APPIC

Atlas of Protein Protein Interactions in Cancer

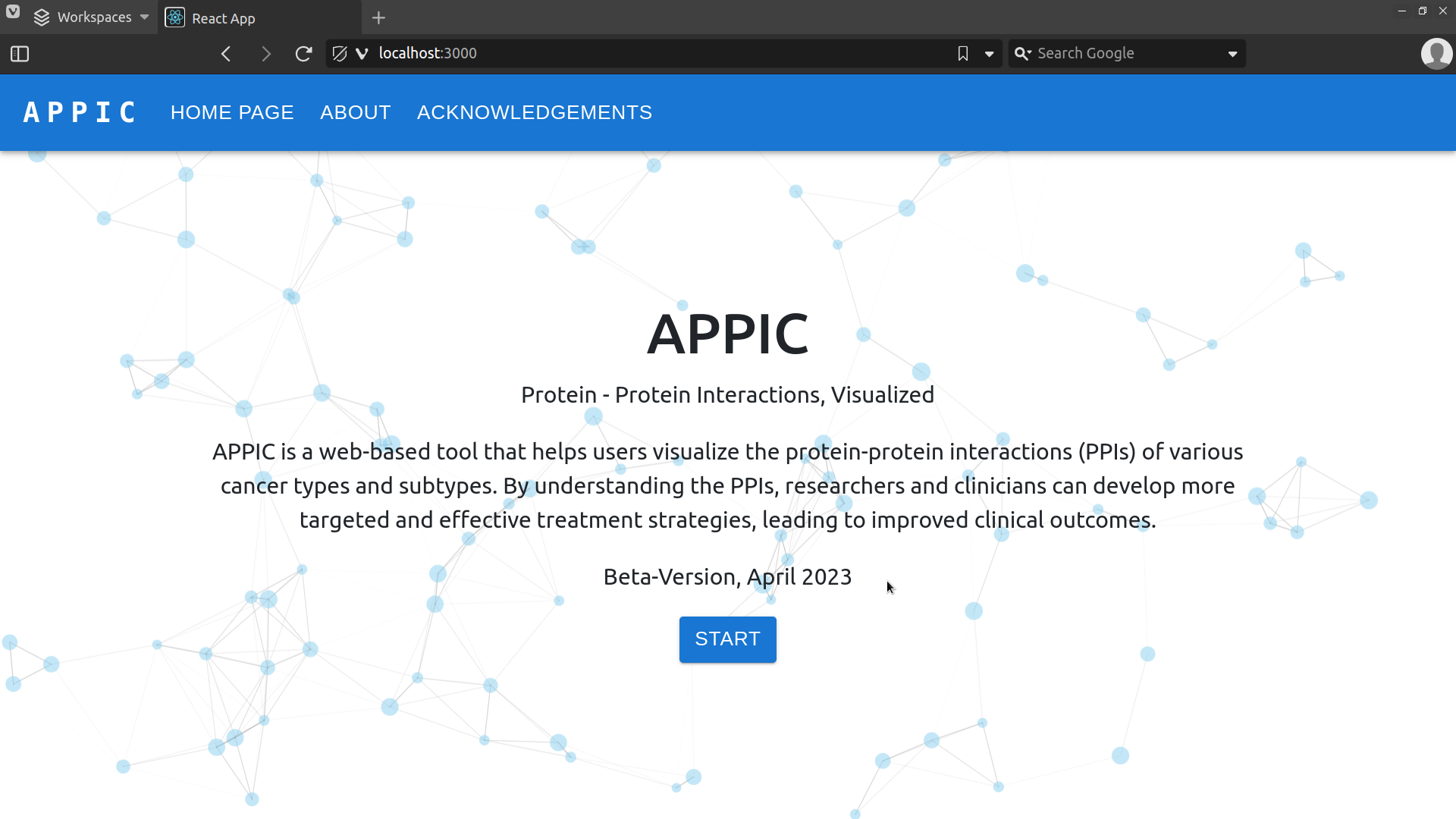
User Guide

version 1.0

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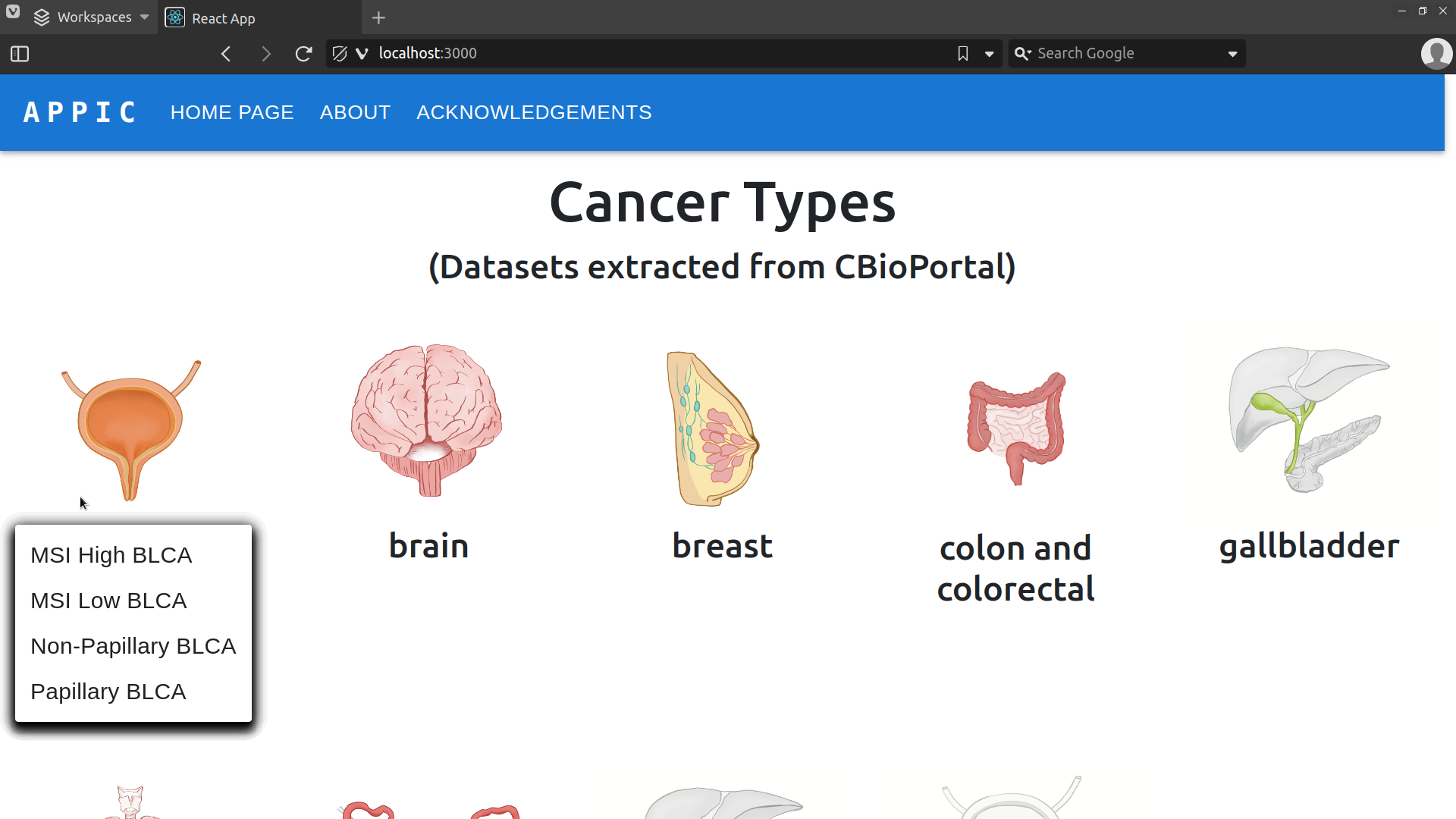
**Start**

The web tool starts at this landing page. To start searching different cancer subtypes, click “START”

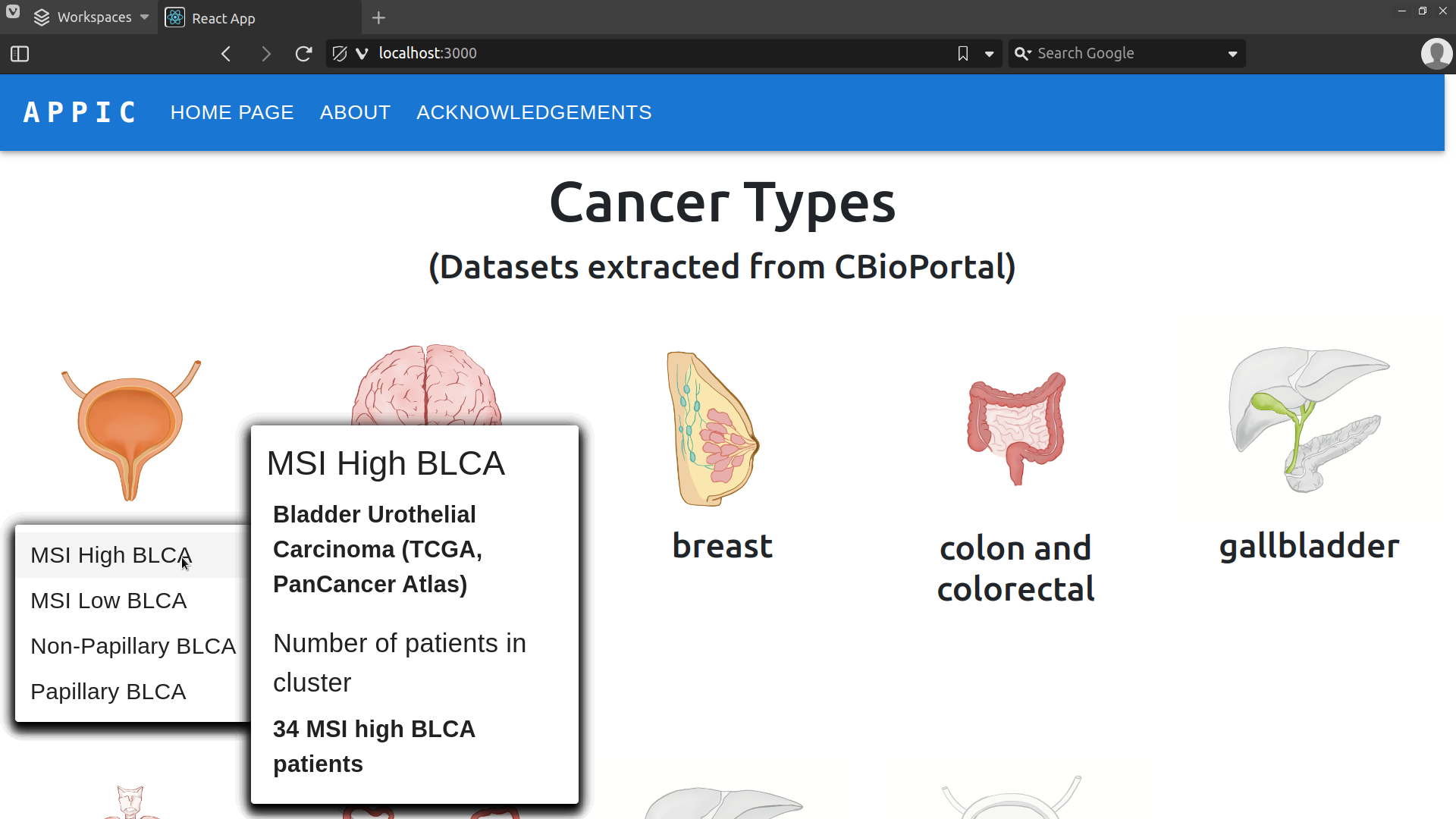


**Body Diagram Page**

After clicking “START”, the web tool will bring you to this page. Here, you can click on each organ which will drop down a list of different subtypes within that tissue.

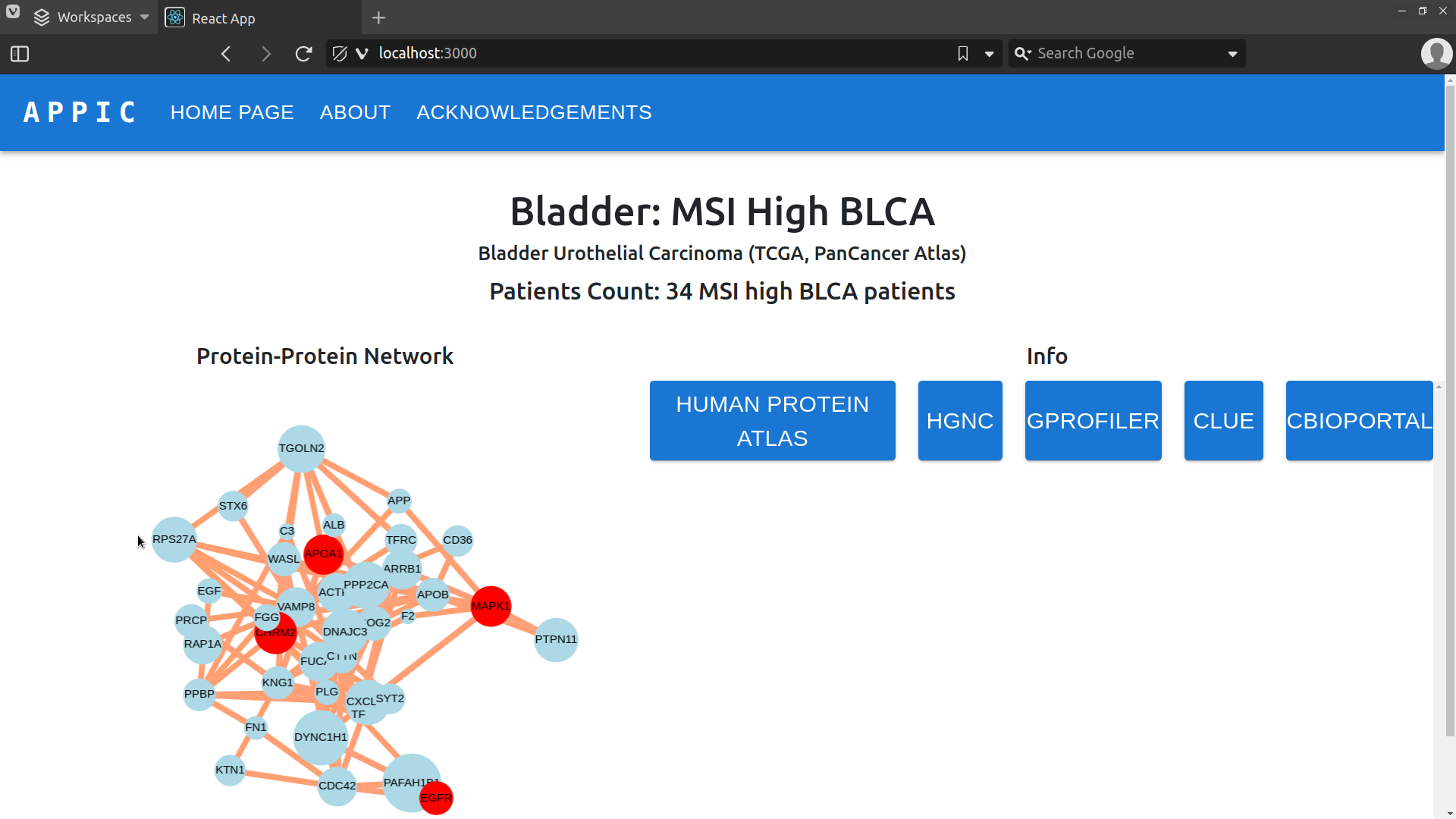


Users can also hover their mouse over each subtype to open a popup box which describes the dataset used to create the cancer subtype. Clicking on a cancer subtype will bring the user to the network diagram page.



**Network Diagram Page**

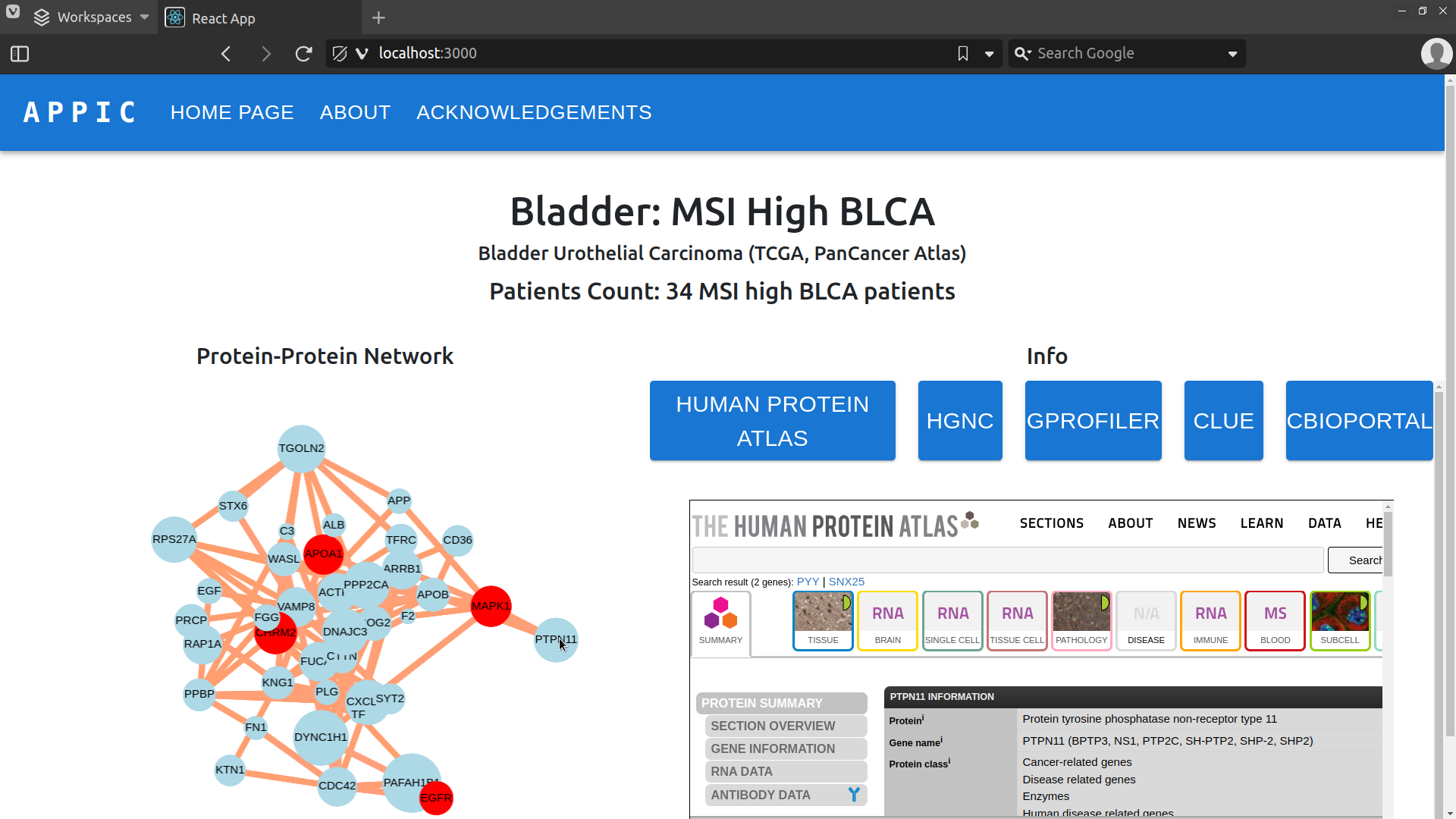
Here, the protein-protein interaction network for this cancer subtype is displayed on the left. Nodes colored in red indicate existing drug targets (see Clue.io database notes).



On the right hand side are the several databases linked to the protein-protein interaction network. Users can click on each button to view results from the databases.

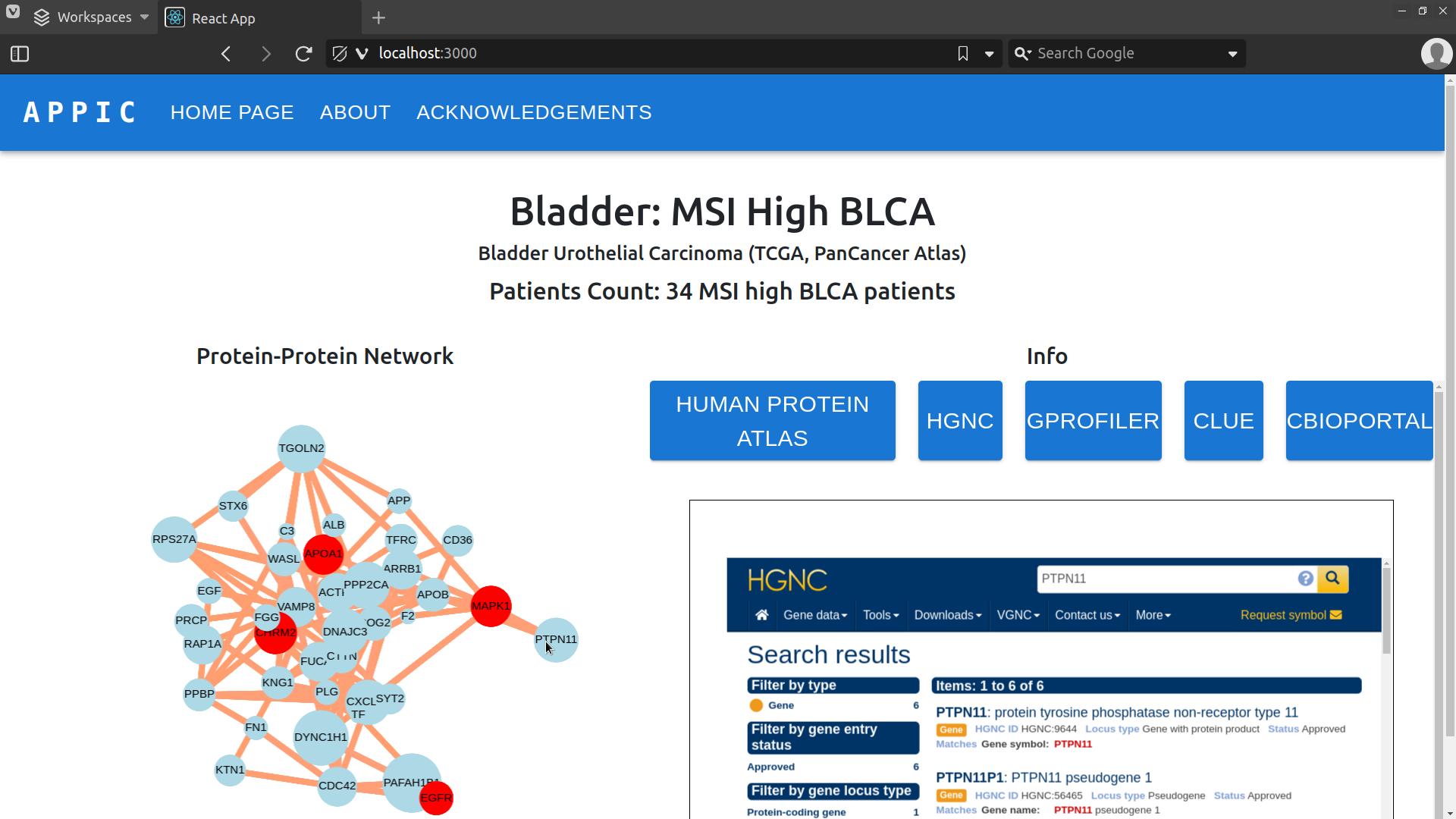
**Human Protein Atlas**

Users should click on a node in the network diagram to create a response.

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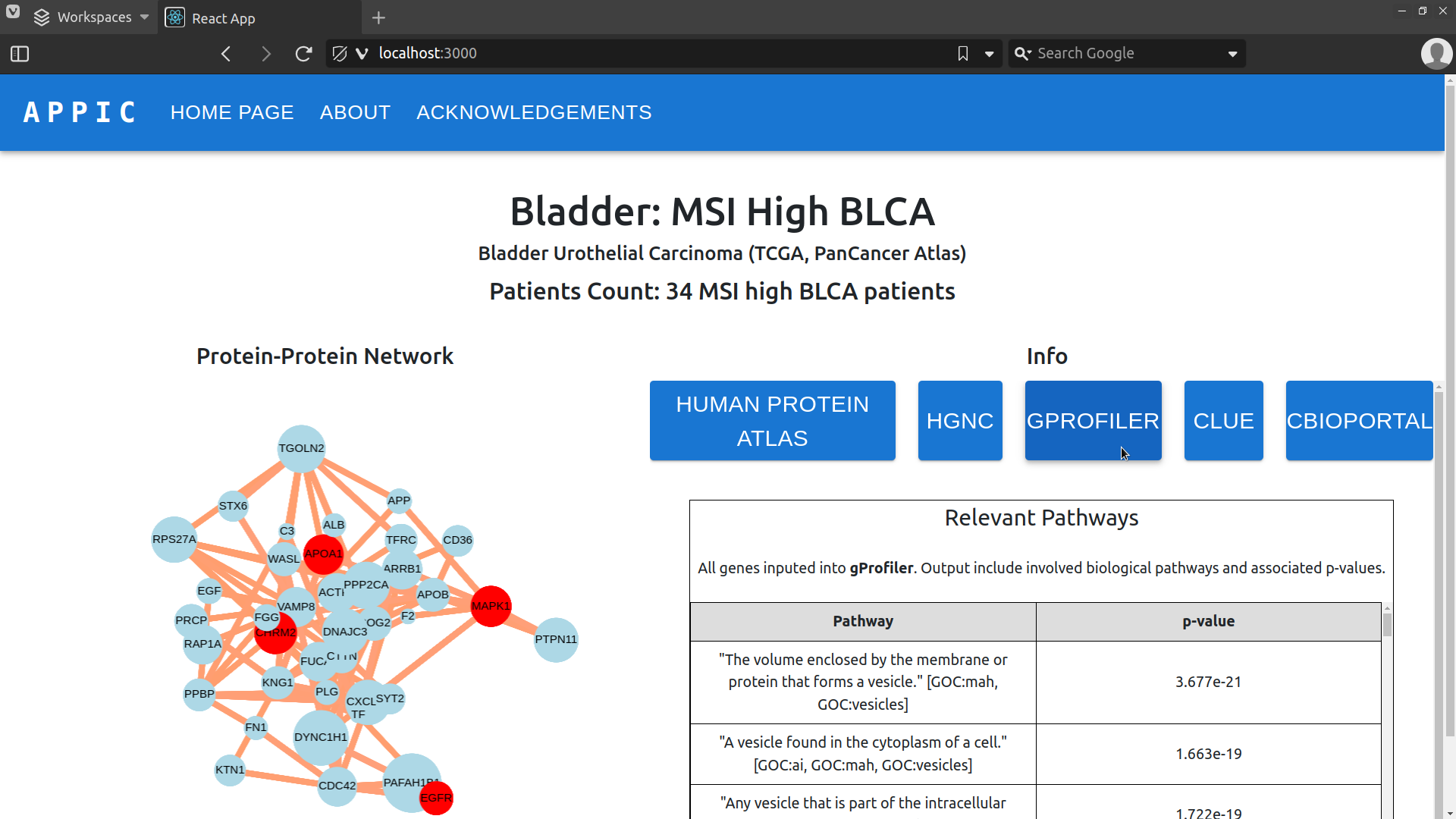
**HGNC**

Users should click on a node in the network diagram to create a response.



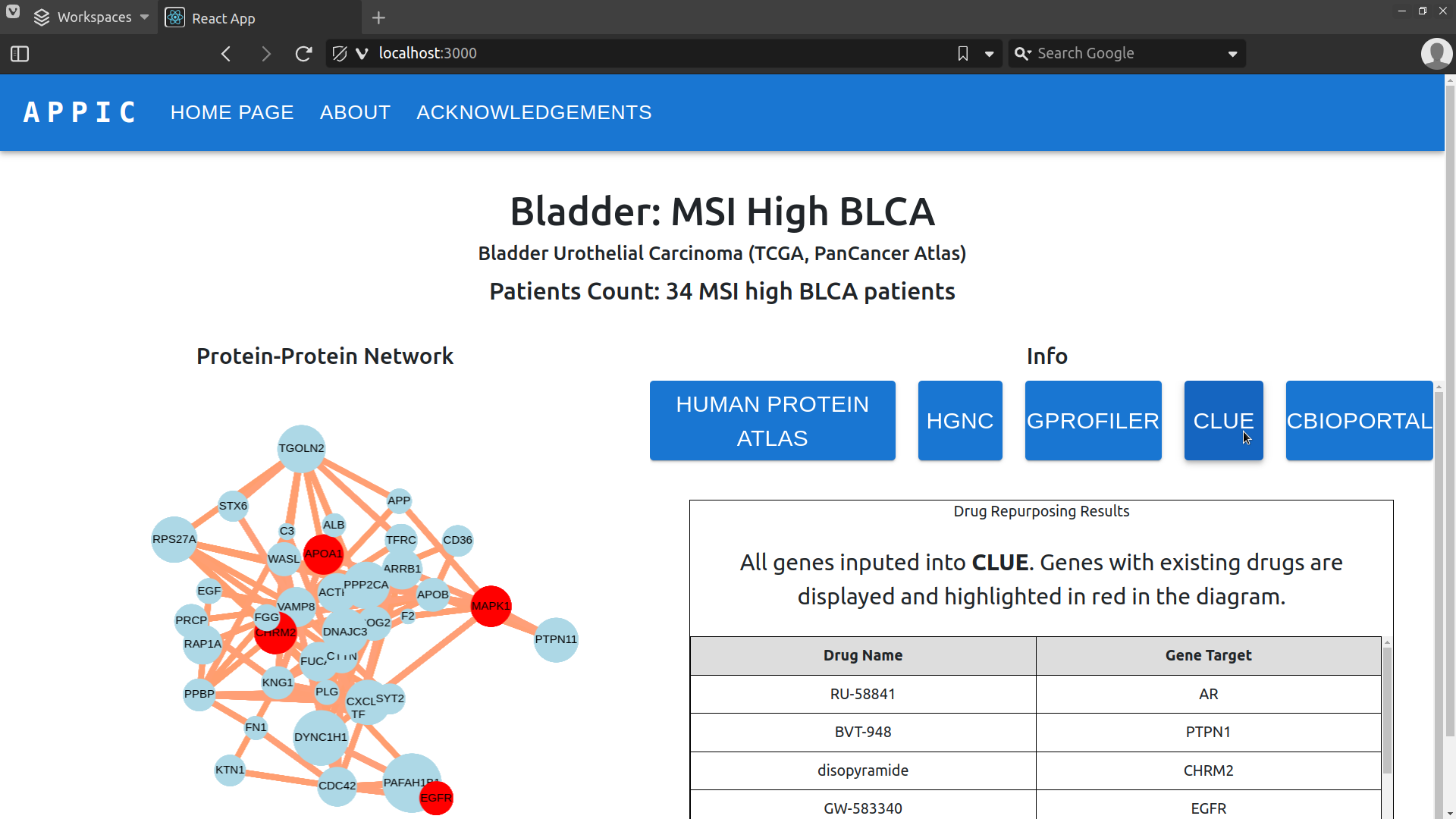
**Gprofiler**

All proteins are passed into gProfiler. The output is a table that represent biological pathways related to the proteins in the protein-protein interaction network. Biological pathways are ordered by p-value. Please note the table can take up to 10 seconds to populate.



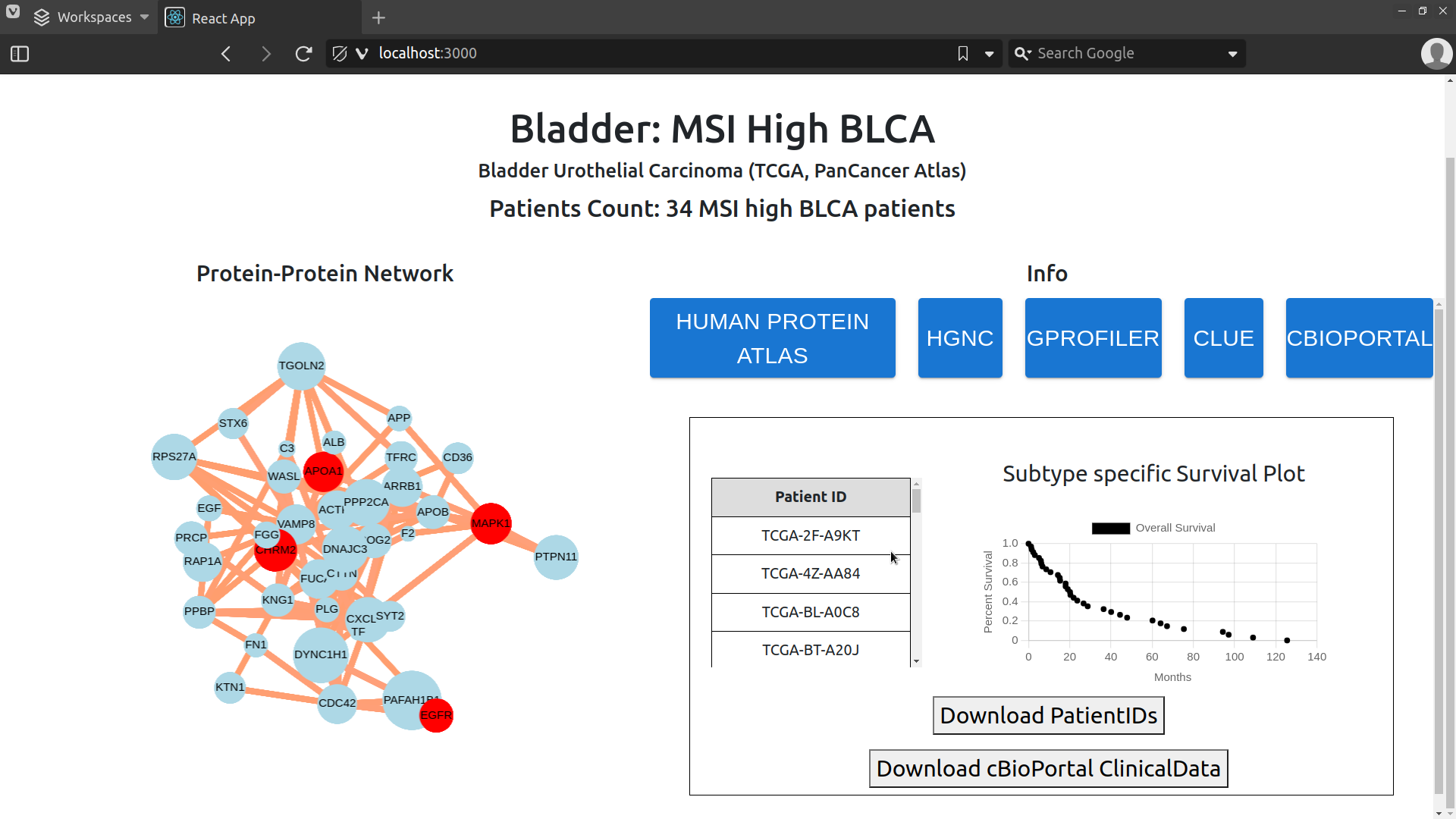
**Clue**

All proteins are searched in the Clue.io database to see if any drugs that target these proteins exist. The drug name and target are included in the table. The gene targets are colored red in the network diagram.

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**CbioPortal**

The specific patient IDs that create the cancer subtype are displayed. The survival plot represents the specific patients in the cancer subtype. Users have the options to download the Patient ID list as well as cBioPortal raw data.

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