Pascaline Gaildrat

List of Publications by Year
in descending order

15	959	687363 13	888059 17
papers	citations	h-index	g-index

17	17	17	1962
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Splicing analyses for variants in MMR genes: best practice recommendations from the European Mismatch Repair Working Group. European Journal of Human Genetics, 2022, 30, 1051-1059.	2.8	7
2	Functional characterization of ABCC8 variants of unknown significance based on bioinformatics predictions, splicing assays, and protein analyses: Benefits for the accurate diagnosis of congenital hyperinsulinism. Human Mutation, 2021, 42, 408-420.	2.5	6
3	Calibration of Pathogenicity Due to Variant-Induced Leaky Splicing Defects by Using BRCA2 Exon 3 as a Model System. Cancer Research, 2020, 80, 3593-3605.	0.9	19
4	Largeâ€scale comparative evaluation of userâ€friendly tools for predicting variantâ€induced alterations of splicing regulatory elements. Human Mutation, 2020, 41, 1811-1829.	2.5	29
5	Assessment of branch point prediction tools to predict physiological branch points and their alteration by variants. BMC Genomics, 2020, 21, 86.	2.8	33
6	Skipping Nonsense to Maintain Function: The Paradigm of BRCA2 Exon 12. Cancer Research, 2020, 80, 1374-1386.	0.9	20
7	Novel diagnostic tool for prediction of variant spliceogenicity derived from a set of 395 combined in silico/in vitro studies: an international collaborative effort. Nucleic Acids Research, 2018, 46, 7913-7923.	14.5	71
8	Detecting splicing patterns in genes involved in hereditary breast and ovarian cancer. European Journal of Human Genetics, 2017, 25, 1147-1154.	2.8	76
9	Assessment of the InSiGHT Interpretation Criteria for the Clinical Classification of 24MLH1andMSH2Gene Variants. Human Mutation, 2017, 38, 64-77.	2.5	29
10	Exonic Splicing Mutations Are More Prevalent than Currently Estimated and Can Be Predicted by Using In Silico Tools. PLoS Genetics, 2016, 12, e1005756.	3.5	133
11	UMD-MLH1/MSH2/MSH6 databases: description and analysis of genetic variations in French Lynch syndrome families. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat036-bat036.	3.0	15
12	Functional Analysis of a Large set of BRCA2 exonÂ7 Variants Highlights the Predictive Value of Hexamer Scores in Detecting Alterations of Exonic Splicing Regulatory Elements. Human Mutation, 2013, 34, 1547-1557.	2.5	47
13	Guidelines for splicing analysis in molecular diagnosis derived from a set of 327 combined in silico/in vitro studies on BRCA1 and BRCA2 variants. Human Mutation, 2012, 33, 1228-1238.	2.5	210
14	Contribution of bioinformatics predictions and functional splicing assays to the interpretation of unclassified variants of the BRCA genes. European Journal of Human Genetics, 2011, 19, 1052-1058.	2.8	112
15	Use of Splicing Reporter Minigene Assay to Evaluate the Effect on Splicing of Unclassified Genetic Variants. Methods in Molecular Biology, 2010, 653, 249-257.	0.9	135