

## Section IV.1: Tracker – Similarity (p129 - p134)

See the full manual [here](#).

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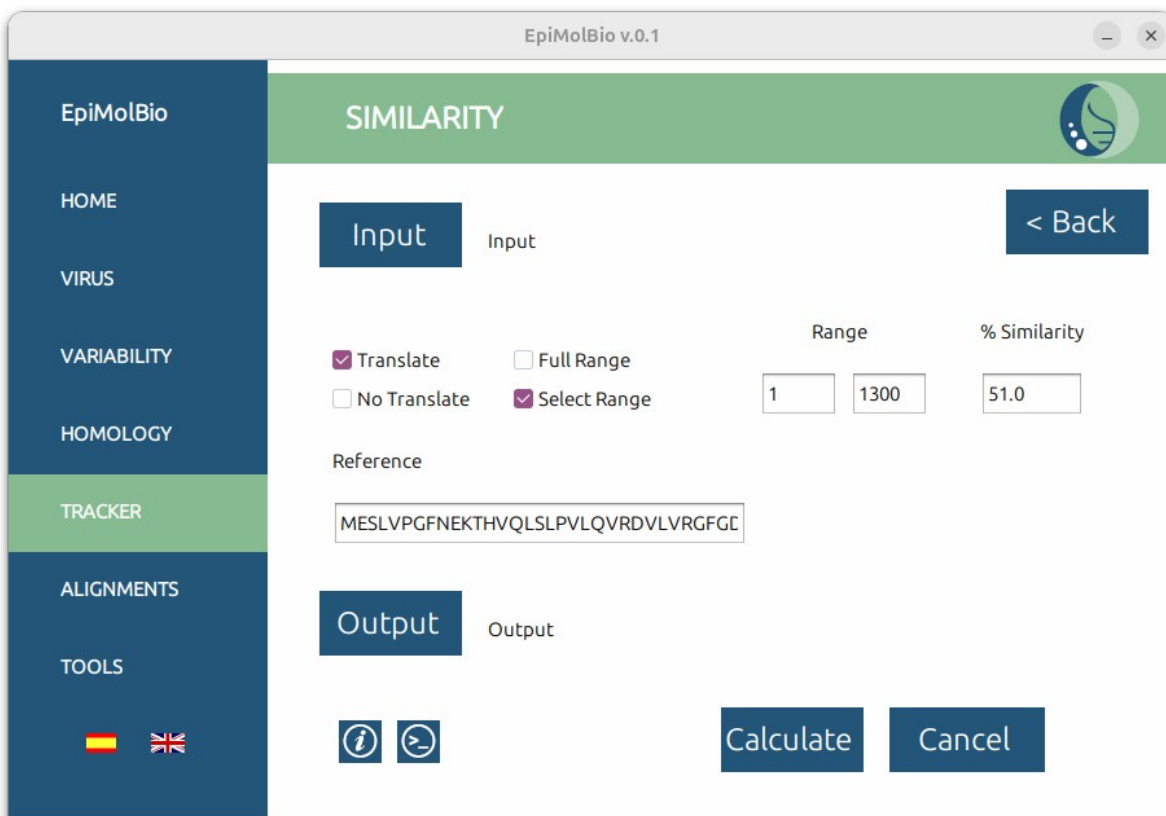
### Example File

File Name: TRACKED SIMILARITY SARS-COV-2 (NSP1).fasta

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### Parameter Selection

- **Translate/No Translate:**
  - *Translate*
- **Full/Select:**
  - *Select Range*
- **Range:**
  - 1 - 1300
- **% Similarity:**
  - 51.0
- **Reference:**
  - MESLVPGFNEKTHVQLSLPVLQVRDVLVRGFGDSVEEVLSEARQHLKDGTCGLVEVEKGVLPQL  
EQPYVFIKRS DARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPHVGEIPVAYRKVLLRKNGNK  
GAGGHRYGADLKSF DLGDELGTD PYEDFQENWNIKHSSGVTRELMRELNGG



The screenshot shows the EpiMolBio v.0.1 SIMILARITY interface. The left sidebar contains navigation links: HOME, VIRUS, VARIABILITY, HOMOLOGUE, TRACKER (highlighted), ALIGNMENTS, and TOOLS. At the bottom of the sidebar are flags for Spanish and English. The main content area has a green header with the title 'SIMILARITY' and a logo. Below the header, there are tabs for 'Input' and 'Output'. The 'Input' tab is active, showing options for 'Translate' (checked), 'Full Range' (unchecked), 'No Translate' (unchecked), and 'Select Range' (checked). There are input fields for 'Range' (1 to 1300) and '% Similarity' (51.0). A 'Reference' text box contains the sequence: MESLVPGFNEKTHVQLSLPVLQVRDVLVRGFGC. At the bottom, there are 'Calculate' and 'Cancel' buttons, along with information and help icons.