Enabling large-scale dataset analysis in the area of reproductive health research through the UniProtKB and Gene Ontology Annotation (GOA) databases

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Research into the biology of reproduction and development is generating large amounts of data, however the interpretation of that data is dependent on the available gene/protein annotations and analysis tools available.

UniProtKB is the world’s leading resource of protein sequences and functional data presenting a comprehensive review of the most current biological information for a protein with links to more than 150 complementary biological repositories.

Swiss-Prot (reviewed entries) is a high quality manually annotated and non-redundant protein sequence database. It combines review of the scientific literature with the use of bioinformatics sequence analysis tools.

When available, an entry for a human protein will show information about diseases and sequence variants.

TrEMBL (unreviewed entries) contains protein sequences associated with computationally generated annotation and large-scale functional characterization.

Goa@ebi.ac.uk  help@uniprot.org

UniProt and QuickGO are updated regularly and can be freely accessed or downloaded from www.uniprot.org and www.ebi.ac.uk/QuickGO/

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