Giulia Babbi

List of Publications by Year
in descending order

22 papers	317 citations	1040056 9 h-index	940533 16 g-index
23 all docs	23 docs citations	23 times ranked	772 citing authors

#	Article	IF	Citations
1	eDGAR: a database of Disease-Gene Associations with annotated Relationships among genes. BMC Genomics, 2017, 18, 554.	2.8	52
2	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	2.5	39
3	Large scale analysis of protein stability in OMIM disease related human protein variants. BMC Genomics, 2016, 17, 397.	2.8	37
4	Mutant MYO1F alters the mitochondrial network and induces tumor proliferation in thyroid cancer. International Journal of Cancer, 2018, 143, 1706-1719.	5.1	35
5	Assessment of blind predictions of the clinical significance of BRCA1 and BRCA2 variants. Human Mutation, 2019, 40, 1546-1556.	2.5	19
6	Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4. Human Mutation, 2017, 38, 1123-1131.	2.5	17
7	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. Human Mutation, 2019, 40, 1392-1399.	2.5	16
8	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. Human Mutation, 2019, 40, 1495-1506.	2.5	16
9	Functional and Structural Features of Disease-Related Protein Variants. International Journal of Molecular Sciences, 2019, 20, 1530.	4.1	15
10	CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases. Human Mutation, 2019, 40, 1373-1391.	2.5	10
11	Assessment of predicted enzymatic activity of Î±â€•N â€acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	2.5	10
12	PhenPath: a tool for characterizing biological functions underlying different phenotypes. BMC Genomics, 2019, 20, 548.	2.8	8
13	Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473.	2.5	8
14	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGIâ€5. Human Mutation, 2019, 40, 1474-1485.	2.5	8
15	Assessing the performance of in silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer. Human Mutation, 2019, 40, 1612-1622.	2.5	8
16	Are machine learning based methods suited to address complex biological problems? Lessons from CAGIâ€5 challenges. Human Mutation, 2019, 40, 1455-1462.	2.5	6
17	Mapping OMIM Diseaseâ€“Related Variations on Protein Domains Reveals an Association Among Variation Type, Pfam Models, and Disease Classes. Frontiers in Molecular Biosciences, 2021, 8, 617016.	3.5	5
18	Highlighting Human Enzymes Active in Different Metabolic Pathways and Diseases: The Case Study of EC 1.2.3.1 and EC 2.3.1.9. Biomedicines, 2020, 8, 250.	3.2	3

#	Article	IF	Citations
19	Huntingtin: A Protein with a Peculiar Solvent Accessible Surface. International Journal of Molecular Sciences, 2021, 22, 2878.	4.1	3
20	A Glance into MTHFR Deficiency at a Molecular Level. International Journal of Molecular Sciences, 2022, 23, 167.	4.1	2
21	Cover Image, Volume 38, Issue 9. Human Mutation, 2017, 38, i.	2.5	0
22	Mouse Genomic Associations With ex vivo Sensitivity to Simulated Space Radiation. SSRN Electronic Journal, 0, , .	0.4	0