

Osman UÄur Sezerman

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

1,002
citations

516215

16
h-index

500791

28
g-index

58
all docs

58
docs citations

58
times ranked

1715
citing authors

#	ARTICLE	IF	CITATIONS
1	A splice site mutation in the <i>TSEN2</i> causes a new syndrome with craniofacial and central nervous system malformations, and atypical hemolytic uremic syndrome. <i>Clinical Genetics</i> , 2022, 101, 346-358.	1.0	4
2	Structural analysis of <i>M1AP</i> variants associated with severely impaired spermatogenesis causing male infertility. <i>PeerJ</i> , 2022, 10, e12947.	0.9	1
3	Is cutaneous microbiota a player in disease pathogenesis? Comparison of cutaneous microbiota in psoriasis and seborrheic dermatitis with scalp involvement. <i>Indian Journal of Dermatology, Venereology and Leprology</i> , 2022, 88, 738-748.	0.2	4
4	Understanding the Role of the Microbiome in Cancer Diagnostics and Therapeutics by Creating and Utilizing ML Models. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 4094.	1.3	2
5	Computational analysis of missense filamin-A variants, including the novel p.Arg484Gln variant of two brothers with periventricular nodular heterotopia. <i>PLoS ONE</i> , 2022, 17, e0265400.	1.1	0
6	Integrated bioinformatics analysis of validated and circulating miRNAs in ovarian cancer. <i>Genomics and Informatics</i> , 2022, 20, e20.	0.4	4
7	A comprehensive study on identifying the structural and functional SNPs of human neuronal membrane glycoprotein M6A (GPM6A). <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 2693-2701.	2.0	8
8	CogNet: classification of gene expression data based on ranked active-subnetwork-oriented KEGG pathway enrichment analysis. <i>PeerJ Computer Science</i> , 2021, 7, e336.	2.7	24
9	A recursive molecular docking coupled with energy-based pose-rescoring and MD simulations to identify hsGC ¹² H-NOX allosteric modulators for cardiovascular dysfunctions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-23.	2.0	1
10	Identifying and elucidating the roles of Y198N and Y204F mutations in the PAH enzyme through molecular dynamic simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-12.	2.0	3
11	Re-analysis of whole-exome sequencing data reveals a novel splicing variant in the <i>SLC2A1</i> in a patient with GLUT1 Deficiency Syndrome 1 accompanied by hemangioma: a case report. <i>BMC Medical Genomics</i> , 2021, 14, 197.	0.7	1
12	Bridging the Bridging Imidazolate in the Bimetallic Center of the Cu/Zn SOD1 and ALS. <i>Frontiers in Chemistry</i> , 2021, 9, 716438.	1.8	5
13	SARS-CoV-2 isolation and propagation from Turkish COVID-19 patients. <i>Turkish Journal of Biology</i> , 2020, 44, 192-202.	2.1	19
14	Probing the Structural Dynamics of the Catalytic Domain of Human Soluble Guanylate Cyclase. <i>Scientific Reports</i> , 2020, 10, 9488.	1.6	4
15	Understanding thermal and organic solvent stability of thermoalkalophilic lipases: insights from computational predictions and experiments. <i>Journal of Molecular Modeling</i> , 2020, 26, 122.	0.8	15
16	High-throughput profiling reveals perturbation of endoplasmic reticulum stress-related genes in atherosclerosis induced by high-cholesterol diet and the protective role of vitamin E. <i>BioFactors</i> , 2020, 46, 653-664.	2.6	7
17	Adaptive phenotypic modulations lead to therapy resistance in chronic myeloid leukemia cells. <i>PLoS ONE</i> , 2020, 15, e0229104.	1.1	21
18	pathfindR: An R Package for Comprehensive Identification of Enriched Pathways in Omics Data Through Active Subnetworks. <i>Frontiers in Genetics</i> , 2019, 10, 858.	1.1	247

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19	Enhancing Enzymatic Properties of Endoglucanase I Enzyme from <i>Trichoderma Reesei</i> via Swapping from Cellobiohydrolase I Enzyme. <i>Catalysts</i> , 2019, 9, 130.	1.6	4
20	Identification of epilepsy related pathways using genome-wide DNA methylation measures: A trio-based approach. <i>PLoS ONE</i> , 2019, 14, e0211917.	1.1	6
21	Comparison of Dendritic Cell Activation by Virus-Based Vaccine Delivery Vectors Emphasizes the Transcriptional Downregulation of the Oxidative Phosphorylation Pathway. <i>Human Gene Therapy</i> , 2019, 30, 429-445.	1.4	2
22	Thermostability of the PYL-PP2C Heterodimer Is Dependent on Magnesium: <i>In Silico</i> Insights into the Link between Heat Stress Response and Magnesium Deficiency in Plants. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 661-672.	2.5	6
23	Prediction of HIV Drug Resistance by Combining Sequence and Structural Properties. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 966-973.	1.9	19
24	Computational drug repurposing to predict approved and novel drug-disease associations. <i>Journal of Molecular Graphics and Modelling</i> , 2018, 85, 91-96.	1.3	14
25	Investigating the structural properties of the active conformation BTL2 of a lipase from <i>Geobacillus thermocatenulatus</i> in toluene using molecular dynamic simulations and engineering BTL2 via in-silico mutation. <i>Journal of Molecular Modeling</i> , 2018, 24, 229.	0.8	10
26	Ligand binding pocket of a novel Allatostatin receptor type C of stick insect, <i>Carausius morosus</i> . <i>Scientific Reports</i> , 2017, 7, 41266.	1.6	6
27	Computational approaches for <i>de novo</i> design and redesign of metal-binding sites on proteins. <i>Bioscience Reports</i> , 2017, 37, .	1.1	33
28	ZK DrugResist 2.0: A TextMiner to extract semantic relations of drug resistance from PubMed. <i>Journal of Biomedical Informatics</i> , 2017, 69, 93-98.	2.5	8
29	Analysis of the interplay between methylation and expression reveals its potential role in cancer aetiology. <i>Functional and Integrative Genomics</i> , 2017, 17, 53-68.	1.4	14
30	Active Subnetwork GA: A Two Stage Genetic Algorithm Approach to Active Subnetwork Search. <i>Current Bioinformatics</i> , 2017, 12, .	0.7	13
31	RACK1 Is an Interaction Partner of ATG5 and a Novel Regulator of Autophagy. <i>Journal of Biological Chemistry</i> , 2016, 291, 16753-16765.	1.6	48
32	Systems Biological Applications for Fungal Gene Expression. <i>Fungal Biology</i> , 2016, , 385-393.	0.3	1
33	Design and characterizations of two novel cellulases through single-gene shuffling of Cel12A (EG3) gene from <i>Trichoderma reesei</i> . <i>Protein Engineering, Design and Selection</i> , 2016, 29, 219-229.	1.0	7
34	Probing the roles of two tryptophans surrounding the unique zinc coordination site in lipase family I.5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 129-142.	1.5	9
35	A novel analysis strategy for integrating methylation and expression data reveals core pathways for thyroid cancer aetiology. <i>BMC Genomics</i> , 2015, 16, S7.	1.2	3
36	Prediction of neddylation sites from protein sequences and sequence-derived properties. <i>BMC Bioinformatics</i> , 2015, 16, S9.	1.2	15

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37	Molecular diversity of LysM carbohydrate-binding motifs in fungi. <i>Current Genetics</i> , 2015, 61, 103-113.	0.8	121
38	Reply to Stoimenis et al. <i>European Journal of Human Genetics</i> , 2015, 23, 1280-1280.	1.4	0
39	Assessment of global and gene-specific DNA methylation in rat liver and kidney in response to non-genotoxic carcinogen exposure. <i>Toxicology and Applied Pharmacology</i> , 2015, 289, 203-212.	1.3	29
40	PANOGA: a web server for identification of SNP-targeted pathways from genome-wide association study data. <i>Bioinformatics</i> , 2014, 30, 1287-1289.	1.8	36
41	Predicting sumoylation sites using support vector machines based on various sequence features, conformational flexibility and disorder. <i>BMC Genomics</i> , 2014, 15, S18.	1.2	16
42	Prediction of peptides binding to MHC class I and II alleles by temporal motif mining. <i>BMC Bioinformatics</i> , 2013, 14, S13.	1.2	27
43	A genetic algorithm approach to active subnetwork search applied to GWAS data. , 2013, , .		0
44	The Identification of Pathway Markers in Intracranial Aneurysm Using Genome-Wide Association Data from Two Different Populations. <i>PLoS ONE</i> , 2013, 8, e57022.	1.1	21
45	MIR376A Is a Regulator of Starvation-Induced Autophagy. <i>PLoS ONE</i> , 2013, 8, e82556.	1.1	45
46	Representation of Protein Secondary Structure Using Bond-Orientational Order Parameters. <i>Lecture Notes in Computer Science</i> , 2012, , 188-197.	1.0	1
47	A New Methodology to Associate SNPs with Human Diseases According to Their Pathway Related Context. <i>PLoS ONE</i> , 2011, 6, e26277.	1.1	52
48	APPLICATION OF AUTOMATIC MUTATIONâ€“GENE PAIR EXTRACTION TO DISEASES. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 1261-1275.	0.3	29
49	Bioinformatics Workflows for Genomic Variant Discovery, Interpretation and Prioritization. , 0, , .		3
50	Investigation of multiple sclerosis-related pathways through the integration of genomic and proteomic data. <i>PeerJ</i> , 0, 9, e11922.	0.9	0
51	Identification of SNP Targeted Pathways From Genome-wide Association Study (GWAS) Data. <i>Protocol Exchange</i> , 0, , .	0.3	7