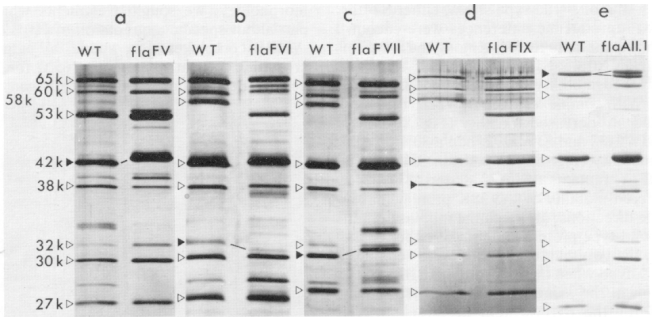
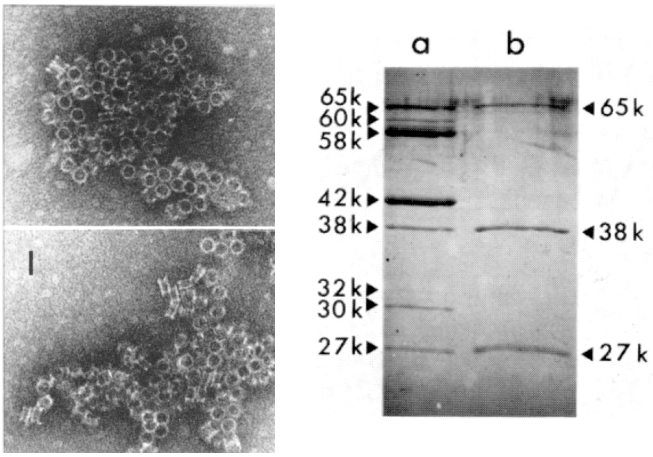
SDS gels to identify HBB gene products in the ts *fla* mutants



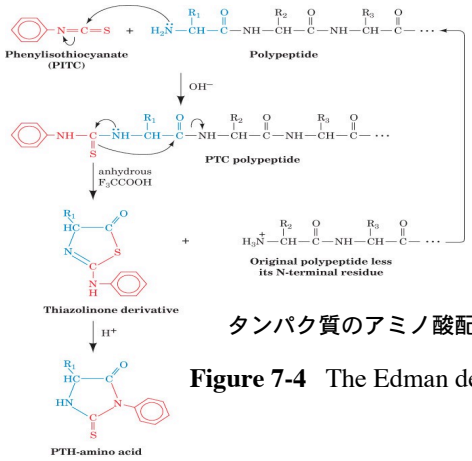
Aizawa et al., J. Bacteriol. (1985)

Ring preparations from HBB



Correspondences among genes, proteins, and structures

Apparent mol wt (10^3)	pI	Gene	Morphological features, functions, or comments
65	6.8–7.3	*flaAII.1*[b]	M ring? Base plate for energy-transducing and switching proteins?
60	5.0	*flaW*[c]	Junction between hook and filament; absent in polyhook-basal body complexes; found as HAP1 in hooks from filamentless mutants
58	4.8	*H2*[d]	Flagellar filament, 1,2 antigen
53	5.2	*H1*[d]	Flagellar filament, i antigen
42	4.7	*flaFV*[e]	Hook protein
38	ca.9	*flaFIX*[b]	P ring portion of outer cylinder?
32	4.5	*flaFVI*[b]	Rod?
30	4.6	*flaFVII*[b]	Rod?
27	7.5	*flaFVIII*?	L ring and wall portion of outer cylinder?
16	5.4	?	?
14	5.5	?	?
12	7.3	?	?[f]
?	?	?	S ring



タンパク質のアミノ酸配列決定

Figure 7-4 The Edman degradation.

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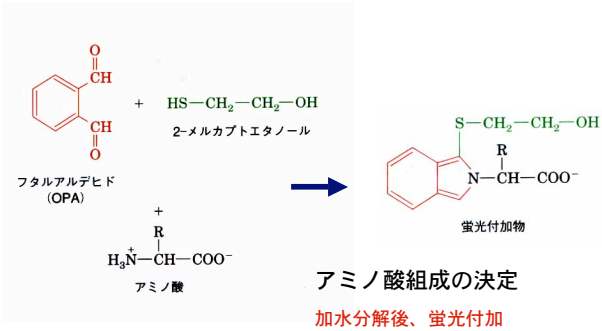
蛍光付加物の作成



アミノ酸組成の決定

加水分解後、蛍光付加物にして分析

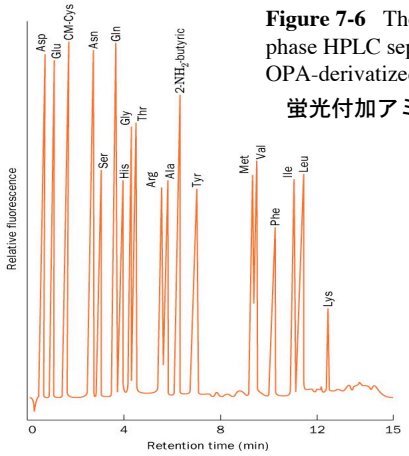


Figure 7-6 The reverse-phase HPLC separation of OPA-derivatized amino acids.

蛍光付加アミノ酸の分析

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Figure 7-6 Amino acid analysis.

Figure 7-7 The amino acid sequence of a polypeptide chain.

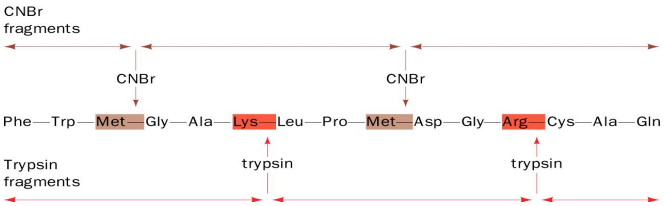


Figure 7-8a The generation of the gas phase ions required for the mass spectrometric analysis of proteins. (*a*) By electrospray ionization (ESI).
LysやArgにプロトン化した電荷により分離（0.5~2電荷／kD）

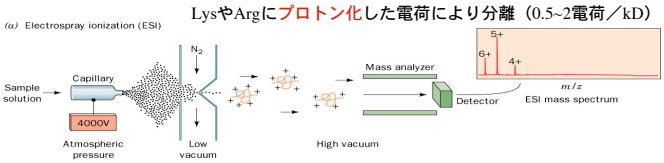


Figure 7-8b The generation of the gas phase ions required for the mass spectrometric analysis of proteins. (*b*) By matrix-assisted laser desorption/ionization (MALDI).

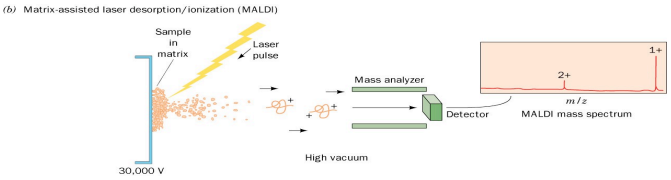


Figure 7-8c The generation of the gas phase ions required for the mass spectrometric analysis of proteins. (*c*) By fast atom bombardment (FAB).

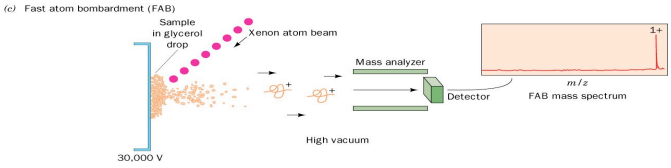
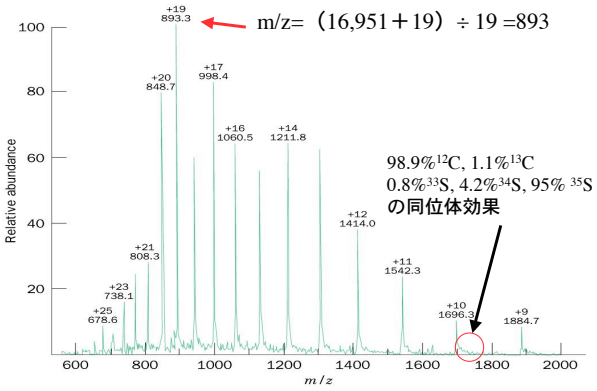
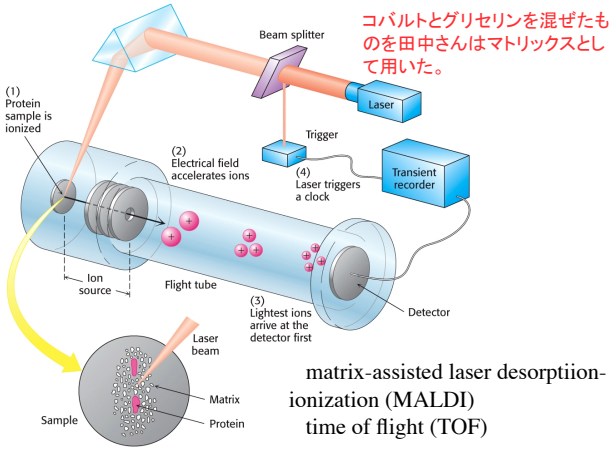


Figure 7-9 The ESI-MS spectrum of the 16,951-D horse heart protein apomyoglobin.



MALDI-TOF mass spectrometry



matrix-assisted laser desorptiion-ionization (MALDI)
time of flight (TOF)

MALDI-TOF mass spectrum of insulin and β–lactoglobulin

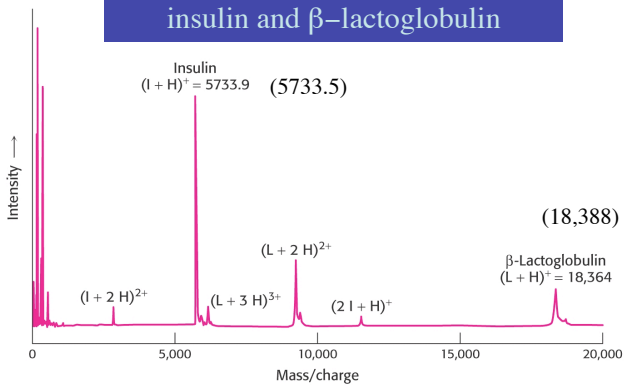


Figure 7-10 The use of a tandem mass spectrometer (MS/MS) in amino acid sequencing.

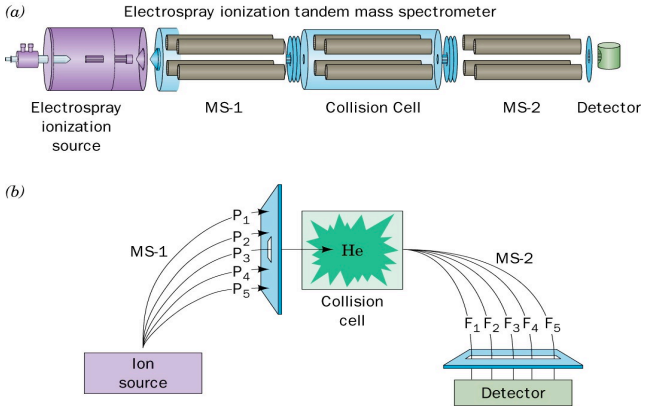


Figure 7-10 The use of a tandem mass spectrometer (MS/MS) in amino acid sequencing.

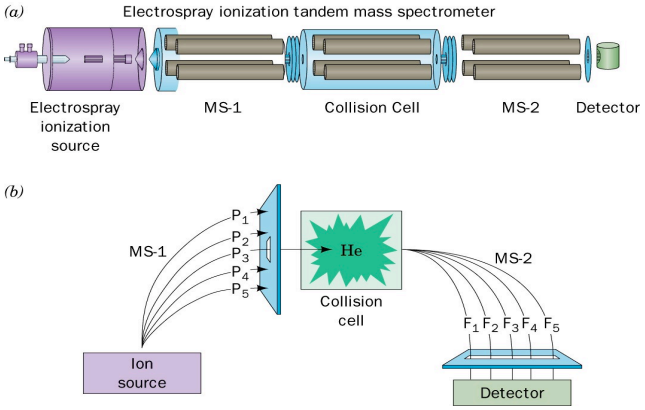
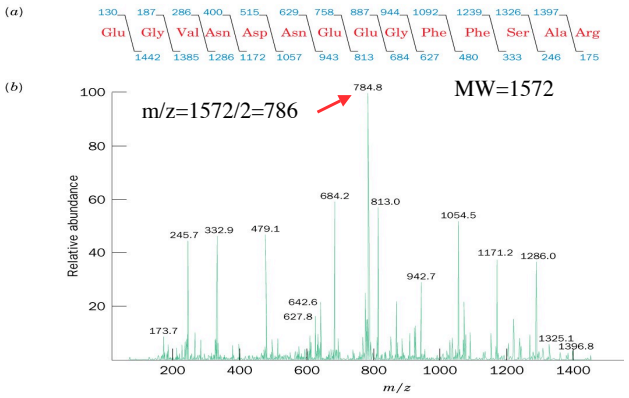
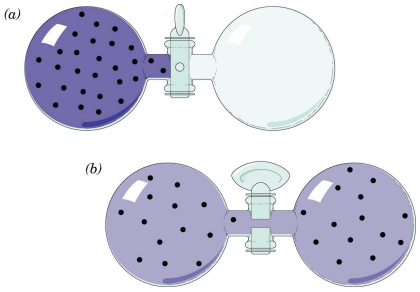


Figure 7-11 The tandem mass spectrum of the doubly charged ion of the 14-residue human [Glu^1]fibrinopeptide B (m/z = 786).



Thermodiynamic Principles



熱力学の法則

1） エンタルピーの定義：H = U + PV

U：エネルギー
P：圧力
V：体積
Q：熱
W：仕事

ΔH = ΔU +PΔV,　ΔU = ΔQ - ΔW
（第一法則）

ΔH = ΔQ - ΔW +PΔV = ΔQ - ΔW'

2） エントロピー：S　dS = dQ/T (可逆過程)

蒸気になるときのエンタルピー変化

水の蒸発のΔH_{vap}=40.7 kJmol^{-1}で T=373 °Kであるから → ΔS_{vap}= 109.1 JK^{-1}

3） ギブスの自由エネルギー：G = H - TS

1N = 1 Kg・m・s^{-2}
[N・m] = [J]

ΔG = ΔH - TΔS（等温条件）

0.24 cal = 1J = 1 Kg・m^2・s^{-2}

1/2・mv^2 = 1/2・(2 kg)・(1 m・s^{-1})^2 = 1 Kg・m^2・s^{-2} = 1Nm

質量2 kgが1 m・s^{-1}の速さで動いているものの運動エネルギーに1Jが対応

化学ポテンシャル

化学ポテンシャル
（部分モル自由エネルギー）

out	in
A_o	A_i

$\mu_o = \mu^\circ + RT \cdot \ln A_o$

$\mu_i = \mu^\circ + RT \cdot \ln A_i$

$\Delta\mu = \mu_i - \mu_o = RT \cdot \ln(A_o/A_i)$

T: Kelvin 温度

R: ガス定数(2cal・mol^{-1}・K^{-1})