Edwin Severin Iversen Jr

List of Publications by Year
in descending order

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16	925	687363 13	940533 16
papers	citations	h-index	g-index

17	17	17	1968
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	An integrative model for the comprehensive classification of BRCA1 and BRCA2 variants of uncertain clinical significance. Npj Genomic Medicine, 2022, 7, .	3.8	4
2	Bridging the gaps: using an NHP model to predict single dose radiation absorption in humans. International Journal of Radiation Biology, 2020, 96, 47-56.	1.8	7
3	A computational model for classification of BRCA2 variants using mouse embryonic stem cell-based functional assays. Npj Genomic Medicine, 2020, 5, 52.	3.8	18
4	Comprehensive annotation of BRCA1 and BRCA2 missense variants by functionally validated sequence-based computational prediction models. Genetics in Medicine, 2019, 21, 71-80.	2.4	52
5	Impact of amino acid substitutions at secondary structures in the BRCT domains of the tumor suppressor BRCA1: Implications for clinical annotation. Journal of Biological Chemistry, 2019, 294, 5980-5992.	3.4	32
6	Assessment of the Clinical Relevance of BRCA2 Missense Variants by Functional and Computational Approaches. American Journal of Human Genetics, 2018, 102, 233-248.	6.2	64
7	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	2.5	9
8	Functional assays provide a robust tool for the clinical annotation of genetic variants of uncertain significance. Npj Genomic Medicine, 2016, 1, .	3.8	70
9	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	1.3	22
10	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44
11	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). Journal of Genetics and Genome Research, 2015, 2, .	0.3	25
12	Erythrocyte folate concentrations, CpG methylation at genomically imprinted domains, and birth weight in a multiethnic newborn cohort. Epigenetics, 2014, 9, 1120-1130.	2.7	73
13	A Computational Method to Classify Variants of Uncertain Significance Using Functional Assay Data with Application to BRCA1. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1078-1088.	2.5	54
14	A Systematic Genetic Assessment of 1,433 Sequence Variants of Unknown Clinical Significance in the BRCA1 and BRCA2 Breast Cancerâ€"Predisposition Genes. American Journal of Human Genetics, 2007, 81, 873-883.	6.2	416
15	Classification of Missense Mutations of Disease Genes. Journal of the American Statistical Association, 2005, 100, 51-60.	3.1	19
16	Population-Calibrated Gene Characterization. Journal of the American Statistical Association, 2005, 100, 399-409.	3.1	16