- Reference protein selection
  - 'Protein database' (Swiss-Prot, trEMBL + personal data)
  - 'Cross-hybridization database' (transcribed regions ENV, PRO, FUN 5'-UTR + CDS + 3'-UTR)

- Extraction of candidate protein sequences
  - BLASTp

- Multiple alignment
  - ClustalW
  - Divergent size filter

- Backtranslation
  - Probe size
  - Inosine (%) threshold
  - Degeneracy threshold

- Specificity checking
  - Expected value threshold

- Cross-hybridizations confirmation
  - BLASTx
  - BLASTn
  - Kane's criteria
  - Enzyme family comparison
  - Clustering cross-hybridizations

- Displayed results