

# NeXO USER MANUAL

## Navigation with OBO-Edit

The NeXO ontology can also be explored using designated ontology editors and browsers such as OBO-Edit (available from <http://www.oboedit.org/>) as shown in the below screenshot. For this purpose we have provided the file NeXO\_x\_x.obo which conforms to the Open Biological and Biomedical Ontology (OBO) format. Using OBO-Edit the NeXO ontology can be explored in three basic ways:

- Using the Ontology Tree Editor
- Using the Graph Editor
- By searching for keywords appearing in NeXO term annotations.

Terms in the NeXO.obo file are annotated with text labels transferred through alignment to GO. The label indicates matchings with score  $\geq 0.1$  to any one of the three GO ontologies: Cellular Component (CC), Biological Process (BP), and Molecular Function (MF). Additional information about the term such as its robustness score, interaction density, and alignment scores are provided in the Comment field.

Each term relationship is annotated with one of two types: “child\_of” or “linked\_to”. The “X child\_of Y” relationship indicates that X is a child of Y in the tree forming the backbone of the NeXO ontology. “X linked to Y” indicates that X was linked to Y by an additional edge in the NeXO DAG.

The screenshot displays the OBO-Edit interface with three main panels:

- Ontology Tree Editor:** A hierarchical tree view of the ontology. The selected term is "CC: SWI/SNF complex | BP: nucleosome mobilization | MF: positive regulation of transcription, DNA-dependent".
- Graph Editor:** A network diagram showing relationships between terms. The selected term is highlighted in blue, and its parent terms are shown in grey.
- Text Editor:** A detailed view of the selected term, including its ID (NeXO:9301), namespace (NeXO), name, definition, comment, and various scores (robustness, density, bootstrap, cc\_score, bp\_score, mf\_score).