

Ogun Adebali

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

1,217
citations

567281

15
h-index

580821

25
g-index

36
all docs

36
docs citations

36
times ranked

1562
citing authors

#	ARTICLE	IF	CITATIONS
1	Cache Domains That are Homologous to, but Different from PAS Domains Comprise the Largest Superfamily of Extracellular Sensors in Prokaryotes. <i>PLoS Computational Biology</i> , 2016, 12, e1004862.	3.2	147
2	Dynamic maps of UV damage formation and repair for the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6758-6763.	7.1	131
3	Differential damage and repair of DNA-adducts induced by anti-cancer drug cisplatin across mouse organs. <i>Nature Communications</i> , 2019, 10, 309.	12.8	131
4	MiST 3.0: an updated microbial signal transduction database with an emphasis on chemosensory systems. <i>Nucleic Acids Research</i> , 2020, 48, D459-D464.	14.5	129
5	Human genome-wide repair map of DNA damage caused by the cigarette smoke carcinogen benzo[a]pyrene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6752-6757.	7.1	76
6	Genome-wide transcription-coupled repair in <i>Escherichia coli</i> is mediated by the Mfd translocase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2116-E2125.	7.1	71
7	CDvist: a webserver for identification and visualization of conserved domains in protein sequences. <i>Bioinformatics</i> , 2015, 31, 1475-1477.	4.1	69
8	Cisplatin-DNA adduct repair of transcribed genes is controlled by two circadian programs in mouse tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4777-E4785.	7.1	65
9	Molecular mechanisms and genomic maps of DNA excision repair in <i>Escherichia coli</i> and humans. <i>Journal of Biological Chemistry</i> , 2017, 292, 15588-15597.	3.4	64
10	Genome-wide mapping of nucleotide excision repair with XR-seq. <i>Nature Protocols</i> , 2019, 14, 248-282.	12.0	48
11	Genome-wide excision repair in <i>Arabidopsis</i> is coupled to transcription and reflects circadian gene expression patterns. <i>Nature Communications</i> , 2018, 9, 1503.	12.8	43
12	Mfd translocase is necessary and sufficient for transcription-coupled repair in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 18386-18391.	3.4	39
13	Single-nucleotide resolution dynamic repair maps of UV damage in <i>Saccharomyces cerevisiae</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3408-E3415.	7.1	36
14	Establishing the precise evolutionary history of a gene improves prediction of disease-causing missense mutations. <i>Genetics in Medicine</i> , 2016, 18, 1029-1036.	2.4	31
15	The Mutation Profile of SARS-CoV-2 Is Primarily Shaped by the Host Antiviral Defense. <i>Viruses</i> , 2021, 13, 394.	3.3	30
16	Phylogenetic analysis of SARS-CoV-2 genomes in Turkey. <i>Turkish Journal of Biology</i> , 2020, 44, 146-156.	0.8	17
17	Nucleotide excision repair capacity increases during differentiation of human embryonic carcinoma cells into neurons and muscle cells. <i>Journal of Biological Chemistry</i> , 2019, 294, 5914-5922.	3.4	16
18	Class III Histidine Kinases: a Recently Accessorized Kinase Domain in Putative Modulators of Type IV Pilus-Based Motility. <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	14

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19	Aquerium: A web application for comparative exploration of domain-based protein occurrences on the taxonomically clustered genome tree. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 72-77.	2.6	14
20	SURF1 related Leigh syndrome: Clinical and molecular findings of 16 patients from Turkey. <i>Molecular Genetics and Metabolism Reports</i> , 2020, 25, 100657.	1.1	10
21	The utility of next-generation sequencing technologies in diagnosis of Mendelian mitochondrial diseases and reflections on clinical spectrum. <i>Journal of Pediatric Endocrinology and Metabolism</i> , 2021, 34, 417-430.	0.9	8
22	Comparative analyses of two primate species diverged by more than 60 million years show different rates but similar distribution of genome-wide UV repair events. <i>BMC Genomics</i> , 2021, 22, 600.	2.8	5
23	CSB-independent, XPC-dependent transcription-coupled repair in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	5
24	Evolutionary association of receptor-wide amino acids with G protein-coupling selectivity in aminergic GPCRs. <i>Life Science Alliance</i> , 2022, 5, e202201439.	2.8	4
25	Genome-wide Excision Repair Map of Cyclobutane Pyrimidine Dimers in <i>Arabidopsis</i> and the Roles of CSA1 and CSA2 Proteins in Transcription-coupled Repair. <i>Photochemistry and Photobiology</i> , 2022, 98, 707-712.	2.5	3
26	PHACT: Phylogeny-Aware Computing of Tolerance for Missense Mutations. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	3
27	Phylostat: A Web-based Tool to Analyze Paralogous Clade Divergence in Phylogenetic Trees. <i>Turkish Journal of Biology</i> , 2021, 45, 667-673.	0.8	0
28	High-resolution Maps of Genome-wide Human Damage and Repair. <i>FASEB Journal</i> , 2018, 32, 647.3.	0.5	0
29	Molecular Biology of SARS-CoV-2. <i>Turkish Journal of Immunology</i> , 2020, 8, 73-88.	0.1	0