

Cell

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<http://web.me.com/whitby/Octahedron/Welcome.html>

Reference

Octahedron1stEd.pdf–bookmark CELL–pages 351-362

Introduction

This material is excerpted from *Octahedron*. It includes lipids, soap film structures and relates them to the lipid-bilayer of the cell membrane. Structures like gap junctions and channels are also touched upon.

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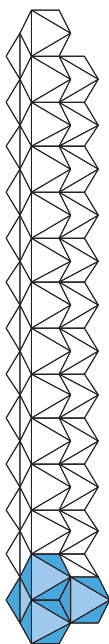
This chapter looks at structures which are important to the assembly of the biological cell. The membrane or enclosure of the cell is a lipid bilayer. Lipids are shown in the first part. Lipids are the constituents of soap films and the film junctions reveal the crystalline association of the lipids. Channels which traverse the cellular membrane are involved in molecular transport and their structures are discussed and related to the membrane structure.

Lipids

Chains of C-atoms in lipids.

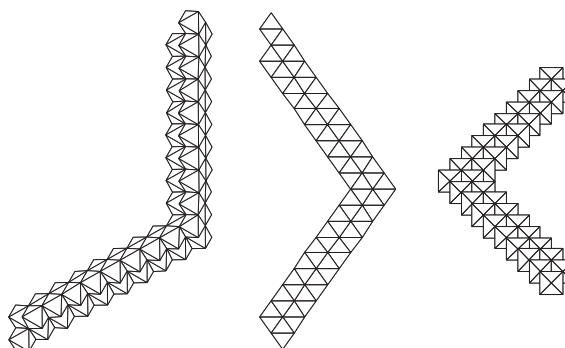
Lipid groups are characterized by chains of C-atoms. The conformation of the chains of some common lipids are indicated here.

Lauric chain



Single bend lipid

Oleic chain

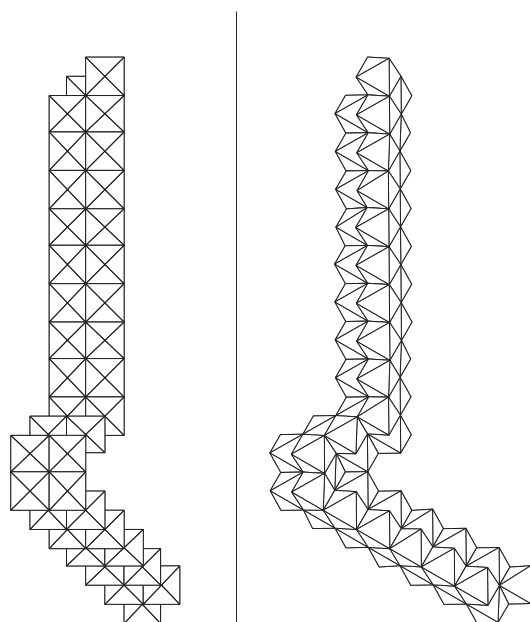


On the left, the oleic chain is oriented so that the bend angle projects as 120° , the true angle

In the middle, the oleic chain is oriented so that the projected bend angle is $180^\circ - \text{atan} \sqrt{8}$ which is about $109^\circ 28' 16''$.

On the right, the oleic chain is oriented so that the bend angle projects at 90° .

Linoleic chain



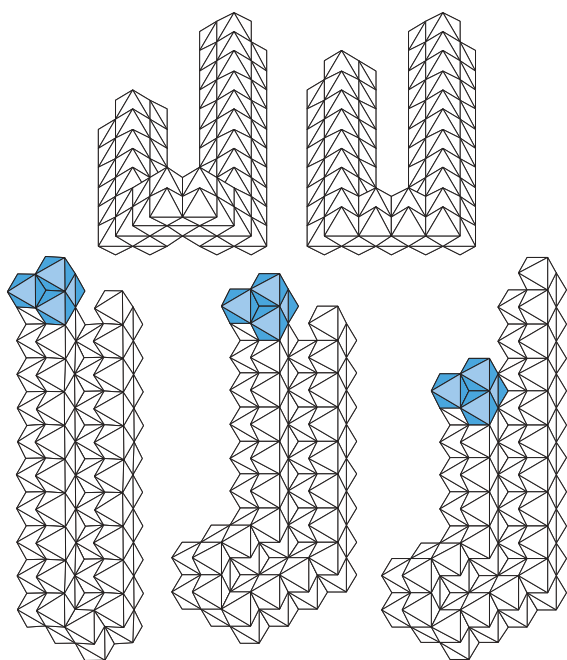
$\text{atan} \sqrt{1/2}$

On the left is a linoleic chain oriented so that the projected bend angle is 135° . This is the angle depicted in Lehninger's *Biochemistry*.¹

On the right a linoleic chain is in the correct orientation to show the true bend angle of 120° which is shown in Stryer's² *Biochemistry*. The two orientations differ by an angle of $\text{atan}\sqrt{2}$ which is approximately $54^\circ 44' 08''$.

Mixed bend lipid

Arachidonic acid³



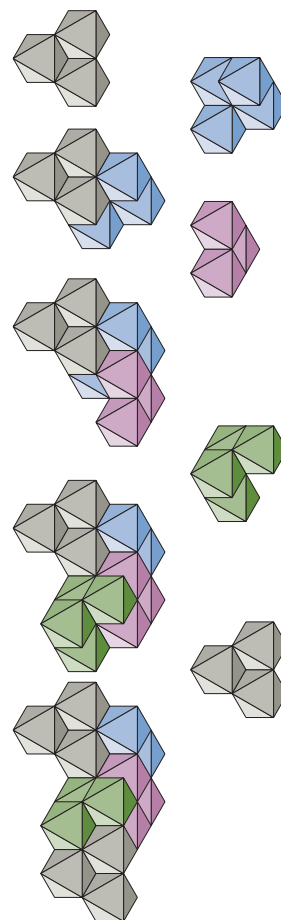
In the upper row, the two legs of each chain are not in contact. The chain on the left has an additional bend that the chain on the right does not have.

In the bottom row the two legs of each chain are in contact. The chain on the left has two

1. A. L. Lehninger, *Biochemistry*, 2d ed. p. 282.
2. Lubert Stryer, *Biochemistry*, 2d ed. p. 226 Fig.10-30.
3. Stuart J. Baum, *Introduction to Organic and Biological Chemistry*, 4th ed., MacMillan, 1987, p. 299.

bends. The middle chain and the chain on the right have three bends each. The free ends of the two legs of the chain on the right are not adjacent.

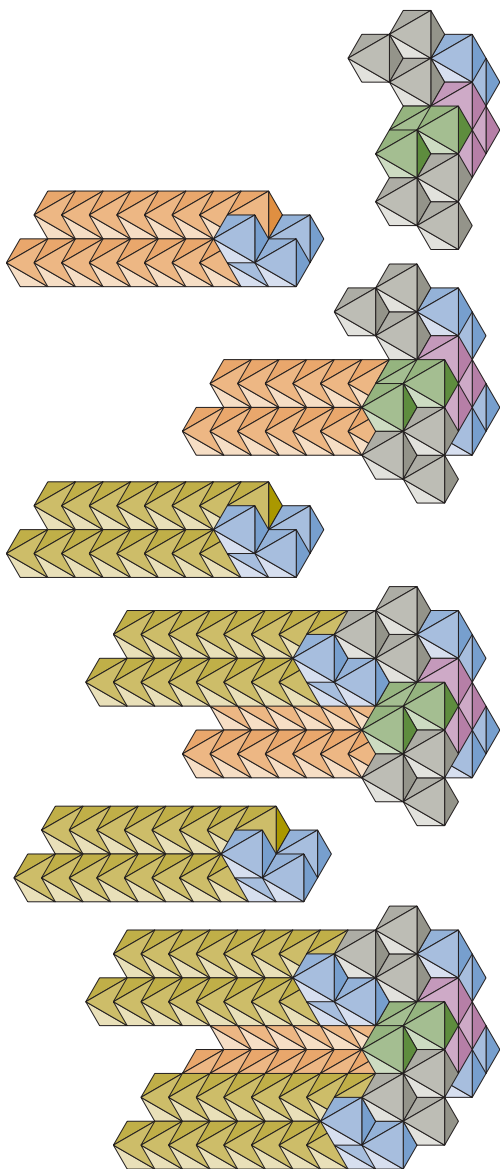
Glycerol



The arrangement of C-atoms and O-atoms of the glycerol unit must accommodate three parallel carbon chains while retaining an attachment place for an H_2PO_4 group. The assembly which is depicted in the figure provides these features. It is notable that the contacts between the C-atoms is edgial. There are no cleft-joints between C-atoms here. The C-atoms are cleftly joined to O-atoms: C-O-C-O-C. The arrangement leaves the central C-atom with one cleft for joining a carbon chain. Each of the two C-atoms at either side has two clefts for joining. One each is used to join a carbon chain. The

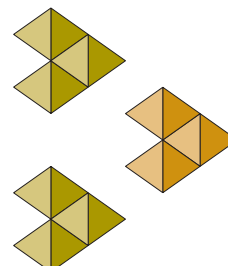
assembly depicted here begins with a C-atom at the top. The adding atoms are in the right hand column. The assembly proceeds atom by atom to the bottom.

Trilauric acid



The assembly of carbon chains to the glycerol assembly is shown in the next figure. The three chains are identical in length, composition, and orientation. Each is terminated by an O-atom which is to be cleftly joined to one of the C-atoms of the glycerol. The first chain is attached to the middle C-atom of the glycerol. The second and third chains are added to the

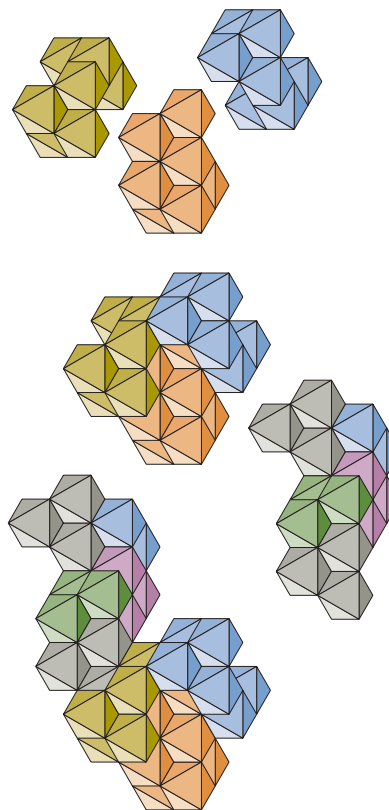
end C-atoms. The open cleft of each of the end C-atoms is seen in the final step of the assembly. The three carbon chains are parallel and are spaced as indicated in the axial view of the combined chains shown below. The viewing



direction is from the glycerol.

Phosphatidic acid

The figure shows the assembly of an H_2PO_4 group at the top. The orange S-atom represents

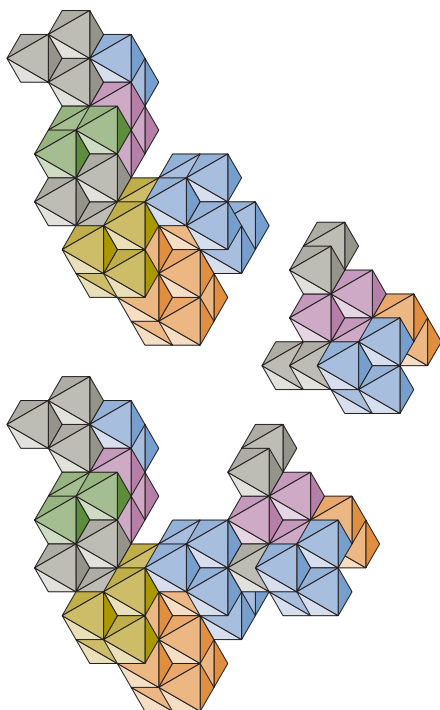


the H_2P portion and this is joined with the O_2 groups colored yellow and blue. The glycerol

group shown on the right joins with the H_2PO_4 group to make the assembly at bottom. The join to the C-atom still permits the attachment of a lipid chain in the manner shown in the trilaureic acid assembly.

Phosphatidyl serine

A serine group is added to the phosphatidic acid group in the next figure. A He-octa of the C-atom of the serine sidechain fills the void in the blue colored O₂-group of the H_2PO_4 portion of the phosphatidic acid assembly. There is more than one orientation in which the serine group can make an equivalent join.



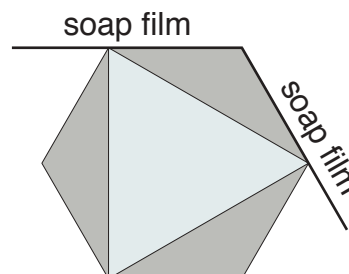
Cell walls

The walls of the cell feature lipids whose chain axes are perpendicular to the surface of the membrane. The chain is defined by the C-atoms which are arranged parallel to an edge of the octahedron. A closed form which will accommodate this octahedral orientation is the rhombic dodecahedron. This form shows up as the underlying structure of soap bubbles. Soap is composed of lipids, too. This suggests that

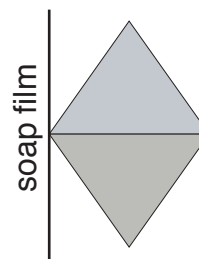
the rhombic dodecahedron is the principal structural form of the cell membrane.

Soap films¹

Joseph Plateau found that the angle between soap film planes is 120° . When two soap films are viewed so that their surfaces and the junc-



tion between them are parallel to the view direction, their relationship to a facial view of a regular octahedron is seen in the figure. Each of the films is tangent to an edge of the octahedron. The relationship of the soap film to an edgial view of a regular octahedron is such that



Soap film referenced to the edgial view of a regular octahedron.

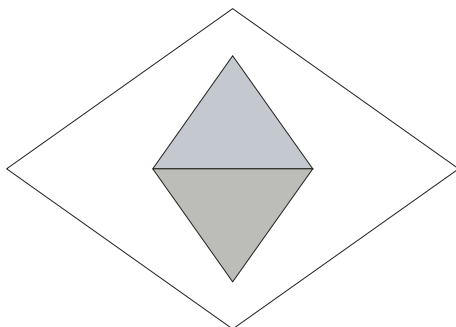
The edgial equator of the octahedron is perpendicular to the soap film plane.

it is normal to the edgial equator. There is *one* closed form of the isometric crystal system whose faces bear the same relationship to the regular octahedron—the *rhombic dodecahedron*.

1. Ian Stewart, Mathematical Recreations "Double Bubble, Toil and Trouble" *Scientific American* January 1998, pages 104 to 107. The article refers to work on soap films by Joseph A. Plateau in the 1830's.

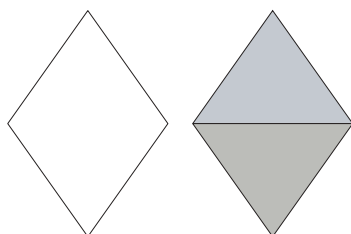
Soap films are rhombic dodecahedral planes

The angle between soap film surfaces at their junction is 120° . The angle between the faces of the rhombic dodecahedron at an edge is 120° . The surface of the face of a rhombic dodecahedron that is a crystalline assembly of regular octahedra is defined by the edges of the regular octahedra of which it is composed. The



edges of the octahedra are parallel to the major diameters of the faces. This relationship is shown in the figure where an edgial view of the octahedron is superimposed upon the rhombic face of a dodecahedron.

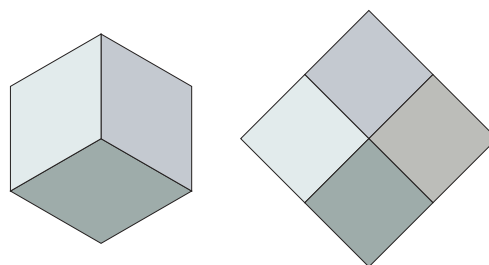
The perimeter of the face of the rhombic dodecahedron and the perimeter of the edgial view of the regular octahedron are geometrically similar. The perimeter of the dodecahedral face is shown here in the same orientation



as the edgial view of the octahedron and the two are of the same size.

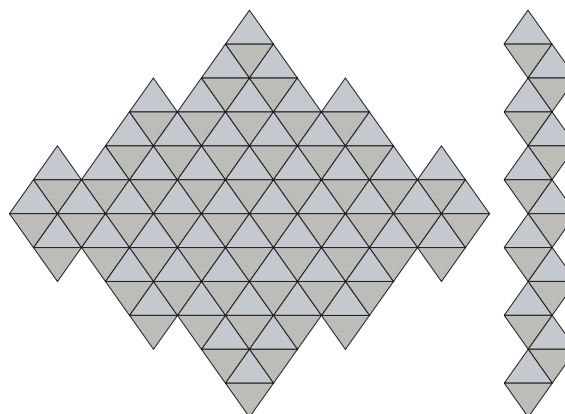
The vertexes of the dodecahedron are of two types—threefold and fourfold. The angle between the edges at a threefold vertex is $180 - \text{atan}\sqrt{8}$, or $109^\circ 28' 16''$; the angle between the edges at a fourfold vertex are $\text{atan}\sqrt{8}$ or $70^\circ 31' 43''$. These interedgial angles are shown truly in the view normal to a

rhombic dodecahedral face.



Rhombic dodecahedral assembly of regular octahedra.

A hollow rhombic dodecahedral shell can be built of regular octahedral panels. The panels

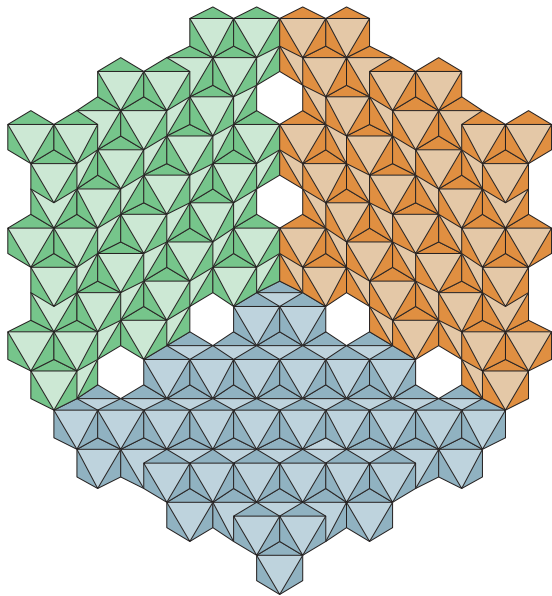


Rhombic dodecahedron: Octahedral panel
Facial view on left, edgial view on right.

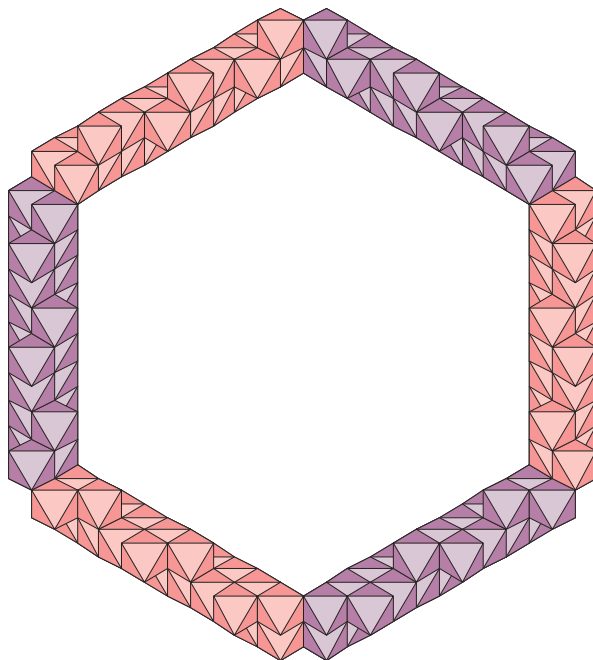
will be two edgial layers thick, the minimum for an assembly. The figure shows the panel in two views, one view is normal to the plane of the panel and the other view is parallel to the plane of the panel. One panel is used for each of the twelve rhombic dodecahedral faces.

Assembling octahedral panels to form a hollow rhombic dodecahedron

The assembly is shown using three sub-assemblies of panels. Three panels are joined at their edges so that the panels are concave toward the viewer. Each of the three panels of the sub-assembly have been colored so that they may be differentiated. They are identical.



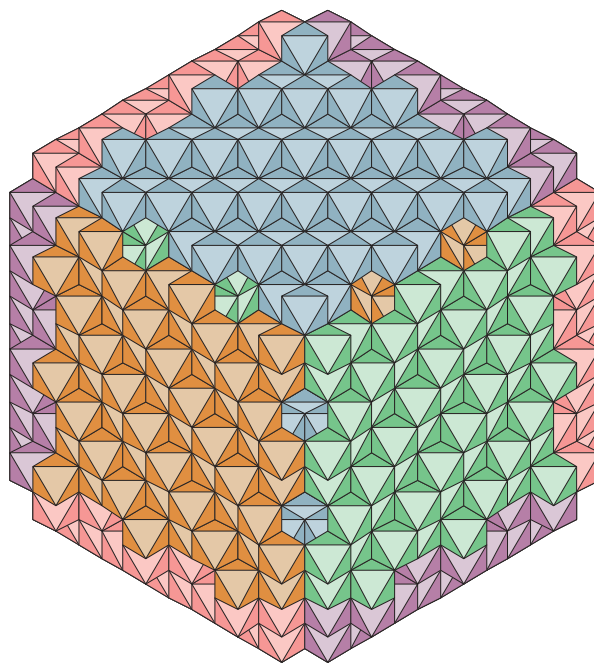
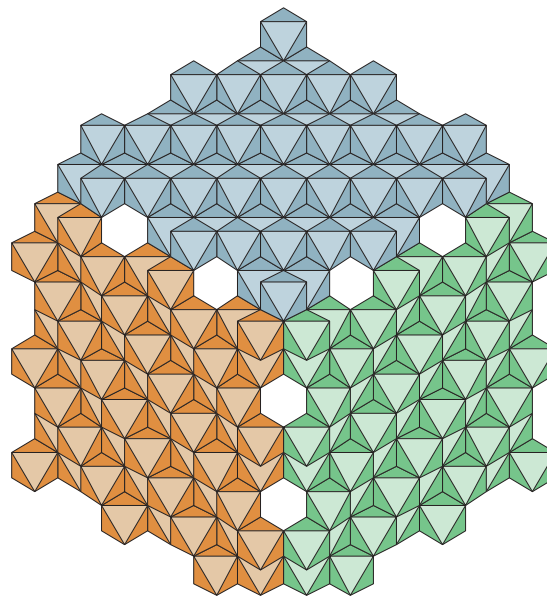
**Rhombic dodecahedral subassembly,
three panels, concave towards.**



Two panels are joined at three places where each of two octahedra of one panel share an edge with two octahedra of the other panel.

The next subassembly consists of six panels which join to one another in a manner which is identical to those of the previous sub-assembly.

bly. The panels here are viewed edgially. Together, the six panels form a regular hexagonal prism.



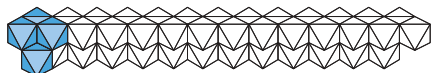
The third and final sub-assembly is identical to the first sub-assembly. It is rotated 180° to the first so that it is convex towards the viewer.

When the three subassemblies are joined so that the edges of their panels are in the same relationship as the panels at the other edges, the resulting appearance is as shown. This is a

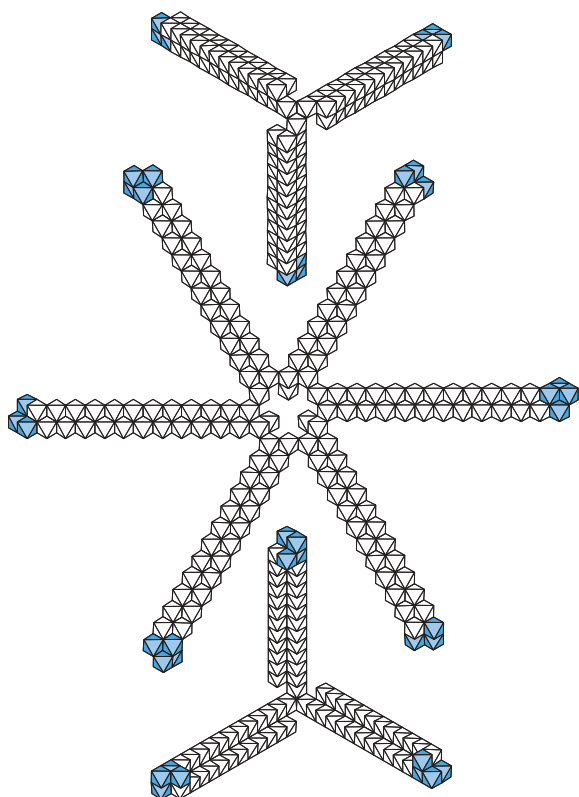
hollow rhombic dodecahedron viewed along one of its threefold axes. While the first two sub-assemblies are somewhat hidden by the third subassembly, portion of each of the panels of the other assemblies can be seen in the full assembly.

Lipid orientations relative to the rhombic dodecahedron

The lauric chain axis is a straight line paral-



lel to an edge diameter of the regular octahedra. The axis is oriented so that it is perpendicular to a plane of the rhombic dodecahedron. To show this relationship, the lauric chains are shown as they relate to each of the subassemblies using octahedral panel to form a hollow rhombic dodecahedron. One chain is depicted for each of the panels each of

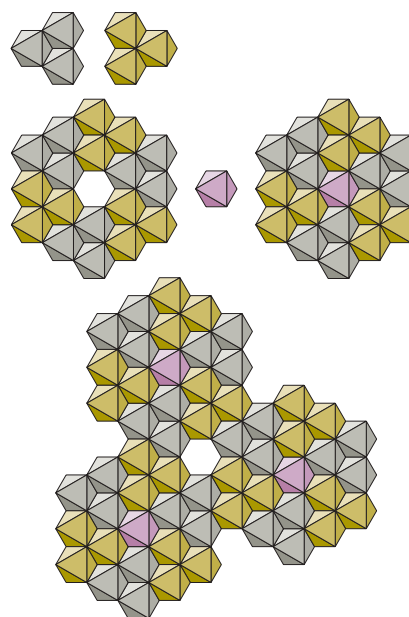


the subassemblies. The sense of each of the chains is that it commences at the exterior of the panel and proceeds away from the panel. In the top group, each of the three chains pro-

ceeds from its junction with the other two chains downward in a direction perpendicular to one of the panels of the concave threefold vertex and beneath the viewing plane. The six chains of the middle group are parallel to the viewing plane and each proceeds in a direction which is normal to one of the panels of the equatorial assembly. The chains of the bottom group proceed towards the viewer from the lower junction and each is perpendicular to one of the three panels of the convex three-vertex.

Porin

Porin is a transmembrane protein which forms channels in the outer membrane of a gram-negative bacterium.¹ Electron micrographs show a pattern which is modelable using regular octahedra. The arrangement of groups of three dark spots surrounded by whitish background fit the pattern depicted here.



The octahedra of the gray hued triplet are in the same relationship as the dark spots which

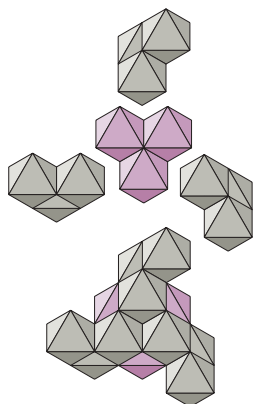
1. Lubert Stryer *Biochemistry*, 2d ed. W. H. Freeman 1981, Fig. 32-33 B <Electron micrograph of negatively stained arrays of porin channels from *E. coli*>, p. 785.

are labeled “channel” in the reference. The spacing of the gray triplets is provided by the yellow triplets to match the arrangement of the electron micrograph. The ring of gray and yellow triplets is the planar CFU which will extend the pattern over the plane. The violet octa is placed at the center of the ring to identify each of the rings in the three ring assembly at the bottom of the figure and to differentiate the ring centers from the octahedral voids which are defined by the ring assemblies.

Gap junctions

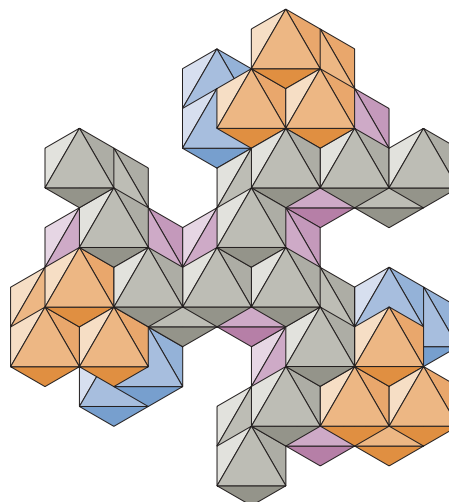
Groups which are analogous to porin form channels in the outer membranes of chloroplasts and mitochondria.¹ Gap junctions are described as having six subunits surrounding a hole of 20A. They are shown in an electron micrograph to be in a hexagonal lattice. They could be of the same form as those shown for porin.

Protein substructures composed of chains of amino acids which proceed normally to a hexagonal plane are two in number. The alpha helix and the epsilon helix. Three alpha helixes can be linked by a four C-atom assembly



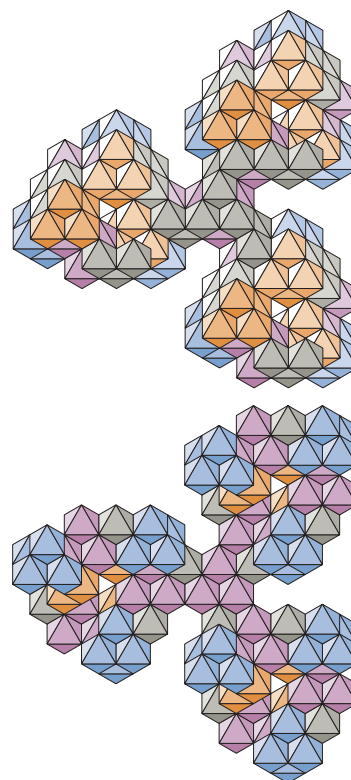
which consists of a central C-atom hub and three C-atom spokes. The C-atoms which compose the are shown above the assembled linker in the figure.

The next figure shows each of the C-atom



spokes of the linker cleftly joined to the alpha carbon of a main chain portion of an amino acid. The three aminoes together are in the three alpha helical orientations.

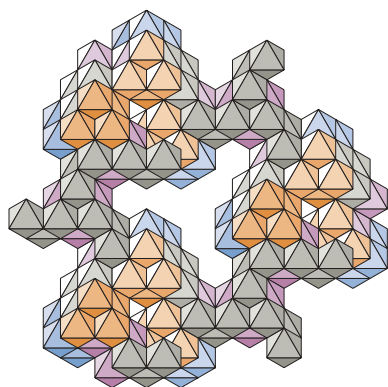
A single turn of an alpha helix has been added to each C-atom spoke of the linker in the next figure. The three helixes are in the same relationship as the three octahedra of the gray



1. Stryer, *ibid.* p.878.

triplet of the porin CFU. The male end of the alpha helix is nearest to the viewer. The obverse view places the female end of the helixes nearest the viewer.

A triplet of alpha helixes in which each helix is in the position of the yellow triplet of the porin CFU is shown here. The helixes are



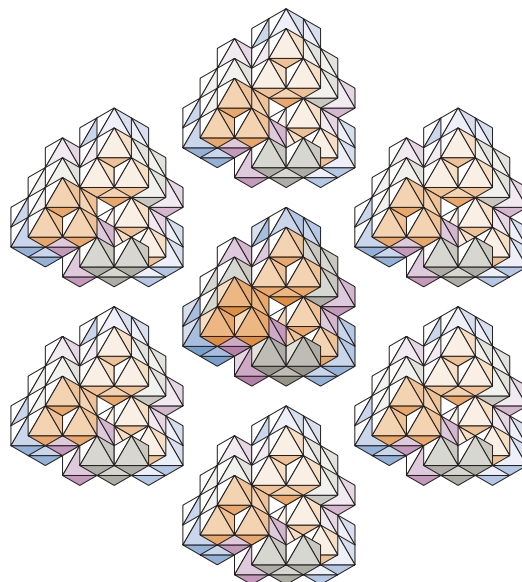
joined at the periphery by three C-atom linkers.

The two types of alpha helical triplet are then joined to form an assembly which is equivalent to the porin CFU depicted with octahedral triplets. The six helical triplets define a channel at the centroid of the assembly which is seen in the figure depicting the assembly on the next page.

Removing the yellow octahedral triplet shows the pattern which was captured in the electron micrograph. This pattern is also seen when the helical triplets which are equivalent to the yellow octahedral triplet are hidden and leave the three helical triplets which represent the gray octahedral triplets.

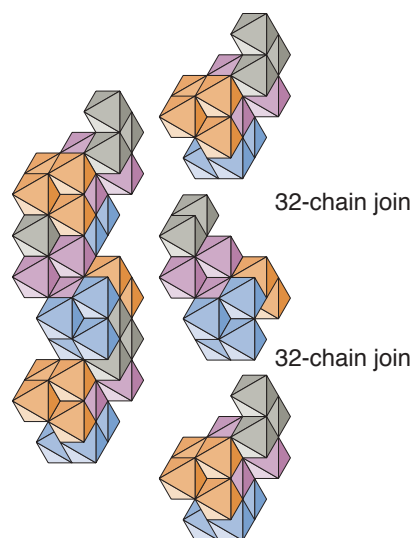
The channel formed by the six alpha helical triplets can accommodate an alpha helical turn. This is shown in the figure. For each of the six triplets, only the helix which is at the periphery of the channel is depicted. The helix in the cen-

ter is identical to the surrounding helixes.

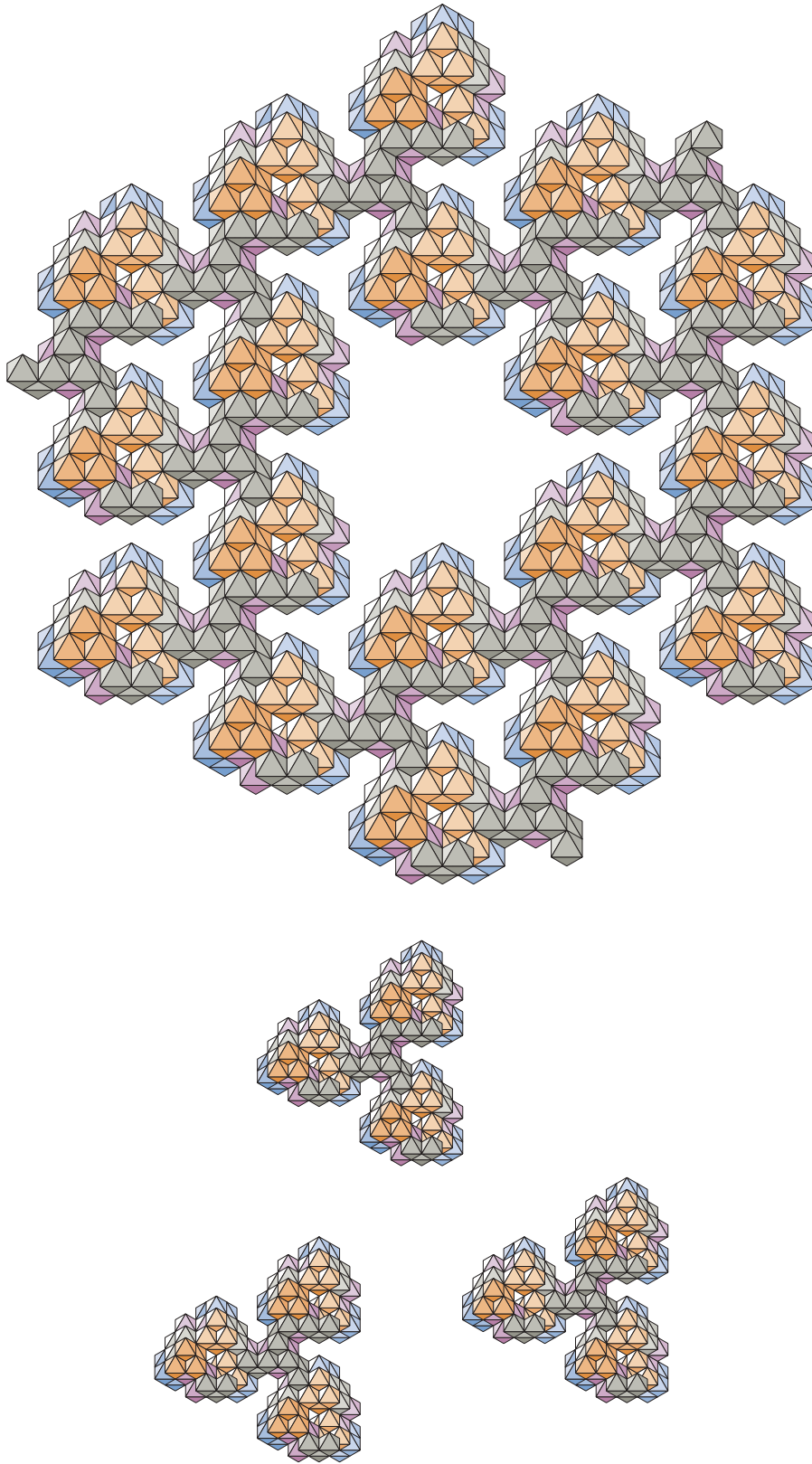


Gramicidin-A channel

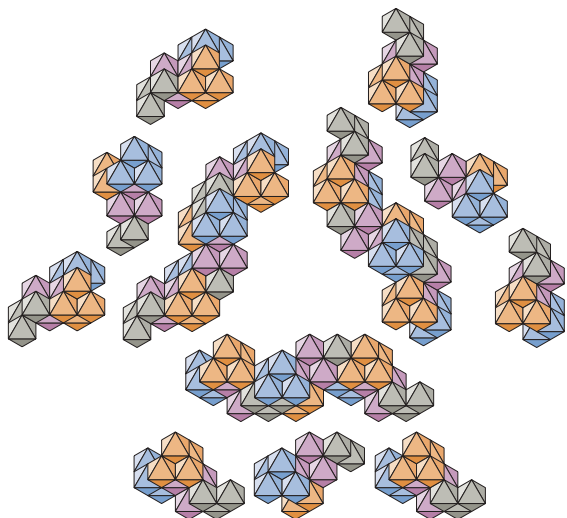
A helix can be built which could act as the gramicidin-A channel. It is an alpha helix which has been expanded by the addition of residues which link to two alpha helical aminoes to form a length of 32-chain. This expansion is shown in the next figure. The aminoes



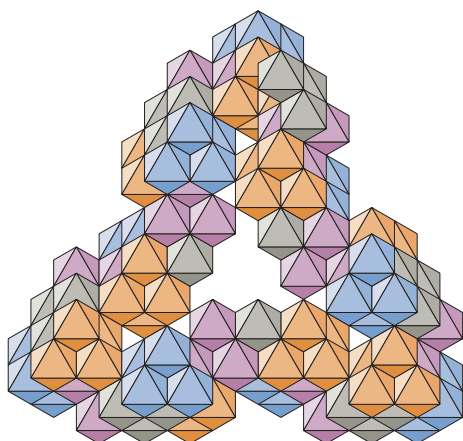
are shown in the right column. The amino at the top is in the same orientation as the amino at the bottom. The middle amino is in an orien-



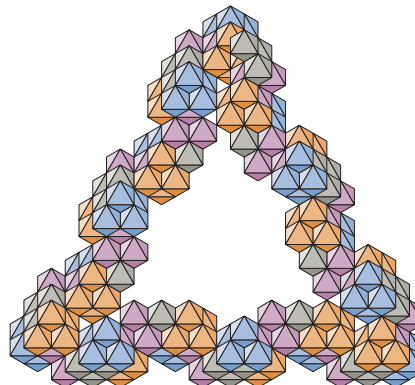
tation which permits the formation of the 32-chain on the left. The helix is built of identical chains which differ in orientation by rotation of 120 or 240 degrees. The assembly of the three legs is shown in this figure. The three



legs are oriented for joining in the alpha helical join. The assembly of the three chains is shown below.



A similar assembly is made using five aminoes per chain which produces a larger channel.



Side chains have been added in each of the external locations. The chains are identical and consist of a straight chain of three C-atoms. Each is cleftly joined to the alpha C-atom of an amino. One chain has been joined to an internal amino location. The chains are seen to be parallel to the 32-chains which make up the helix.

