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	A Glance into MTHFR Deficiency at a Molecular Level. International Journal of Molecular Sciences, 2022, 23, 167.	4.1	2
2	Huntingtin: A Protein with a Peculiar Solvent Accessible Surface. International Journal of Molecular Sciences, 2021, 22, 2878.	4.1	3
3	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
4	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
5	PhenPath: a tool for characterizing biological functions underlying different phenotypes. BMC Genomics, 2019, 20, 548.	2.8	8
6	Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473.	2.5	8
7	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
8	Assessment of blind predictions of the clinical significance of BRCA1 and BRCA2 variants. Human Mutation, 2019, 40, 1546-1556.	2.5	19
9	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
10	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
11	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
12	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
13	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. Human Mutation, 2019, 40, 1495-1506.	2.5	16
14	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
15	Functional and Structural Features of Disease-Related Protein Variants. International Journal of Molecular Sciences, 2019, 20, 1530.	4.1	15
16	Mutant MYO1F alters the mitochondrial network and induces tumor proliferation in thyroid cancer. International Journal of Cancer, 2018, 143, 1706-1719.	5.1	35
17	Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4. Human Mutation, 2017, 38, 1123-1131.	2.5	17
18	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

#	Article	IF	Citations
19	Cover Image, Volume 38, Issue 9. Human Mutation, 2017, 38, i.	2.5	0
20	eDGAR: a database of Disease-Gene Associations with annotated Relationships among genes. BMC Genomics, 2017, 18, 554.	2.8	52
21	Large scale analysis of protein stability in OMIM disease related human protein variants. BMC Genomics, 2016, 17, 397.	2.8	37
22	Mouse Genomic Associations With ex vivo Sensitivity to Simulated Space Radiation. SSRN Electronic Journal, 0, , .	0.4	0