# Basic function



Blast

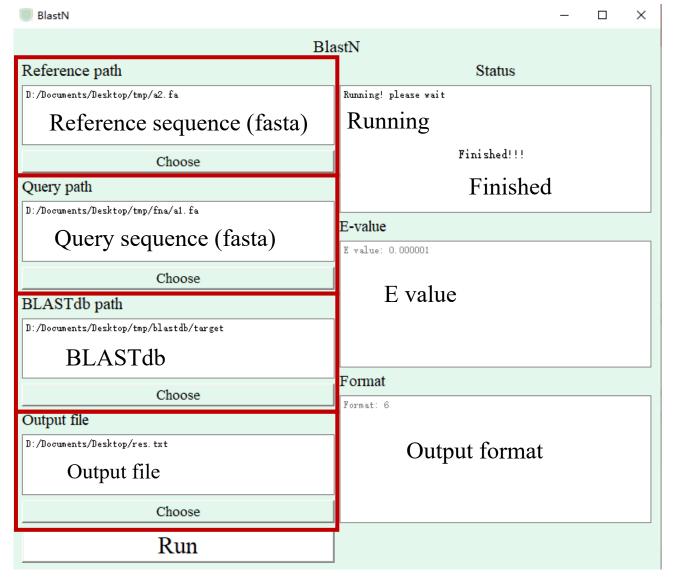
Alignment

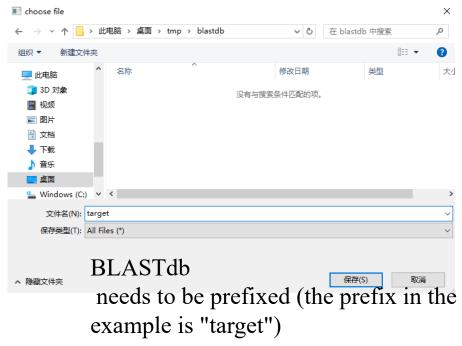
Build tree

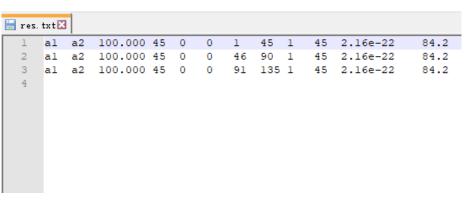
Activity

#### BlastN



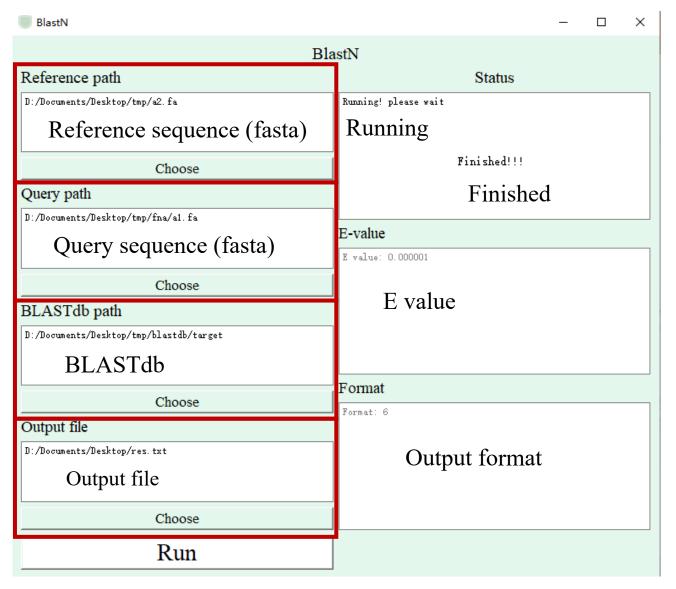




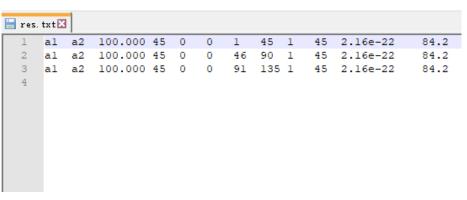


#### BlastP

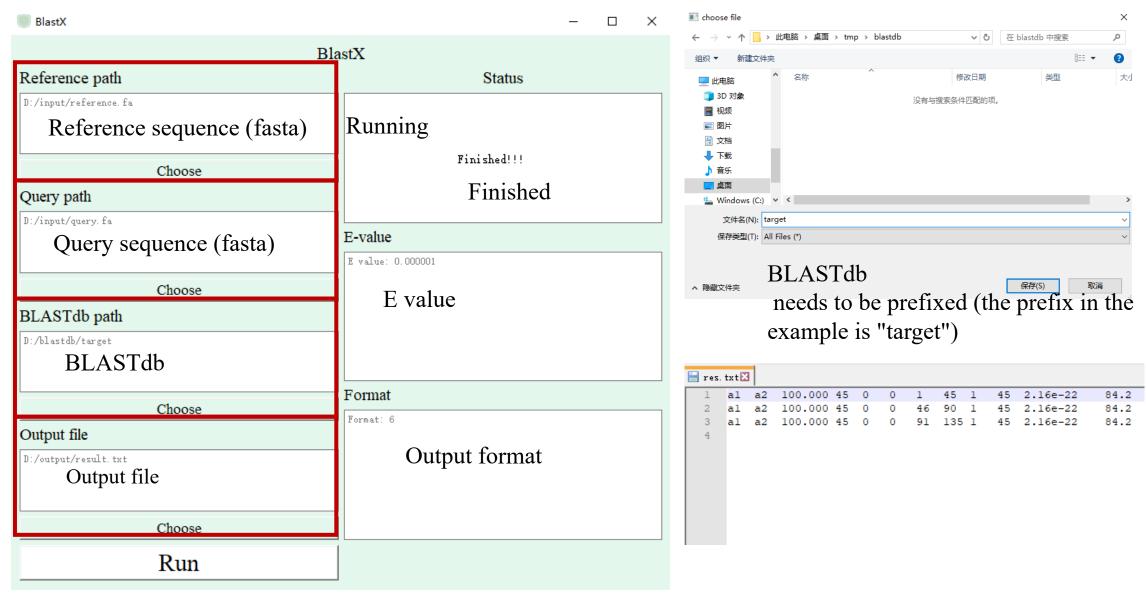






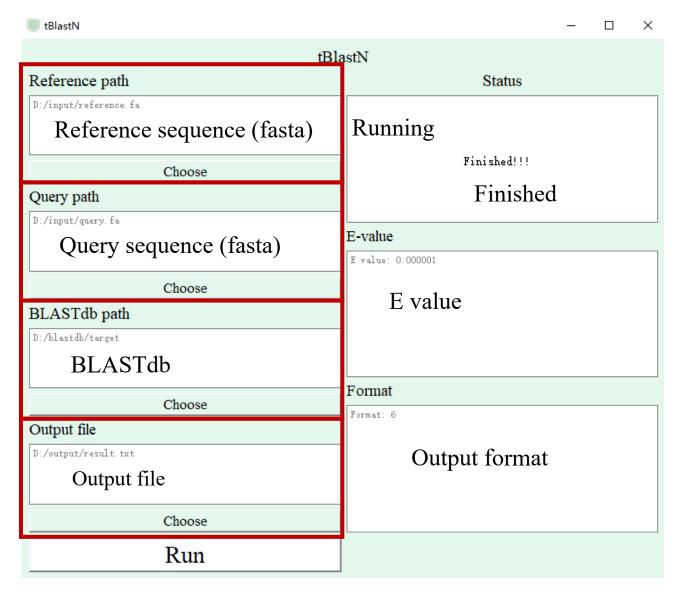


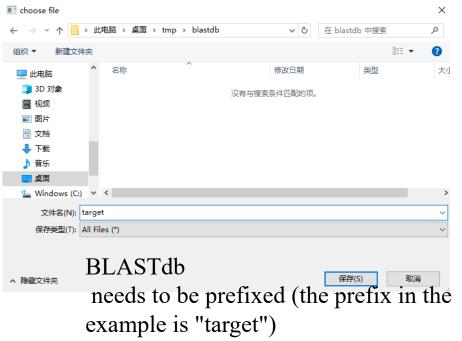


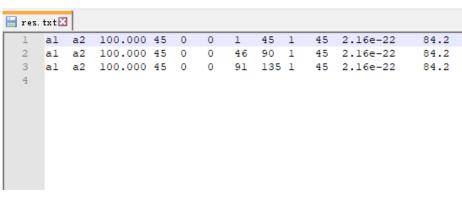


### tBlastN



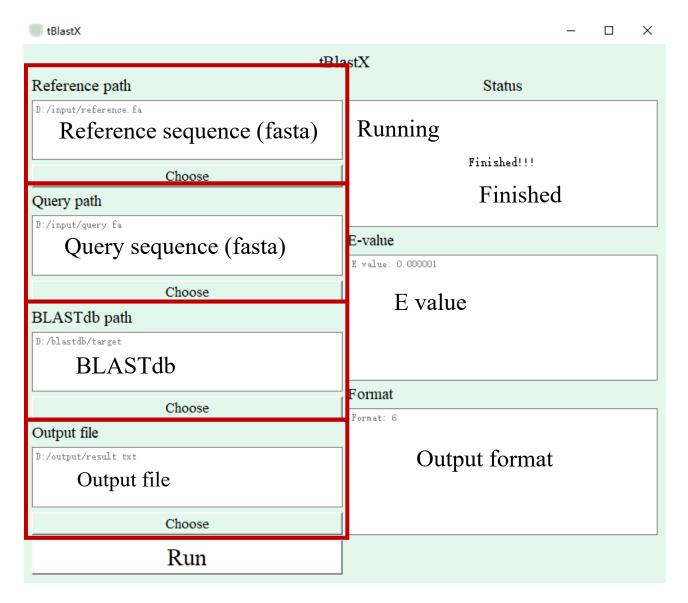


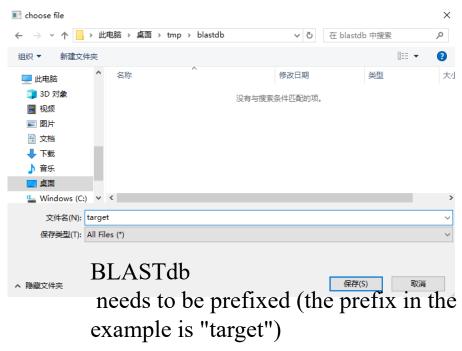


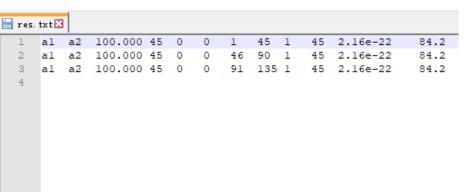


### tBlastX



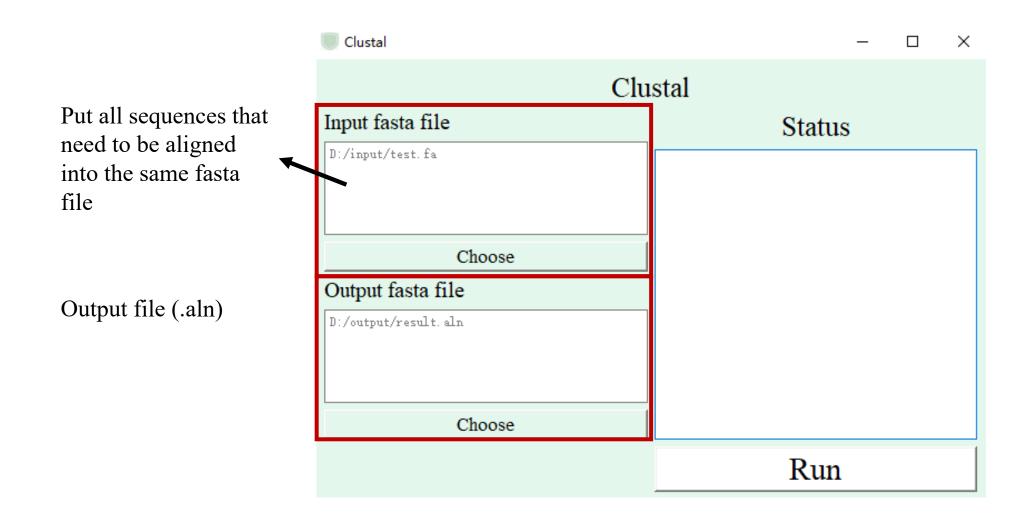






# Alignment - Clustal for example





## Build Tree - Fasttree for example



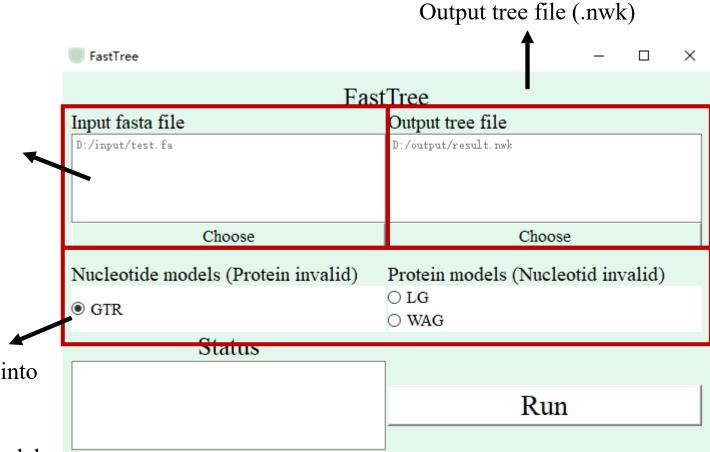
Put all sequences that need to be aligned into the same fasta file

Different construction models, divided into nucleic acids and proteins:

GTR: General Time Reversible Model

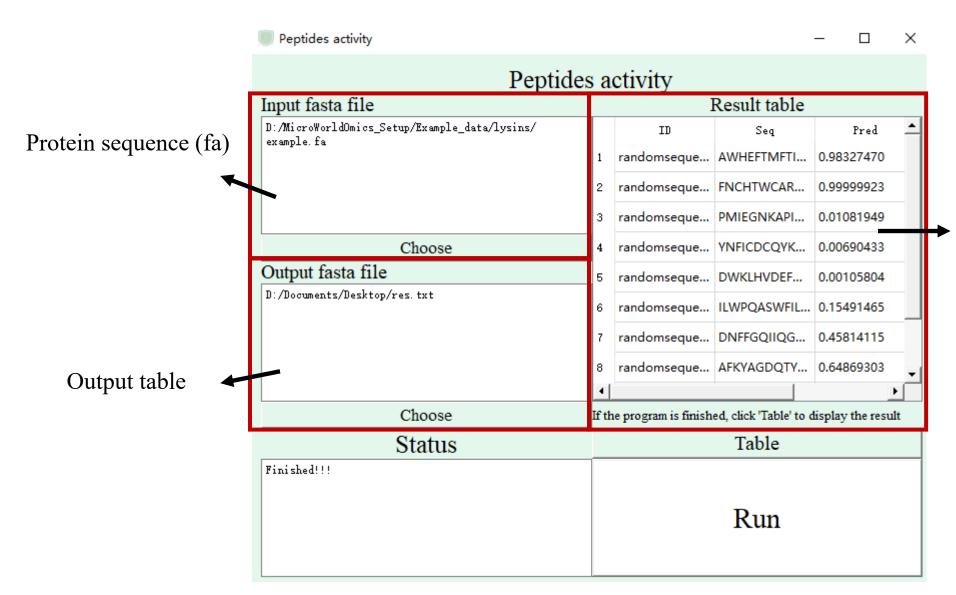
LG: Le and Gascuel

WAG: Whelan & Goldman



## Peptides activity

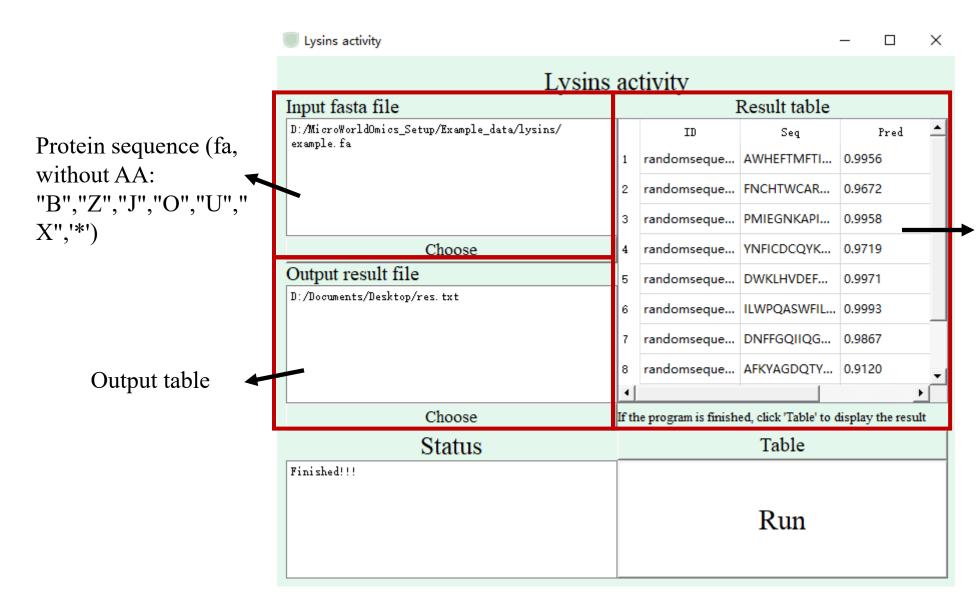




The result table shows that the first column is the protein ID, the second column is the sequence, and the third column is the activity score (0-1). A score close to 1 indicates better activity

## Lysins activity





The result table shows that the first column is the protein ID, the second column is the sequence, and the third column is the activity score (0-1). A score close to 1 indicates better activity