medicine</i> , 2022, 24, S328.	2.4	0
99	Effects of germline and somatic events in candidate BRCA-like genes on breast-tumor signatures. , 2020, 15, e0239197.		0
100	Effects of germline and somatic events in candidate BRCA-like genes on breast-tumor signatures. , 2020, 15, e0239197.		0
101	Effects of germline and somatic events in candidate BRCA-like genes on breast-tumor signatures. , 2020, 15, e0239197.		0
102	Effects of germline and somatic events in candidate BRCA-like genes on breast-tumor signatures. , 2020, 15, e0239197.		0