Steven M Harrison

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6996048/publications.pdf

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30 papers	3,872 citations	257450 24 h-index	477307 29 g-index
37 all docs	37 docs citations	37 times ranked	5879 citing authors

#	Article	IF	Citations
1	ClinGen Variant Curation Interface: a variant classification platform for the application of evidence criteria from ACMG/AMP guidelines. Genome Medicine, 2022, 14, 6.	8.2	34
2	Whole-genome sequencing as an investigational device for return of hereditary disease risk and pharmacogenomic results as part of the All of Us Research Program. Genome Medicine, 2022, 14, 34.	8.2	27
3	Harmonizing variant classification for return of results in the All of Us Research Program. Human Mutation, 2022, 43, 1114-1121.	2.5	7
4	Recommendations for clinical interpretation of variants found in non-coding regions of the genome. Genome Medicine, 2022, 14, .	8.2	65
5	International consensus guidelines for constitutional sequence variant interpretation. , 2021, , 29-40.		0
6	DNA-based screening and population health: a points to consider statement for programs and sponsoring organizations from the American College of Medical Genetics and Genomics (ACMG). Genetics in Medicine, 2021, 23, 989-995.	2.4	43
7	Recommendations for reporting of secondary findings in clinical exome and genome sequencing, 2021 update: a policy statement of the American College of Medical Genetics and Genomics (ACMG). Genetics in Medicine, 2021, 23, 1391-1398.	2.4	145
8	ACMG SF v3.0 list for reporting of secondary findings in clinical exome and genome sequencing: a policy statement of the American College of Medical Genetics and Genomics (ACMG). Genetics in Medicine, 2021, 23, 1381-1390.	2.4	356
9	Creation of an Expert Curated Variant List for Clinical Genomic Test Development and Validation. Journal of Molecular Diagnostics, 2021, 23, 1500-1505.	2.8	2
10	Recommendations for application of the functional evidence PS3/BS3 criterion using the ACMG/AMP sequence variant interpretation framework. Genome Medicine, 2020, 12, 3.	8.2	312
11	Fitting a naturally scaled point system to the ACMG/AMP variant classification guidelines. Human Mutation, 2020, 41, 1734-1737.	2.5	105
12	Best practices for the analytical validation of clinical whole-genome sequencing intended for the diagnosis of germline disease. Npj Genomic Medicine, 2020, 5, 47.	3.8	67
13	Overview of Specifications to the ACMG/AMP Variant Interpretation Guidelines. Current Protocols in Human Genetics, 2019, 103, e93.	3.5	88
14	A survey assessing adoption of the ACMG-AMP guidelines for interpreting sequence variants and identification of areas for continued improvement. Genetics in Medicine, 2019, 21, 1699-1701.	2.4	35
15	Evaluating the Clinical Validity of Hypertrophic Cardiomyopathy Genes. Circulation Genomic and Precision Medicine, 2019, 12, e002460.	3.6	267
16	Is â€˜likely pathogenicâ€™ really 90% likely? Reclassification data in ClinVar. Genome Medicine, 2019, 11, 72.	8.2	78
17	Modeling the ACMG/AMP variant classification guidelines as a Bayesian classification framework. Genetics in Medicine, 2018, 20, 1054-1060.	2.4	366
18	Adaptation and validation of the ACMG/AMP variant classification framework for MYH7-associated inherited cardiomyopathies: recommendations by ClinGenâ€™s Inherited Cardiomyopathy Expert Panel. Genetics in Medicine, 2018, 20, 351-359.	2.4	283

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19	The ACMG/AMP reputable source criteria for the interpretation of sequence variants. Genetics in Medicine, 2018, 20, 1687-1688.	2.4	152
20	BRCA Challenge: BRCA Exchange as a global resource for variants in BRCA1 and BRCA2. PLoS Genetics, 2018, 14, e1007752.	3.5	148
21	ClinGen's GenomeConnect registry enables patientâ€centered data sharing. Human Mutation, 2018, 39, 1668-1676.	2.5	25
22	Updated recommendation for the benign standâ€alone ACMG/AMP criterion. Human Mutation, 2018, 39, 1525-1530.	2.5	102
23	ClinGen Variant Curation Expert Panel experiences and standardized processes for disease and geneâ€level specification of the ACMG/AMP guidelines for sequence variant interpretation. Human Mutation, 2018, 39, 1614-1622.	2.5	132
24	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
25	Recommendations for interpreting the loss of function PVS1 ACMG/AMP variant criterion. Human Mutation, 2018, 39, 1517-1524.	2.5	511
26	ClinVar Miner: Demonstrating utility of a Web-based tool for viewing and filtering ClinVar data. Human Mutation, 2018, 39, 1051-1060.	2.5	81
27	ClinGen Pathogenicity Calculator: a configurable system for assessing pathogenicity of genetic variants. Genome Medicine, 2017, 9, 3.	8.2	59
28	Clinical laboratories collaborate to resolve differences in variant interpretations submitted to ClinVar. Genetics in Medicine, 2017, 19, 1096-1104.	2.4	200
29	ClinVar Is a Critical Resource to Advance Variant Interpretation. Oncologist, 2017, 22, 1562-1562.	3.7	15
30	Using ClinVar as a Resource to Support Variant Interpretation. Current Protocols in Human Genetics, 2016, 89, 8.16.1-8.16.23.	3.5	89