

Esti Yeger-Lotem

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

9,579
citations

236833

25
h-index

265120

42
g-index

50
all docs

50
docs citations

50
times ranked

19759
citing authors

#	ARTICLE	IF	CITATIONS
1	The differential activity of biological processes in tissues and cell subsets can illuminate disease-related processes and cell-type identities. <i>Bioinformatics</i> , 2022, 38, 1584-1592.	1.8	7
2	The TissueNet v.3 Database: Protein-protein Interactions in Adult and Embryonic Human Tissue contexts. <i>Journal of Molecular Biology</i> , 2022, 434, 167532.	2.0	6
3	The Organ-Disease Annotations (ODiseA) Database of Hereditary Diseases and Inflicted Tissues. <i>Journal of Molecular Biology</i> , 2022, 434, 167619.	2.0	6
4	The landscape of molecular chaperones across human tissues reveals a layered architecture of core and variable chaperones. <i>Nature Communications</i> , 2021, 12, 2180.	5.8	62
5	Small heat-shock protein HSPB3 promotes myogenesis by regulating the lamin B receptor. <i>Cell Death and Disease</i> , 2021, 12, 452.	2.7	16
6	Unraveling the hidden role of a uORF-encoded peptide as a kinase inhibitor of PKCs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	32
7	Mechanisms of tissue and cell-type specificity in heritable traits and diseases. <i>Nature Reviews Genetics</i> , 2020, 21, 137-150.	7.7	105
8	A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020, 183, 269-283.e19.	13.5	243
9	The GTEx Consortium atlas of genetic regulatory effects across human tissues. <i>Science</i> , 2020, 369, 1318-1330.	6.0	2,385
10	Dosage-sensitive molecular mechanisms are associated with the tissue-specificity of traits and diseases. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 4024-4032.	1.9	6
11	Differential network analysis of multiple human tissue interactomes highlights tissue-selective processes and genetic disorder genes. <i>Bioinformatics</i> , 2020, 36, 2821-2828.	1.8	28
12	A reference map of the human binary protein interactome. <i>Nature</i> , 2020, 580, 402-408.	13.7	724
13	Aging promotes reorganization of the CD4 T cell landscape toward extreme regulatory and effector phenotypes. <i>Science Advances</i> , 2019, 5, eaaw8330.	4.7	182
14	Large-scale analysis of human gene expression variability associates highly variable drug targets with lower drug effectiveness and safety. <i>Bioinformatics</i> , 2019, 35, 3028-3037.	1.8	24
15	ResponseNet v.3: revealing signaling and regulatory pathways connecting your proteins and genes across human tissues. <i>Nucleic Acids Research</i> , 2019, 47, W242-W247.	6.5	11
16	RSRC1 mutation affects intellect and behaviour through aberrant splicing and transcription, downregulating IGFBP3. <i>Brain</i> , 2018, 141, 961-970.	3.7	20
17	The DifferentialNet database of differential protein-protein interactions in human tissues. <i>Nucleic Acids Research</i> , 2018, 46, D522-D526.	6.5	71
18	Role of duplicate genes in determining the tissue-selectivity of hereditary diseases. <i>PLoS Genetics</i> , 2018, 14, e1007327.	1.5	33

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19	Integrating Rio1 activities discloses its nutrient-activated network in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2018, 46, 7586-7611.	6.5	19
20	MotifNet: a web-server for network motif analysis. <i>Bioinformatics</i> , 2017, 33, 1907-1909.	1.8	18
21	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213.	13.7	3,500
22	Identifying <i>cis</i> -mediators for <i>trans</i> -eQTLs across many human tissues using genomic mediation analysis. <i>Genome Research</i> , 2017, 27, 1859-1871.	2.4	72
23	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome Research</i> , 2017, 27, 1843-1858.	2.4	139
24	The TissueNet v.2 database: A quantitative view of protein-protein interactions across human tissues. <i>Nucleic Acids Research</i> , 2017, 45, D427-D431.	6.5	55
25	An Asymmetrically Balanced Organization of Kinases versus Phosphatases across Eukaryotes Determines Their Distinct Impacts. <i>PLoS Computational Biology</i> , 2017, 13, e1005221.	1.5	31
26	Algorithms for Regular Tree Grammar Network Search and Their Application to Mining Human-viral Infection Patterns. <i>Journal of Computational Biology</i> , 2016, 23, 165-179.	0.8	2
27	A Differentiation Transcription Factor Establishes Muscle-Specific Proteostasis in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2016, 12, e1006531.	1.5	35
28	Human protein interaction networks across tissues and diseases. <i>Frontiers in Genetics</i> , 2015, 6, 257.	1.1	76
29	MyProteinNet: build up-to-date protein interaction networks for organisms, tissues and user-defined contexts. <i>Nucleic Acids Research</i> , 2015, 43, W258-W263.	6.5	49
30	A combination of gene expression ranking and co-expression network analysis increases discovery rate in large-scale mutant screens for novel <i>Arabidopsis thaliana</i> abiotic stress genes. <i>Plant Biotechnology Journal</i> , 2015, 13, 501-513.	4.1	33
31	Algorithms for Regular Tree Grammar Network Search and Their Application to Mining Human-Viral Infection Patterns. <i>Lecture Notes in Computer Science</i> , 2015, , 53-65.	1.0	0
32	Comparative Analysis of Human Tissue Interactomes Reveals Factors Leading to Tissue-Specific Manifestation of Hereditary Diseases. <i>PLoS Computational Biology</i> , 2014, 10, e1003632.	1.5	70
33	Cancer Evolution Is Associated with Pervasive Positive Selection on Globally Expressed Genes. <i>PLoS Genetics</i> , 2014, 10, e1004239.	1.5	93
34	The TissueNet database of human tissue protein-protein interactions. <i>Nucleic Acids Research</i> , 2013, 41, D841-D844.	6.5	54
35	ResponseNet2.0: revealing signaling and regulatory pathways connecting your proteins and genes now with human data. <i>Nucleic Acids Research</i> , 2013, 41, W198-W203.	6.5	25
36	A context-sensitive framework for the analysis of human signalling pathways in molecular interaction networks. <i>Bioinformatics</i> , 2013, 29, i210-i216.	1.8	8

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37	ResponseNet: revealing signaling and regulatory networks linking genetic and transcriptomic screening data. <i>Nucleic Acids Research</i> , 2011, 39, W424-W429.	6.5	76
38	Compounds from an unbiased chemical screen reverse both ER-to-Golgi trafficking defects and mitochondrial dysfunction in Parkinson's disease models. <i>DMM Disease Models and Mechanisms</i> , 2010, 3, 194-208.	1.2	159
39	Bridging high-throughput genetic and transcriptional data reveals cellular responses to alpha-synuclein toxicity. <i>Nature Genetics</i> , 2009, 41, 316-323.	9.4	266
40	Chromosomal organization is shaped by the transcription regulatory network. <i>Trends in Genetics</i> , 2005, 21, 138-142.	2.9	69
41	Alignment of metabolic pathways. <i>Bioinformatics</i> , 2005, 21, 3401-3408.	1.8	193
42	Network motifs in integrated cellular networks of transcription-regulation and protein-protein interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5934-5939.	3.3	479
43	Detection of regulatory circuits by integrating the cellular networks of protein-protein interactions and transcription regulation. <i>Nucleic Acids Research</i> , 2003, 31, 6053-6061.	6.5	34
44	Dynamic voting for consistent primary components. , 1997, , .		35
45	The AS/400 cluster engine: A case study. , 0, , .		6