

Resource Summary Report

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Appyters

RRID:SCR_021245

Type: Tool

Proper Citation

Appyters (RRID:SCR_021245)

Resource Information

URL: <https://appyters.maayanlab.cloud>

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Description: Collection of web-based software applications that enable users to execute bioinformatics workflows without coding. Turns Jupyter notebooks into fully functional standalone web-based bioinformatics applications. Each Appyter application introduces data entry form for uploading or fetching data, as well as for selecting options for various settings. Once user presses Submit, Appyter is executed in cloud and user is presented with Jupyter Notebook report that contain results. Report includes markdown text, interactive and static figures, and source code. Appyter users can share the link to the output report, as well as download the fully executable notebook for execution on other platforms.

Resource Type: web application, software resource

Defining Citation: [DOI:10.1016/j.patter.2021.100213](https://doi.org/10.1016/j.patter.2021.100213)

Keywords: Jupyter Notebooks, data-driven web apps collection, Jupyter Notebook results report

Funding: NCI U24 CA224260;
NHLBI U54 HL127624;
NIH Office of the Director OT2 OD030160

Availability: Free, Available for download, Freely available

Resource Name: Appyters

Resource ID: SCR_021245

Alternate URLs: <https://github.com/MaayanLab/appyter>,
<https://github.com/MaayanLab/appyter-catalog>

License: Attribution-NonCommercial-ShareAlike 4.0 International

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260728T043617+0000

Ratings and Alerts

No rating or validation information has been found for Appyters.

No alerts have been found for Appyters.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Watson PM, et al. (2025) Loss of ARID1A leads to a cold tumor phenotype via suppression of IFN γ signaling. Scientific reports, 15(1), 8716.

Sonnleitner ST, et al. (2025) Decoding the transcriptome from bulk RNA of infection-naïve versus imprinted patients with SARS-CoV-2 Omicron B.1.1.529. Microbiology spectrum, 13(8), e0291424.

Kołodziejczak-Guglas I, et al. (2025) Proteomic-based stemness score measures oncogenic dedifferentiation and enables the identification of druggable targets. Cell genomics, 5(6), 100851.

Schmerer N, et al. (2025) A searchable atlas of pathogen-sensitive lncRNA networks in human macrophages. Nature communications, 16(1), 4733.

Feret N, et al. (2025) Temporal Analysis of Tear Fluid Proteome Reveals Critical Corneal Repair Events After Photorefractive Surgery. Investigative ophthalmology & visual science, 66(13), 49.

Easwaran S, et al. (2025) A genome-wide association study implicates the olfactory system in Drosophila melanogaster diapause-associated lifespan extension and fecundity. eLife, 13.

Balcioglu O, et al. (2024) Mcam stabilizes luminal progenitor breast cancer phenotypes via Ck2 control and Src/Akt/Stat3 attenuation. bioRxiv : the preprint server for biology.

Balcioglu O, et al. (2024) Mcam stabilizes a luminal progenitor-like breast cancer cell state via Ck2 control and Src/Akt/Stat3 attenuation. NPJ breast cancer, 10(1), 80.

Monson KR, et al. (2024) Tyrosine Protein Kinase SYK-Related Gene Signature in Baseline Immune Cells Associated with Adjuvant Immunotherapy-Induced Immune-Related Adverse Events in Melanoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(19), 4412.