BLAST
Find closest seq in large DB, transfer annotations

InterProScan
Apply >50,000 signatures & HMMs

MEGERSTCFYY
FWAWLPINAWE
LPMEEEFSTPI
LNRRFLAWAFL

Input: amino acid sequence

- **Amylase activity**

- **Exported protein**

Output: annotation with a subset of >10,000 multi-hot labels

Apply single deep neural network

ProteInfer