Database with sequences and annotations

Non-redundant Database (Uniref90)

Filtering by evidence codes

Filtering predicted proteins

BLAST (Blastp/Blastx)

Search for a highly similar sequence

Search for an ortholog

Sma3s algorithm

Sequence to annotate

Most probable gene name and description

All significant Blast hits by “length vs % identity” + annotation enrichment

Annotation report

Functional categories

Annotations: GO, keywords, EC numbers and pathways