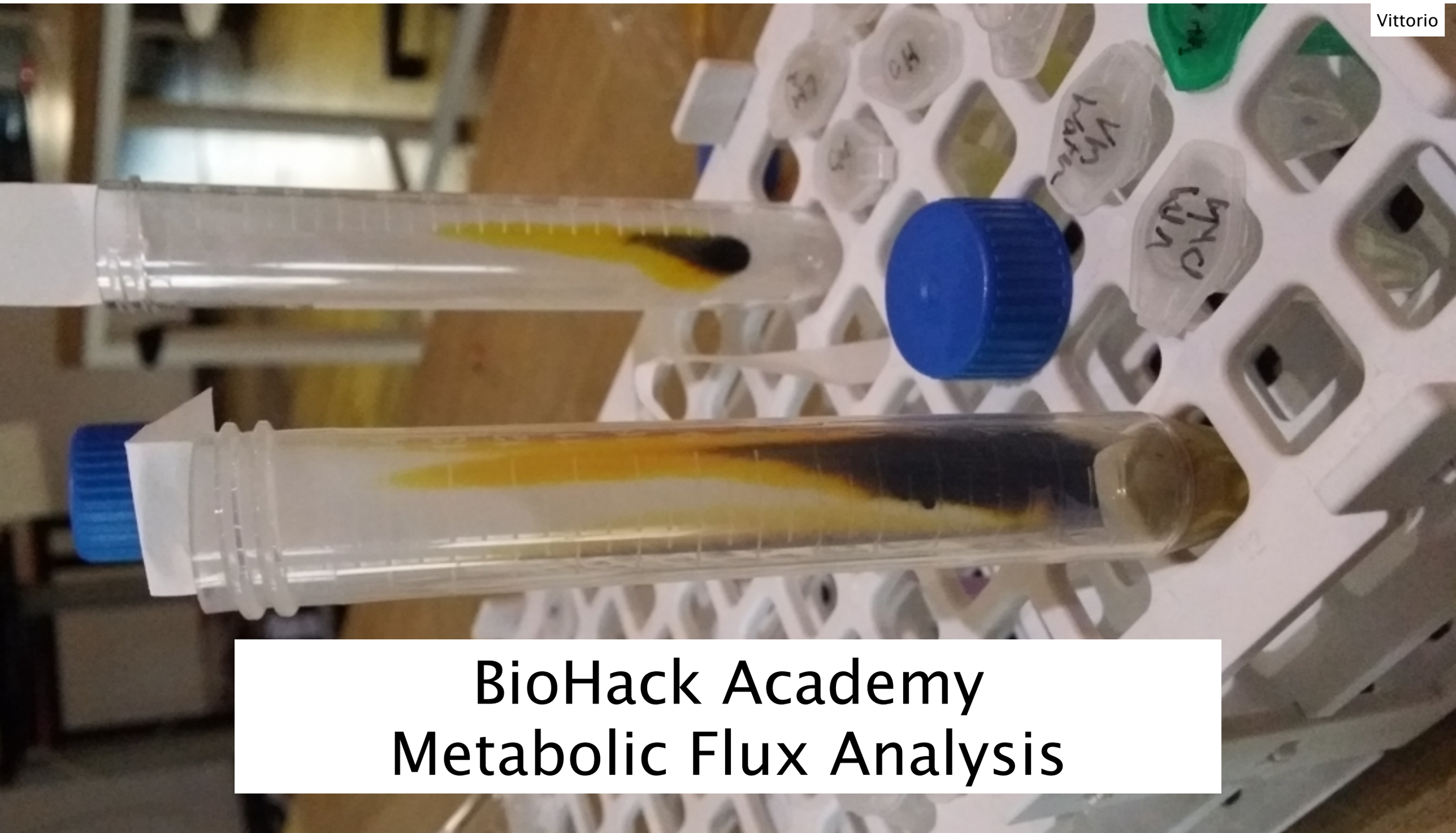
waag society

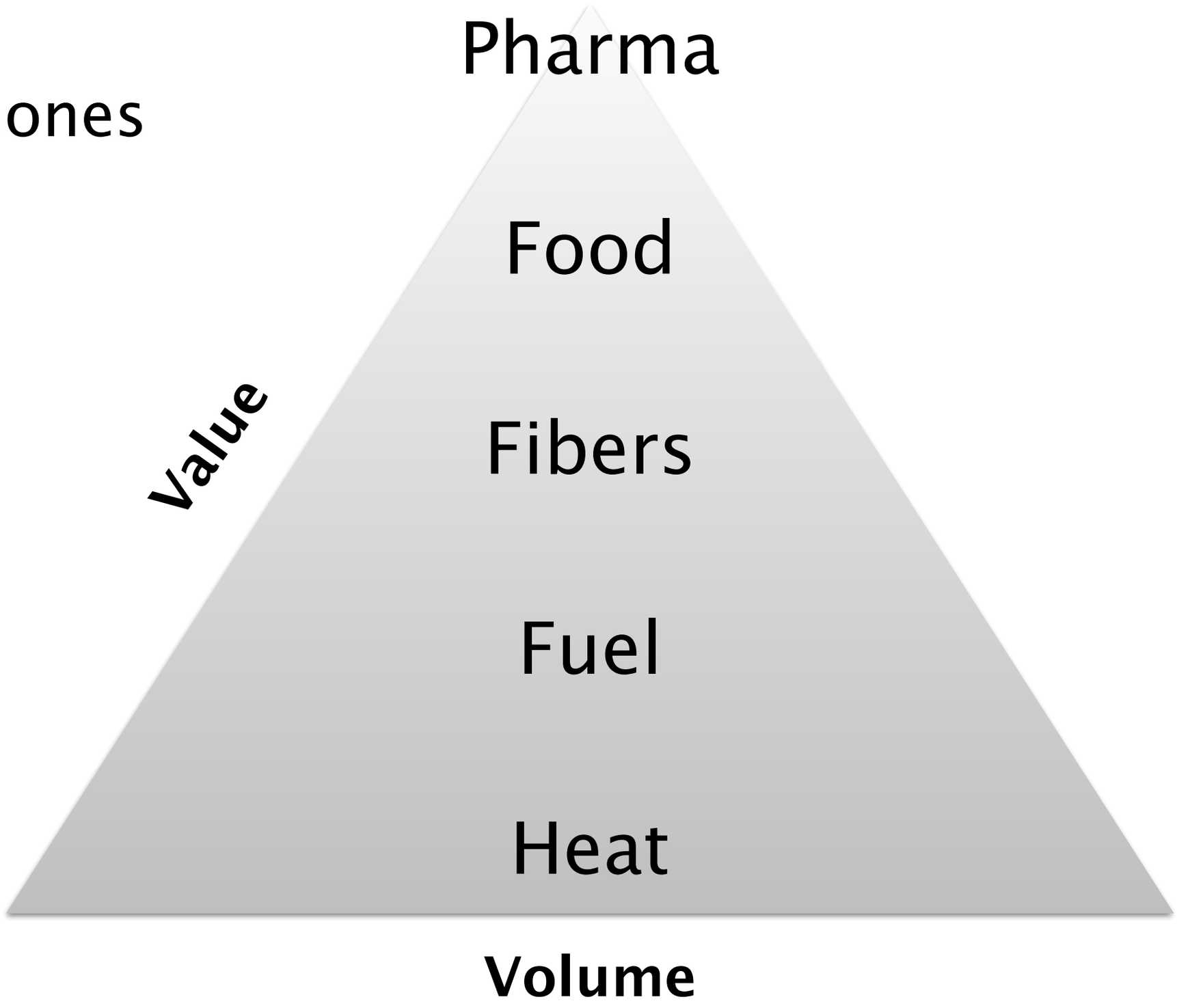
institute for art, science and technology




# BioHack Academy
# Metabolic Flux Analysis

# Bioreactor value pyramid

- Antibiotics
- Steroids / hormones
- Vitamins
- Proteins
- Sugars
- Acids



# Bioreactor value pyramid

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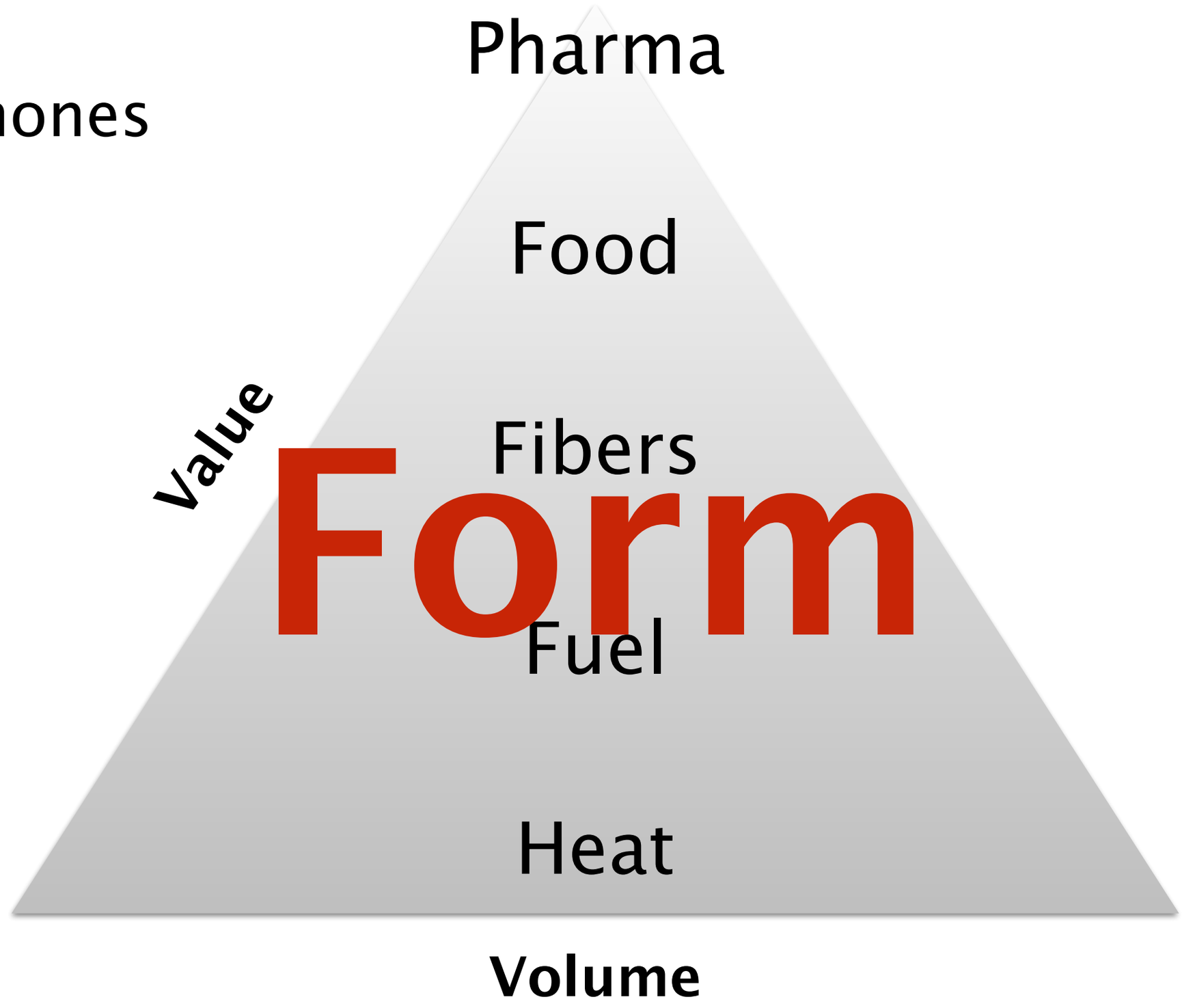
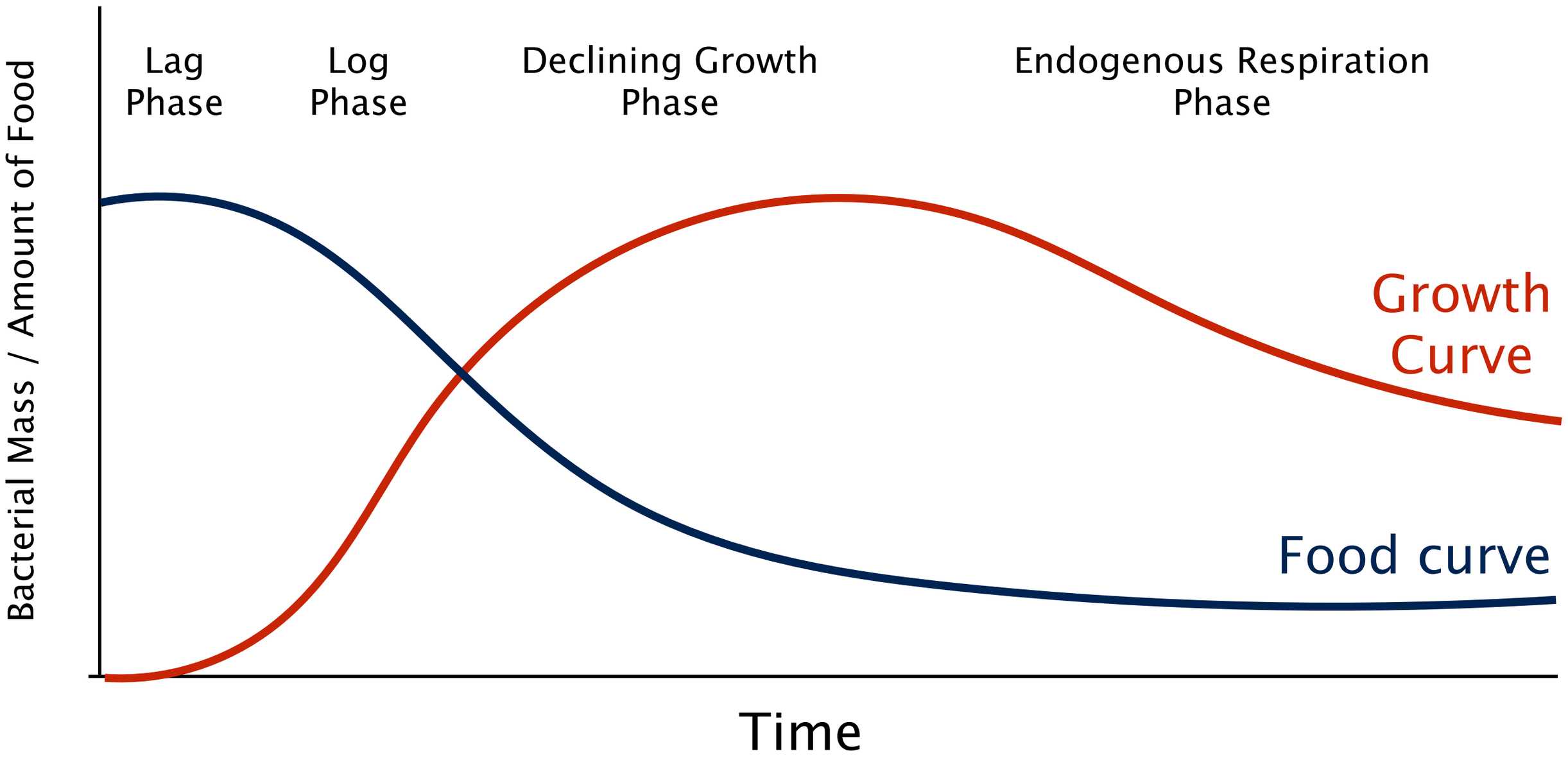
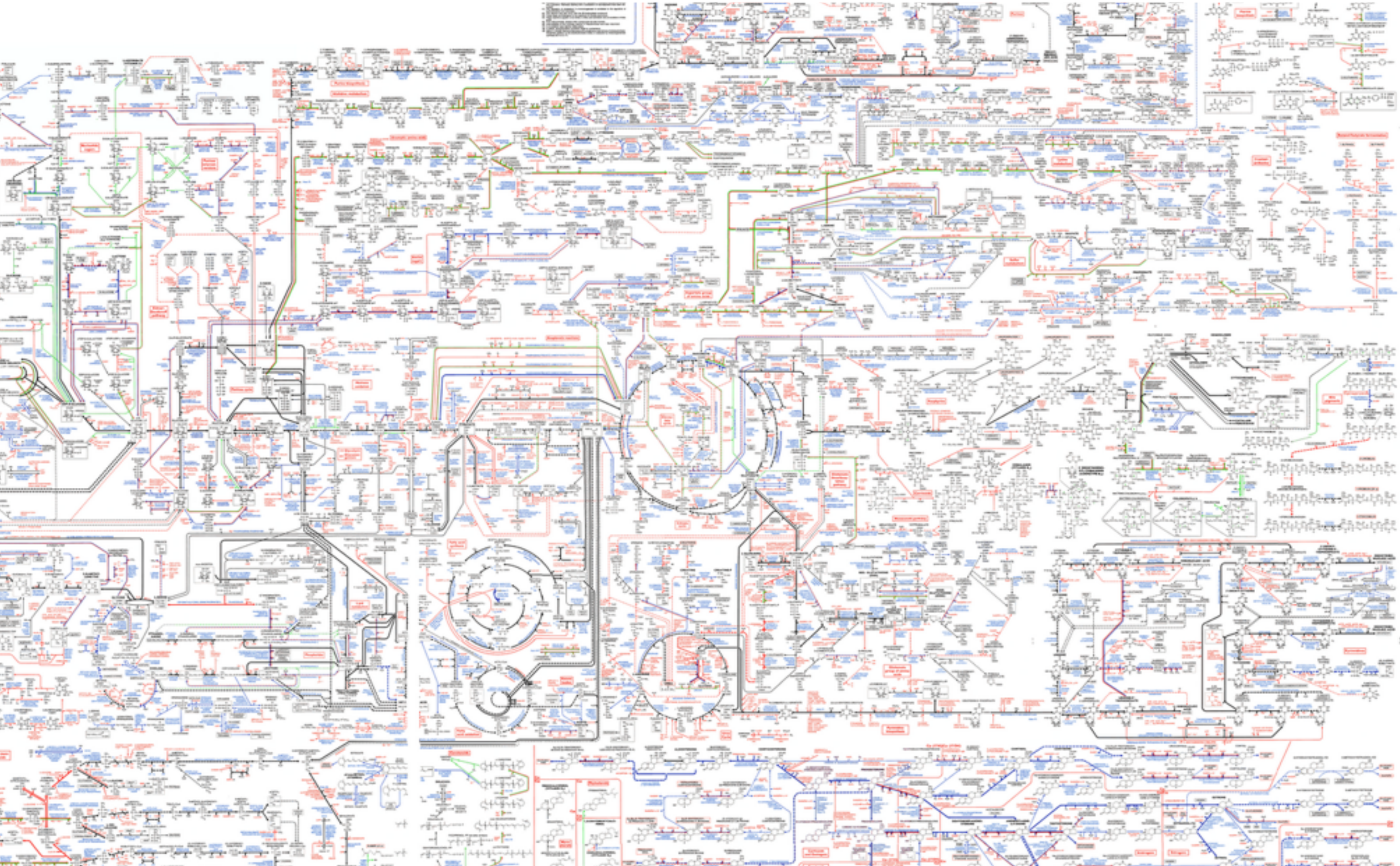


# Bacterial growth curve – Batch



# Metabolic Pathways



# Production pathway?

Tryptophan

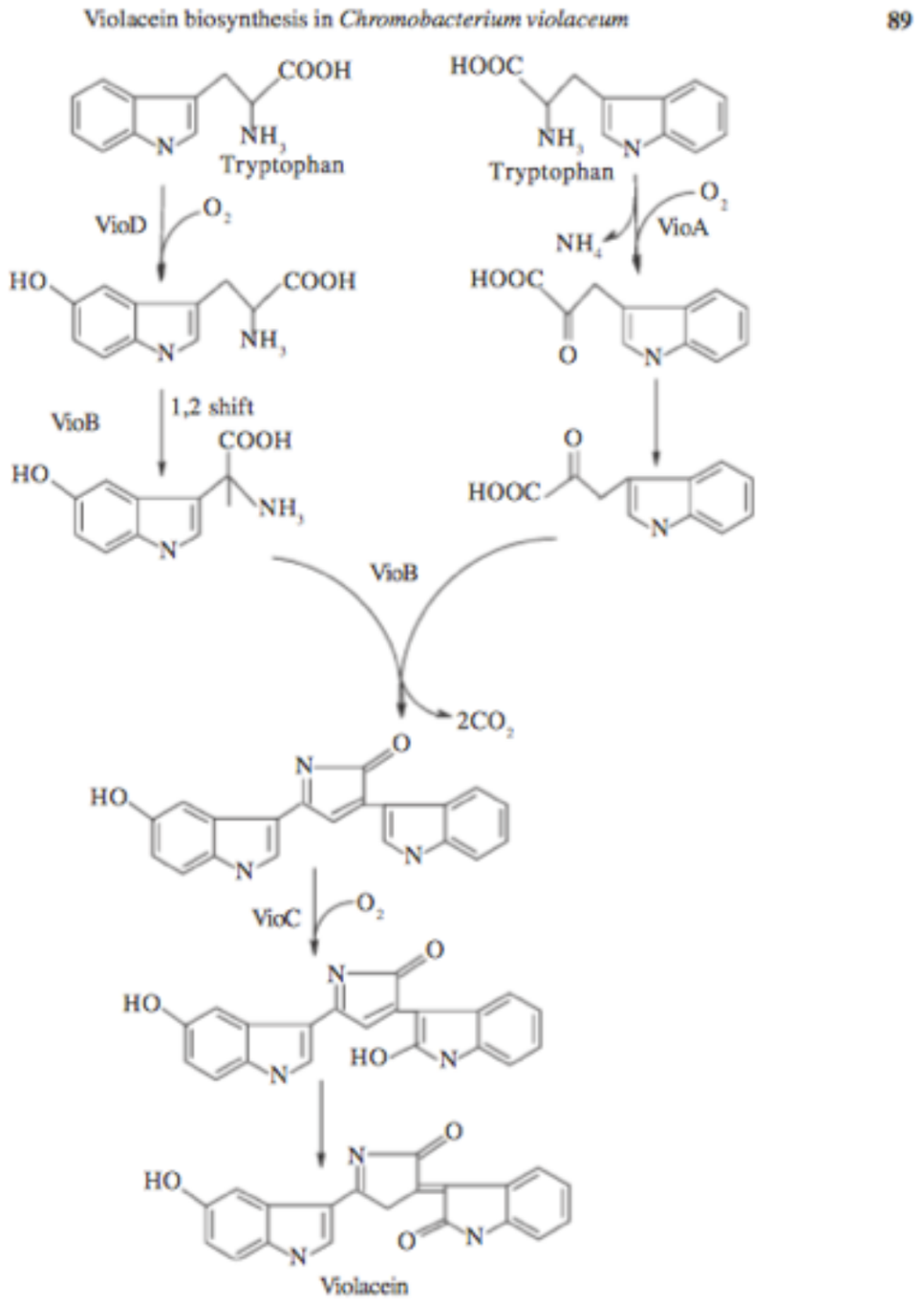


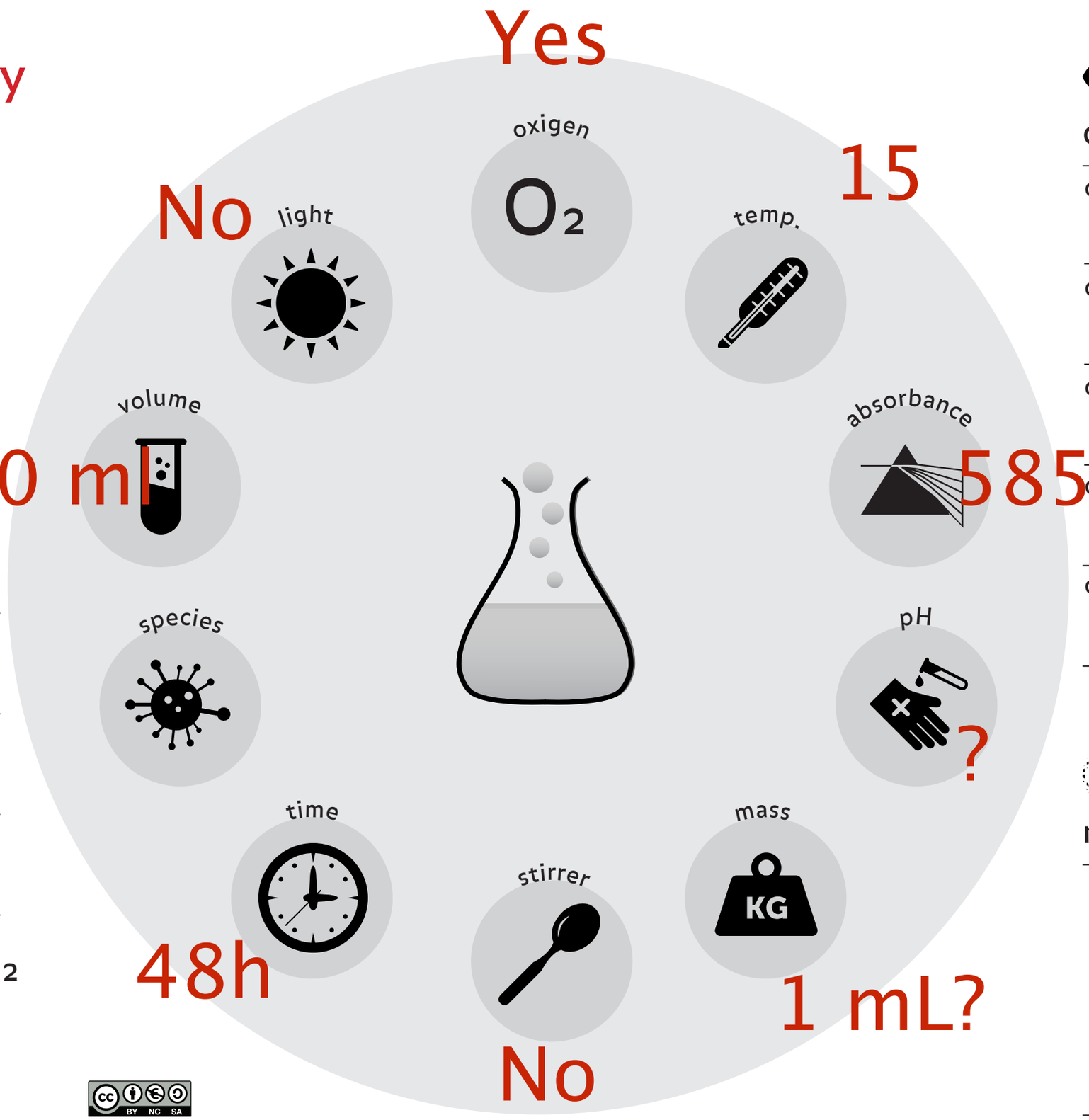

**Figure 2.** Violacein biosynthesis, as proposed by August et al., 2000. VioA, VioB, VioC, and VioD are the gene products of the biosynthesis operon, encoding nucleotide-dependent monooxygenases and a protein similar to a polyketide synthase (VioB).

Antonio, R.V. and Creczynski-Pasa, T.B. (2004) Genetics analysis of violacein biosynthesis by C. violaceum. Genet Mol Res 3, 85-91.

# J. Lividum canvas

BioFactory
canvas

open wetlab
waag society




input

C

N

P

$O_2$

S

Nutrient
Broth
Glycerol
Tryptoph.

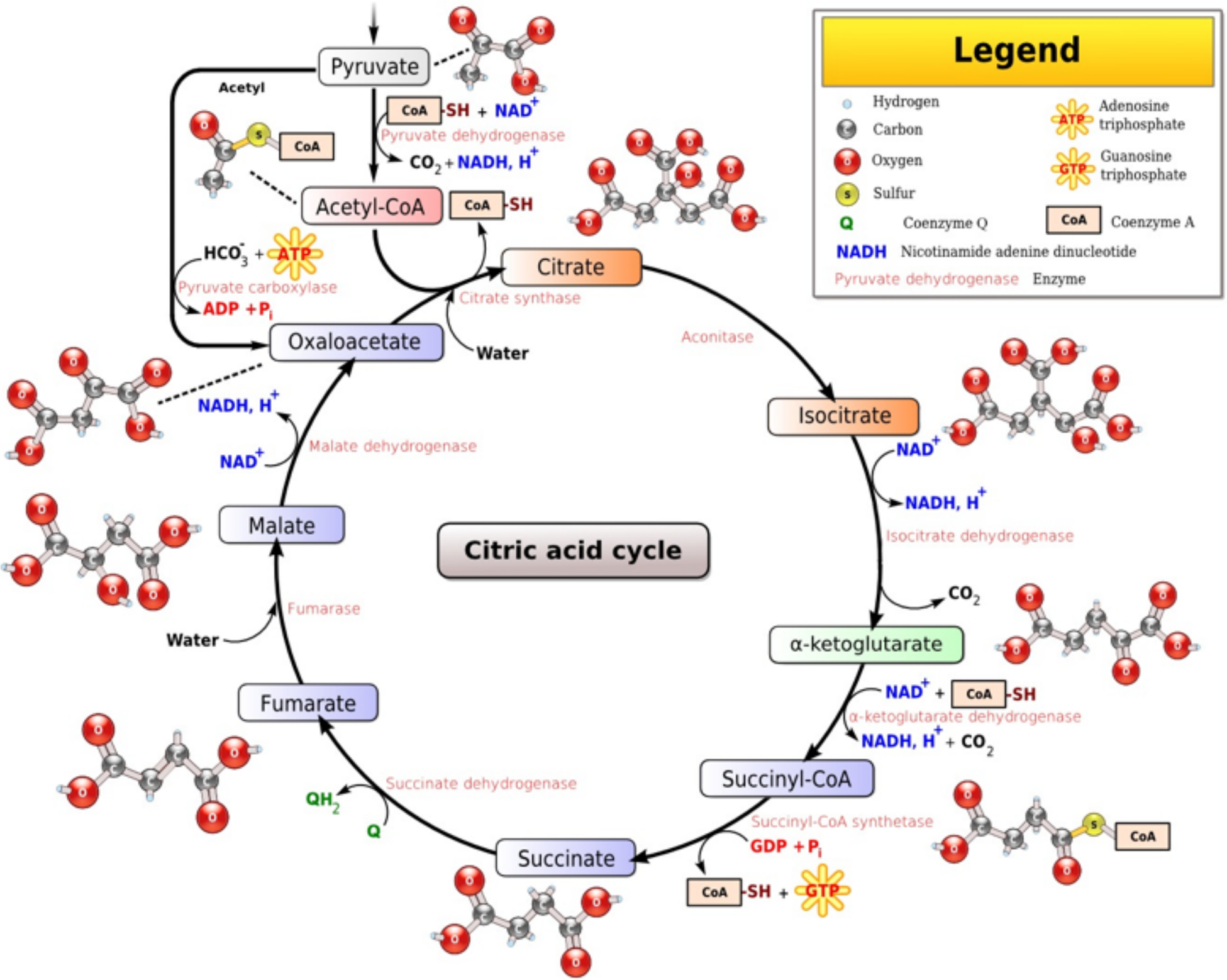
observations

| | |
|---|---|
| day # | |
| day # | |
| day # | |
| day # | |

material

CC BY NC SA

# Citric Acid Cycle

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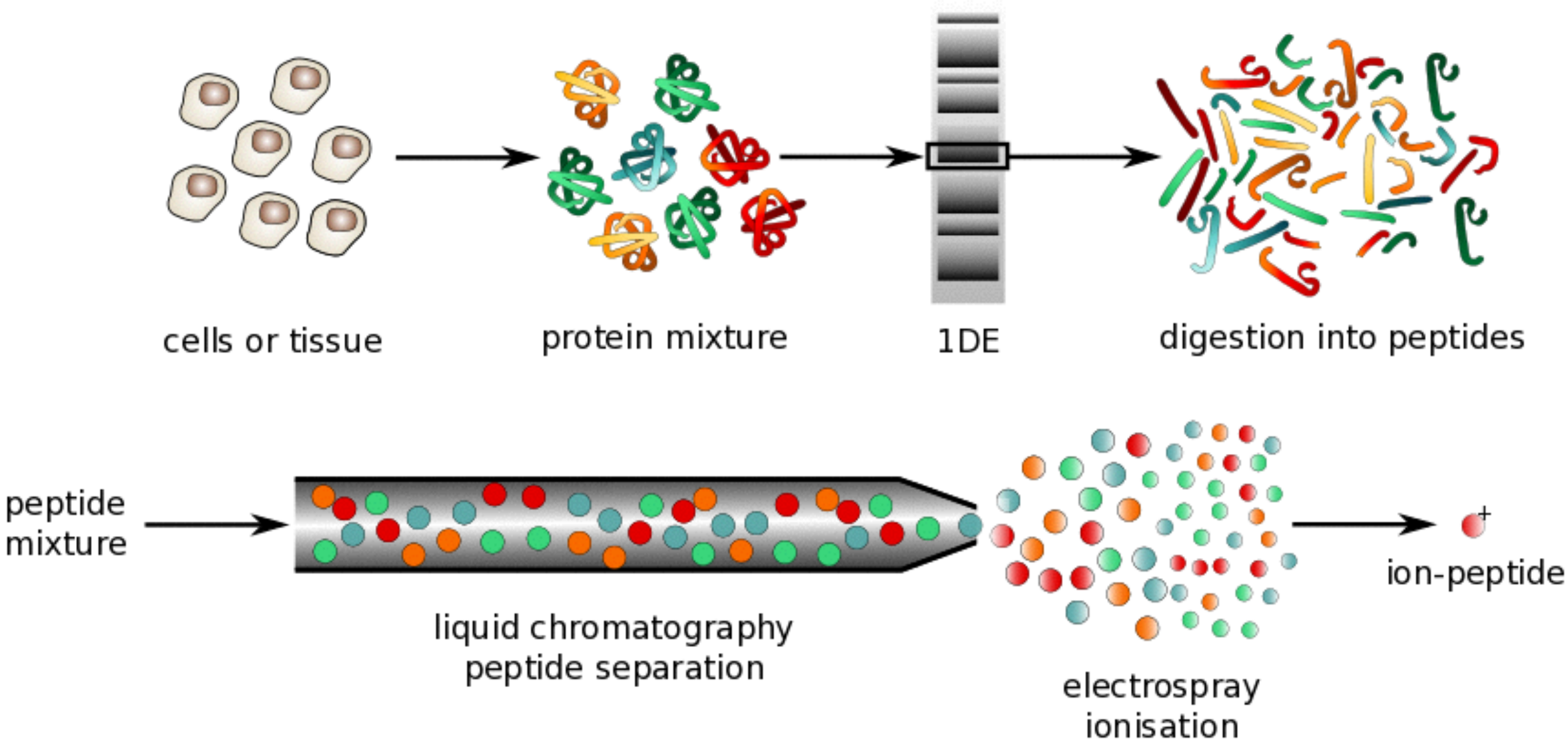
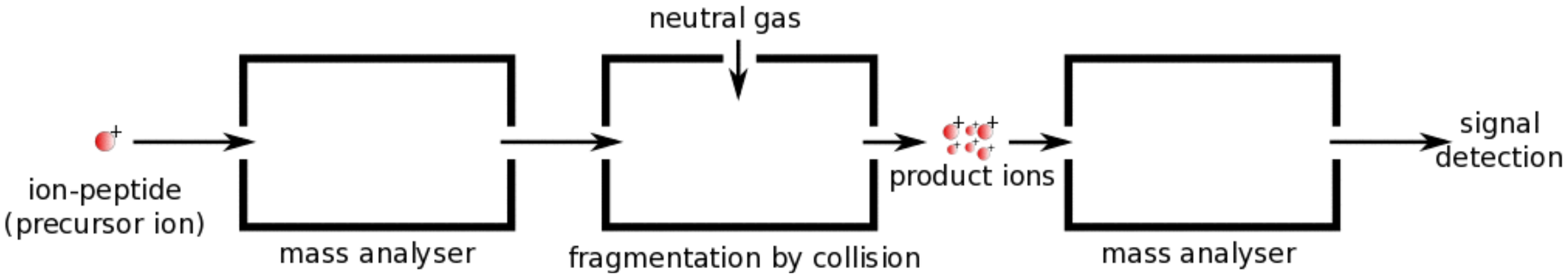
# Mass spectrometry




Philippe Hupé - CC-BY-SA 3.0

# Mass spectrometry

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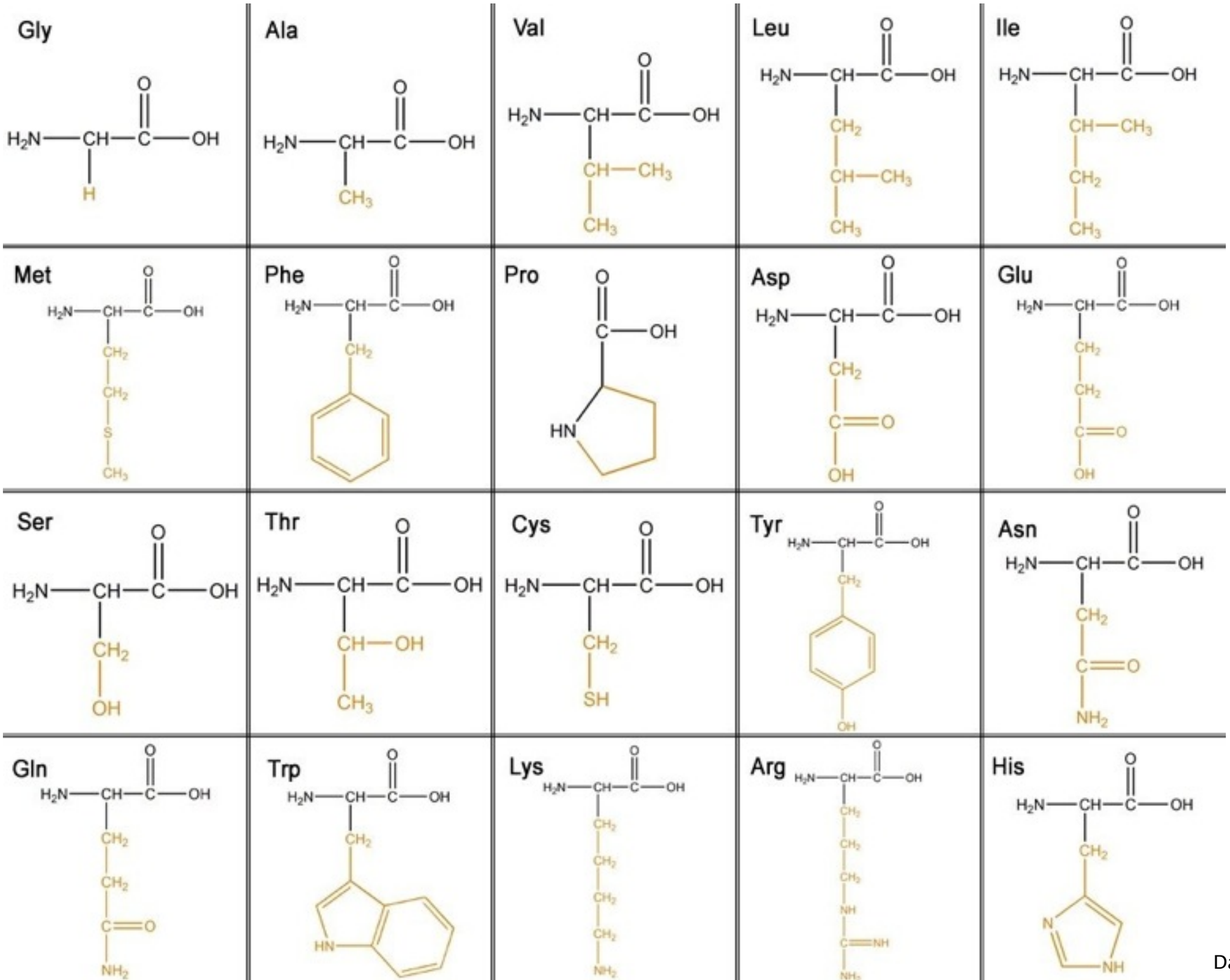
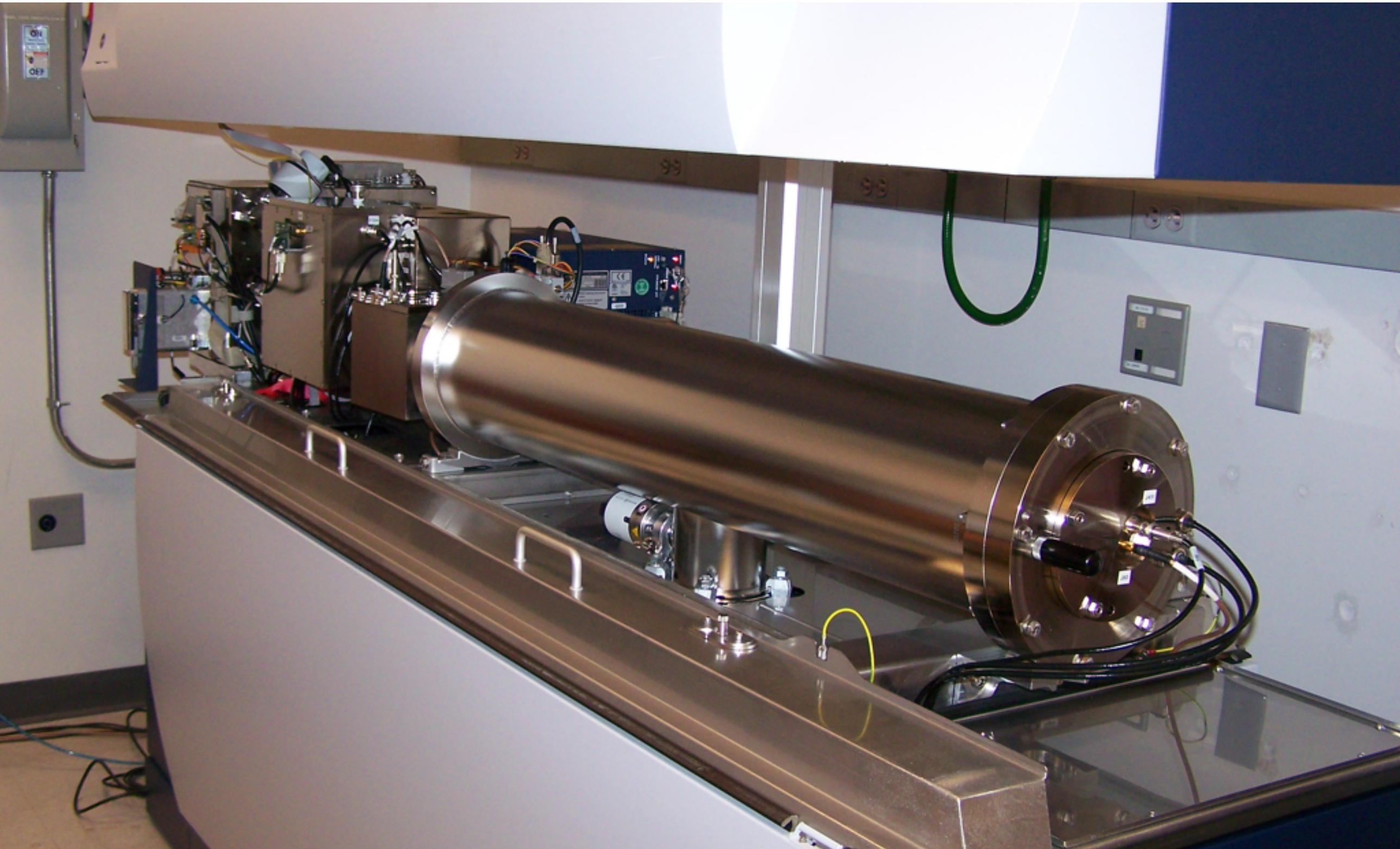
# Amino acids, the building blocks

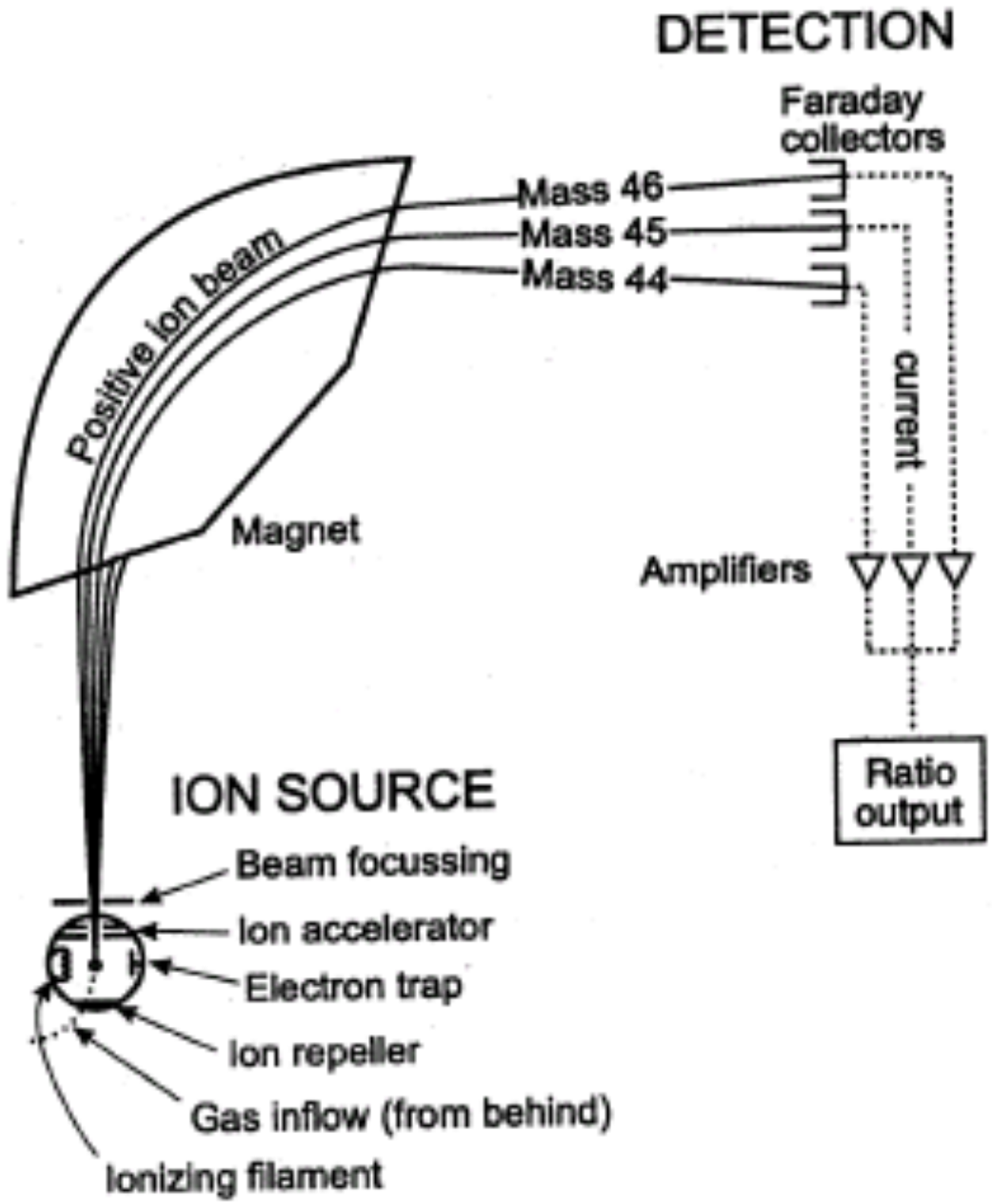



Dalibor Bosits CC-BY-SA 3.0

# Mass spectrometer

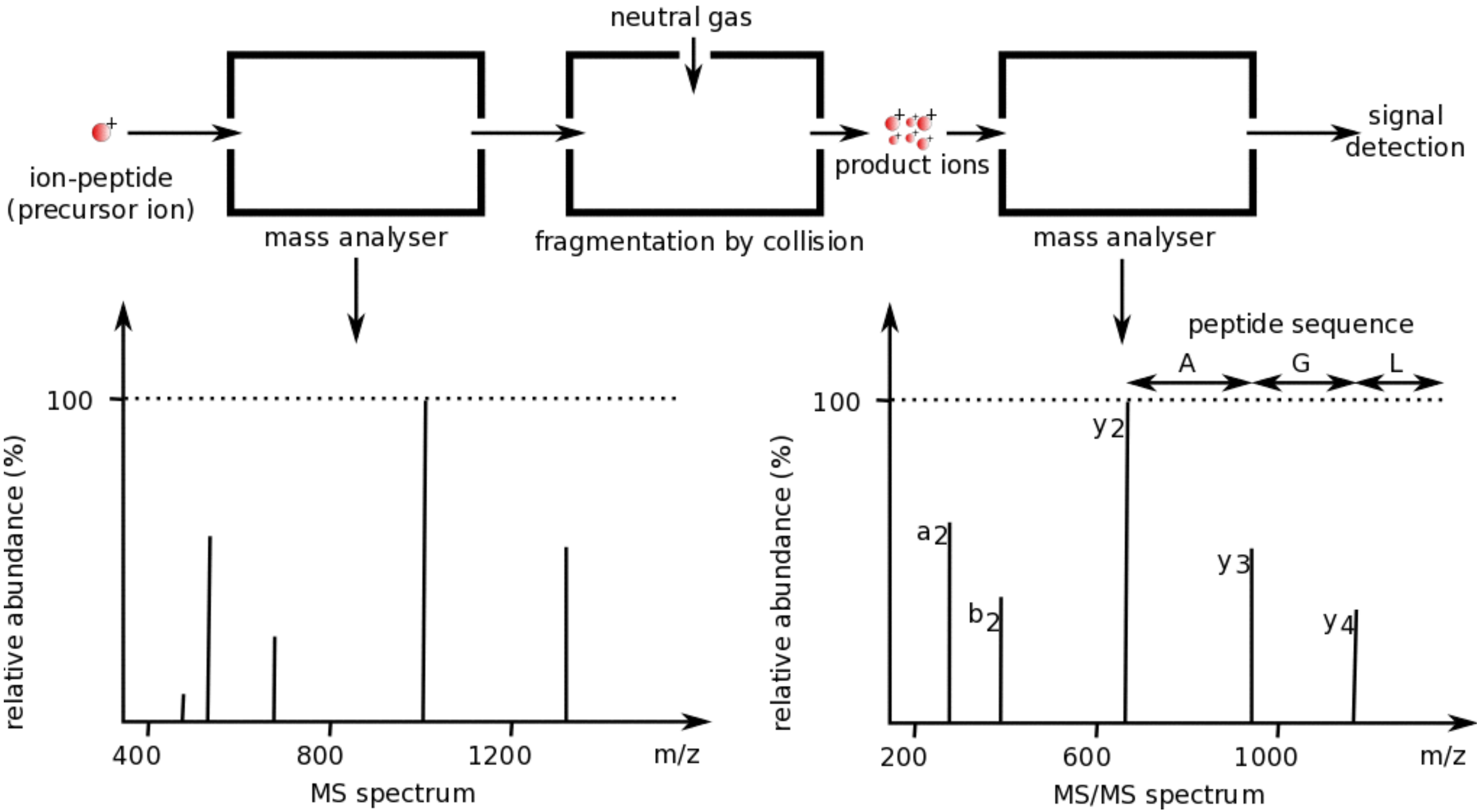


# Inside the machine




Public Domain

# Mass spectrometry

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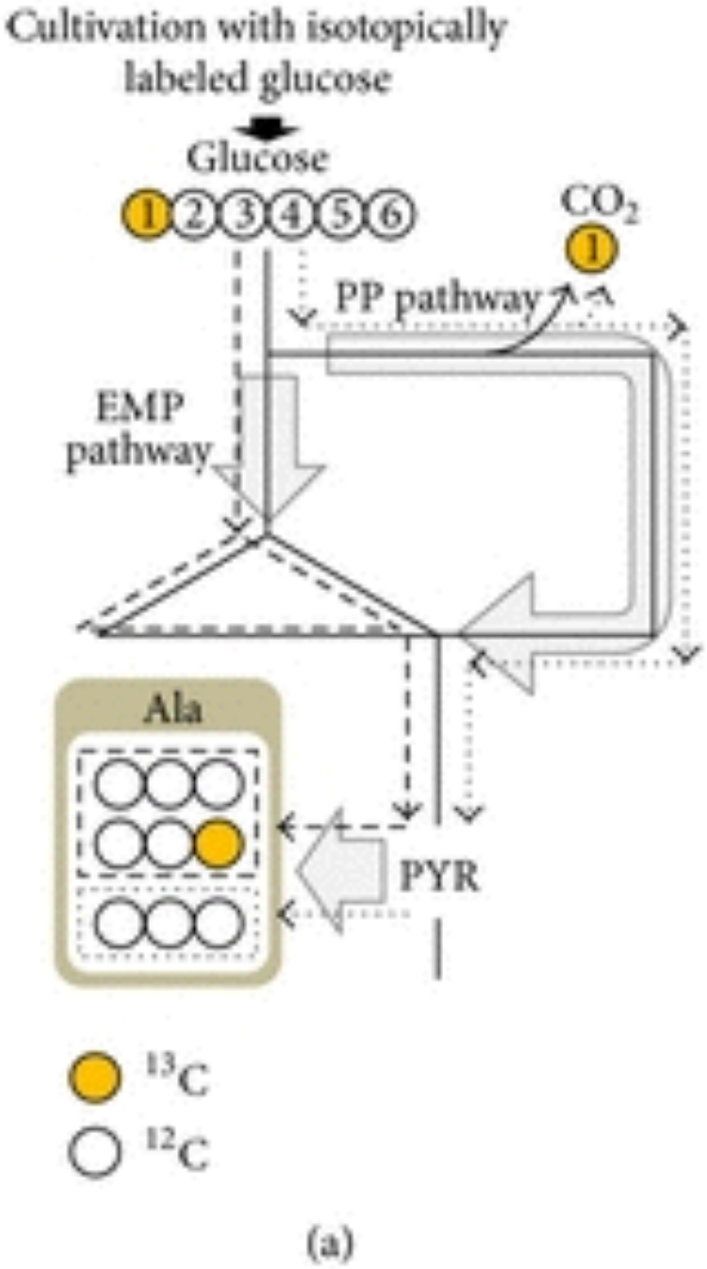
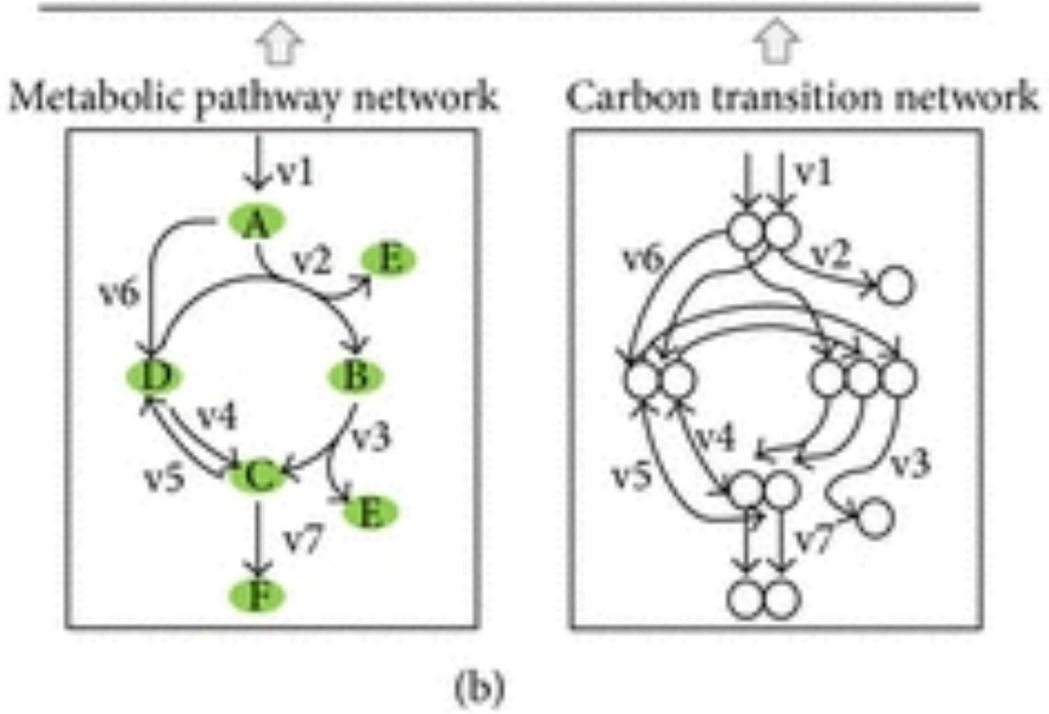
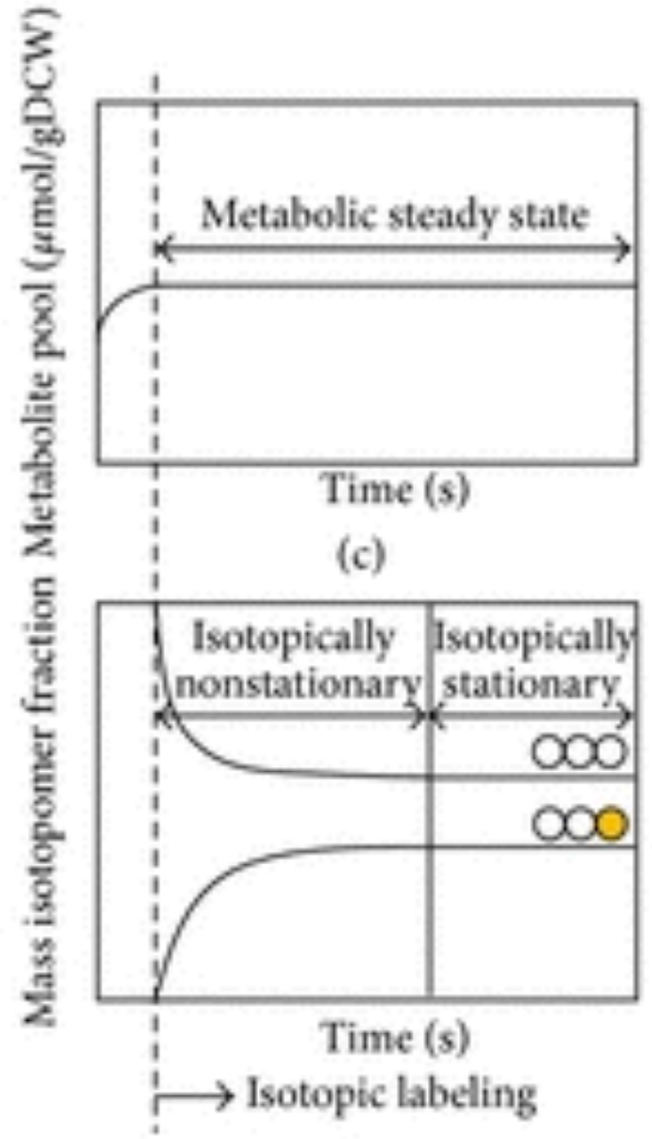
# C13 labeling




Metabolic_network.xlsx

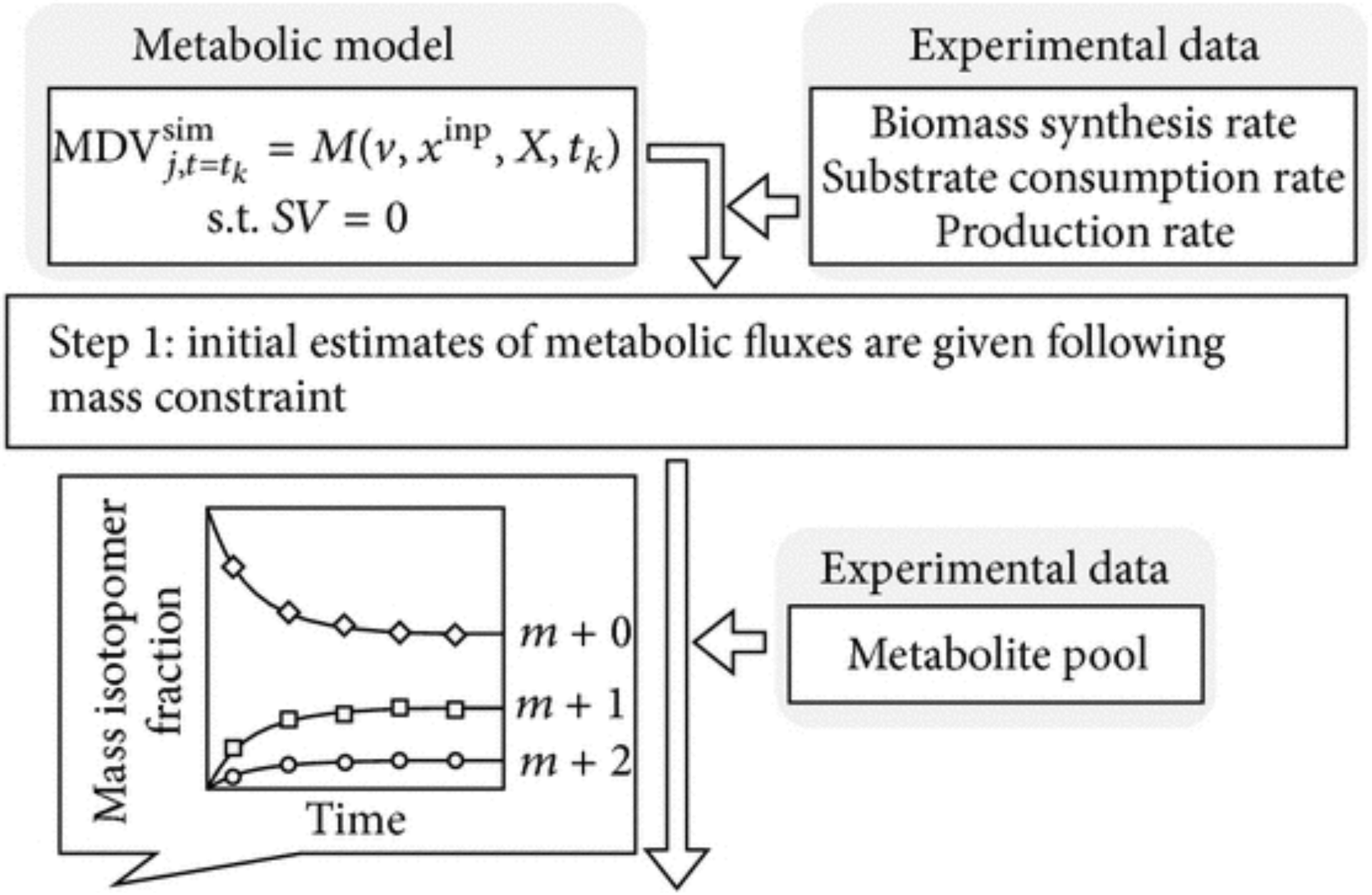
| FluxID | Rxns | NetFlux | Carbon_transitions |
|---|---|---|---|
| r1 | Sub_A ⟶ A | 0 | ab ⟶ ab |
| r2 | A + D ⟶ B + [E] | 0 | ab + cd ⟶ adc + b |
| r3 | B ⟶ C + [E] | 0 | abc ⟶ ab + c |
| r4 | D ⟶ C | 1 | ab ⟶ ba |
| r5 | C ⟶ D | 1 | ab ⟶ ba |
| r6 | A ⟶ D | 0 | ab ⟶ ab |
| r7 | C ⟶ [F] | 0 | ab ⟶ ab |




Shuichi Kajihata, Chikara Furusawa, Fumio Matsuda, and Hiroshi Shimizu, "OpenMebius: An Open Source Software for Isotopically Nonstationary 13C-Based Metabolic Flux Analysis," BioMed Research International, vol. 2014, Article ID 627014, 10 pages, 2014. doi:10.1155/2014/627014

# Metabolic modeling

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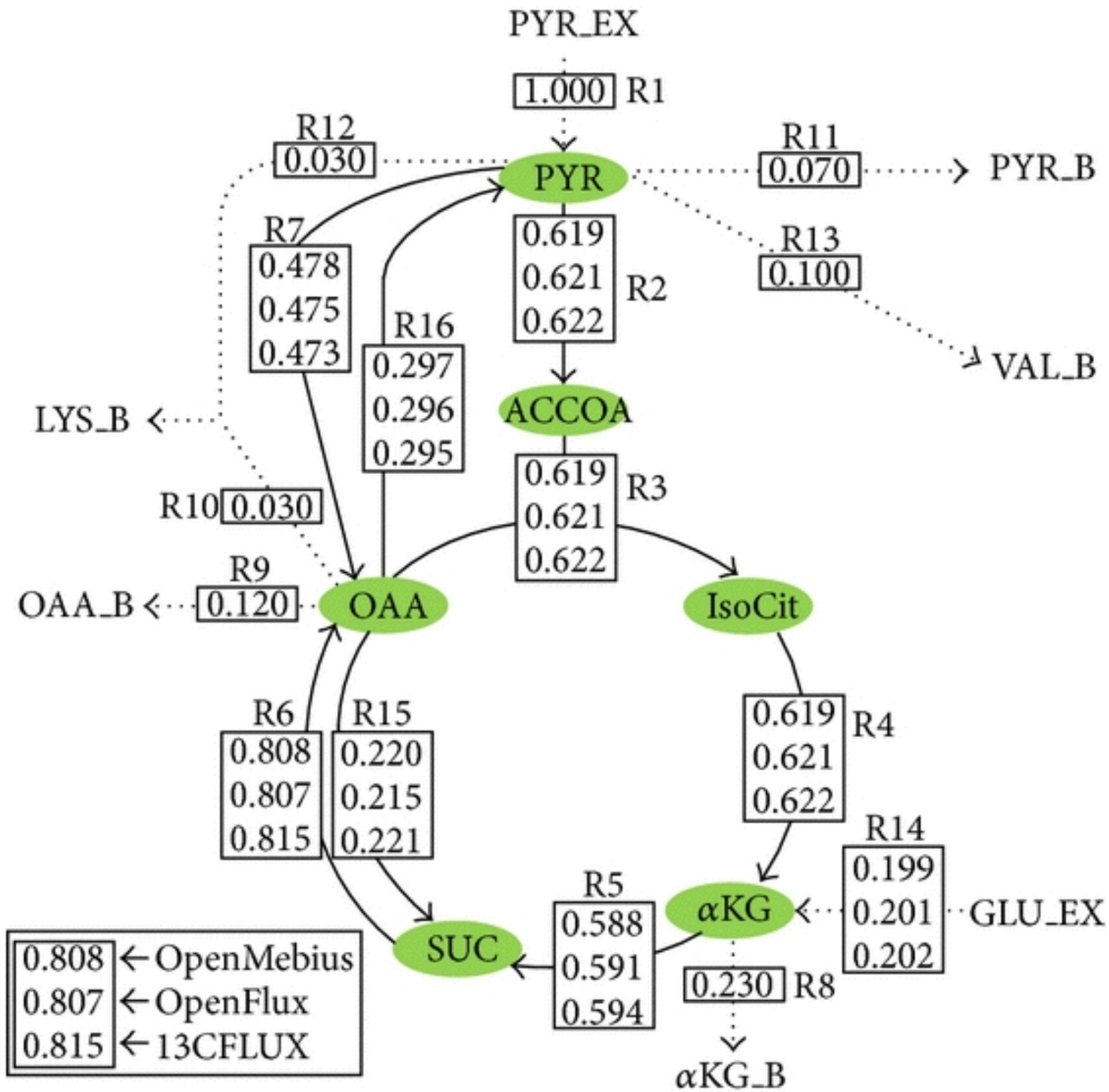
# Flux estimations

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# MFA Software

- 13CFLUX
- 13CFLUX2
- C13
- Metran
- FIA
- influx_s
- OpenFLUX

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