

Esti Yeger-Lotem

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6357606/publications.pdf>

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 | Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213. | 13.7 | 3,500 |
| 2 | The GTEx Consortium atlas of genetic regulatory effects across human tissues. <i>Science</i> , 2020, 369, 1318-1330. | 6.0 | 2,385 |
| 3 | A reference map of the human binary protein interactome. <i>Nature</i> , 2020, 580, 402-408. | 13.7 | 724 |
| 4 | 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 |
| 5 | 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 |
| 6 | A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020, 183, 269-283.e19. | 13.5 | 243 |
| 7 | Alignment of metabolic pathways. <i>Bioinformatics</i> , 2005, 21, 3401-3408. | 1.8 | 193 |
| 8 | 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 |
| 9 | 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 |
| 10 | Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome Research</i> , 2017, 27, 1843-1858. | 2.4 | 139 |
| 11 | Mechanisms of tissue and cell-type specificity in heritable traits and diseases. <i>Nature Reviews Genetics</i> , 2020, 21, 137-150. | 7.7 | 105 |
| 12 | Cancer Evolution Is Associated with Pervasive Positive Selection on Globally Expressed Genes. <i>PLoS Genetics</i> , 2014, 10, e1004239. | 1.5 | 93 |
| 13 | ResponseNet: revealing signaling and regulatory networks linking genetic and transcriptomic screening data. <i>Nucleic Acids Research</i> , 2011, 39, W424-W429. | 6.5 | 76 |
| 14 | Human protein interaction networks across tissues and diseases. <i>Frontiers in Genetics</i> , 2015, 6, 257. | 1.1 | 76 |
| 15 | 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 |
| 16 | The DifferentialNet database of differential protein-protein interactions in human tissues. <i>Nucleic Acids Research</i> , 2018, 46, D522-D526. | 6.5 | 71 |
| 17 | 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 |
| 18 | Chromosomal organization is shaped by the transcription regulatory network. <i>Trends in Genetics</i> , 2005, 21, 138-142. | 2.9 | 69 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | The TissueNet database of human tissue protein-protein interactions. <i>Nucleic Acids Research</i> , 2013, 41, D841-D844. | 6.5 | 54 |
| 22 | 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 |
| 23 | Dynamic voting for consistent primary components. , 1997, , . | | 35 |
| 24 | A Differentiation Transcription Factor Establishes Muscle-Specific Proteostasis in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2016, 12, e1006531. | 1.5 | 35 |
| 25 | 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 |
| 26 | 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 |
| 27 | Role of duplicate genes in determining the tissue-selectivity of hereditary diseases. <i>PLoS Genetics</i> , 2018, 14, e1007327. | 1.5 | 33 |
| 28 | 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 |
| 29 | 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 |
| 30 | 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 |
| 31 | 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 |
| 32 | 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 |
| 33 | RSRC1 mutation affects intellect and behaviour through aberrant splicing and transcription, downregulating IGFBP3. <i>Brain</i> , 2018, 141, 961-970. | 3.7 | 20 |
| 34 | 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 |
| 35 | MotifNet: a web-server for network motif analysis. <i>Bioinformatics</i> , 2017, 33, 1907-1909. | 1.8 | 18 |
| 36 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | 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 |
| 40 | The AS/400 cluster engine: A case study. , 0, , . | | 6 |
| 41 | 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 |
| 42 | 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 |
| 43 | The Organ-Disease Annotations (ODiseA) Database of Hereditary Diseases and Inflicted Tissues. <i>Journal of Molecular Biology</i> , 2022, 434, 167619. | 2.0 | 6 |
| 44 | 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 |
| 45 | 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 |