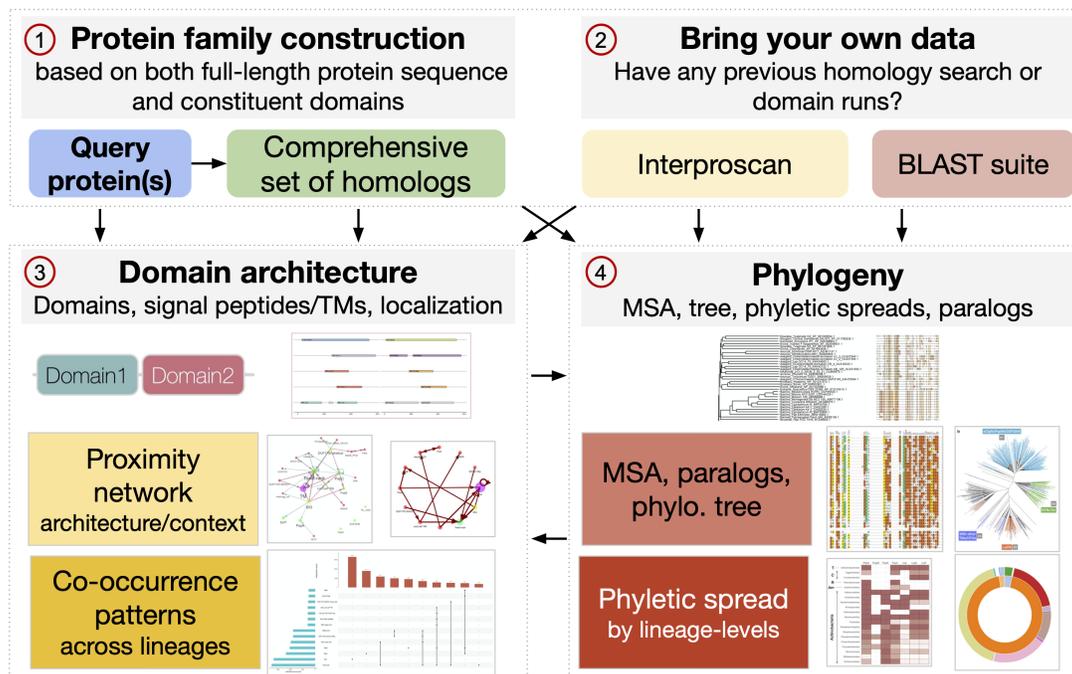




# MolEvolvR: A web-app for molecular evolution and phylogeny



**The MolEvolvR web-app integrates molecular evolution and phylogenetic protein characterization under one-roof.**

MolEvolvR allows users to start with protein(s) of interest and perform the full analysis (1+3+4), only protein characterization (1+3), only homology searches (1+4), or start with external outputs from BLAST or Interproscan for further analysis, summarization, and visualization (2+3+4). MolEvolvR is interactive, queryable, and customizable.

## Start your Analysis

### Abstract

Studying proteins through the lens of evolution can help identify conserved features and lineage-specific variants, and consequently, their functions. MolEvolvR is a web-app that enables researchers to run a general-purpose computational workflow for characterizing the molecular evolution and phylogeny of their proteins of interest. The web-app accepts inputs in multiple formats: protein/domain sequences (FASTA/AccNum), homologous proteins (e.g., BLAST output, MSA), or motif/domain scans (e.g., InterProScan output). MolEvolvR returns detailed data about homologs along with dynamic graphical summaries such as multiple sequence alignment, phylogenetic trees, domain architectures, domain proximity networks, phyletic spreads, and co-occurrence patterns across lineages. Thus, MolEvolvR provides a powerful, easy-to-use interface for computationally characterizing proteins.

# How to Cite

## **MolEvolvR: A web-app for characterizing proteins using molecular evolution and phylogeny**

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