BioStructX Module Navigator – User Guide

What You See

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

```
+--------------------------+   +--------------------------+
| Module 1 Name            |   | Module 2 Name            |
| Brief description here   |   | Brief description here   |
| ■ Open Module 1          |   | ■ Open Module 2          |
+--------------------------+   +--------------------------+
```

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