Lipika R Pal

List of Publications by Year
in descending order

34 papers	664 citations	687363 13 h-index	642732 23 g-index
40 all docs	40 docs citations	40 times ranked	1242 citing authors

#	Article	IF	Citations
1	Synthetic lethality-based prediction of anti-SARS-CoV-2 targets. IScience, 2022, 25, 104311.	4.1	7
2	Genomeâ€scale metabolic modeling reveals SARSâ€CoVâ€2â€induced metabolic changes and antiviral targets. Molecular Systems Biology, 2021, 17, e10260.	7.2	26
3	Matching whole genomes to rare genetic disorders: Identification of potential causative variants using phenotypeâ€weighted knowledge in the CAGI SickKids5 clinical genomes challenge. Human Mutation, 2020, 41, 347-362.	2.5	4
4	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
5	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	2.5	5
6	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
7	Back Cover, Volume 40, Issue 9. Human Mutation, 2019, 40, ii.	2.5	0
8	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
9	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. Human Mutation, 2019, 40, 1495-1506.	2.5	16
10	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	2.5	10
11	Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAGIâ€5 intellectual disability challenge. Human Mutation, 2019, 40, 1330-1345.	2.5	11
12	Harnessing formal concepts of biological mechanism to analyze human disease. PLoS Computational Biology, 2018, 14, e1006540.	3.2	14
13	The Product Guides the Process: Discovering Disease Mechanisms. Studies in Applied Philosophy, Epistemology and Rational Ethics, 2018, , 101-117.	0.3	4
14	Determination of disease phenotypes and pathogenic variants from exome sequence data in the CAGI 4 gene panel challenge. Human Mutation, 2017, 38, 1201-1216.	2.5	5
15	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	2.5	13
16	CAGI4 SickKids clinical genomes challenge: A pipeline for identifying pathogenic variants. Human Mutation, 2017, 38, 1169-1181.	2.5	11
17	CAGI4 Crohn's exome challenge: Marker SNP versus exome variant models for assigning risk of Crohn disease. Human Mutation, 2017, 38, 1225-1234.	2.5	15
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	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.	2.5	14
20	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. Human Mutation, 2017, 38, 1266-1276.	2.5	14
21	Reply to HU et al.: On the interpretation of gasdermin-B expression quantitative trait loci data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7863-E7864.	7.1	0
22	Lessons from the CAGIâ€4 Hopkins clinical panel challenge. Human Mutation, 2017, 38, 1155-1168.	2.5	6
23	Consensus Genome-Wide Expression Quantitative Trait Loci and Their Relationship with Human Complex Trait Disease. OMICS A Journal of Integrative Biology, 2016, 20, 400-414.	2.0	46
24	Insights from GWAS: emerging landscape of mechanisms underlying complex trait disease. BMC Genomics, 2015, 16, S4.	2.8	16
25	Genetic Basis of Common Human Disease: Insight into the Role of Missense SNPs from Genome-Wide Association Studies. Journal of Molecular Biology, 2015, 427, 2271-2289.	4.2	44
26	Protein Characterization of a Candidate Mechanism SNP for Crohn's Disease: The Macrophage Stimulating Protein R689C Substitution. PLoS ONE, 2011, 6, e27269.	2.5	24
27	A Top-Down Approach to Infer and Compare Domain-Domain Interactions across Eight Model Organisms. PLoS ONE, 2009, 4, e5096.	2.5	13
28	Structural Insights into the Substrate Binding and Stereoselectivity of Giardia Fructose-1,6-bisphosphate Aldolase[,]. Biochemistry, 2009, 48, 3186-3196.	2.5	30
29	Tracing the origin of functional and conserved domains in the human proteome: implications for protein evolution at the modular level. BMC Evolutionary Biology, 2006, 6, 91.	3.2	12
30	DMAPS: a database of multiple alignments for protein structures. Nucleic Acids Research, 2006, 34, D273-D276.	14.5	6
31	310-Helix adjoining Î±-helix and Î²-strand: Sequence and structural features and their conservation. Biopolymers, 2005, 78, 147-162.	2.4	25
32	Expanded turn conformations: Characterization and sequence-structure correspondence in Î±-turns with implications in helix folding. Proteins: Structure, Function and Bioinformatics, 2004, 55, 305-315.	2.6	39
33	Sequence and Structure Patterns in Proteins from an Analysis of the Shortest Helices: Implications for Helix Nucleation. Journal of Molecular Biology, 2003, 326, 273-291.	4.2	71
34	Variants of 310-helices in proteins. Proteins: Structure, Function and Bioinformatics, 2002, 48, 571-579.	2.6	42