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An Approach to the Design of Molecular Solids. A Symmetry Analysis of the Problem

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An Approach to the Design of Molecular Solids. A Symmetry Analysis of the Problem.

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Abstract

In a molecular crystal, intermolecular interactions will correspond to specific symmetry elements. If one chooses molecules carefully, one can reliably predict specific intermolecular interactions and the corresponding symmetry operations. The symmetry operations of one and two dimensional networks of molecules can be combined to form rod and layer groups respectively. In many cases of chemical interest the sequence of moving from a molecule to a one dimensional array, then on to two and three dimensions corresponds directly to the symmetry combinations leading from the point group to rod group, to layer group and on to the space group. The structures of a number of disubstituted urea derivatives were determined and are used to illustrate these ideas of molecular design.

Keywords: hydrogen bonding, symmetry analysis, molecular design, group theory, ureas

Introduction.

When one wishes to solve a problem of molecular design one is supported by the work of generations of chemists who have developed the theories of molecular structure and reactivity necessary for rational molecular design as well as the synthetic tools needed for the implementation of the design. However, when one turns to a problem requiring the design of a molecular solid, the problem is considerably more complex and the analogous tools are not well developed.

The analysis of the alternate possible packings of molecules in a solid and a prediction of a final crystal structure requires a consideration of the various possible molecular conformations as well as the energies of the various intermolecular interactions. The problem is that these intermolecular energies are so small and there are so many of them.¹

Various approaches to the problem have been adopted. In his classic work Kitaigorodskii gave a detailed analysis of molecular structures based upon the principle of molecular close packing.² He was able to show that the most common space groups were those that allowed molecules of a general shape to close pack.

Others have given more attention to the nature of the intermolecular bonding interactions, with detailed analyses of hydrogen bonding patterns the most common. Hydrogen bonds are among the strongest intermolecular bonds found in molecular solids. They are reasonably specific and predictable. Many solid state design efforts are based upon hydrogen bond patterns.³

The detailed analysis of observed hydrogen bond patterns is a very important component of molecular crystallography. Systematic studies such as those based upon the graph theory techniques of Etter can be very useful.⁴ Less well appreciated is the power of a rigorous symmetry analysis of hydrogen bond patterns as well as other intermolecular interactions.

Symmetry Analysis.

The fundamental building block of a crystal is the asymmetric unit. In molecular crystallography this asymmetric unit is an asymmetric assembly of atoms. The asymmetric assembly corresponds most often to a single molecule, but it may consist of multiple molecules or in certain cases just a portion of a symmetrical molecule.

Consider first the simplest and most common situation with an asymmetric assembly consisting of a single molecule. Symmetry requires that all other molecules within the crystal have structures that are identical or enantiomorphic to the structure of the asymmetric assembly. Every molecule in the crystal can be related to every other molecule in the crystal by some symmetry operation. This rule is well known, but it has a corollary rule that is perhaps not so well appreciated: *In a molecular crystal, if all molecules are identical or enantiomorphic, then all intermolecular interactions will correspond to a specific symmetry operation.*

A given intermolecular interaction will have only certain symmetry operations that are chemically possible. If one chooses molecules carefully one can reliably predict specific intermolecular interactions and the corresponding symmetry operations as well. If multiple intermolecular interactions are combined to build up a network of molecules, the corresponding symmetry operations will combine according to the rules of group theory to specify the predicted symmetry group of the network. To make an analysis of this type, one must first understand how the various symmetry operations combine.

Within a crystal there are two types of symmetry operations, conventional point group operations such as inversion, reflection or rotation, and translation operations corresponding to screw axes, glide planes and simple translations. If the molecule of the asymmetric assembly forms an intermolecular interaction with another molecule related by a conventional symmetry element such as a center of inversion, then the resulting dimer will be a symmetric assembly, or supramolecule, belonging to a higher point group.

For example, a typical carboxylic acid, such as benzoic acid, will crystallize with no imposed crystallographic symmetry, and a single molecule will belong to the asymmetric point group C_1 . By far the most common hydrogen bond pattern for such a molecule leads to a centrosymmetric dimer of symmetry C_i .

Things are more interesting if the added symmetry operation is a translation operation. As an illustration consider secondary amides that characteristically form linear networks of hydrogen bonds. A close examination of such amides in the Cambridge Data Base⁵ reveals that in almost every case this hydrogen bond network will be generated by one of three different symmetry operations, Figure 1. The three possible networks are generated by a simple translation, **1a**, a two-fold screw axis, **1b**, or a glide plane, **1c**.

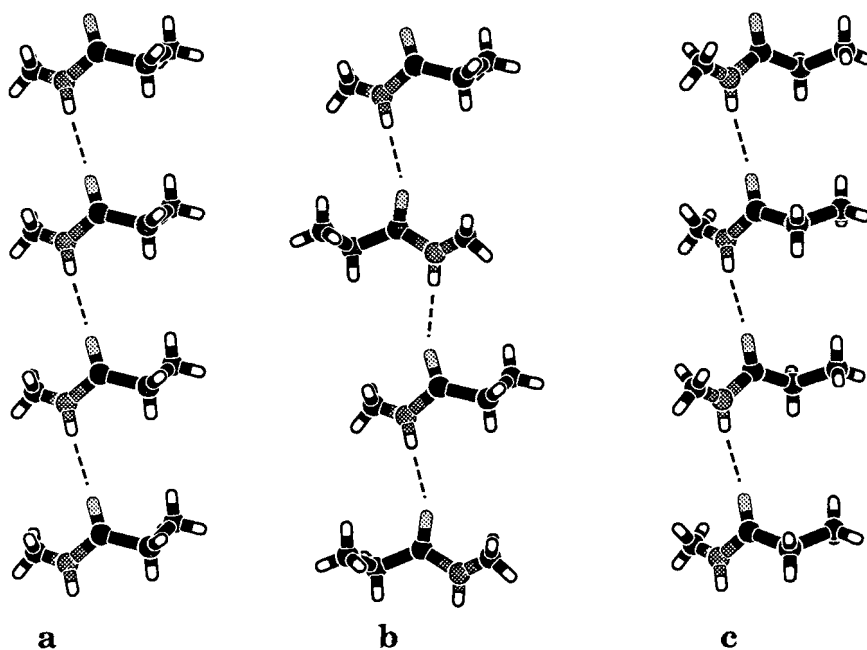


Figure 1. The three common hydrogen bond networks found for secondary amides. The symmetric assembly shown in **a** has rod group symmetry $P1$, **b** has rod group symmetry $P2_1$ and **c** has rod group symmetry Pa .

Table 1. The 22 Low Order Rod Groups.

1.	$P1$	9.	$P1m$	16.	$Pma2$
2.	$P\bar{1}$	10.	$P1a$	17.	$P2mm$
3.	$P2$	11.	$P12/m$	18.	$P2aa$
4.	$P2_1$	12.	$P12/a$	19.	$P2_1ma$
5.	Pm	13.	$P222$	20.	$Pmmm$
6.	$P2/m$	14.	$P2_122$	21.	$Pmma$
7.	$P2_1/m$	15.	$Pmm2$	22.	$Pmaa$
8.	$P12$				

If just one translational symmetry operation is added to a point group the resulting group is called a rod group.⁶ The rod groups are not widely used and are not well known. There are 75 rod groups possible within the constraints of crystallography. If one excludes high order axes of three fold or greater order there are 22 low order rod groups (Table 1). A one dimensional network of molecules found in any triclinic, monoclinic or orthorhombic crystal can be classified as belonging to one of the 22 low order rods. The amide networks of Figure 1 are symmetric assemblies belonging to the $P1$, $P2_1$ and Pa rod groups.

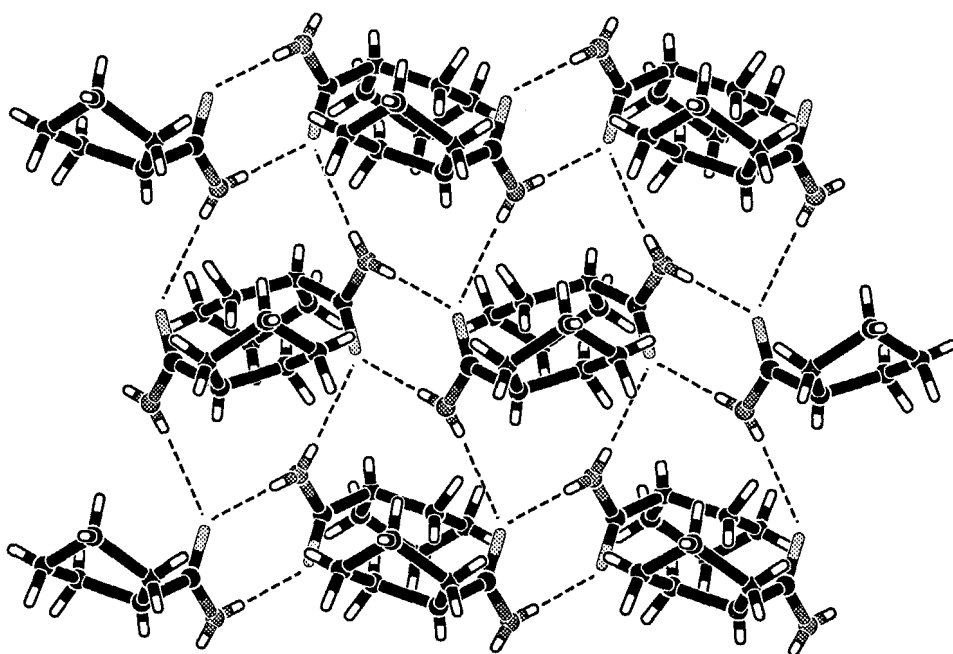


Figure 2. The crystal structure of cyclopentanecarboxamide.⁷ In the vertical direction molecules hydrogen bond to form a linear network via the carbonyl oxygen atom and the anti hydrogen atom; the rod symmetry is Pa . The amide groups also form cyclic dimers to amides of neighboring rods; the added center of symmetry combines with the original glide plane to yield a layer symmetry of $P2_1/a$.

If additional symmetry operations are added to a rod group, the new group may be a different rod group, a two dimensional layer group or three dimensional space group. Leiserowtz and Hagler have used similar ideas to provide a very thorough symmetry analysis of the packing of primary amides.⁸ In a typical example a network of primary amides with rod group symmetry $P1$ is related to another by centers of symmetry, forming a network of cyclic hydrogen bonded dimers of rod group symmetry, $P\bar{1}$.

Many primary amides form two dimensional structures as shown in Figure 2. When centers of symmetry are added to a symmetric assembly of primary amides with rod group symmetry, P_2 , the resulting network has layer group symmetry $P2_1/a$.

The layer groups are also unfamiliar to most chemists and crystallographers although they have been used by surface scientists.^{5a,9} They are formed by adding two directions of translational symmetry to a point group. There are 80 layer groups possible within the restraints of crystallography. Any two dimensional network of molecules found within any crystal will have layer symmetry corresponding to one of the 80 groups.

Note that one should not confuse the layer groups with the more commonly encountered plane groups. The 17 crystallographic plane groups are true two-dimensional groups, the third dimension does not exist. The 80 layer groups are three dimensional, but with only two directions of translational symmetry. The plane groups can be used to classify projections of a two dimensional molecular array, but only layer groups can properly classify a real two dimensional array of three dimensional molecules.

The rules for combining point groups, rod groups, layer groups and space groups have not been worked out and do not appear in the literature. The rules are obviously complex. The build up will not always be stepwise. In some cases one must go directly from a point group to a layer group or a space group without the formation of an intermediate rod group. Fortunately, in most cases of chemical interest, the attractive sequence of moving from a molecule to a one dimensional array, then on to two and three dimensions corresponds directly to the symmetry combinations leading from the point group to rod group, to layer group and on to the space group.

Applications.

In our own work we sought a family of molecules that would form predictable two dimensional layers in the crystalline state.¹⁰ Our strategy was to choose molecules that would give us chemical control of the crystal symmetry. This is possible if one chooses molecules which will have specific symmetries associated with their intermolecular interactions.

N,N'-disubstituted ureas are well known to form linear arrays via self complementary hydrogen bonds. If the substituents are identical then the molecular symmetry is often C_2 . Most commonly, the neighboring molecule in the hydrogen bonded array is related by a simple translation yielding a symmetrical assembly of rod group symmetry $P2$ and a characteristic repeat distance of about 4.6Å.

For a controlled layer structure we chose to use carboxylic acid functionalities, well known to form dimers about centers of symmetry. Combining these two functionalities each with a preferred intermolecular chemistry and an associated preferred symmetry operation leads one to predict the layer structure shown in Figure 3. The rod group symmetry of the linear urea array is $P2$; the carboxylic acid dimers form about inversion centers. The predicted layer group symmetry is $P2/a$. The predicted space group is not as obvious since there are no strong intermolecular bonds predicted between layers. The two most likely space groups would seem to be $P2/c$ if the layers are related by simple translation or $C2/c$ if the layers are related by additional centers of symmetry.

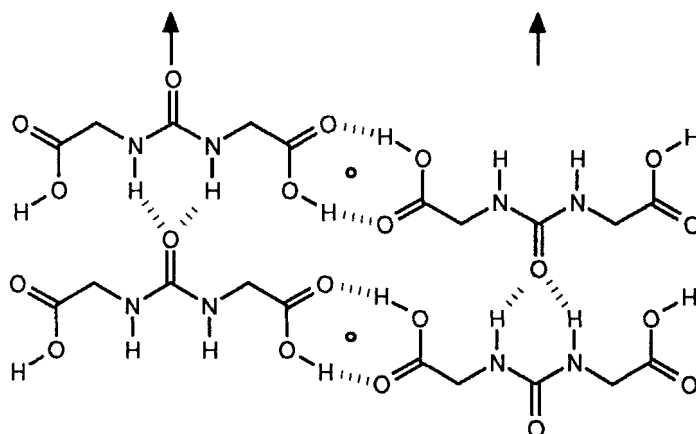


Figure 3. The proposed P2/a layer structure formed by a ureylenedicarboxylic acid.

In our initial work¹⁰ we studied a series of urylenedicarboxylic acids derived from glycine, β -alanine, 4-aminobutyric acid and the dipeptide glycylglycine. Each formed the predicted network with P2/a layer group symmetry. The space group in the first three cases was C2/c. Figure 4 shows the structure of the urea derived from 4-aminobutyric acid. In the case of the molecule derived from glycylglycine the two-fold axis was lost and the resulting space group symmetry dropped to P $\bar{1}$, but with a clear pseudo symmetry the overall structure is quite similar to the others.

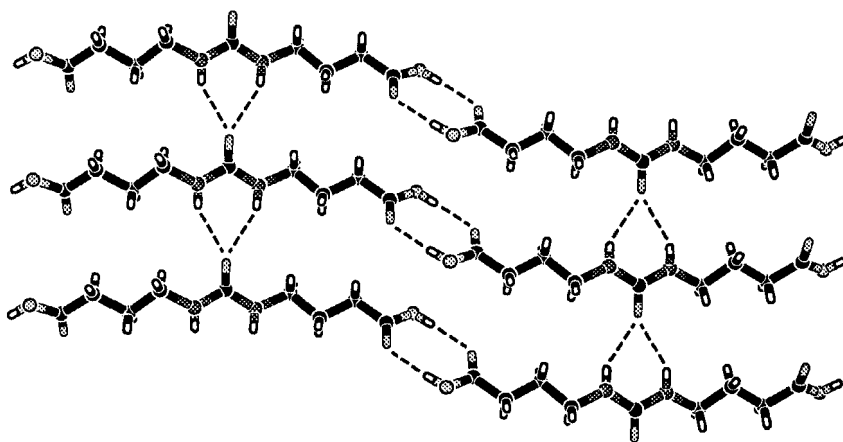


Figure 4. The crystal structures of the urea derived from 4-aminobutyric acid. The layer group symmetry is P2/a and the space group symmetry is C2/c.

A related structure has been published by Hollingsworth who determined the structure of the 1:1 adduct of urea with adiponitrile.¹¹ A two dimensional array of layer group symmetry P2/a was formed that is quite similar to the layer structures formed by the symmetric ureylenedicarboxylic acids. However in the case of the adiponitrile/urea adduct the P2/a layers pack via simple translation in the third dimension, and the final space group is P2/c instead of C2/c.

More recently we have studied the amide analogues of the ureylenedicarboxylic acids.¹² We anticipated similar structures since the amide functionality is also known to dimerize about a center of symmetry. The urea derived from the amide of 4-aminobutyric acid does indeed have the P2/a layer and C2/c space group symmetries.

The structure of the diamide of the urea derived from glycine gave a different result. The urea hydrogen bonds formed the expected one dimensional array of rod group symmetry P2. Instead of dimerizing about a center of symmetry the amide functionalities formed a helix about a 2_1 screw axis, Figure 5. The combination of the original P2 rod group with a 2_1 screw axis gives the layer group symmetry C2 for this two dimensional array. The amides each use their anti hydrogens to form additional hydrogen bonds to adjacent layers related to the original layer by inversion centers. The space group is thus again C2/c, even though the layer and rod group symmetries of the chemically important substructures are different.

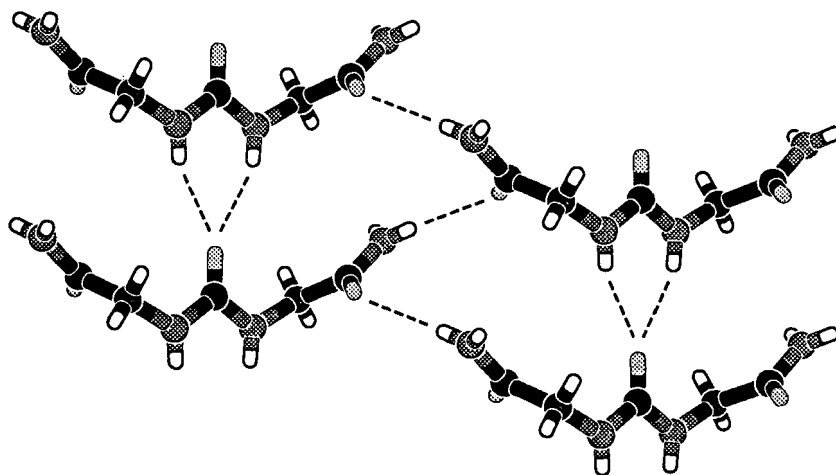
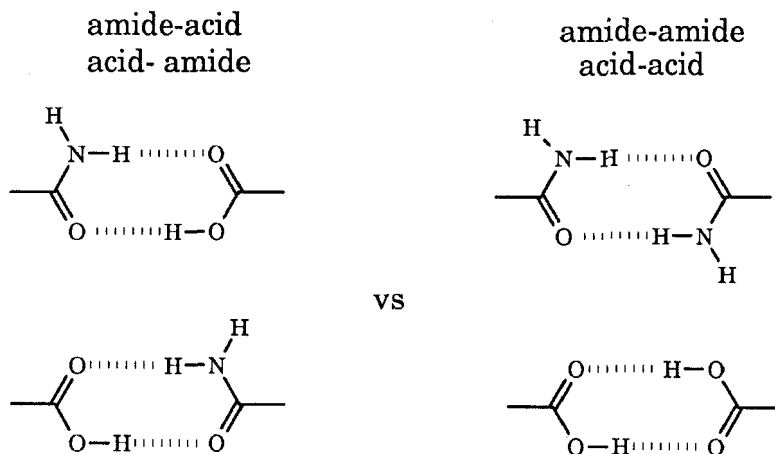


Figure 5. The crystal structures of the urea derived from the amide of glycine. The layer group symmetry is C2 and the space group symmetry is C2/c.

Our initial studies all involved symmetrical molecules with C_2 point group symmetry. Monoamide derivatives of the urylenedicarboxylic acids lack the C_2 symmetry element. From a survey of the literature and from some of our own work we expected that energetics might prefer hydrogen bond patterns featuring a mixed acid-amide cyclic dimer instead of the alternative of centrosymmetric acid-acid and amide-amide dimers. We anticipated a P1 layer group with only translational symmetry.



The monoamide derivatives of the ureas derived from glycine and from 4-aminobutyric acid both gave unexpected results inconsistent with our designs. The molecules both crystallized with the same P2/a layer group symmetry and C2/c space group symmetry as did their diacid precursors. In both cases the molecules disorder about the two fold axis. Infrared analysis is most consistent with cyclic acid-amide dimers, but, because of the disorder this can not be verified from the x-ray experiment. These structures thus carry a significant chemical warning. Even though the hydrogen bond patterns of an acid and an amide would be considered to be significantly different, the overall pseudo symmetry and molecular shape seems to be more important and two functionalities adopt similar environments as the molecule disorders. Molecular modelers should take note.

When the two ends of the molecule are made more different, disorder can not take place. Figure 6 shows the layer structure adopted by the unsymmetrical urea formed from β -alanine and the amide of glycine. In this case there are two molecules per asymmetric unit, the layer group symmetry is $P\bar{1}$ and the space group is also $P\bar{1}$.

Figure 7 shows the isomer with the amide group of the β -alanine end of the molecule. In this case the layer has only P1 layer group symmetry as originally anticipated. The amide anti hydrogen bond forms within the plane breaking the normal pattern of two urea hydrogen bonds. The inter layer symmetry is quite complex and the space group symmetry is $P2_1/c$.

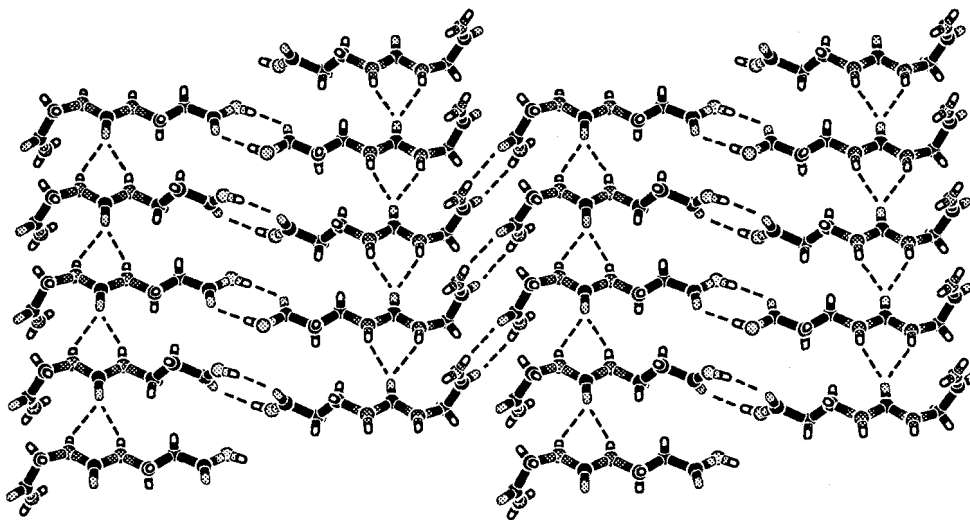


Figure 6. The crystal structure of the urea formed from the amide of glycine and β -alanine. The structure has $P\bar{1}$ layer group symmetry as well as $P\bar{1}$ space group symmetry. There are two molecules in the asymmetric unit.

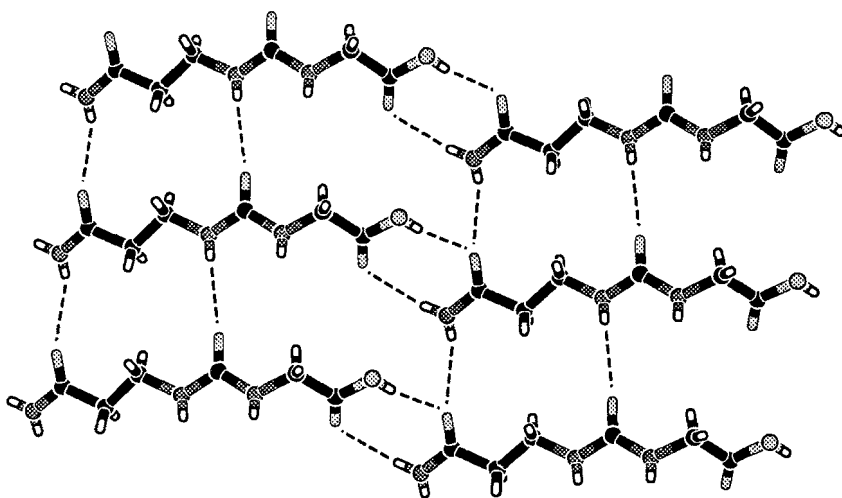


Figure 7. The crystal structure of the urea formed from the amide of β -alanine and glycine. The structure has $P1$ layer group symmetry and $P2_1/c$ space group symmetry.

As a final example consider the chiral urea formed from the amide of glycine and phenyl alanine. The layer structure shown in Figure 8 has only translation symmetry, layer group P1, but γ is equal to 90° . The P1 layer group has only translational symmetry and there is no chemical or symmetry requirement for the 90° angle within the layer. However, adjacent layers are related alternately by two fold and two-fold screw axes giving an overall space group symmetry of C2 for the three dimensional structure. The layer packing thus requires the 90° angle. We anticipate that other chiral molecules of this type will also form simple layer structures with only translational symmetry. They are the subject of our continuing studies.

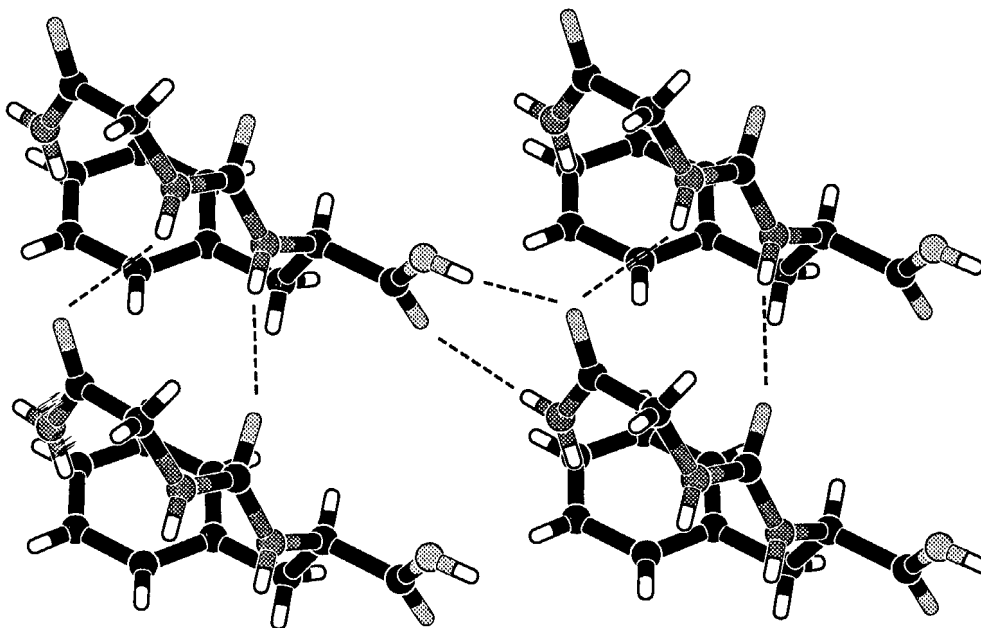


Figure 8. The crystal structure of the chiral urea formed from the amide of glycine and phenylalanine. The structure has P1 layer group symmetry and C2 space group symmetry.

Conclusions.

A systematic symmetry analysis based upon the chemistry of the molecule under study can be a useful approach to the design of molecular solids. In a molecular crystal, if all molecules are identical or enantiomorphic, then all intermolecular interactions will correspond to a specific symmetry operation. The ultimate structure of any molecular solid depends upon the chemistry of the intermolecular interactions. These interactions are weak, but by combining our chemical knowledge with the necessary symmetry constraints we can make useful predictions.

In most cases of chemical interest the attractive sequence of moving from a molecule to a one dimensional array, then on to two and three dimensions corresponds directly to the symmetry combinations leading from the point group to rod group, to layer group and on to the space group.

We have found that these ideas work well. In the symmetric ureylenedicarboxylic acids, hydrogen bonds are well matched and specific layered structures form as anticipated. With amides and mixed acid amide molecules it is more difficult to anticipate the observed intermolecular contacts and some structures were thus unanticipated. The introduction of chirality into a structure limits the number of possible intermolecular interactions and increases the prospect of a successful design.

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