

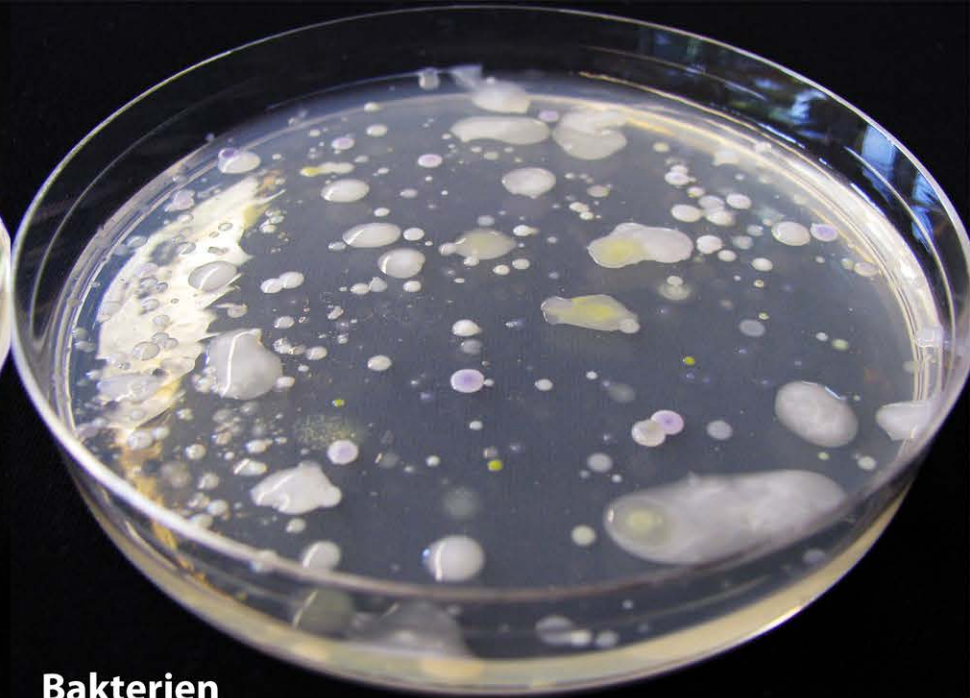


Quantifizierung von
Bakterien und Pilzen

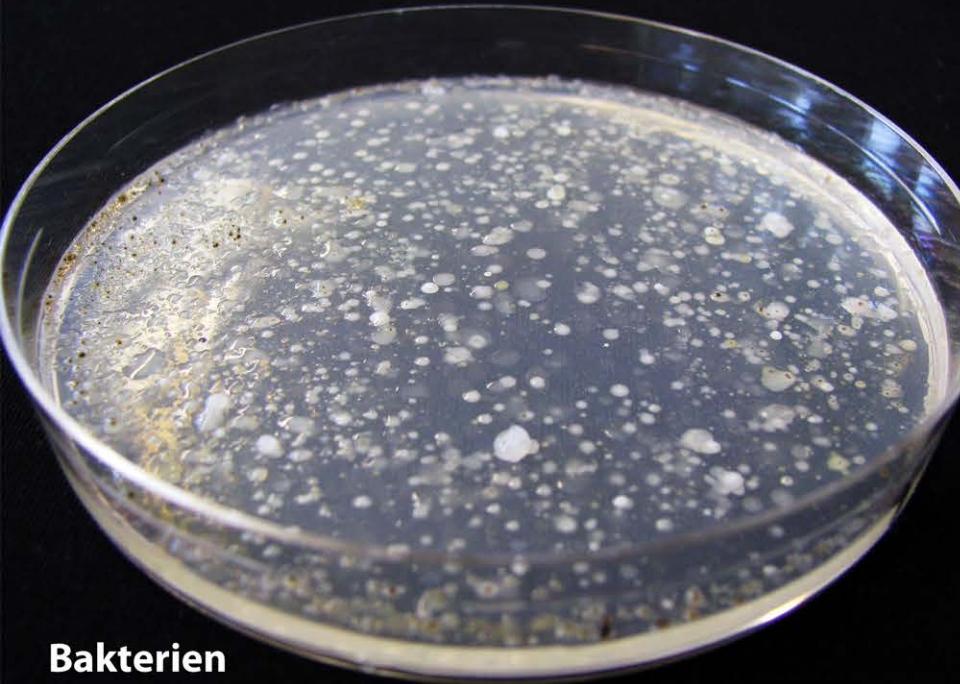
Phospho Lipid Fettsäure Analysen



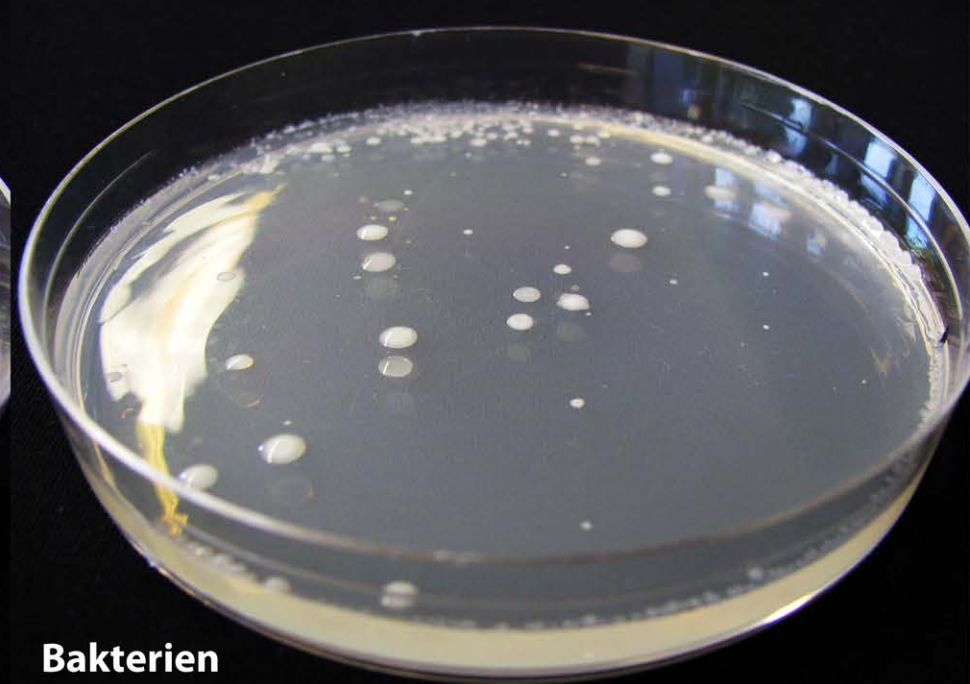
Pilze



Bakterien

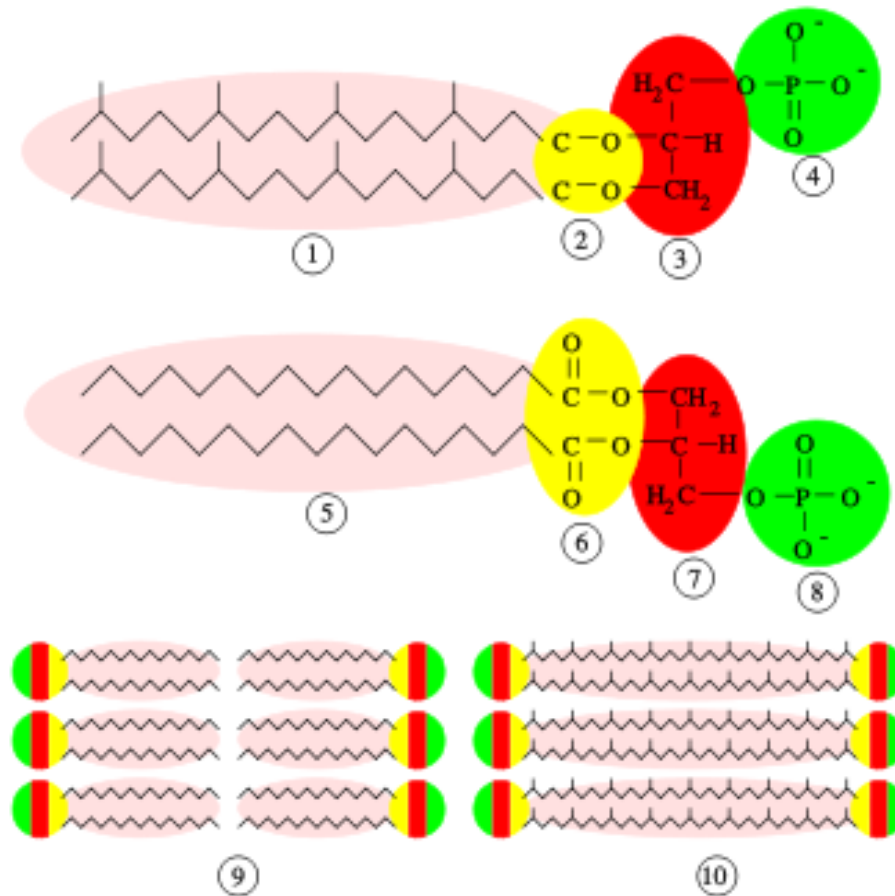


Bakterien



Bakterien

Membranen



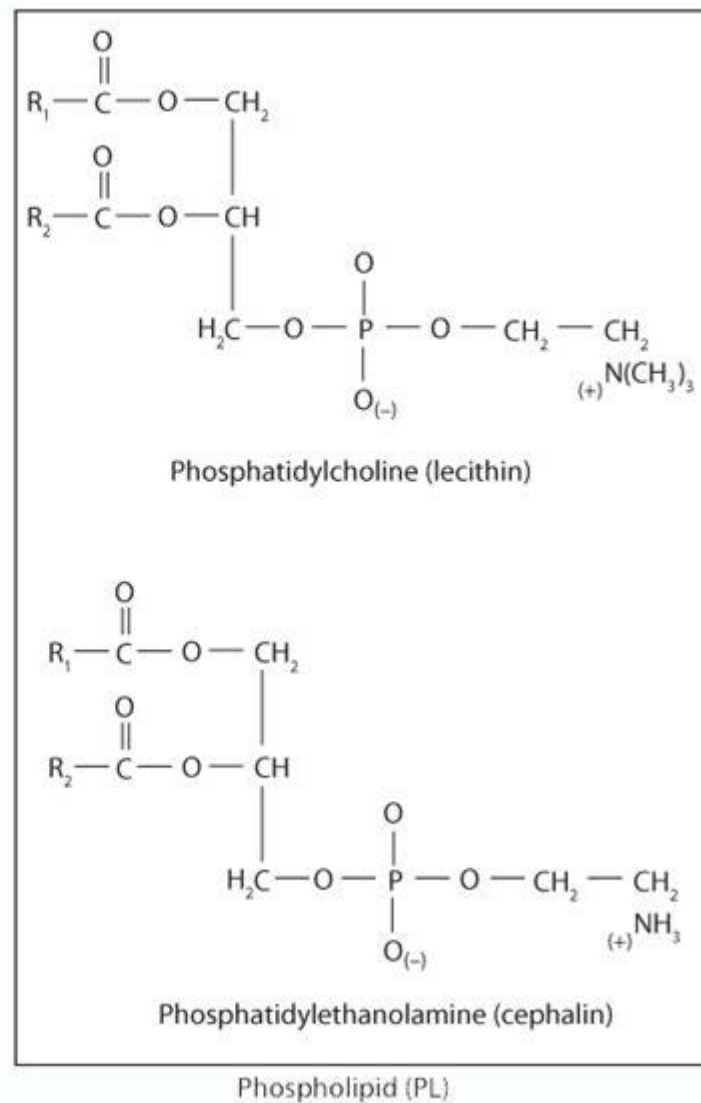
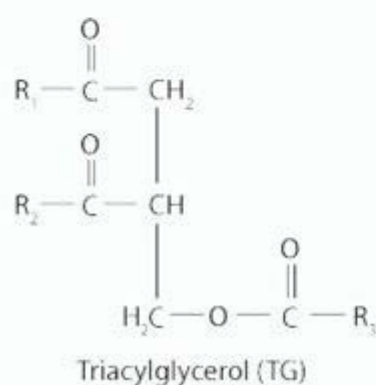
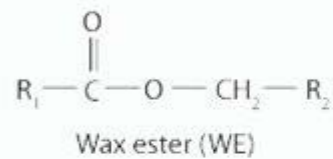
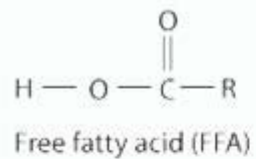
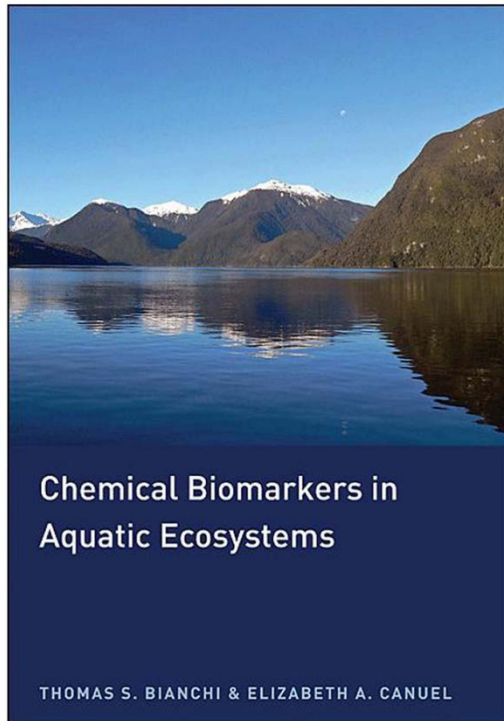
Oben: Phospholipid Archaeen, **1** Isopren Seitenkette,

2 Etherbindung, **3** L-glycerol, **4** Phosphatreste.

Mitte: ein bakterielles und ein eukaryotisches Phospholipid: **5** Fettsäure, **6**

Esterbindung, **7** D-glycerol, **8** Phosphatreste.

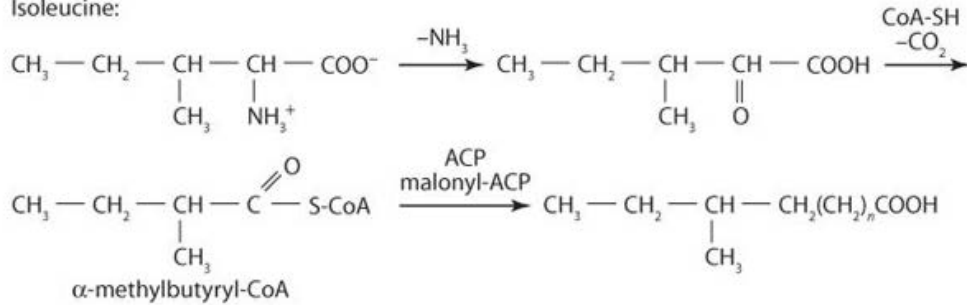
Unten: **9** Lipid Bilayer von Bakterien und Eukaryoten, **10** Lipid Monolayer der Archaeen.



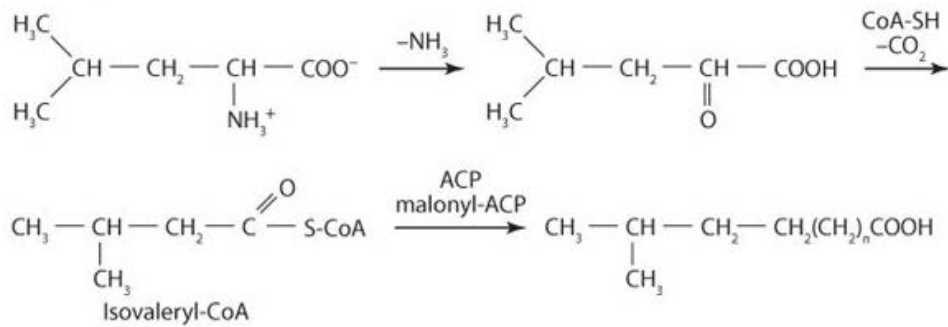
Phospholipide

Fettsäuren mit verzweigten Ketten

Isoleucine:



Leucine:



Valine:

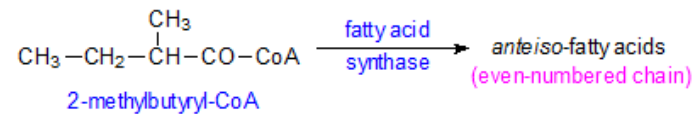
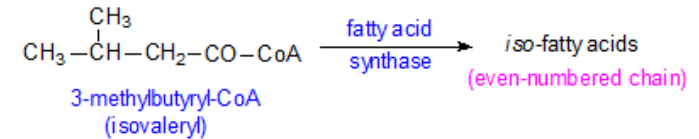
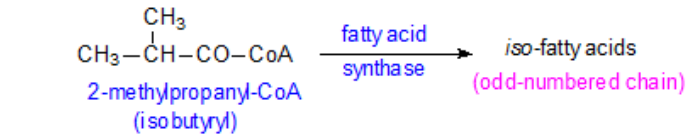
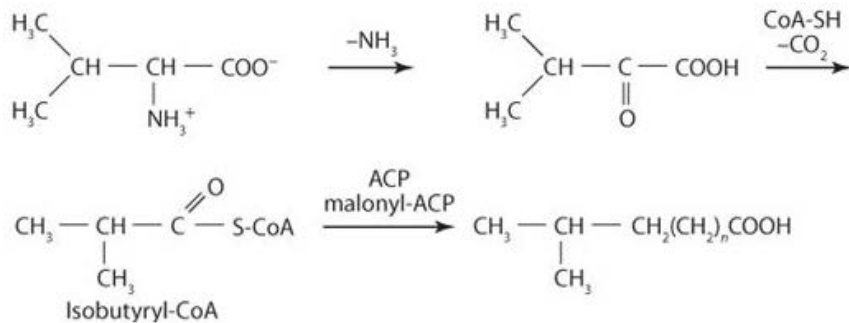


Table 8.1

Structural features of fatty acids and their use as source indicators

*Feature**Source***Short chain (14:0, 16:0, 18:0)**

Nonspecific (marine and terrigenous; bacteria, plants, and animals)

Long chain (24:0, 26:0, 28:0)

Higher (vascular) plants

Monounsaturated short chain (16:1 and 18:1)Generally, nonspecific
However, isomers may be source-specific

18:1 ω 7 (*cis*-vaccenic) is abundant in, but not exclusive to, bacteria
 18:1 ω 9 (oleic acid) animals, higher plants and algae
 16:1 ω 7: bacteria
 16:1 ω 9: algal

Polyunsaturated

20:4, 20:5, 22:4, 22:5, 22:6

Marine and aquatic phytoplankton, zooplankton and fish

18:2 and 18:3

Higher plants and algae

Methylbranched chains (iso and anteiso)

Bacteria

Internally branched and cycloalkyl10-methyl isomers of 16:0 and 18:0
cyclopropyl 17:0 and 19:0Fungi and bacteria
Eubacteria**Hydroxy** α -hydroxy (2-hydroxy)
 β -hydroxy (3-hydroxy)Intermediates in oxidation of monocarboxylic acids
Mostly bacteria, some cyanobacteria (predominantly C₁₄-C₁₆) and some microalgaeC₁₅ and C₁₇ β -hydroxy

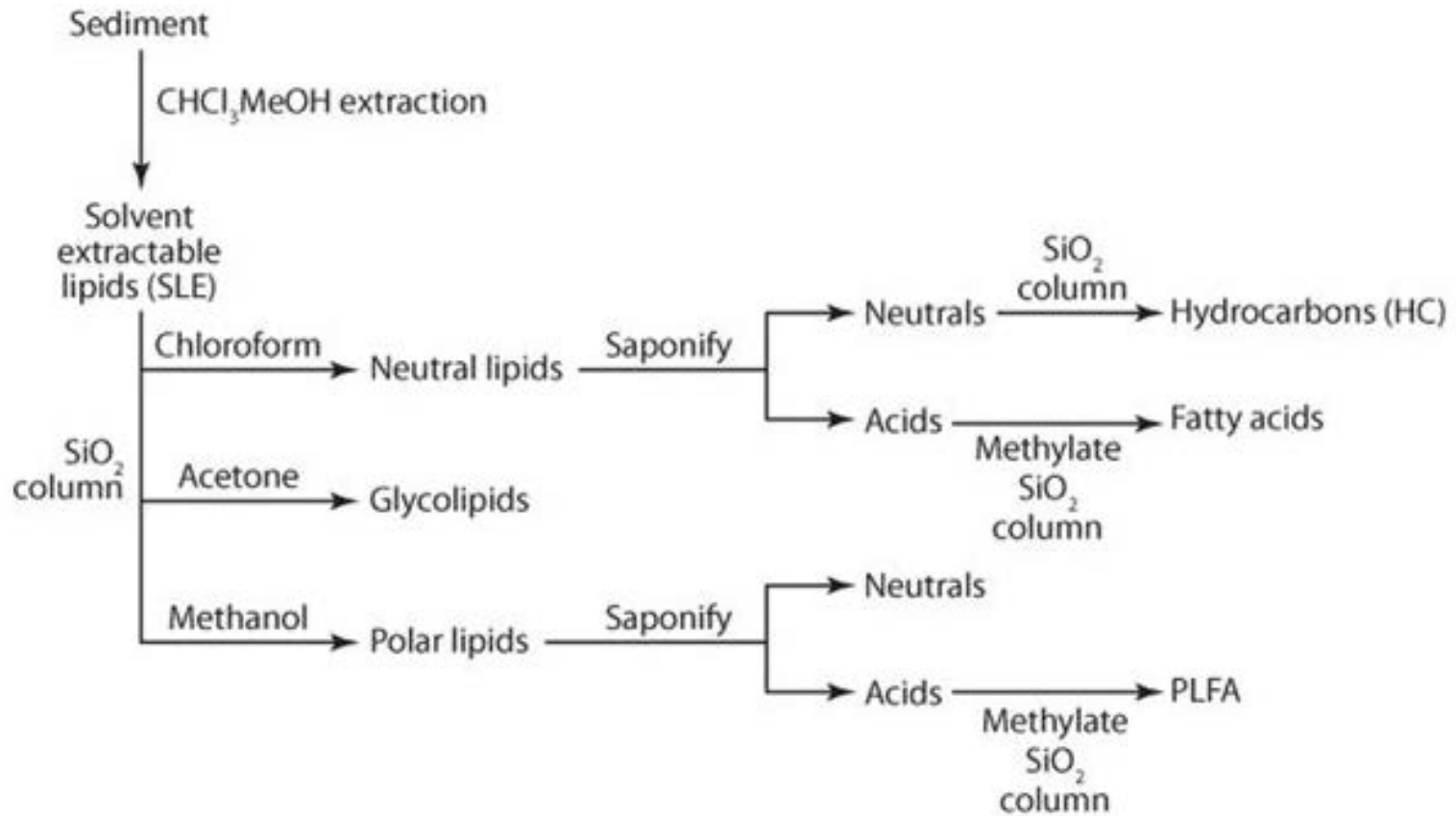
Bacteria

C₂₆ to C₃₀ β -hydroxy

Eustigmatophytes

Diacids α , ω diacidsHigher plants
Bacterial oxidation of other compounds

Extraktion



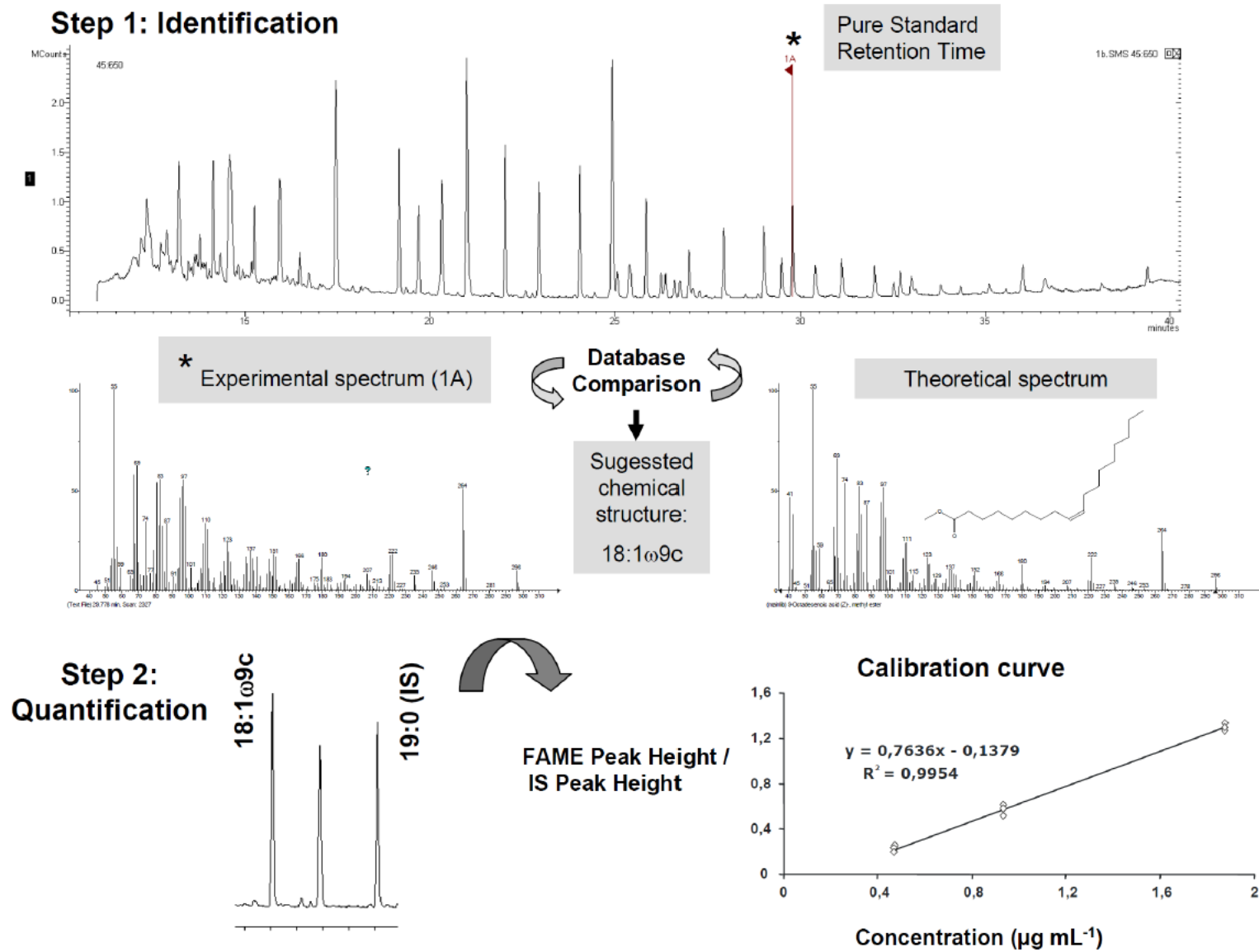


Figure 3. Identification and quantification of FAMES by means of gas chromatography-mass spectrometry.