

# Kevin M Bowling

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11519312/publications.pdf>

Version: 2024-02-01

20  
papers

2,182  
citations

516561

16  
h-index

752573

20  
g-index

25  
all docs

25  
docs citations

25  
times ranked

5993  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamic DNA methylation across diverse human cell lines and tissues. <i>Genome Research</i> , 2013, 23, 555-567.	2.4	614
2	Performance of ACMG-AMP Variant-Interpretation Guidelines among Nine Laboratories in the Clinical Sequencing Exploratory Research Consortium. <i>American Journal of Human Genetics</i> , 2016, 98, 1067-1076.	2.6	432
3	Analysis of DNA Methylation in a Three-Generation Family Reveals Widespread Genetic Influence on Epigenetic Regulation. <i>PLoS Genetics</i> , 2011, 7, e1002228.	1.5	256
4	Genomic diagnosis for children with intellectual disability and/or developmental delay. <i>Genome Medicine</i> , 2017, 9, 43.	3.6	188
5	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. <i>American Journal of Human Genetics</i> , 2016, 98, 1051-1066.	2.6	137
6	Secondary findings from clinical genomic sequencing: prevalence, patient perspectives, family history assessment, and health-care costs from a multisite study. <i>Genetics in Medicine</i> , 2019, 21, 1100-1110.	1.1	111
7	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.	1.1	68
8	Mutations in EBF3 Disturb Transcriptional Profiles and Cause Intellectual Disability, Ataxia, and Facial Dysmorphism. <i>American Journal of Human Genetics</i> , 2017, 100, 117-127.	2.6	62
9	Variant Classification Concordance using the ACMG-AMP Variant Interpretation Guidelines across Nine Genomic Implementation Research Studies. <i>American Journal of Human Genetics</i> , 2020, 107, 932-941.	2.6	51
10	De novo mutations in MED13, a component of the Mediator complex, are associated with a novel neurodevelopmental disorder. <i>Human Genetics</i> , 2018, 137, 375-388.	1.8	46
11	Direct Binding of GTP Cyclohydrolase and Tyrosine Hydroxylase. <i>Journal of Biological Chemistry</i> , 2008, 283, 31449-31459.	1.6	41
12	Eliciting preferences on secondary findings: the Preferences Instrument for Genomic Secondary Results. <i>Genetics in Medicine</i> , 2017, 19, 337-344.	1.1	36
13	A typical N-terminal Extensions Confer Novel Regulatory Properties on GTP Cyclohydrolase Isoforms in <i>Drosophila melanogaster</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 33302-33312.	1.6	24
14	Genomic sequencing identifies secondary findings in a cohort of parent study participants. <i>Genetics in Medicine</i> , 2018, 20, 1635-1643.	1.1	24
15	Variants in TCF20 in neurodevelopmental disability: description of 27 new patients and review of literature. <i>Genetics in Medicine</i> , 2019, 21, 2036-2042.	1.1	23
16	Characterizing reduced coverage regions through comparison of exome and genome sequencing data across 10 centers. <i>Genetics in Medicine</i> , 2018, 20, 855-866.	1.1	22
17	Approaches to carrier testing and results disclosure in translational genomics research: The clinical sequencing exploratory research consortium experience. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2018, 6, 898-909.	0.6	15
18	Clinical utility of genomic sequencing. <i>Current Opinion in Pediatrics</i> , 2019, 31, 732-738.	1.0	14

#	ARTICLE	IF	CITATIONS
19	Identifying rare, medically relevant variation via population-based genomic screening in Alabama: opportunities and pitfalls. <i>Genetics in Medicine</i> , 2021, 23, 280-288.	1.1	9
20	How secondary findings are made. , 2020, , 59-75.		0