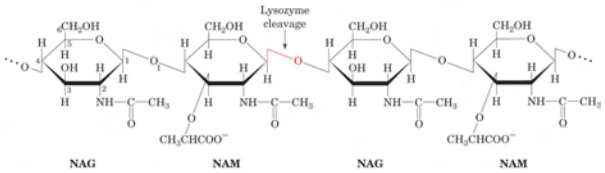
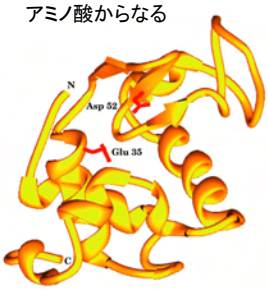
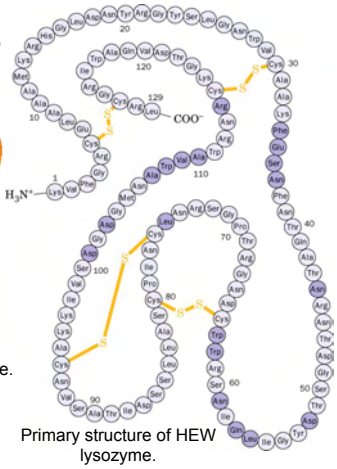
Figure 15-8 The alternating NAG–NAM polysaccharide component of bacterial cell walls.



分子量14.7 kDaで129個のアミノ酸からなる

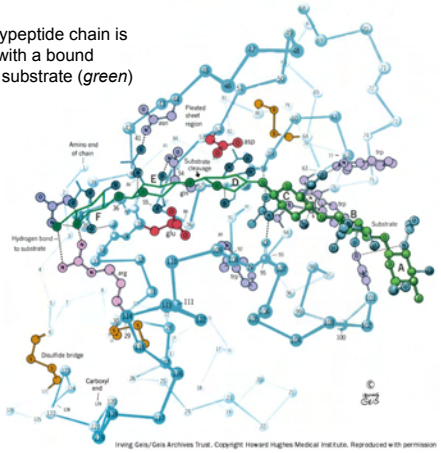


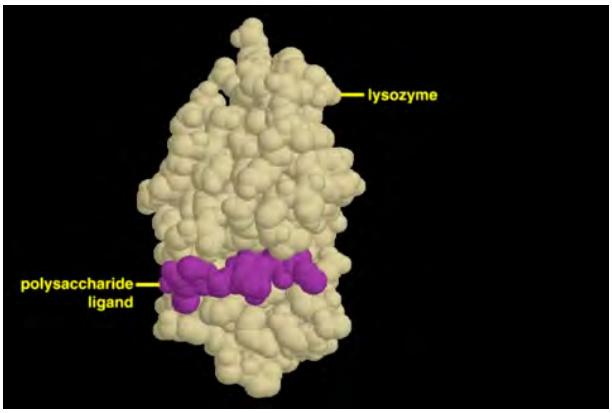
X-Ray structure of HEW lysozyme.



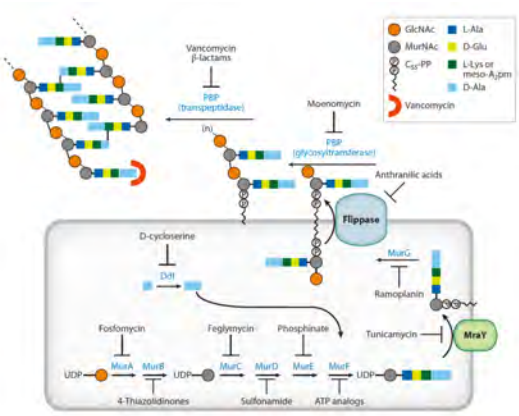
Primary structure of HEW lysozyme.

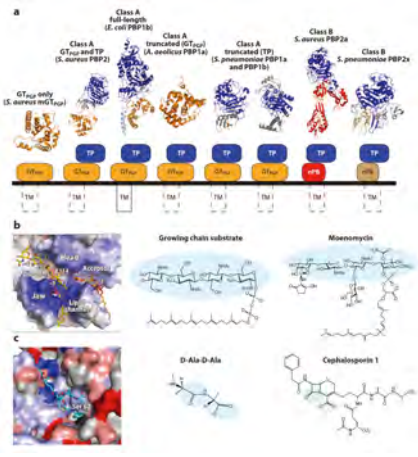
The polypeptide chain is shown with a bound $(NAG)_6$ substrate (*green*)



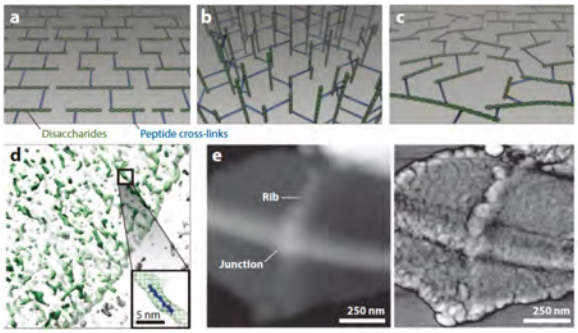


Summary of the peptidoglycan biosynthesis pathway

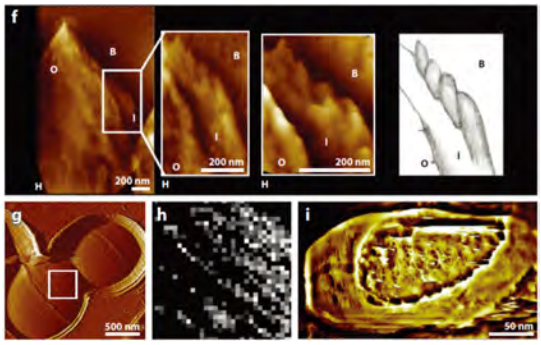




Structural summary of high-molecular-weight penicillin-binding proteins (PBPs). (*a*) Representative members from the different PBPs are shown in ribbon format. From left to right, the items from the Protein Data Bank (PDB) shown are *S. aureus* monofunctional glycosyltransferase peptidoglycan polymerization (mGTPGP) (PDB code 3HZS), *S. aureus* PBP2 (PDB code 2OLU), *E. coli* PBP1b (PDB code 3FWM), *A. aeolicus* PBP1a (PDB code 2OQO), *Streptococcus pneumoniae* PBP1a (PDB code 2C6W), *S. pneumoniae* PBP1b (PDB code 2BG1), *S. aureus* PBP2a (PDB code 1VQQ), and *S. pneumoniae* PBP2x (PDB code 1QME), and they are represented by a domain-based schematic below their structures. (*b*) Model for a productive complex of the GT peptidoglycan polymerization (GTPGP) domain from *S. aureus* PBP2 with the acceptor lipid II and donor glycan chain. Shown next to the structure (*left*) are the molecular structures of lipid IV (*middle*; E-*Z* stereochemical designation of *cis/trans* bonds of isoprenyl groups not shown) and the donor strand analog moenomycin (*right*). (*c*) Complex structure of the *Streptomyces* R61 D,D carboxypeptidase/transpeptidase (TP) acylated by cephalosporin 1 (PDB code 1HVB) (*left*). The molecular structure of the natural TP substrate D-Ala-D-Ala is shown (*middle*) along with the mimicking β-lactam substrate analog cephalosporin 1, bound in the active site (*right*). The blue highlighted regions represent the functional groups on the substrate molecule and their corresponding groups on the antibiotic that are used to mimic these groups.

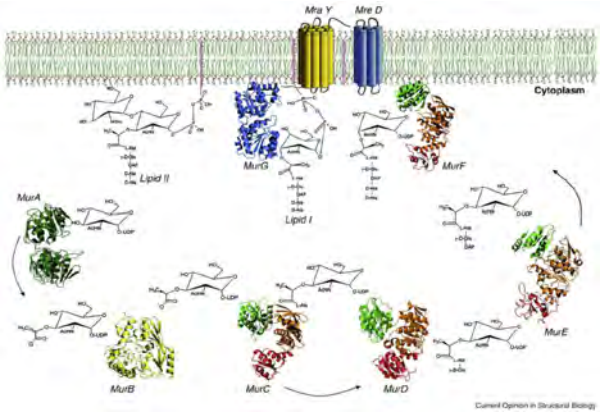


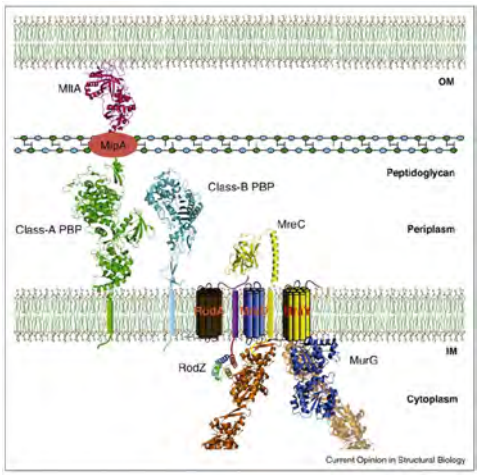
Conceptual models of peptidoglycan organization include the (*a*) layered, (*b*) scaffold, and (*c*) disorganized layered arrangements. Panels *a-c* depict the disaccharides as green pills and the stretched peptide cross-links as blue sticks. It is contested whether the glycans run parallel or antiparallel to each other, although see Sharif et al. (173) for an examination of the *S. aureus* peptidoglycan. (*d*) Electron cryotomography of sacculi isolated from *C. crescentus* strain CB15N, with a putative glycan 9-mer atomic model placed in density (*inset*). (*e*) Atomic force microscopy (AFM; left side of image is height, right side is phase components) image of *S. aureus* division planes, showing the inherited rib and junction peptidoglycan "piecrust" features characteristic of division in successive 90◦ planes.



(*f*) AFM of the inner-facing surface of a *B. subtilis* peptidoglycan layer with increasing magnification and a schematic (*far right side*), revealing the "twisted cable" architecture (*feature* I, *background B*) in all four panels. Panels *g* and *h* show the use of AFM and secondary cell wall polymer mutants to probe the nanoscale architecture of cell wall peptidoglycans in living gram-positive bacteria, using a topographic imaging peptidoglycan localized as parallel lines [visible in both *g* and *h* panels, deflection image and adhesion force map (from the square area shown in *g*), respectively, on the surface of these mutants. (*i*) AFM image of a single *Bacillus atrophaeus* spore germinating under native conditions; the peptidoglycan cell wall structure is evident in the center of the image.

細胞質におけるペプチドグリカンプレカーサーの合成





電荷をもった物質の濃度差の持つエネルギー

$$\Delta\tilde{\mu}_A^{\pm z} = \Delta\mu + \Delta G = RT \cdot \ln(A_O/A_i) + zF(V_O - V_i)$$

V_o= 0 mVとすると

$$\Delta\tilde{\mu}_A^{\pm z} = -zF \cdot V_i + RT \cdot \ln(A_O/A_i)$$

ここで平衡時を考えると $\Delta\tilde{\mu}_A^{\pm z} = 0$

$$zF \cdot V_i = RT \cdot \ln(A_O/A_i)$$

$$V_i = RT/zF \cdot \ln(A_O/A_i)$$ ------ネルンストの式

V_o= 0 mVとしたときの平衡時の電気化学ポテンシャル

平衡電位を求める

$$RT/zF = \frac{\frac{\text{ジュール}}{\text{mol}\cdot\text{K}^\circ}\,\text{K}^\circ}{(z)\,\frac{\text{ジュール}}{\text{ボルト}\cdot\text{mol}}} = \text{ボルト}$$

平衡電位（ΔΨ）$= RT/zF \cdot \ln(A_O/A_i)$

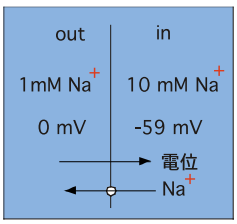
$$= \frac{8.314 \times 298}{1 \times 96500} \times 2.303 \cdot \log(A_O/A_i)$$

$$= 0.059 \cdot \log(A_O/A_i)\text{---volt}$$

平衡膜電位の実際例

平衡電位（ΔΨ）= 0.059・log(1 / 1 0)

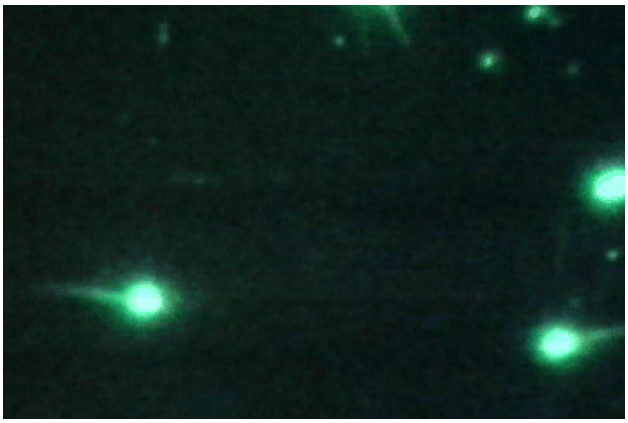
= -59 mV ----拡散電位



釣り合った状態（平衡電位）

1 ΔpH = -59 mV

バクテリアの運動



ATP量とべん毛運動