

Emre Guney

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

2,567
citations

331670
21
h-index

289244
40
g-index

56
all docs

56
docs citations

56
times ranked

4466
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcription Factor NRF2 as a Therapeutic Target for Chronic Diseases: A Systems Medicine Approach. <i>Pharmacological Reviews</i> , 2018, 70, 348-383.	16.0	441
2	Network-based in silico drug efficacy screening. <i>Nature Communications</i> , 2016, 7, 10331.	12.8	394
3	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019, 10, 2674.	12.8	240
4	Sex and gender differences and biases in artificial intelligence for biomedicine and healthcare. <i>Npj Digital Medicine</i> , 2020, 3, 81.	10.9	225
5	From single drug targets to synergistic network pharmacology in ischemic stroke. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7129-7136.	7.1	132
6	Architectures and Functional Coverage of Protein-Protein Interfaces. <i>Journal of Molecular Biology</i> , 2008, 381, 785-802.	4.2	106
7	HotSpring: database of computational hot spots in protein interfaces. <i>Nucleic Acids Research</i> , 2007, 36, D662-D666.	14.5	102
8	Tissue Specificity of Human Disease Module. <i>Scientific Reports</i> , 2016, 6, 35241.	3.3	99
9	Exploiting Protein-Protein Interaction Networks for Genome-Wide Disease-Gene Prioritization. <i>PLoS ONE</i> , 2012, 7, e43557.	2.5	87
10	Biana: a software framework for compiling biological interactions and analyzing networks. <i>BMC Bioinformatics</i> , 2010, 11, 56.	2.6	85
11	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. <i>Nature Communications</i> , 2016, 7, 12460.	12.8	73
12	Integrating personalized gene expression profiles into predictive disease-associated gene pools. <i>Npj Systems Biology and Applications</i> , 2017, 3, 10.	3.0	54
13	A diseasome cluster-based drug repurposing of soluble guanylate cyclase activators from smooth muscle relaxation to direct neuroprotection. <i>Npj Systems Biology and Applications</i> , 2018, 4, 8.	3.0	45
14	Integrating Structure to Protein-Protein Interaction Networks That Drive Metastasis to Brain and Lung in Breast Cancer. <i>PLoS ONE</i> , 2013, 8, e81035.	2.5	38
15	GUILDify: a web server for phenotypic characterization of genes through biological data integration and network-based prioritization algorithms. <i>Bioinformatics</i> , 2014, 30, 1789-1790.	4.1	36
16	FN14 and GRP94 expression are prognostic/predictive biomarkers of brain metastasis outcome that open up new therapeutic strategies. <i>Oncotarget</i> , 2015, 6, 44254-44273.	1.8	35
17	iFrag: A Protein-Protein Interface Prediction Server Based on Sequence Fragments. <i>Journal of Molecular Biology</i> , 2017, 429, 382-389.	4.2	33
18	A Transcriptome-proteome Integrated Network Identifies Endoplasmic Reticulum thiol oxidoreductase (ERp57) as a Hub that Mediates Bone Metastasis. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2111-2125.	3.8	32

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19	Proximal Pathway Enrichment Analysis for Targeting Comorbid Diseases via Network Endopharmacology. <i>Pharmaceuticals</i> , 2018, 11, 61.	3.8	32
20	GUILDify v2.0: A Tool to Identify Molecular Networks Underlying Human Diseases, Their Comorbidities and Their Druggable Targets. <i>Journal of Molecular Biology</i> , 2019, 431, 2477-2484.	4.2	32
21	Genetic and functional characterization of disease associations explains comorbidity. <i>Scientific Reports</i> , 2017, 7, 6207.	3.3	28
22	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype. <i>PLoS Biology</i> , 2020, 18, e3000885.	5.6	23
23	Networks of Protein-Protein Interactions: From Uncertainty to Molecular Details. <i>Molecular Informatics</i> , 2012, 31, 342-362.	2.5	22
24	Thrombin stimulates insulin secretion via protease-activated receptor-3. <i>Islets</i> , 2015, 7, e1118195.	1.8	20
25	REPRODUCIBLE DRUG REPURPOSING: WHEN SIMILARITY DOES NOT SUFFICE. , 2017, 22, 132-143.		18
26	Network, Transcriptomic and Genomic Features Differentiate Genes Relevant for Drug Response. <i>Frontiers in Genetics</i> , 2018, 9, 412.	2.3	18
27	The eTRANSafe Project on Translational Safety Assessment through Integrative Knowledge Management: Achievements and Perspectives. <i>Pharmaceuticals</i> , 2021, 14, 237.	3.8	17
28	The human hepatocyte TXG-MAPr: gene co-expression network modules to support mechanism-based risk assessment. <i>Archives of Toxicology</i> , 2021, 95, 3745-3775.	4.2	16
29	Î ⁹ -tetrahydrocannabinol modulates the proteasome system in the brain. <i>Biochemical Pharmacology</i> , 2018, 157, 159-168.	4.4	11
30	An ensemble learning approach for modeling the systems biology of drug-induced injury. <i>Biology Direct</i> , 2021, 16, 5.	4.6	11
31	Analysis of the Robustness of Network-Based Disease-Gene Prioritization Methods Reveals Redundancy in the Human Interactome and Functional Diversity of Disease-Genes. <i>PLoS ONE</i> , 2014, 9, e94686.	2.5	11
32	Revisiting Cross-Validation of Drug Similarity Based Classifiers Using Paired Data. <i>Genomics and Computational Biology</i> , 2017, 4, 100047.	0.7	10
33	Galaxy InteractOMIX: An Integrated Computational Platform for the Study of Protein-Protein Interaction Data. <i>Journal of Molecular Biology</i> , 2021, 433, 166656.	4.2	9
34	Investigating Side Effect Modules in the Interactome and Their Use in Drug Adverse Effect Discovery. <i>Springer Proceedings in Complexity</i> , 2017, , 239-250.	0.3	6
35	Toward PWAS: discovering pathways associated with human disorders. <i>BMC Bioinformatics</i> , 2011, 12, .	2.6	5
36	Extending Signaling Pathways with Protein-Protein Interaction Networks. Application to Apoptosis. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 245-256.	2.0	5

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37	Heterogeneity in Fragile X Syndrome Highlights the Need for Precision Medicine-Based Treatments. Frontiers in Psychiatry, 2021, 12, 722378.	2.6	4
38	The ISCB Student Council Internship Program: Expanding computational biology capacity worldwide. PLoS Computational Biology, 2018, 14, e1005802.	3.2	4
39	Understanding Cancer Progression Using Protein Interaction Networks. , 2012, , 167-195.		1
40	A systems biology approach to cGMP suggests a prominent role for sGC in stroke: Validation by mechanism-based activation of apo-sGC in non-steal dosing conveys neuroprotection and increased survival. BMC Pharmacology & Toxicology, 2015, 16, .	2.4	1
41	A needle for Alzheimerâ€™s in a haystack of claims data. Nature Aging, 2021, 1, 1083-1085.	11.6	1
42	Title is missing!. , 2020, 18, e3000885.		0
43	Title is missing!. , 2020, 18, e3000885.		0
44	Title is missing!. , 2020, 18, e3000885.		0
45	Title is missing!. , 2020, 18, e3000885.		0
46	Title is missing!. , 2020, 18, e3000885.		0
47	Title is missing!. , 2020, 18, e3000885.		0
48	Title is missing!. , 2020, 18, e3000885.		0
49	Implications of sex-specific differences on clinical studies of human health. , 2022, , 11-33.		0
50	Introduction: The relevance of sex and gender in precision medicine and the role of technologies and artificial intelligence. , 2022, , 1-8.		0