Brian H Shirts

List of Publications by Year
in descending order

102	3,984	186265 28	133252 59
papers	citations	h-index	g-index

109	109	109	8541
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Molecular diagnosis of childhood immune dysregulation, polyendocrinopathy, and enteropathy, and implications for clinical management. Journal of Allergy and Clinical Immunology, 2022, 149, 327-339.	2.9	22
2	Inherited TP53 Variants and Risk of Prostate Cancer. European Urology, 2022, 81, 243-250.	1.9	40
3	eP097: The utility of CSF-derived cell free DNA in molecular diagnostics for the Megalencephaly-capillary Malformation (MCAP) syndrome: A case report. Genetics in Medicine, 2022, 24, S63-S64.	2.4	1
4	eP493: Population genetic screening study participants intend to share test results with family members. Genetics in Medicine, 2022, 24, S313-S314.	2.4	0
5	Laboratory-related outcomes from integrating an accessible delivery model for hereditary cancer risk assessment and genetic testing in populations with barriers to access. Genetics in Medicine, 2022, 24, 1196-1205.	2.4	6
6	eP514: Extending cascade screening using genealogy, DTC genetics and social media â€“ the ConnectMyVariant exploratory pilot study. Genetics in Medicine, 2022, 24, S328.	2.4	0
7	An algorithm for optimal testing in coâ€segregation analysis. Human Mutation, 2022, 43, 547-556.	2.5	2
8	Implementation of pharmacogenomic clinical decision support for health systems: a cost-utility analysis. Pharmacogenomics Journal, 2022, 22, 188-197.	2.0	4
9	Harmonizing variant classification for return of results in the All of Us Research Program. Human Mutation, 2022, 43, 1114-1121.	2.5	7
10	Socioeconomic Status and Interest in Genetic Testing in a US-Based Sample. Healthcare (Switzerland), 2022, 10, 880.	2.0	7
11	Relationship between genetic knowledge and familial communication of CRC risk and intent to communicate CRCP genetic information: insights from FamilyTalk eMERGE III. Translational Behavioral Medicine, 2021, 11, 563-572.	2.4	1
12	Design of a study to implement population-based risk assessment for hereditary cancer genetic testing in primary care. Contemporary Clinical Trials, 2021, 101, 106257.	1.8	5
13	The FamilyTalk randomized controlled trial: patient-reported outcomes in clinical genetic sequencing for colorectal cancer. Cancer Causes and Control, 2021, 32, 483-492.	1.8	2
14	Infobuttons for Genomic Medicine: Requirements and Barriers. Applied Clinical Informatics, 2021, 12, 383-390.	1.7	3
15	Multiplexing mutation rate assessment: determining pathogenicity of Msh2 variants in Saccharomyces cerevisiae. Genetics, 2021, 218, .	2.9	12
16	What improves the likelihood of people receiving genetic test results communicating to their families about genetic risk?. Patient Education and Counseling, 2021, 104, 726-731.	2.2	11
17	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. Genetics in Medicine, 2021, 23, 1673-1680.	2.4	40
18	Prospective Statewide Study of Universal Screening for Hereditary Colorectal Cancer: The Ohio Colorectal Cancer Prevention Initiative. JCO Precision Oncology, 2021, 5, 779-791.	3.0	31

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19	Closing the gap: Systematic integration of multiplexed functional data resolves variants of uncertain significance in BRCA1, TP53, and PTEN. American Journal of Human Genetics, 2021, 108, 2248-2258.	6.2	42
20	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. Nature Communications, 2020, 11, 3644.	12.8	55
21	Family-specific genetic variants: Principles, detection, and clinical interpretation. , 2020, , 73-104.		0
22	Systematic misclassification of missense variants in BRCA1 and BRCA2 â€œcoldspotsâ€• Genetics in Medicine, 2020, 22, 825-830.	2.4	32
23	Exploring relativesâ€™ perceptions of participation, ethics, and communication in a patientâ€driven study for hereditary cancer variant reclassification. Journal of Genetic Counseling, 2020, 29, 857-866.	1.6	4
24	Effects of germline and somatic events in candidate BRCA-like genes on breast-tumor signatures. PLoS ONE, 2020, 15, e0239197.	2.5	13
25	Complexities of Next-Generation Sequencing in Solid Tumors: Case Studies. Journal of the National Comprehensive Cancer Network: JNCCN, 2020, 18, 1150-1155.	4.9	5
26	Effects of germline and somatic events in candidate BRCA-like genes on breast-tumor signatures. , 2020, 15, e0239197.		0
27	Effects of germline and somatic events in candidate BRCA-like genes on breast-tumor signatures. , 2020, 15, e0239197.		0
28	Effects of germline and somatic events in candidate BRCA-like genes on breast-tumor signatures. , 2020, 15, e0239197.		0
29	Effects of germline and somatic events in candidate BRCA-like genes on breast-tumor signatures. , 2020, 15, e0239197.		0
30	Modified captureâ€“recapture estimates of the number of families with Lynch syndrome in Central Ohio. Familial Cancer, 2019, 18, 67-73.	1.9	7
31	Experiences of patients seeking to participate in variant of uncertain significance reclassification research. Journal of Community Genetics, 2019, 10, 189-196.	1.2	23
32	Exploring the effect of ascertainment bias on genetic studies that use clinical pedigrees. European Journal of Human Genetics, 2019, 27, 1800-1807.	2.8	12
33	Insurance coverage does not predict outcomes of genetic testing: The search for meaning in payer decisions for germline cancer tests. Journal of Genetic Counseling, 2019, 28, 1208-1213.	1.6	14
34	Technical, Biological, and Systems Barriers for Molecular Clinical Decision Support. Clinics in Laboratory Medicine, 2019, 39, 281-294.	1.4	3
35	Comparison of CDH1 Penetrance Estimates in Clinically Ascertained Families vs Families Ascertained for Multiple Gastric Cancers. JAMA Oncology, 2019, 5, 1325.	7.1	109
36	Incorporating user feedback in the design of a genetics analysis tool: A two-part approach. Journal of Biomedical Informatics, 2019, 95, 103204.	4.3	0

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37	Patient goals, motivations, and attitudes in a patientâ€driven variant reclassification study. Journal of Genetic Counseling, 2019, 28, 558-569.	1.6	5
38	Clinical exome sequencing vs. usual care for hereditary colorectal cancer diagnosis: A pilot comparative effectiveness study. Contemporary Clinical Trials, 2019, 84, 105820.	1.8	6
39	Characterization of splice-altering mutations in inherited predisposition to cancer. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26798-26807.	7.1	34
40	Patients' perspectives of variants of uncertain significance and strategies for uncertainty management. Journal of Genetic Counseling, 2019, 28, 313-325.	1.6	46
41	Outcomes of 92 patient-driven family studies for reclassification of variants of uncertain significance. Genetics in Medicine, 2019, 21, 1435-1442.	2.4	34
42	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. Cancer Discovery, 2018, 8, 730-749.	9.4	367
43	Hereditary cancer gene panel test reports: wide heterogeneity suggests need for standardization. Genetics in Medicine, 2018, 20, 1438-1445.	2.4	12
44	Assessment of Tumor Sequencing as a Replacement for Lynch Syndrome Screening and Current Molecular Tests for Patients With Colorectal Cancer. JAMA Oncology, 2018, 4, 806.	7.1	136
45	A comparison of cosegregation analysis methods for the clinical setting. Familial Cancer, 2018, 17, 295-302.	1.9	19
46	Proffered Papers and Posters Presented at the Seventh International Symposium on Hereditary Breast and Ovarian Cancerâ€"BrcA: From the Personal to the Population. Current Oncology, 2018, 25, 224-262.	2.2	2
47	Postmortem Somatic Sequencing of Tumors From Patients With Suspected Lynch Syndrome Has Clinical Utility for Surviving Relatives. JCO Precision Oncology, 2018, 2, 1-7.	3.0	1
48	Rare loss of function variants in candidate genes and risk of colorectal cancer. Human Genetics, 2018, 137, 795-806.	3.8	10
49	Scaling resolution of variant classification differences in ClinVar between 41 clinical laboratories through an outlier approach. Human Mutation, 2018, 39, 1641-1649.	2.5	50
50	Efficient Detection of Copy Number Mutations in PMS2 Exons with a Close Homolog. Journal of Molecular Diagnostics, 2018, 20, 512-521.	2.8	7
51	Using Somatic Mutations from Tumors to Classify Variants in Mismatch Repair Genes. American Journal of Human Genetics, 2018, 103, 19-29.	6.2	36
52	Features of Patients With Hereditary Mixed Polyposis Syndrome Caused by Duplication of GREM1 and Implications for Screening and Surveillance. Gastroenterology, 2017, 152, 1876-1880.e1.	1.3	34
53	Power of pedigree likelihood analysis in extended pedigrees to classify rare variants of uncertain significance in cancer risk genes. Familial Cancer, 2017, 16, 611-620.	1.9	7
54	Prevalence and Spectrum of Germline Cancer Susceptibility Gene Mutations Among Patients With Early-Onset Colorectal Cancer. JAMA Oncology, 2017, 3, 464.	7.1	510

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55	Knowledge for Precision Medicine. JAMA - Journal of the American Medical Association, 2017, 318, 1649.	7.4	47
56	A survey of current practices for genomic sequencing test interpretation and reporting processes in US laboratories. Genetics in Medicine, 2017, 19, 575-582.	2.4	68
57	Practical considerations for implementing genomic information resources. Applied Clinical Informatics, 2016, 07, 870-882.	1.7	21
58	Applying Ancestry and Sex Computation as a Quality Control Tool in Targeted Next-Generation Sequencing. American Journal of Clinical Pathology, 2016, 145, 308-315.	0.7	9
59	CADD score has limited clinical validity for the identification of pathogenic variants in noncoding regions in a hereditary cancer panel. Genetics in Medicine, 2016, 18, 1269-1275.	2.4	45
60	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. American Journal of Human Genetics, 2016, 98, 1051-1066.	6.2	137
61	Family-Specific Variants and the Limits of Human Genetics. Trends in Molecular Medicine, 2016, 22, 925-934.	6.7	30
62	Family Studies for Classification of Variants of Uncertain Classification: Current Laboratory Clinical Practice and a New Webâ€Based Educational Tool. Journal of Genetic Counseling, 2016, 25, 1146-1156.	1.6	26
63	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. Journal of Genetic Counseling, 2016, 25, 515-519.	1.6	5
64	Physician perspectives of CYP2C19 and clopidogrel drug-gene interaction active clinical decision support alerts. International Journal of Medical Informatics, 2016, 86, 117-125.	3.3	16
65	Improving performance of multigene panels for genomic analysis of cancer predisposition. Genetics in Medicine, 2016, 18, 974-981.	2.4	80
66	The genomic CDS sandbox: An assessment among domain experts. Journal of Biomedical Informatics, 2016, 60, 84-94.	4.3	4
67	Modeling the costs of clinical decision support for genomic precision medicine. AMIA Summits on Translational Science Proceedings, 2016, 2016, 60-4.	0.4	5
68	Clinical laboratory analytics: Challenges and promise for an emerging discipline. Journal of Pathology Informatics, 2015, 6, 9.	1.7	15
69	A bayesian approach to laboratory utilization management. Journal of Pathology Informatics, 2015, 6, 10.	1.7	7
70	Development of clinical decision support alerts for pharmacogenomic incidental findings from exome sequencing. Genetics in Medicine, 2015, 17, 939-942.	2.4	25
71	Next-Generation Sequencing Panels for the Diagnosis of Colorectal Cancer and Polyposis Syndromes: A Cost-Effectiveness Analysis. Journal of Clinical Oncology, 2015, 33, 2084-2091.	1.6	118
72	CSER and eMERGE: current and potential state of the display of genetic information in the electronic health record. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1231-1242.	4.4	73

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73	Actionable exomic incidental findings in 6503 participants: challenges of variant classification. Genome Research, 2015, 25, 305-315.	5.5	313
74	Pragmatic and Ethical Challenges of Incorporating the Genome into the Electronic Health Record. Current Genetic Medicine Reports, 2014, 2, 201-211.	1.9	10
75	The 2013 symposium on pathology data integration and clinical decision support and the current state of field. Journal of Pathology Informatics, 2014, 5, 2.	1.7	14
76	Large numbers of individuals are required to classify and define risk for rare variants in known cancer risk genes. Genetics in Medicine, 2014, 16, 529-534.	2.4	21
77	Deep sequencing with intronic capture enables identification of an APC exon 10 inversion in a patient with polyposis. Genetics in Medicine, 2014, 16, 783-786.	2.4	13
78	Do We Now Know What Inappropriate Laboratory Utilization Is?. American Journal of Clinical Pathology, 2014, 141, 774-783.	0.7	71
79	Using Patients Like My Patient for Clinical Decision Support: Institution-Specific Probability of Celiac Disease Diagnosis Using Simplified Near-Neighbor Classification. Journal of General Internal Medicine, 2013, 28, 1565-1572.	2.6	8
80	Actionable, Pathogenic Incidental Findings in 1,000 Participantsâ€™ Exomes. American Journal of Human Genetics, 2013, 93, 631-640.	6.2	342
81	Laboratory informatics based evaluation of methylene tetrahydrofolate reductase C677T genetic test overutilization. Journal of Pathology Informatics, 2013, 4, 33.	1.7	3
82	Seropositivity Rates for Measles, Mumps, and Rubella IgG and Costs Associated with Testing and Revaccination. Vaccine Journal, 2013, 20, 443-445.	3.1	11
83	Vitamin D dependent effects of APOA5 polymorphisms on HDL cholesterol. Atherosclerosis, 2012, 222, 167-174.	0.8	20
84	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. Thrombosis Research, 2012, 130, e134-e138.	1.7	0
85	Utilization and utility of clinical laboratory reports with graphical elements. Journal of Pathology Informatics, 2012, 3, 26.	1.7	6
86	Cervical Ribs Are More Prevalent in Stillborn Fetuses than in Live-Born Infants and Are Strongly Associated with Fetal Aneuploidy. Pediatric and Developmental Pathology, 2011, 14, 431-437.	1.0	28
87	Simultaneous Genotyping of rs12979860 and rs8099917 Variants Near the IL28B Locus Associated with HCV Clearance and Treatment Response. Journal of Molecular Diagnostics, 2011, 13, 446-451.	2.8	26
88	Evaluation of the geneâ€“age interactions in HDL cholesterol, LDL cholesterol, and triglyceride levels: The impact of the SORT1 polymorphism on LDL cholesterol levels is age dependent. Atherosclerosis, 2011, 217, 139-141.	0.8	31
89	Partitioning Reference Intervals by Use of Genetic Information. Clinical Chemistry, 2011, 57, 475-481.	3.2	13
90	A Population-Based Description of Familial Clustering of Pancreatic Cancer. Clinical Gastroenterology and Hepatology, 2010, 8, 812-816.	4.4	19

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91	Grey matter changes associated with host genetic variation and exposure to Herpes Simplex Virus 1 (HSV1) in first episode schizophrenia. Schizophrenia Research, 2010, 118, 232-239.	2.0	18
92	Informatics methods for laboratory evaluation of HPV ordering patterns with an example from a nationwide sample in the United States, 2003-2009. Journal of Pathology Informatics, 2010, 1, 26.	1.7	6
93	Pilot Study of Linking Web-Based Supplemental Interpretive Information to Laboratory Test Reports. American Journal of Clinical Pathology, 2009, 132, 818-823.	0.7	8
94	Provider Management of and Satisfaction With Laboratory Testing in the Nursing Home Setting: Results of a National Internet-Based Survey. Journal of the American Medical Directors Association, 2009, 10, 161-166.e3.	2.5	17
95	A network of dopaminergic gene variations implicated as risk factors for schizophrenia. Human Molecular Genetics, 2008, 17, 747-758.	2.9	124
96	Antibodies to cytomegalovirus and Herpes Simplex Virus 1 associated with cognitive function in schizophrenia. Schizophrenia Research, 2008, 106, 268-274.	2.0	84
97	Changing interpretations, stable genes: responsibilities of patients, professionals, and policy makers in the clinical interpretation of complex genetic information. Genetics in Medicine, 2008, 10, 778-783.	2.4	35
98	Are exposure to cytomegalovirus and genetic variation on chromosome 6p joint risk factors for schizophrenia?. Annals of Medicine, 2007, 39, 145-153.	3.8	28
99	Polymorphisms in MICB are associated with human herpes virus seropositivity and schizophrenia risk. Schizophrenia Research, 2007, 94, 342-353.	2.0	40
100	A comprehensive genetic association and functional study of TNF in schizophrenia risk. Schizophrenia Research, 2006, 83, 7-13.	2.0	21
101	Association study of IL10, IL1Î², and IL1RN and schizophrenia using tag SNPs from a comprehensive database: Suggestive association with rs16944 at IL1Î². Schizophrenia Research, 2006, 88, 235-244.	2.0	52
102	Cell culture analysis of the regulatory frameshift event required for the expression of mammalian antizymes. Genes To Cells, 2001, 6, 931-941.	1.2	32