Osman UÄŸr Sezerman

List of Publications by Year
in descending order

51 papers	1,002 citations	516710 16 h-index	501196 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 <scp><i>TSEN2</i></scp> causes a new syndrome with craniofacial and central nervous system malformations, and atypical hemolytic uremic syndrome. Clinical Genetics, 2022, 101, 346-358.	2.0	4
2	Structural analysis of <i>M1AP</i> variants associated with severely impaired spermatogenesis causing male infertility. PeerJ, 2022, 10, e12947.	2.0	1
3	Is cutaneous microbiota a player in disease pathogenesis? Comparison of cutaneous microbiota in psoriasis and seborrheic dermatitis with scalp involvement. Indian Journal of Dermatology, Venereology and Leprology, 2022, 88, 738-748.	0.6	4
4	Understanding the Role of the Microbiome in Cancer Diagnostics and Therapeutics by Creating and Utilizing ML Models. Applied Sciences (Switzerland), 2022, 12, 4094.	2.5	2
5	Computational analysis of missense filamin-A variants, including the novel p.Arg484Gln variant of two brothers with periventricular nodular heterotopia. PLoS ONE, 2022, 17, e0265400.	2.5	0
6	Integrated bioinformatics analysis of validated and circulating miRNAs in ovarian cancer. Genomics and Informatics, 2022, 20, e20.	0.8	4
7	A comprehensive study on identifying the structural and functional SNPs of human neuronal membrane glycoprotein M6A (GPM6A). Journal of Biomolecular Structure and Dynamics, 2021, 39, 2693-2701.	3.5	8
8	CogNet: classification of gene expression data based on ranked active-subnetwork-oriented KEGG pathway enrichment analysis. PeerJ Computer Science, 2021, 7, e336.	4.5	24
9	A recursive molecular docking coupled with energy-based pose-rescoring and MD simulations to identify hsGC Î²H-NOX allosteric modulators for cardiovascular dysfunctions. Journal of Biomolecular Structure and Dynamics, 2021, , 1-23.	3.5	1
10	Identifying and elucidating the roles of Y198N and Y204F mutations in the PAH enzyme through molecular dynamic simulations. Journal of Biomolecular Structure and Dynamics, 2021, , 1-12.	3.5	3
11	Re-analysis of whole-exome sequencing data reveals a novel splicing variant in the SLC2A1 in a patient with GLUT1 Deficiency Syndrome 1 accompanied by hemangioma: a case report. BMC Medical Genomics, 2021, 14, 197.	1.5	1
12	Bridging the Bridging Imidazolate in the Bimetallic Center of the Cu/Zn SOD1 and ALS. Frontiers in Chemistry, 2021, 9, 716438.	3.6	5
13	SARS-CoV-2 isolation and propagation from Turkish COVID-19 patients. Turkish Journal of Biology, 2020, 44, 192-202.	0.8	19
14	Probing the Structural Dynamics of the Catalytic Domain of Human Soluble Guanylate Cyclase. Scientific Reports, 2020, 10, 9488.	3.3	4
15	Understanding thermal and organic solvent stability of thermoalkalophilic lipases: insights from computational predictions and experiments. Journal of Molecular Modeling, 2020, 26, 122.	1.8	15
16	Highâ€throughput profiling reveals perturbation of endoplasmic reticulum stressâ€related genes in atherosclerosis induced by highâ€cholesterol diet and the protective role of vitamin E. BioFactors, 2020, 46, 653-664.	5.4	7
17	Adaptive phenotypic modulations lead to therapy resistance in chronic myeloid leukemia cells. PLoS ONE, 2020, 15, e0229104.	2.5	21
18	pathfindR: An R Package for Comprehensive Identification of Enriched Pathways in Omics Data Through Active Subnetworks. Frontiers in Genetics, 2019, 10, 858.	2.3	247

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19	Enhancing Enzymatic Properties of Endoglucanase I Enzyme from Trichoderma Reesei via Swapping from Cellobiohydrolase I Enzyme. Catalysts, 2019, 9, 130.	3.5	4
20	Identification of epilepsy related pathways using genome-wide DNA methylation measures: A trio-based approach. PLoS ONE, 2019, 14, e0211917.	2.5	6
21	Comparison of Dendritic Cell Activation by Virus-Based Vaccine Delivery Vectors Emphasizes the Transcriptional Downregulation of the Oxidative Phosphorylation Pathway. Human Gene Therapy, 2019, 30, 429-445.	2.7	2
22	Thermostability of the PYLâ€"PP2C Heterodimer Is Dependent on Magnesium: *In Silico* Insights into the Link between Heat Stress Response and Magnesium Deficiency in Plants. Journal of Chemical Information and Modeling, 2018, 58, 661-672.	5.4	6
23	Prediction of HIV Drug Resistance by Combining Sequence and Structural Properties. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 966-973.	3.0	19
24	Computational drug repurposing to predict approved and novel drug-disease associations. Journal of Molecular Graphics and Modelling, 2018, 85, 91-96.	2.4	14
25	Investigating the structural properties of the active conformation BTL2 of a lipase from Geobacillus thermocatenulatus in toluene using molecular dynamic simulations and engineering BTL2 via in-silico mutation. Journal of Molecular Modeling, 2018, 24, 229.	1.8	10
26	Ligand binding pocket of a novel Allatostatin receptor type C of stick insect, Carausius morosus. Scientific Reports, 2017, 7, 41266.	3.3	6
27	Computational approaches for *de novo* design and redesign of metal-binding sites on proteins. Bioscience Reports, 2017, 37, .	2.4	33
28	ZK DrugResist 2.0: A TextMiner to extract semantic relations of drug resistance from PubMed. Journal of Biomedical Informatics, 2017, 69, 93-98.	4.3	8
29	Analysis of the interplay between methylation and expression reveals its potential role in cancer aetiology. Functional and Integrative Genomics, 2017, 17, 53-68.	3.5	14
30	Active Subnetwork GA: A Two Stage Genetic Algorithm Approach to Active Subnetwork Search. Current Bioinformatics, 2017, 12, .	1.5	13
31	RACK1 Is an Interaction Partner of ATG5 and a Novel Regulator of Autophagy. Journal of Biological Chemistry, 2016, 291, 16753-16765.	3.4	48
32	Systems Biological Applications for Fungal Gene Expression. Fungal Biology, 2016, , 385-393.	0.6	1
33	Design and characterizations of two novel cellulases through single-gene shuffling of Cel12A (EG3) gene from *Trichoderma reseei*. Protein Engineering, Design and Selection, 2016, 29, 219-229.	2.1	7
34	Probing the roles of two tryptophans surrounding the unique zinc coordination site in lipase family I.5. Proteins: Structure, Function and Bioinformatics, 2016, 84, 129-142.	2.6	9
35	A novel analysis strategy for integrating methylation and expression data reveals core pathways for thyroid cancer aetiology. BMC Genomics, 2015, 16, S7.	2.8	3
36	Prediction of neddylation sites from protein sequences and sequence-derived properties. BMC Bioinformatics, 2015, 16, S9.	2.6	15

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37	Molecular diversity of LysM carbohydrate-binding motifs in fungi. Current Genetics, 2015, 61, 103-113.	1.7	121
38	Reply to Stoimenis et al. European Journal of Human Genetics, 2015, 23, 1280-1280.	2.8	0
39	Assessment of global and gene-specific DNA methylation in rat liver and kidney in response to non-genotoxic carcinogen exposure. Toxicology and Applied Pharmacology, 2015, 289, 203-212.	2.8	29
40	PANOGA: a web server for identification of SNP-targeted pathways from genome-wide association study data. Bioinformatics, 2014, 30, 1287-1289.	4.1	36
41	Predicting sumoylation sites using support vector machines based on various sequence features, conformational flexibility and disorder. BMC Genomics, 2014, 15, S18.	2.8	16
42	Prediction of peptides binding to MHC class I and II alleles by temporal motif mining. BMC Bioinformatics, 2013, 14, S13.	2.6	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. PLoS ONE, 2013, 8, e57022.	2.5	21
45	MIR376A Is a Regulator of Starvation-Induced Autophagy. PLoS ONE, 2013, 8, e82556.	2.5	45
46	Representation of Protein Secondary Structure Using Bond-Orientational Order Parameters. Lecture Notes in Computer Science, 2012, , 188-197.	1.3	1
47	A New Methodology to Associate SNPs with Human Diseases According to Their Pathway Related Context. PLoS ONE, 2011, 6, e26277.	2.5	52
48	APPLICATION OF AUTOMATIC MUTATIONâ€"GENE PAIR EXTRACTION TO DISEASES. Journal of Bioinformatics and Computational Biology, 2007, 05, 1261-1275.	0.8	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. PeerJ, 0, 9, e11922.	2.0	0
51	Identification of SNP Targeted Pathways From Genome-wide Association Study (GWAS) Data. Protocol Exchange, 0, , .	0.3	7