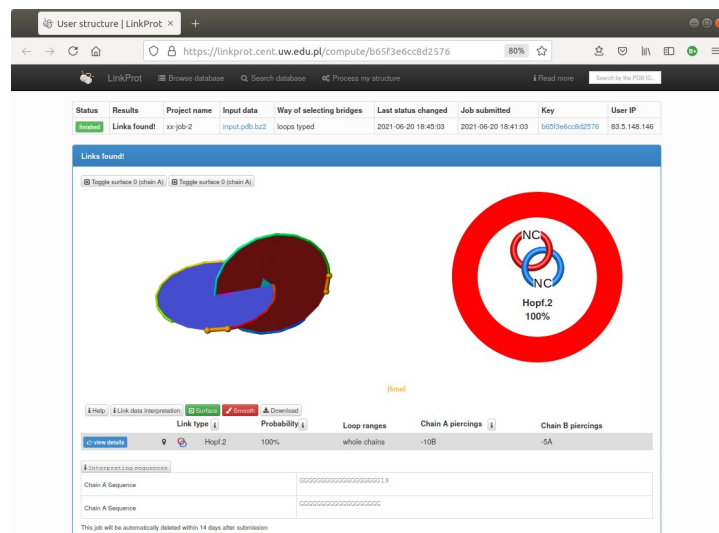


1. Please, open the page of the **Linkprot database**: <https://linkprot.cent.uw.edu.pl>, and click "**Process my structure**" button in the top menu or at the bottom of the page. It will direct you to the **submit menu**.
2. First two fields are optional: **job name** and **e-mail address**. Providing "**job name**" would be helpful in the case of running several jobs to distinguish between them. If the e-mail address is provided, a link to the results of the job will be send to this address after the job is submitted.
3. Before uploading the structure for the job, one has to determine the **input data format**. The server accepts two formats: **PDB**, and **XYZ**. For details of both formats one can click the light blue "**iHelp**" button. In the calculations only positions of C-alpha atoms are used; therefore, it is sufficient to provide only positions of these atoms in one of these formats.
4. **[EXAMPLE-1: PDB, link-1-3.pdb, whole chains, chain names: A, B]**. Let's start with a simple example of the Hopf link. The system is provided in the PDB format. Here it is obligatory to provide names of the chains, since the structure may contain more than two chains.



5. Results of [EXAMPLE-1: PDB, link-1-3.pdb, whole chains, chain names: A, B]: can be found under this link: <https://linkprot.cent.uw.edu.pl/compute/b65f3e6cc8d2576>. It is possible to manipulate the structure (surface on/off), orange bar and spheres indicate connected points. Below the structure view window, there are details of linking, for example piercing points (numbers of amino acids/beads).
6. **[PDB, 2lfk-MDL1.pdb, A: 24-51, A: 52-69 (Protein with a Hopf link)]**. (2LFK: protease inhibitor TdPI). The numbers of amino acids introduced in the fields are related to the numbering of residues in the PDB file! The result of calculations is can be found here: <https://linkprot.cent.uw.edu.pl/compute/cbddd3d1dc2d0d9>

