

## RetroPath2.0 parameters for Naringenin

Below are listed the RetroPath2.0 parameters in order to reproduce the naringenin results. See “*RetroPath2.0\_tutorial*” file for a step-by-step guide.

### Case A

- Input
  - Pathway length: 5
  - Source: path to “*naringenin/source.csv*” file (naringenin)
  - Sink: path to “*naringenin/sink\_A.csv*” file (tyrosyne and phenylalanine compounds)
  - Rules: path to “*naringenin/rules.csv*” file
- Output
  - Result folder: path to the desired output folder (should exists before execution)
- Result expected
  - No scope found since side-products of some reactions are not in sink.

### Case B

- Input
  - Pathway length: 5
  - Source: path to “*naringenin/source.csv*” file (naringenin)
  - Sink: path to “*naringenin/sink\_B.csv*” file (all *E. coli* compounds)
  - Rules: path to “*naringenin/rules.csv*” file
- Output
  - Result folder: path to the desired output folder (should exists before execution)
- Result expected
  - The generated metabolic graph (*.json* file in the result folder) can be visualized using the Scope Viewer.