Lipika R Pal

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4018937/publications.pdf

Version: 2024-02-01

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	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
2	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
3	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
4	Variants of 310-helices in proteins. Proteins: Structure, Function and Bioinformatics, 2002, 48, 571-579.	2.6	42
5	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
6	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
7	Structural Insights into the Substrate Binding and Stereoselectivity of Giardia Fructose-1,6-bisphosphate Aldolase[,]. Biochemistry, 2009, 48, 3186-3196.	2.5	30
8	Genomeâ€scale metabolic modeling reveals SARSâ€CoVâ€2â€induced metabolic changes and antiviral targets. Molecular Systems Biology, 2021, 17, e10260.	7.2	26
9	310-Helix adjoining Î±-helix and Î²-strand: Sequence and structural features and their conservation. Biopolymers, 2005, 78, 147-162.	2.4	25
10	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
11	Insights from GWAS: emerging landscape of mechanisms underlying complex trait disease. BMC Genomics, 2015, 16, S4.	2.8	16
12	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. Human Mutation, 2019, 40, 1495-1506.	2.5	16
13	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
14	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
15	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
16	Harnessing formal concepts of biological mechanism to analyze human disease. PLoS Computational Biology, 2018, 14, e1006540.	3.2	14
17	A Top-Down Approach to Infer and Compare Domain-Domain Interactions across Eight Model Organisms. PLoS ONE, 2009, 4, e5096.	2.5	13
18	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	2.5	13

#	Article	IF	Citations
19	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
20	CAGI4 SickKids clinical genomes challenge: A pipeline for identifying pathogenic variants. Human Mutation, 2017, 38, 1169-1181.	2.5	11
21	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
22	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
23	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
24	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	2.5	10
25	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
26	Synthetic lethality-based prediction of anti-SARS-CoV-2 targets. IScience, 2022, 25, 104311.	4.1	7
27	DMAPS: a database of multiple alignments for protein structures. Nucleic Acids Research, 2006, 34, D273-D276.	14.5	6
28	Lessons from the CAGIâ€4 Hopkins clinical panel challenge. Human Mutation, 2017, 38, 1155-1168.	2.5	6
29	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
30	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	2.5	5
31	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
32	The Product Guides the Process: Discovering Disease Mechanisms. Studies in Applied Philosophy, Epistemology and Rational Ethics, 2018, , 101-117.	0.3	4
33	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
34	Back Cover, Volume 40, Issue 9. Human Mutation, 2019, 40, ii.	2.5	0