How to use the NODE pages.

Each of the bars are clickable to show the detailed information.

The magenta bars represent PDB clusters. The PDB cluster represented by the magenta bar clicked contain two PDB chains, 1g3j A and C, in this case.

Please also refer to the glossary for the terms “NODE”, “PDB cluster”, “at least rule” etc.
The "complex" buttons are linked to the EDGE pages. The "Seq" buttons show the region in color. The prediction section presents the order/disorder prediction and domain assignments. The color samples for the bar diagram are here. You can jump to the network map. In this case, IID00039 is colored in yellow. The prediction section presents the order/disorder prediction and domain assignments. The "Seq" buttons show the region in color. The color samples for the bar diagram are here. You can jump to the network map. In this case, IID00039 is colored in yellow.
How to use the EDGE pages.

The region from 133 to 664 of Catenin beta-1 is shown in the J-mol applet.

Catenin beta-1 is shown in green, while Adenomatous polyposis coli protein is in pink.

The structure shown is the representative one in the PDB cluster. You can select other models in the pull down menu.

You can jump to the network map.
How to use the network pages.

- You can enlarge and reduce the map by the middle wheel on a mouse (win & mac) or two finger scroll (mac). Also, you can grasp the network by dragging the mouse and modify its shape as you want to be.

- Each “node” is clickable to see the node page.

- Each “edge” is clickable to see the edge page.

- The protein from which the network is generated is in yellow.

- Moving the pointer on a node gives the protein name.

- Green ones are proteins with at least one ProS.

- Moving the pointer on a edge gives the PDB ID with the pair of chain names.