

Bio-Analytic Resource for Plant Biology (BAR)

<http://bar.utoronto.ca>

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Recent activities and newly developed tools and/or resources

The Bio-Analytic Resource is a collection of user-friendly web-based tools for working with functional genomics and other data for hypothesis generation and confirmation. Most are designed with the plant (mainly Arabidopsis) researcher in mind. Data sets include: * 175 million gene expression measurements (100 million from A.th.), plus “expressologs” (homologs showing similar patterns of expression in equivalent tissues) for many genes across 12 species. View expression patterns with our popular eFP Browsers or newer ePlant tools. * 70,944 predicted protein-protein interactions plus 83,626 experimentally determined PPIs and ~2.8 million protein-DNA interactions, which can be explored with our new Arabidopsis Interactions Viewer 2 tool. * 29,180 predicted protein tertiary structures and experimentally determined structures for 402 Arabidopsis proteins.* Millions of non-synonymous SNPs from the 1001 Arabidopsis Genomes project, now delivered via the 1001 Genomes API.* Documented subcellular localizations for 11.7k proteins, predicted localization for most of Arabidopsis proteome, from the SUBA database at the University of Western Australia.* Thalemine (Pasha *et al.*, 2020).

The Bio-Analytic Resource worked with Ute Roessner’s group in Australia to develop an Arabidopsis Lipid Map eFP Browser for visualizing the amount of any one of hundreds of lipids across 7 different tissues (Kehelpannala *et al.*, 2021). It also worked collaboratively with Patrick Schaefer’s group at the University of Warwick to develop a cell-type specific immunity view for roots in ePlant (Rich-Griffin *et al.*, 2020). A Plant Reactome (Tello-Ruiz *et al.*, 2018) pathways viewer was added to ePlant (Waese-Perlman *et al.*, 2021). The BAR also rolled out two new tools for exploring gene regulatory networks and natural variation: AGENT (Lau *et al.*, 2021) and Variant Viewer (Cumming *et al.*, 2021), respectively. Last but not least, based on the Marcotte Lab’s co-fractionation mass spectrometry to identify protein complexes in 13 plant species, including Arabidopsis (McWhite *et al.*, 2020), we loaded the Arabidopsis data consisting of 21,910 interactions into the BAR’s Arabidopsis Interactions Viewer database (<http://bar.utoronto.ca/interactions2>). The numbers listed above reflect this addition. For non-Arabidopsis researchers, we worked with Robert Schaffer’s group in New Zealand to set up/host an Actinidia eFP Browser, also known as kiwifruit. Check it out here: http://bar.utoronto.ca/efp_actinidia/cgi-bin/efpWeb.cgi (Brian *et al.*, 2021). And we also work with Thorsten Schnurbusch’s group and colleagues in Germany to set up a barley floral meristem eFP view (Thiel *et al.*, 2021) in our Barley ePlant at http://bar.utoronto.ca/eplant_barley/. New expression views were added for several other species including tomato, soybean and rice.

Planned future activities

A custom eFP view in ePlant for a researcher’s own RNA-seq data is in the works, along with “Gaia” (kind of like Siri or Alexa, but for Arabidopsis information) as part of an award from Genome Canada: check out a beta version at <http://bar.utoronto.ca/gaia>.

In addition to bringing together search results from many different tools, Gaia indexes 67,291 Arabidopsis papers with 155,175 figures of which 11,205 are genetic models – these were identified using a triplet network. We extracted 9,457 unique terms from the models by OCR using the Google Vision AI. Thus Gaia is able to identify if your favourite gene is present in an image – you can also search to see if it co-occurs with another search term in a figure. Several new ePlants are also planned as part of the Genome Canada project, and an ecosystem viewer will also be developed. The aforementioned AGENT tool was also funded by this grant. The BAR participated in the 2020 American Society of Plant Biology (ASPB) virtual Plant Biology conference, as part of the Plant AgData Outreach booth and in the Plant Bioinformatics workshop.

Please provide a paragraph describing the general impact of the COVID19 pandemic on your activities

We were able to continue developing BAR tools and data sets when BAR staff started working from home. A letter describing a collaborative effort with TAIR and NCGR to rescue/resuscitate Araport was published in The Plant Cell (Pasha *et al.*, 2020). Note: the McWhite *et al.* (2020) and Tello-Ruiz *et al.* (2018) publications are not BAR publications.

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