REVEL: An Ensemble Method for Predicting the Pathog

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Citation Report

#	Article	IF	Citations
1	Structural, Functional, and Clinical Characterization of a NovelPTPN11Mutation Cluster Underlying Noonan Syndrome. Human Mutation, 2017, 38, 451-459.	1.1	39
2	Sexual dimorphisms in genetic loci linked to body fat distribution. Bioscience Reports, 2017, 37, .	1.1	58
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4	Robust and rapid algorithms facilitate large-scale whole genome sequencing downstream analysis in an integrative framework. Nucleic Acids Research, 2017, 45, gkx019.	6.5	36
5	Missense variant pathogenicity predictors generalize well across a range of functionâ€specific prediction challenges. Human Mutation, 2017, 38, 1092-1108.	1.1	39
6	Identification of 8 Novel Mutations in Nephrogenesis-Related Genes in Chinese Han Patients with Unilateral Renal Agenesis. American Journal of Nephrology, 2017, 46, 55-63.	1.4	11
7	Ensemble variant interpretation methods to predict enzyme activity and assign pathogenicity in the CAGI4 NAGLU (Human Nâ€acetylâ€glucosaminidase) and UBE2I (Human SUMOâ€ligase) challenges. Human Mutation, 2017, 38, 1109-1122.	1.1	14
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13	Higher-than-expected population prevalence of potentially pathogenic germlineTP53variants in individuals unselected for cancer history. Human Mutation, 2017, 38, 1723-1730.	1.1	40
14	Optimizing genomic medicine in epilepsy through a gene-customized approach to missense variant interpretation. Genome Research, 2017, 27, 1715-1729.	2.4	150
15	The prevalence of DICER1 pathogenic variation in population databases. International Journal of Cancer, 2017, 141, 2030-2036.	2.3	75
16	IDUA mutational profile and genotypeâ€“phenotype relationships in UK patients with Mucopolysaccharidosis Type I. Human Mutation, 2017, 38, 1555-1568.	1.1	16
17	Settling the score: variant prioritization and Mendelian disease. Nature Reviews Genetics, 2017, 18, 599-612.	7.7	213
18	Exome Pool-Seq in neurodevelopmental disorders. European Journal of Human Genetics, 2017, 25, 1364-1376.	1.4	77

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20	Loss-of-Function and Gain-of-Function Mutations in KCNQ5 Cause Intellectual Disability or Epileptic Encephalopathy. American Journal of Human Genetics, 2017, 101, 65-74.	2.6	99
21	Patterns of Novel Alleles and Genotype/Phenotype Correlations Resulting from the Analysis of 108 Previously Undetected Mutations in Patients Affected by Neurofibromatosis Type I. International Journal of Molecular Sciences, 2017, 18, 2071.	1.8	11
22	Exome Sequencing Identified a Novel FBN2 Mutation in a Chinese Family with Congenital Contractural Arachnodactyly. International Journal of Molecular Sciences, 2017, 18, 626.	1.8	8
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