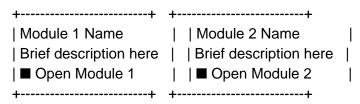
BioStructX Module Navigator – User Guide

What You See

You'll see a grid layout with cards, each representing a module:



How It Works

Each module card displays:

- Name Title of the tool (e.g., Protein Viewer, Ligand Clustering)
- Description What the module does
- ■ Open button Launches the module

Clicking the ■ Open button for a module:

- 1. Stores your selection in memory (st.session_state)
- 2. Automatically reloads the app with that module active

Step-by-Step Usage

- 1. Launch the App (e.g., via streamlit run biostructx_home.py)
- 2. Scroll to the Module Selector Grid
- 3. Read Descriptions to find the module you need
- 4. Click Open [Module Name]
- 5. The app will reload and show the selected tool's interface

Example Modules

```
| Module | Description |
|------|
|-------|
| Protein Viewer | View 3D structures and get UniProt data |
| Ligand Similarity | Cluster and compare chemical structures |
| Binding Affinity Predictor | Predict ligand-protein interaction strength |
| Evolutionary Divergence | Align and compare protein sequences and structures |
```

Switching Modules

To go back and select a different module, click the ■ Home or ■ BioStructX link in the sidebar or top navigatio