

Augustin Luna

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

8,260
citations

201674

27
h-index

243625

44
g-index

58
all docs

58
docs citations

58
times ranked

15524
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | CellMiner Cross-Database (CellMinerCDB) version 1.2: Exploration of patient-derived cancer cell line pharmacogenomics. <i>Nucleic Acids Research</i> , 2021, 49, D1083-D1093. | 14.5 | 104 |
| 2 | CellBox: Interpretable Machine Learning for Perturbation Biology with Application to the Design of Cancer Combination Therapy. <i>Cell Systems</i> , 2021, 12, 128-140.e4. | 6.2 | 67 |
| 3 | A pan-cancer survey of cell line tumor similarity by feature-weighted molecular profiles. <i>Cell Reports Methods</i> , 2021, 1, 100039. | 2.9 | 8 |
| 4 | Synthetic biology open language visual (SBOL Visual) version 2.3. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, . | 1.5 | 6 |
| 5 | Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. <i>Patterns</i> , 2021, 2, 100257. | 5.9 | 44 |
| 6 | COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387. | 7.2 | 53 |
| 7 | Analyzing causal relationships in proteomic profiles using CausalPath. <i>STAR Protocols</i> , 2021, 2, 100955. | 1.2 | 7 |
| 8 | Author-sourced capture of pathway knowledge in computable form using Biofactoid. <i>ELife</i> , 2021, 10, . | 6.0 | 11 |
| 9 | Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. <i>Nucleic Acids Research</i> , 2020, 48, D489-D497. | 14.5 | 161 |
| 10 | SCLC-CellMiner: A Resource for Small Cell Lung Cancer Cell Line Genomics and Pharmacology Based on Genomic Signatures. <i>Cell Reports</i> , 2020, 33, 108296. | 6.4 | 86 |
| 11 | AlignmentViewer: Sequence Analysis of Large Protein Families. <i>F1000Research</i> , 2020, 9, 213. | 1.6 | 5 |
| 12 | AlignmentViewer: Sequence Analysis of Large Protein Families. <i>F1000Research</i> , 2020, 9, 213. | 1.6 | 7 |
| 13 | netboxr: Automated discovery of biological process modules by network analysis in R. <i>PLoS ONE</i> , 2020, 15, e0234669. | 2.5 | 2 |
| 14 | Synthetic biology open language visual (SBOL visual) version 2.2. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, . | 1.5 | 7 |
| 15 | Systems biology graphical notation markup language (SBCNML) version 0.3. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, . | 1.5 | 21 |
| 16 | netboxr: Automated discovery of biological process modules by network analysis in R. , 2020, 15, e0234669. | | 0 |
| 17 | netboxr: Automated discovery of biological process modules by network analysis in R. , 2020, 15, e0234669. | | 0 |
| 18 | netboxr: Automated discovery of biological process modules by network analysis in R. , 2020, 15, e0234669. | | 0 |

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| 19 | netboxr: Automated discovery of biological process modules by network analysis in R. , 2020, 15, e0234669. | | 0 |
| 20 | Communicating Structure and Function in Synthetic Biology Diagrams. ACS Synthetic Biology, 2019, 8, 1818-1825. | 3.8 | 30 |
| 21 | Synthetic Biology Open Language Visual (SBOL Visual) Version 2.1. Journal of Integrative Bioinformatics, 2019, 16, . | 1.5 | 8 |
| 22 | Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. Journal of Integrative Bioinformatics, 2019, 16, . | 1.5 | 43 |
| 23 | LLGL2 rescues nutrient stress by promoting leucine uptake in ER+ breast cancer. Nature, 2019, 569, 275-279. | 27.8 | 99 |
| 24 | Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. IScience, 2019, 21, 664-680. | 4.1 | 52 |
| 25 | Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18. | 28.9 | 1,670 |
| 26 | Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10. | 28.9 | 2,111 |
| 27 | Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3. | 6.4 | 119 |
| 28 | A Landscape of Metabolic Variation across Tumor Types. Cell Systems, 2018, 6, 301-313.e3. | 6.2 | 123 |
| 29 | CellMinerCDB for Integrative Cross-Database Genomics and Pharmacogenomics Analyses of Cancer Cell Lines. IScience, 2018, 10, 247-264. | 4.1 | 117 |
| 30 | Synthetic Biology Open Language Visual (SBOL Visual) Version 2.0. Journal of Integrative Bioinformatics, 2018, 15, . | 1.5 | 21 |
| 31 | The NCI-60 Methylome and Its Integration into CellMiner. Cancer Research, 2017, 77, 601-612. | 0.9 | 48 |
| 32 | The digital revolution in phenotyping. Briefings in Bioinformatics, 2016, 17, 819-830. | 6.5 | 41 |
| 33 | Tumor immune microenvironment characterization in clear cell renal cell carcinoma identifies prognostic and immunotherapeutically relevant messenger RNA signatures. Genome Biology, 2016, 17, 231. | 8.8 | 746 |
| 34 | rCellMiner: exploring molecular profiles and drug response of the NCI-60 cell lines in R. Bioinformatics, 2016, 32, 1272-1274. | 4.1 | 39 |
| 35 | An Integrated Metabolic Atlas of Clear Cell Renal Cell Carcinoma. Cancer Cell, 2016, 29, 104-116. | 16.8 | 531 |
| 36 | PaxtoolsR: pathway analysis in R using Pathway Commons. Bioinformatics, 2016, 32, 1262-1264. | 4.1 | 43 |

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|----|---|------|-----------|
| 37 | Systems Biology Graphical Notation: Activity Flow language Level 1 Version 1.2. Journal of Integrative Bioinformatics, 2015, 12, 340-381. | 1.5 | 35 |
| 38 | Alterations of DNA repair genes in the NCI-60 cell lines and their predictive value for anticancer drug activity. DNA Repair, 2015, 28, 107-115. | 2.8 | 55 |
| 39 | Predicted Role of NAD Utilization in the Control of Circadian Rhythms during DNA Damage Response. PLoS Computational Biology, 2015, 11, e1004144. | 3.2 | 15 |
| 40 | Using drug response data to identify molecular effectors, and molecular "omic" data to identify candidate drugs in cancer. Human Genetics, 2015, 134, 3-11. | 3.8 | 27 |
| 41 | Software support for SBGN maps: SBGN-ML and LibSBGN. Bioinformatics, 2012, 28, 2016-2021. | 4.1 | 74 |
| 42 | Gene Expression Profiles of the NCI-60 Human Tumor Cell Lines Define Molecular Interaction Networks Governing Cell Migration Processes. PLoS ONE, 2012, 7, e35716. | 2.5 | 28 |
| 43 | Evidence of statistical epistasis between DISC1, CIT and NDEL1 impacting risk for schizophrenia: biological validation with functional neuroimaging. Human Genetics, 2010, 127, 441-452. | 3.8 | 93 |
| 44 | The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942. | 17.5 | 613 |
| 45 | The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741. | 17.5 | 828 |
| 46 | An Evaluation of Power and Type I Error of Single-Nucleotide Polymorphism Transmission/Disequilibrium-Based Statistical Methods under Different Family Structures, Missing Parental Data, and Population Stratification. American Journal of Human Genetics, 2007, 80, 178-185. | 6.2 | 13 |
| 47 | Exploring causal relationships in proteomic profiles in Cytoscape using the CausalPath App. F1000Research, 0, 11, 458. | 1.6 | 0 |