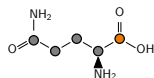


Cumulative explained mass flow (0-99%)

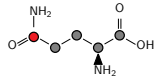
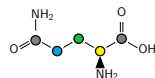


Figure 1: A schematic diagram of the metabolic map of the TCA cycle and its associated pathways. The cycle is represented by a large loop with various branches. The main cycle includes cit[m], icit[c], co2[c→s], succoa[m], suc[m], fum[m], mal[c], and mal[m]. Branches include cit[m] to asp[m] and oaa[m], cit[m] to glu[m] and akg[m], and succoa[m] to oaa[m]. The diagram is color-coded by AEFM: AEFM 1 (blue), AEFM 2 (red), AEFM 3 (green), AEFM 4 (yellow), and AEFM 5 (brown). A legend at the bottom left identifies these colors. A chemical structure of a molecule with two amino groups and a carboxyl group is shown at the bottom right.



The diagram illustrates a metabolic network with nodes representing metabolites (green), enzymes (blue), and cofactors (orange). The network includes various metabolic pathways, such as glycolysis and gluconeogenesis, and is labeled with 'Source' and 'Sink'.

Diagram illustrating the AEFM 1-5 pathway. The pathway is shown as a series of colored loops and straight segments. The top part shows a cycle involving oaa, asp, cit, and mal. The bottom part shows a linear segment involving akg and glu. The legend indicates five AEFMs: AEFM 1 (blue), AEFM 2 (red), AEFM 3 (green), AEFM 4 (orange), and AEFM 5 (brown). A chemical structure of a branched amino acid is shown at the bottom right.



The diagram illustrates the metabolic pathways connecting the Cytosol and Mitochondria, specifically focusing on the TCA cycle and its associated shuttles. The Cytosol is shown on the left, and the Mitochondria are shown on the right, separated by a double-line boundary.

Key Components:

- Non-canonical TCA cycle (Cytosol):** Includes metabolites $gln[s]$, $asp[c]$, $akg[c]$, $glu[c]$, and $oaa[c]$. These are connected by orange arrows, indicating a non-canonical pathway.
- Malate-aspartate shuttle:** Shown as an orange box, it facilitates the exchange of $mal[c]$ and $asp[c]$ between the Cytosol and Mitochondria.
- Canonical TCA cycle (Mitochondria):** Includes metabolites $cit[m]$, $icit[c]$, $co2[c]$, $co2[m]$, $succo[m]$, $suc[m]$, $fum[m]$, $mal[m]$, $glu[m]$, $akg[m]$, and $asp[m]$. These are connected by red arrows, indicating the canonical pathway.
- Shuttles:**
 - Malate-aspartate shuttle:** Transfers $mal[c]$ to $mal[m]$ and $asp[c]$ to $asp[m]$.
 - Other shuttles:** $gln[s]$ is converted to $gln[m]$ and then to $asp[c]$. $icit[c]$ is converted to $icit[m]$ and then to $co2[m]$.

The diagram uses color-coding: orange for the non-canonical cycle and malate-aspartate shuttle, and red for the canonical cycle and other shuttles. Blue circles represent metabolites, and green circles represent metabolites that are part of the canonical cycle. The labels $gln[s]$, $asp[c]$, $akg[c]$, $glu[c]$, and $oaa[c]$ are in the Cytosol, while $cit[m]$, $icit[c]$, $co2[c]$, $co2[m]$, $succo[m]$, $suc[m]$, $fum[m]$, $mal[m]$, $glu[m]$, $akg[m]$, and $asp[m]$ are in the Mitochondria.