

## Hydrogen Bonding and Molecular Assemblies\*

Biserka Kojić-Prodić,\*\* Zoran Štefanić, and Mladen Žinić

Ruđer Bošković Institute, Bijenička c. 54, P.O. Box 180, HR-10002 Zagreb, Croatia

RECEIVED JULY 24, 2003; REVISED OCTOBER 7, 2003; ACCEPTED OCTOBER 28, 2003

The old concept of complementarity, connected with the process of molecular recognition represents a simple approach to understanding molecular assembling. The noncovalent interactions governing (self)assemblies are fundamental to supramolecular chemistry and crystal engineering. Among noncovalent interactions governing molecular assembling, hydrogen bonding plays the leading role. A few examples of molecular assembling relevant to life processes and (bio)nano materials reveal the importance of this phenomenon. Systematic analysis of hydrogen bonding patterns, as a function of proton donor and acceptor properties, and stereochemical parameters, including chirality, is presented for a large number of di(amino acid) and di(amino alcohol) derivatives with oxalyl, phthaloyl, and fumaroyl bridges. Particular attention will be given to the molecular topology of such hydrogen bonded assemblies in terms of crystal engineering.

### Key words

- complementarity principle
  - molecular assembling
    - hydrogen bonding
- supramolecular assemblies
- oxalyl and phthaloyl derivatives of amino acids

*The reason why we are on a higher imaginative level is not because we have finer imagination, but because we have better instruments.*

A. W. Whitehead (1861–1947)

## INTRODUCTION

The essence of the packing principle founded on the shape-induced recognition-complementarity principle, as described by Kitaigorodsky 1955 in *Organicheskaya kristalloghimiya*, is actual nowadays (Figure 1).<sup>1</sup> However, Kitaigorodsky's conclusion that three symmetry elements: an inversion centre, a screw axis and a glide plane govern the close packing cannot be taken as a general rule.<sup>2,3</sup> For recognition between identical molecules, as it is the case in the majority of crystal structures, dissimilar parts of the molecules come into close contacts: bumps fit into hollows just as a key fits into a lock (Figure 2).<sup>4</sup> The close crystal packing within a crystal lattice is based on

this principle, introduced even before Kitaigorodsky; approximately 50 B.C. the Roman philosopher and poet Titus Lucretius Carus exposed the complementarity principle in his work *De Rerum Natura (The Nature of Things)*, a comprehensive exposition of the Epicurean world-view. New concepts of the complementarity principle emerged through the process of molecular recognition described by E. Fischer<sup>4</sup> (1894) as »Schlüssel-Schloss-Prinzip« (key-lock analogy) (applied a few years later by Ehrlich<sup>5</sup> in immunology and modified for the enzyme mechanism as a dynamic version of »glove-hand« (1994) by Koshland).<sup>6</sup> Molecular recognition, a crucial step in molecular assembling, turns to be a *spiritus movens* for new sophisticated materials highly exploited in (bio)nanotechnology.<sup>7</sup>

\* Presented as a plenary lecture at the Twelfth Croatian-Slovenian Crystallographic Meeting held in the Plitvice Lakes National Park, Croatia, June 19–22, 2003.

\*\* Author to whom correspondence should be addressed. (E-mail: kojic@rudjer.irb.hr)

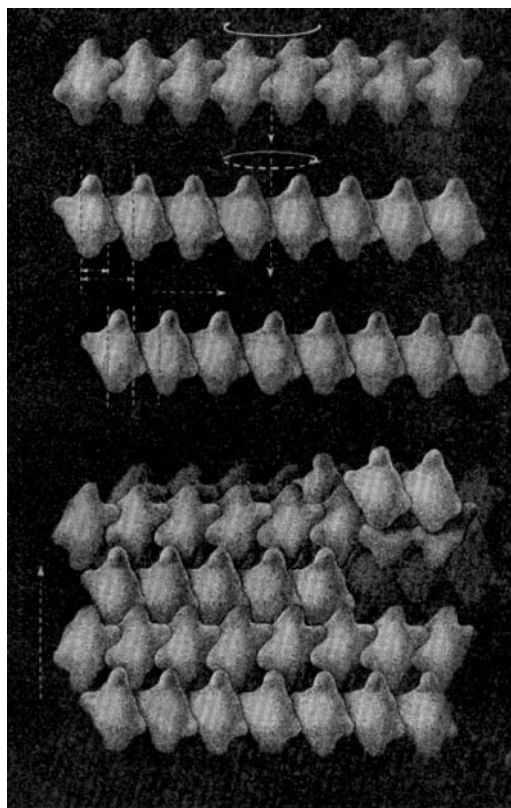


Figure 1. The essence of the packing principle founded on the shape-induced recognition-complementarity principle introduced by Kitaigorodsky, 1955.

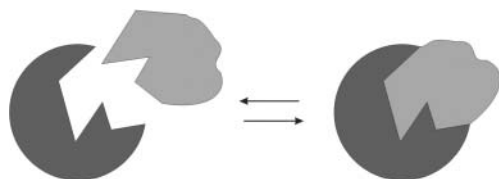


Figure 2. A »lock-key« scenario in biological systems and supra-molecular chemistry.

## SELF-ASSEMBLING

In general, self-assembly is the autonomous organization of components into patterns or structures without human intervention. Self-assembling processes are common to animate (Figure 3) and inanimate (Figure 4) objects in nature where they can be seen as the appearance of order from disorder.<sup>8</sup> Living cells self-assemble but cells themselves include self-assemblies of non-living objects such as ribosome units. Self-assembling has been used as a strategy to produce novel (bio)nanomaterials. Using the dynamic principle this term can be extended even further, *e.g.*, to computer networks and planetary systems, but these will be out of the scope of this paper. Two main classes of self-assemblies can be recognized: static, non-dissipating energy and dynamic, dissipating energy. Molecular crystals and globular proteins are formed by static self-assembly; in general, all types of self-assemblies in

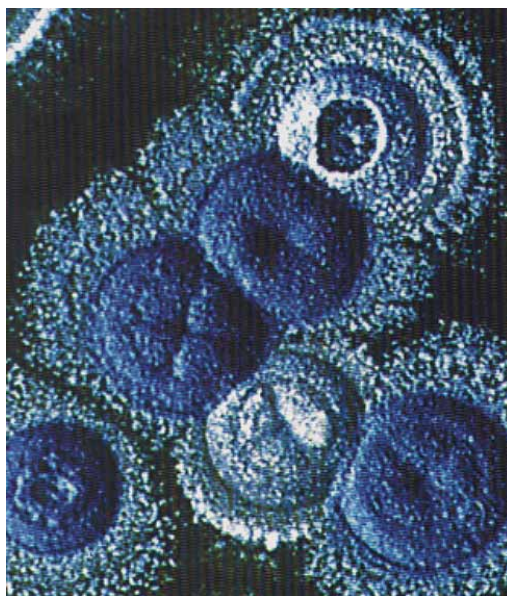


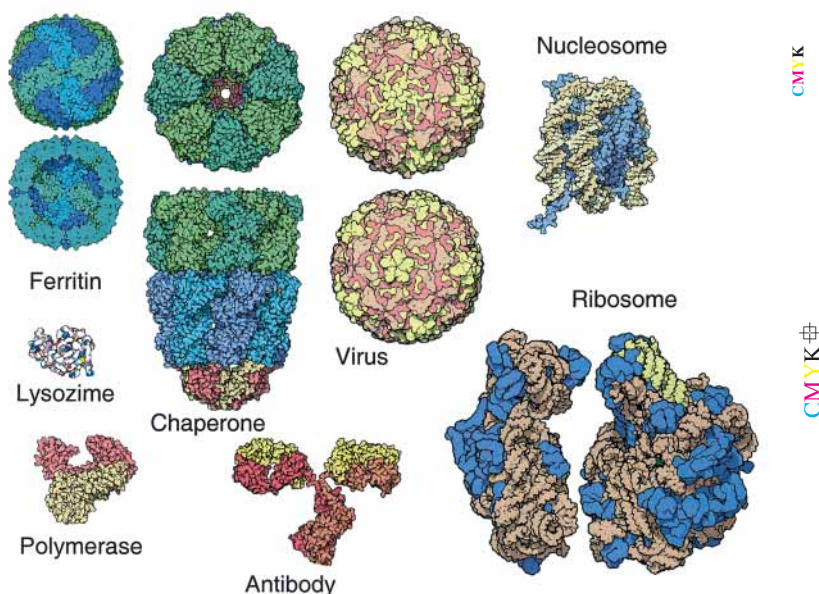
Figure 3. An assembly of *Streptomyces glaucescens* bacteria.

chemistry belong to this class. Current understanding of self-assemblies comes from static systems. However, the most important aspect of self-assembling is its central role in life processes: how does life emerge from a cascade of chemical reactions passing through assembling and disassembling?

## Interactions Governing Molecular Assemblies

According to the above-described principle of complementarity, molecular assemblies will be created through noncovalent interactions between counter parts of each molecule. There are two main classes of these interactions acting among organic molecules: isotropic, medium-range that define molecular shape, size, and close packing; and anisotropic, long-range forces, and electrostatic in nature. Isotropic, van der Waals interactions are usually considered to be dispersive and repulsive forces. Dispersive forces are attractive and are produced as the result of interactions between fluctuating multipoles in adjacent molecules. Their magnitude is proportional to the inverse sixth power of the interatomic distance ( $r^{-6}$ ) and approximately proportional to the size of the molecule. Repulsive forces balance the dispersive ones and in most cases can be modelled by  $r^{-12}$ . Balance between these two interactions and contributors from electrostatic forces have been used for the atom-to-atom potential method (molecular mechanics), energy of the system by a sum of pair-wise van der Waals interactions ( $V(r_{ij})$ ) calculated using a Lennard-Jones or Buckingham potential. Kitaigorodsky used this simple approach to molecular crystals to develop the close-packing principle. However, this simplified approach is valid mainly for non-aromatic hydrocarbons whereas the packing of aromatic hydrocarbons should be viewed through stacking of planar aromatic rings, offset

Figure 4. Macromolecular assemblies as inanimate objects present in the living organisms.



stacking and herringbone arrangements using  $C-H \cdots \pi$  and  $\pi \cdots \pi$  interactions. Packing of aliphatic side-chains in molecular crystals is under the influence of van der Waals forces; for long aliphatic chains hydrophobic interactions are pronounced and more  $CH_2$  groups can be used as synthons in crystal engineering. Nowadays, there are various modifications and methods adjusted to the molecule studied, but reviewing them would be out of the scope of the paper.

Anisotropic interactions involve mostly heteroatoms and are strongly directional and as such they are essential in molecular recognition. Hydrogen bonding is a directional interaction essential for a great number of supramolecular constructions. In spite of the seminal role of hydrogen bonding, it is not simple to offer its comprehensive and strict definition. Spectroscopic and diffraction techniques employing more sensitive detectors provide more accurate data and detect very fine dynamic ef-

fects, thus changing our concepts on hydrogen bonding. To view the hydrogen bond as an incipient proton transfer reaction, a stable hydrogen bond  $X-H \cdots Y$  is the »frozen« state of the reaction  $X-H \cdots Y \rightleftharpoons X^- \cdots H-Y^+$  (or other possibilities).<sup>9</sup> To respect this »dynamical state« of hydrogen bond definition, we would rather catalogue hydrogen bonds of interest in the crystal packing of the studied class of compounds. The conventional hydrogen bonds of the type  $O-H \cdots O$ ,  $N-H \cdots O$  (energies 20–40  $\text{kJ mol}^{-1}$ ) usually termed as the strong ones, dictate molecular assembling in the studied class, but they also prevail in biological molecules. However, weaker  $C-H \cdots O$ ,  $C-H \cdots \pi$ , and  $\pi \cdots \pi$  (energies 2–20  $\text{kJ mol}^{-1}$ ) do the fine-tuning of intermolecular interactions. In strong hydrogen bonds where X is highly electronegative (O, N), it withdraws the electron density from the hydrogen atoms, leaving them with a significant positive charge and leading to a coulombic interaction with the electronegative acceptor

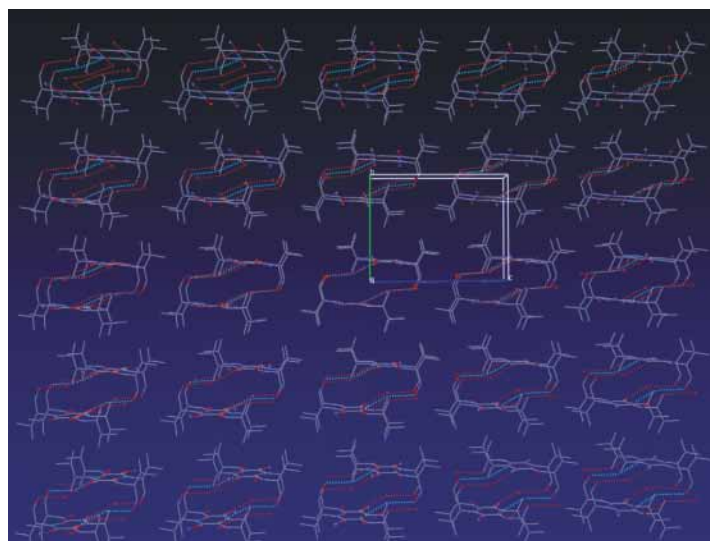
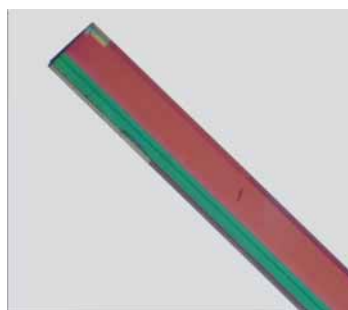


Figure 5. Crystal packing and the twin crystal of *rac*-(*R,R*)-*N,N'*-oxalyl-divalinol,<sup>16</sup> an example of homomeric one-dimensional supramolecular assembly. The crystal is the supramolecule: a lump of matter of macroscopic dimensions, millions of molecules long, held together in a periodic arrangement by just the same kind of noncovalent interactions (J. Dunitz)<sup>13</sup>.



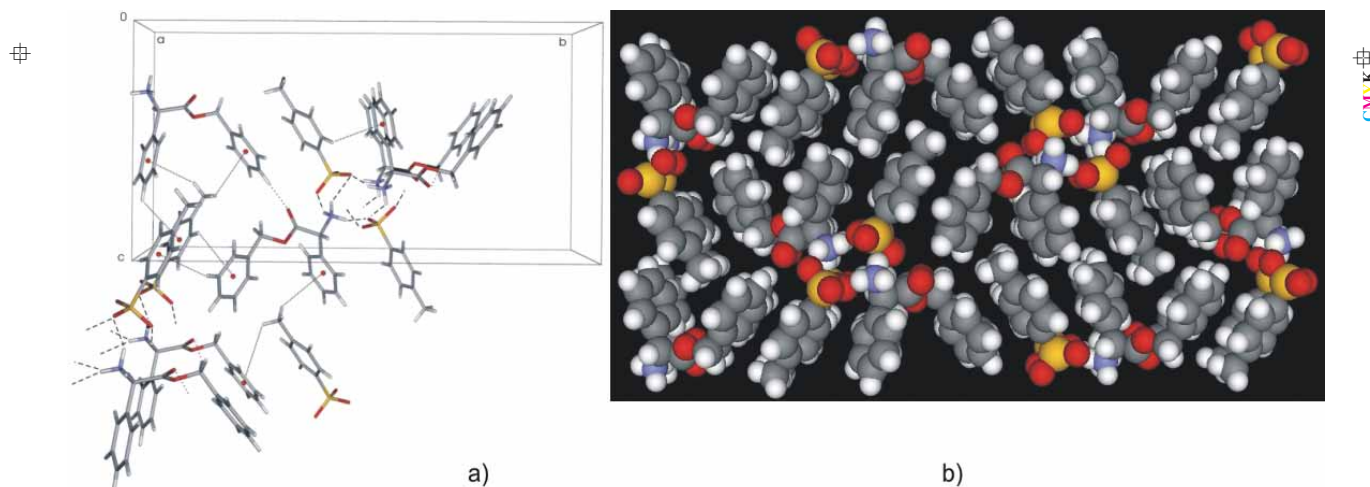


Figure 6. a) A heteromeric assembly in the crystal structure of [2(benzyloxy)-2-oxo-1-phenylethyl]ammonium 4-methyl-1-benzensulphonate governed by: N–H $\cdots$ O hydrogen bonds between cation and anion, C–H $\cdots$ O, CH $\cdots$  $\pi$ , and  $\pi\cdots\pi$  interactions. b) Complementarity principle illustrated by a space-filling model of the crystal packing shown in 6a.

atom A. The distinctive geometrical features are distances X $\cdots$ A and H $\cdots$ A, the angle X–H $\cdots$ A ( $\theta$ ), H $\cdots$ A–Y angle ( $\varphi$ ), and the planarity of the XHAY system.<sup>10</sup> Values X $\cdots$ A are usually in the range 1.80 to 2.00 Å for N–H $\cdots$ O and between 1.60 to 1.80 Å for O–H $\cdots$ O bonds. Ranges for  $\theta$  and  $\varphi$  occur about 150–160° and about 120–130°, respectively (The Cambridge Structural Database, version 5.24, including updates until April 2003).<sup>11</sup>

#### Self-assemblies in Supramolecular Chemistry and Crystal Engineering

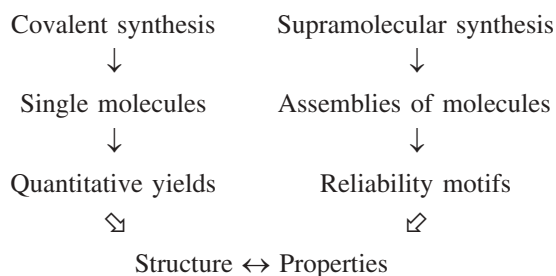
»The consequences of directed and selective hydrogen bond interactions on sets of molecules are to a solid-state chemist what a new synthesis is to a solution chemist« (M. Etter).<sup>12</sup>

In the chemical recognition processes, including supramolecular and biomolecular ones, there are interactions between chemically different or identical molecules (or enantiomers). Assemblies of the identical copies of the same molecule represent homomeric architecture (Figure 5). »The crystal is, in a sense, the supermolecule *par excellence*: a lump of matter, of macroscopic dimensions, millions of molecules long, held together in a periodic arrangement by just the same kind of noncovalent bonding interactions as are responsible for molecular recognition and complexation at all levels« (J. Dunitz).<sup>13</sup> The assemblies composed of binary and ternary systems through noncovalent interactions generate heteromeric architectures; a heteromeric ionic assembly is illustrated by the crystal packing of [2(benzyloxy)-2-oxo-1-phenylethyl]ammonium 4-methyl-1-benzensulphonate (Figures 6a and 6b).<sup>14</sup> They produce sophisticated multipurpose materials useful in nanotechnology, representing a more refined and versatile level of crystal engineering. Thus, crystal engineering aims to produce reliable connections between molecular and supramolecular structures. Princi-

ples of crystal engineering are analogous to those of supramolecular chemistry. Using molecular recognition, one manipulates intermolecular interactions in the crystal to obtain the desired architecture of the molecular assemblies in the crystal.<sup>15</sup> Crystal engineering should recognize and design synthons that are robust enough to be used in various networks with high predictability and reliability. Corey's general definition, introduced in 1967, among seven axioms essential for organic synthesis and its methodology states:«... possible routes are derivable by recognition of structural units within molecules which can be formed and/or assembled by known or conceivable synthetic operations;...these units are designated as synthons«. <sup>16</sup> In light of Corey's definition, Desiraju<sup>2</sup> said: »supramolecular synthons are structural units within supermolecules that can be formed and/or assembled by known or conceivable synthetic operations involving intermolecular interactions«. The synthons used for the present class of compounds are oxalamide groups, carboxyl groups, and phthalamide groups (Scheme 1).<sup>17–19</sup>

In contrast to classical chemical synthesis primarily based on covalent (or ionic) interactions, supramolecular synthesis is chemistry beyond the molecule, based on noncovalent, directional interactions (such as hydrogen bonds including CH $\cdots$  $\pi$ , and  $\pi\cdots\pi$  interactions).

Comparison between covalent and supramolecular syntheses was given concisely by Aakeröy *et al.*:<sup>20</sup>



A striking fact is that physical, chemical and biological properties of building units are different from those of the supramolecule represented as a molecular assembly at a high level: the most familiar examples are graphite, diamond, and carbon nanotubes (fullerene molecules) as carbon assemblies (Figure 7). Among the biological examples, mention can be made of amyloid proteins that self-assemble into fibrous structures under pathological conditions related to Alzheimer's disease.<sup>21</sup>

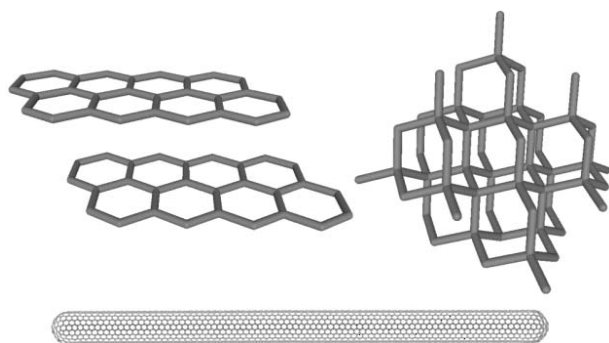
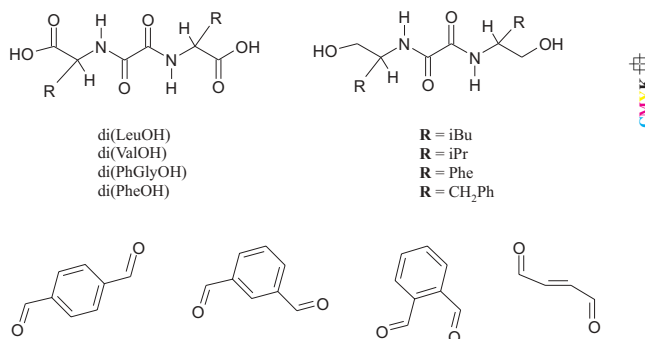


Figure 7. A very common example of the three distinctive assemblies of carbon atoms with different properties: graphite, diamond and carbon nanotubes (fullerene) assemblies.

#### Molecular Organization in Crystals of Di(amino acid) and Di(amino alcohol) Oxalamide and Phthalamide Derivatives

In the crystals of this class of compounds,<sup>17–19,22</sup> the dominant, noncovalent directional interaction governing molecular assemblies is hydrogen bonding realized *via* oxalamide (phthalamide) bridges having both donor and acceptor functionalities, and terminal carboxyl, hydroxy or amide groups.



Scheme 1. Chemical diagrams.

To change the internal organization of molecular assemblies, oxalamide bridges with *trans* disposed carbonyl groups were replaced by *N,N'*-phthalamide, *N,N'*-isophthalamide and *N,N'*-terephthalamide, and *N,N'*-fumaramide groups.<sup>22</sup> The aromatic spacer with different substitution sites (phthaloyl isomers) or the double bond of fumaroyl influence the separation distance of donor and acceptor sites, changing the topology of the hydrogen bonding network. The terminal carboxyl groups were replaced by hydroxy or amide groups, both capable of extending the hydrogen bonding network in two dimensions. Esterification of the carboxyl group removes the donor functionality at the terminal sites but leaves their acceptor functions. In the structures of (*S,S*)-*N,N'*-terephthaloyl-dileucine methyl ester and its valine analogue, a large spacer influences a different topology of the hydrogen bond network: the molecules are oriented perpendicular to each other, forming the two-dimensional wavy network of hydrogen bonds (Figures 8a and 8b).<sup>22</sup> The complementarity principle also governs CH $\cdots$  $\pi$  interactions occurring between the aromatic spacer and the terminal aliphatic groups (Figure 9).

In addition to the above described molecular »tailoring«, the chirality and symmetry elements influence an

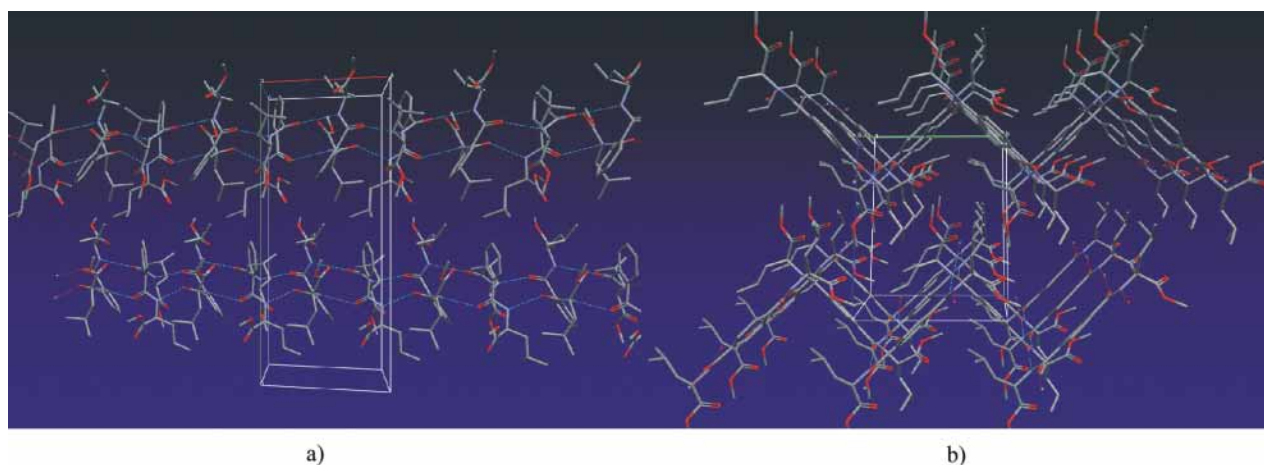


Figure 8. a)  $\alpha$ -network of (*S,S*)-*N,N'*-terephthaloyl-dileucine methyl ester. Esterification prevents formation of a two-dimensional network whereas a large spacer terephthaloyl group changes the topology of the hydrogen bonded network. b) The valine-analogue structure of an isotypical crystal packing.

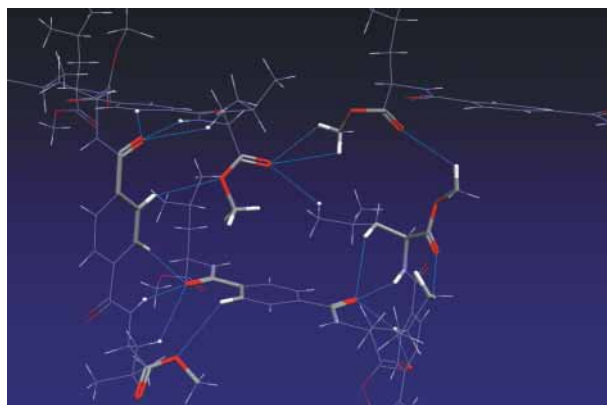


Figure 9. In the crystal structure of *(S,S)*-*N,N'*-terephthaloyl-dileucine methyl ester<sup>19</sup> dominated by hydrogen bonds C–H··· $\pi$  interactions between aromatic spacer and terminal methyl groups are also present.

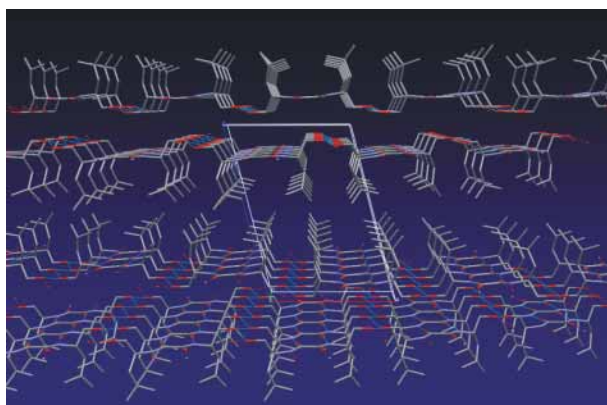


Figure 10. Two-dimensional hydrogen bonding network of *(S,S)*-*N,N'*-oxalyl-dileucinol<sup>18</sup> with enantiomeric bilayers, including well pronounced hydrophobic channels.

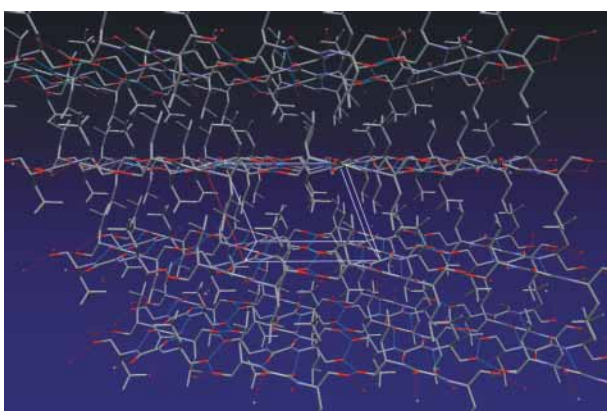


Figure 11. Hydrophobic groups in the crystal structure of *meso*-*N,N'*-oxalyl-dileucinol<sup>18</sup> arranged on both sides of the hydrogen bonded molecular backbone.

arrangement of alkyl groups around the molecular backbone. Thus, the separation of hydrophilic and hydrophobic layers depends on these arrangements. In the enantiomeric structures, the enantiomeric bilayers are formed

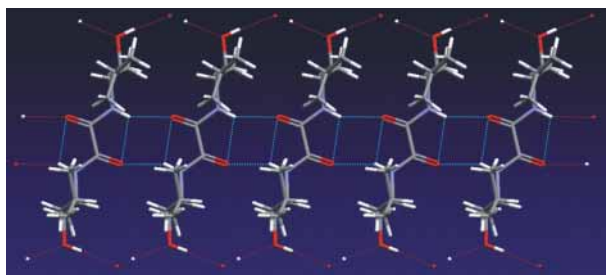


Figure 12. Typical »ladder« pattern realized by intra and intermolecular N–H···O hydrogen bonds.

with the strict separation of hydrophilic and hydrophobic layers (alkyl groups are on the same side of the molecular backbone) (Figure 10). In contrast, in the *meso*-forms, such as *(R,S)*-*N,N'*-oxalyl-dileucinol with alkyl groups alternating on both sides of the molecular backbone, bilayers are formed with less pronounced hydrophobic channels (Figure 11).<sup>18</sup>

#### Structural Elements Created through Hydrogen Bonding

Hydrogen bonds are often formed in a hierarchical fashion: best donor to best acceptor; second-best donor to second-best acceptor, *etc.*<sup>23</sup> In these structures, intermolecular hydrogen bonds can be represented by the following categories in accord with the hierarchical criterion: a) N–H···O between oxalamide groups, b) O–H···O between carboxyl groups, c) between oxalamide and carboxyl groups, and d) between carboxyl groups and chain substituted donor/acceptor groups. The structural hydrogen-bonded element present in the majority of oxalamide structures is the »ladder« pattern (Figure 12) generated by intermolecular hydrogen bonds N–H···O of oxalamide groups. This pattern also includes intramolecular hydrogen bonds N–H···O of a *pseudo*-C<sub>5</sub> ring structure typical of retropeptides with intramolecular hydrogen bonds.<sup>24</sup> Using the graph-set notation,<sup>15,25</sup> the »ladder« structure includes  $R_2^2$  (10),  $C_2^2$  (10), and  $S(5)$  building units. A rather rare example of a two-fold symmetry  $R_2^2$  (10) hydrogen bonded dimer was observed in the structure of *N,N'*-bis[(1*S*)-2-azido-1-(2-methylpropyl)ethyl]oxalamide (Figure 13).<sup>19</sup> Inspection of the Cambridge Structural Database<sup>11</sup> revealed a single example of such a motif in the structure of *N*-hydroxyoxamide.<sup>26</sup> In contrast, centrosymmetric hydrogen bonded dimers formed by carboxylic acids are highly populated but such a motif cannot be generated in the crystal structures of chiral compounds. However, crystal structures of the racemates studied by us revealed the centrosymmetric tandem hydrogen bonds between two hydroxy groups (of a terminal carboxyl group<sup>17</sup> or a terminal alcohol group)<sup>18</sup> of two molecules (Figure 14). It implies that such a hydrogen bond connects molecules of opposite chirality. The tandem hydrogen bonds are not so common<sup>10,11</sup> but they were found in this class of compounds, notably in some racemate

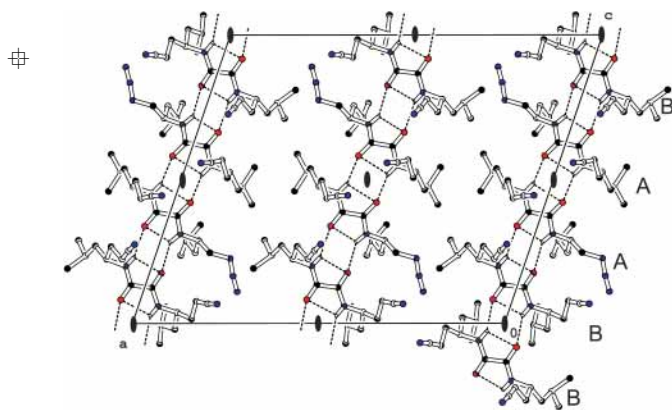


Figure 13. In the crystal structure of *N,N'*-bis[(1*S*)-2-azido-1-(2-methylpropyl)ethyl]oxalamide,<sup>19</sup> as part of the »ladder« pattern, there are symmetrically three different dimers (A...A, B...B with a crystallographic twofold symmetry and A...B dimer with an approximate twofold symmetry).

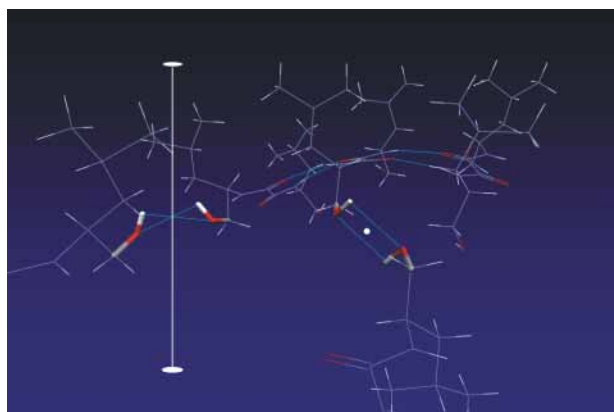


Figure 14. Tandem hydrogen bonds in the crystal structure of *rac*-(*R,R*)-*N,N'*-oxalyl-dileucinol<sup>18</sup> related by a two-fold axis and the centre of inversion.

structures.<sup>18</sup> This configuration leads to too close contacts between H atoms, and disorder can occur. To discuss its geometry, one needs low-temperature data and

even better neutron diffraction data. In the crystal structure of *rac*-(*R,R*)-*N,N'*-oxalyl-dileucinol<sup>18</sup> in the space group *C2/c*, a typical pattern occurs due to the presence of 1+1/2 crystallographically independent molecules. As a consequence of symmetry operations, the »ladder« pattern is composed of molecular triads of opposite chirality: molecules operated by a twofold rotation or translation keep the same chirality whereas those operated by inversion or glide plane change the chirality (Figures 15a and 15b). In this structure, terminal hydroxy groups are involved in two types of tandem hydrogen bonds: the centrosymmetrical tandem connecting molecules of opposite chirality and the twofold symmetry one connecting molecules of the same chirality (Figure 14). However, a different hydrogen bonded pattern occurred in the structure of *rac*-(*R,R*)-*N,N'*-oxalyl-divalinalol<sup>18</sup> (Figure 16). Two compounds of chemically analogous groups, one having a leucyl and the other a valyl group, generate different hydrogen bonded structural elements leading to different crystal packing. The terminal alcohol groups (with *syn*-hydrogen) do not complete the two-dimensional  $\beta$ -network; one of them forms the hydrogen bond whereas the other one donates a proton to the carbonyl group of oxalamide moiety closing a centrosymmetric ring connecting molecules of opposite chirality. Thus, chiral layers are formed. A similar pattern was observed in the structure of *rac*-(*R,R*)-*N,N'*-oxalyl-diphenylglycine structure.<sup>17</sup> This example illustrates that crystal engineering is not a straightforward procedure, and that crystal structure prediction is far from a routine task.<sup>27,28</sup>

*Classification of Crystal Packing: One-dimensional  $\alpha$ -network, Two-dimensional  $\beta$ -network, Three-dimensional  $\gamma$ -network of *N,N'*-di(amino acid) Oxalamides (and Phthalamides) and Their Amino Alcohol Analogues*

Oxalamide was recognized as a good synthon and was intensively used in crystal engineering by Coe, Fowler,

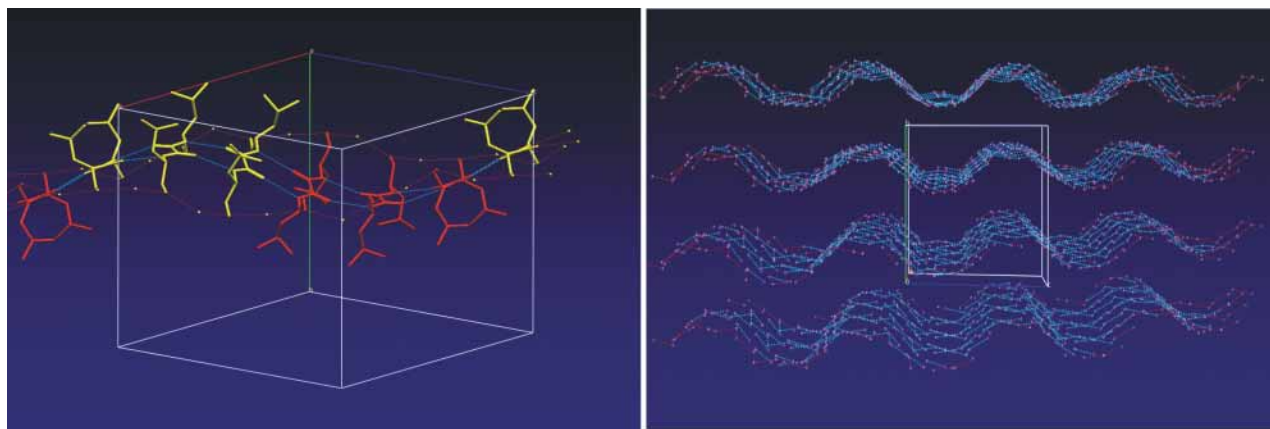


Figure 15. a) In the crystal structure *rac*-(*R,R*)-*N,N'*-oxalyl-dileucinol<sup>18</sup> the »ladder« pattern is composed of molecular triads of opposite chirality: molecules operated by twofold rotation (or translation) keep the same chirality (yellow) whereas those operated by inversion (or a glide plane) change the chirality (red). b) A two-dimensional wavy hydrogen bonded network was obtained.

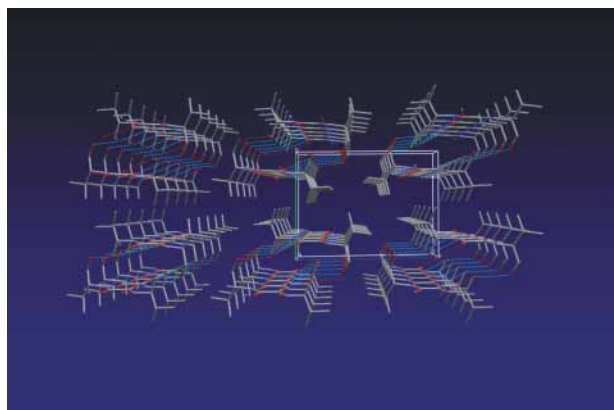


Figure 16. *rac*-(*R,R*)-*N,N'*-oxalyl-divalinal structure with pronounced enantiomeric layers.<sup>18</sup>

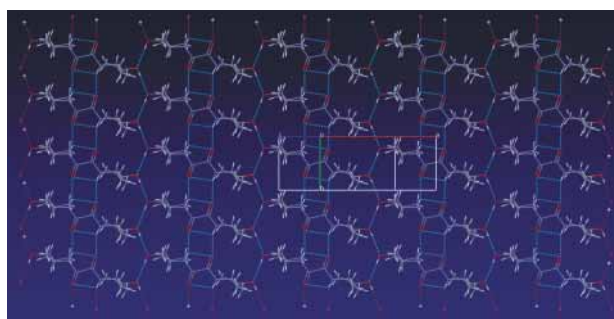


Figure 17. Two-dimensional  $\beta$ -beta-network of (*S,S*)-*N,N'*-oxalyl-dileucinol.<sup>18</sup>

and Lauher.<sup>29</sup> They proposed strategies for generating one-, two-, and three-dimensional molecular assemblies. The oxalamide group serves as a synthon to assemble molecules through N–H $\cdots$ O hydrogen bonds into the one dimensional  $\alpha$ -network (Figure 13). With sophisticated »tailoring« of the molecules, *i.e.*, chemically introduced carboxyl (or amide) groups at the terminal part of the molecules, O–H $\cdots$ O hydrogen bonds will complete the hydrogen bonding network in two-dimensions,  $\beta$ -network (Figure 17). However, crystal engineering cannot be straightforward: instead of the above described hydrogen bond network, the alternative one can be formed using O–H $\cdots$ O hydrogen bonds between the oxalamide and the carboxyl group (or alcohol groups). Thus, a different crystal packing occurs, as a new polymorph with the  $\beta$ -network or a three-dimensional  $\gamma$ -network.<sup>18,29</sup> The three-dimensional  $\gamma$ -network occurs in the case of substitution of a donor group at a side chain. A good example is the molecule of (*R,R*)-*N,N'*-oxalyl-di(*p*-hydroxyphenylglycinol) with substituted PhOH at both *C $\alpha$*  of glycine (introducing chirality), producing the  $\gamma$ -network<sup>30</sup> with intensive hydrogen bonding: only one oxalamide nitrogen acts as donor to a terminal hydroxy group, terminal OH groups are hydrogen bonded to each other whereas one of them is in contact with the *p*-hydroxyphenyl group; *p*-hydroxyphenyl groups act as proton donors to

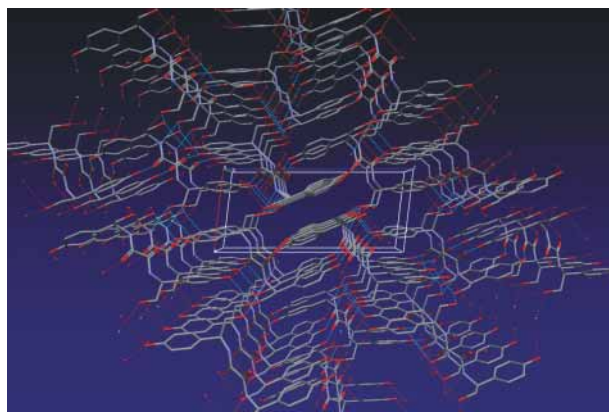


Figure 18. The  $\gamma$ -network of (*R,R*)-*N,N'*-oxalyl-di(*p*-hydroxyphenylglycinol) with the intensive hydrogen bonding network including CH $\cdots$  $\pi$  contacts: between methylene group and an aromatic ring (a separation distance from H to the centroid of the aromatic ring 2.966 Å) and between two aromatic rings (with an angle to the centroid separation distances of 2.978 and 3.001 Å).<sup>30</sup>

oxalamide CO groups. Additional CH $\cdots$  $\pi$  interactions contribute to the crystal packing forces (Figure 18). The only example of the  $\gamma$ -network was obtained by Coe *et al.*<sup>29</sup> through introduction of an additional synthon, a peptide group producing the retrotetrapeptide OH-Gly-Gly-CO-CO-Gly-Gly-OH: oxalamide groups are hydrogen bonded by N–H $\cdots$ O interactions in one direction, generating a typical »ladder« pattern, carboxyl groups are connected by the O–H $\cdots$ O hydrogen bond, and in the third direction are N–H $\cdots$ O hydrogen bonds between the peptide groups.<sup>30</sup> However, in the *rac*-(*R,R*)-*N,N'*-oxalyl-divalinal structure, the hydrogen bonding of terminally located alcohol groups is different from any of the previously described structures; they do not complete either the two-dimensional  $\beta$ -network or the  $\gamma$ -network. One hydroxy group closes a hydrogen bonded centrosymmetric ring dimer and the other one donates a proton to the carbonyl of the oxalamide group, forming an intramolecular hydrogen bond. These rings are stacked one over the other, generating layers of opposite chirality, *meso*-bilayers (Figure 16). This type of network was classified as the  $\alpha$ -network by Chang *et al.*<sup>31</sup>

## RELATIONSHIP BETWEEN MOLECULAR ASSEMBLIES AND PHYSICAL PROPERTIES

The class of compounds studied predominantly exhibit one- or two-dimensional molecular assemblies in the crystals, and in very few cases the three-dimensional  $\gamma$ -network using donor-acceptor complementarity. Some of these organic molecules are gelators of water and less polar organic solvents and their mixtures.<sup>17,18,22</sup> In the majority of cases, chiral molecules exhibit this property. However, in the described class of compounds, *rac*-(*R,R*)-*N,N'*-oxalyl-dileucinol is a much better gelator of aro-



matic solvents than its *S,S*-enantiomer. This phenomenon can be explained by formation of the enantiomeric bilayers in this solvent, while in other solvents the racemate organizes into a *meso*-bilayer (Figures 10, 16).<sup>18</sup> Their molecular assemblies are organized into aggregates entrapping the solvent molecules. If one wants to produce gels, crystallization of self-assembled aggregates must be avoided; a good balance between order and disorder has to be found. In an optimal case, self-assembled molecules should form fibroid aggregates *via* an anisotropic growth process; a length of fibre can be on a micrometer scale whereas its diameter is of a nanometer size (Figure 19). The delicate balance between fibre-fibre and fibre-solvent interactions is essential for obtaining a stable gel. In addition to the required sophisticated gelator design, the solvent polarity and polarizability should be adjusted as



Figure 19. TEM image of (*S,S*)-oxalyl-dileucinol toluene gel negatively stained by dipotassium phosphotungstate (right), and an application of gel – Haribo bonbons (left).

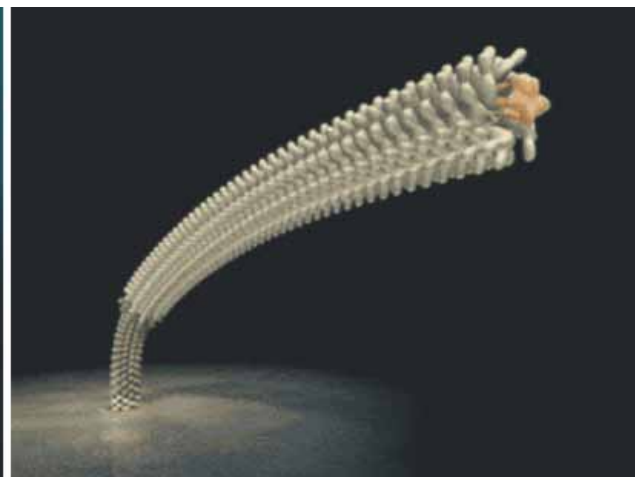


Figure 20. Movement of *Salmonella* bacteria using flagella (20 nm in diameter and over ten thousands nm in length). The flagellar filament is a tubular bundle of 11 proto-filaments, each being an axial array of flagellin subunits (Keiichi Namba, <http://www.npn.jst.go.jp>).

well. However, there is no strict rule, and it is still a matter of trial and error procedures.

In general, (self)-assembly is a strategy for organizing matter on large scales from nanometers to micrometers.<sup>32</sup> (Self)-assembly can find application in crystallization on various scales; robotics and manufacturing (nanotools,<sup>33</sup> Figure 20); nanomaterials such as porous network materials, helical superstructures,<sup>34</sup> nanotubes and wires (Figure 21); microelectronics and microdevices based on two- and three-dimensional systems; netted systems such as computers, (bio)sensors, nervous systems and many other examples.

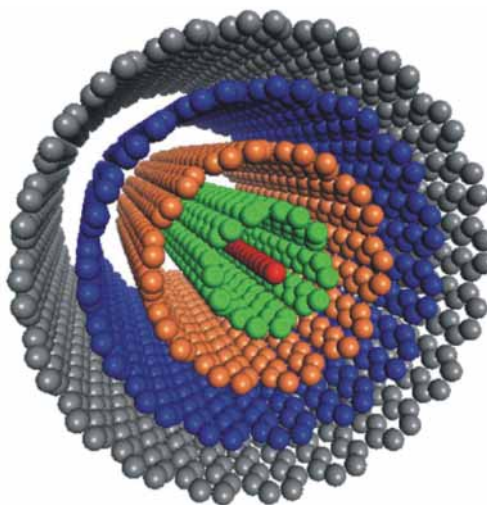


Figure 21. Carbon nanowire (red) inside a carbon nanotube: a single strand of carbon atoms is contained in a multi-walled carbon nanotube (Zhao *et al.*, <http://www.aip.org/mgr/png/2003/186.htm>).

*The important thing in science  
is not so much to obtain new facts as  
to discover new ways of thinking about them.*

W. L. Bragg

*Acknowledgements.* – The work presented was supported by the Ministry of Science and Technology of the Republic of Croatia, projects 0098036 and 0098053. The authors thank Prof. dr. A. Meden, Faculty of Chemistry and Chemical Technology, University of Ljubljana, for X-ray intensity data of the two samples (details will be published elsewhere). The attractive Figure 4 compiled from data stored in the Protein Data Bank by Prof. Dr. N. Ban, Institute for Molecular Biology and Biophysics, Swiss Federal Institute of Technology, ETH, Zürich, and Prof. Dr. D. S. Goodsell, The Scripps Research Institute, USA was kindly offered for this article. The authors appreciate valuable discussion given by Dr. D. Kirin, Rudjer Bošković Institute, Zagreb, Croatia.

## REFERENCES

1. A. I. Kitaigorodsky, *Organicheskaya kristalloghiya*, Izdatelstvo Akademii Nauk SSSR-a, Moskva 1955, pp. 139–236.
2. G. R. Desiraju, *Angew. Chem., Int. Ed. Engl.* **34** (1995) 2311–2327.
3. A. Nangia and G. R. Desiraju, *Acta Crystallogr., Sect. A* **54** (1998) 934–944.
4. E. Fischer, *Ber. Dtsch. Chem. Ges.* **27** (1894) 2985–2993.
5. P. Ehrlich, *Proc. R. Soc. London* **66** (1900) 424–448.
6. D. E. Koshland, *Angew. Chem., Int. Ed. Engl.* **33** (1994) 2375–2378.
7. D. Braga, F. Grepioni, and A. G. Orpen, *Crystal Engineering: From Molecules and Crystals to Materials*, Kluwer, Dordrecht, 1999.
8. G. M. Whitesides and B. Grzybowski, *Science* **295** (2002) 2418–2421.
9. T. Steiner, *Angew. Chem., Int. Ed. Engl.* **41** (2002) 48–76.
10. G. A. Jeffrey and W. Saenger, *Hydrogen Bonding in Biological Structures*, Springer, Berlin, 1991, pp. 103–110; 24, 40, 83.
11. F. H. Allen, *Acta Crystallogr., Sect. B* **58** (2002) 380–388.
12. M. Etter, *J. Phys. Chem.* **95** (1991) 4601–4610.
13. J. D. Dunitz, *Thoughts on Crystals as Supramolecules* in: G. R. Desiraju (Ed.), *The Crystal as a Supramolecular Entity*, Wiley and Sons, New York, 1996, pp. 1–30.
14. Z. Štefanić, M. Jokić, B. Kojić-Prodić, and M. Žinić, unpublished work.
15. W. D. S. Motherwell, G. P. Shields, and F. H. Allen, *Acta Crystallogr., Sect. B* **55** (1999) 1044–1056.
16. E. J. Corey, *Pure Appl. Chem.* **14** (1967) 19–37.
17. J. Makarević, M. Jokić, B. Perić, V. Tomišić, B. Kojić-Prodić, and M. Žinić, *Chem. Eur. J.* **7/15** (2001) 3328–3341.
18. J. Makarević, M. Jokić, Z. Raza, Z. Štefanić, B. Kojić-Prodić, and M. Žinić, *Chem. Eur. J.* **9** (2003) 2–15.
19. Z. Štefanić, B. Kojić-Prodić, Z. Džolić, D. Katalenić, M. Žinić, and A. Meden, *Acta Crystallogr., Sect. C* **59** (2003) 286–288.
20. C. B. Aakeröy, A. M. Beatty, and B. A. Helfrich, *Angew. Chem., Int. Ed. Engl.* **40/17** (2001) 3240–3242.
21. H. Inouye, J. E. Bond, S. P. Deverin, A. Lim, C. E. Costello, D. A. Kirschner, *Biophys. J.* **8** (2002) 1716–1727.
22. Z. Štefanić, B. Kojić-Prodić, M. Jokić, J. Makarević, and M. Žinić, 18th Assembly of Croatian Chemists and Technical Engineers, 16–19 February, 2003 Zagreb, C30 (to be published).
23. M. C. Etter, *Acc. Chem. Res.* **23** (1990) 120–139.
24. I. L. Karle, D. Ranganathan, K. Shah, and N. K. Vaish, *Int. J. Peptide Protein Res.* **46** (1994) 160–165.
25. J. Bernstein, R. E. Davies, L. Shimoni, and N.-L. Chang, *Angew. Chem. Int. Ed. Engl.* **34** (1995) 1555–1573.
26. I. K. Larsen, *Acta Chem. Scand., Ser. B* **34** (1980) 209–212.
27. S. L. Price, *Crystal Structure Predictions*, in: J. L. Atwood and J. W. Steed (Eds.), *Encyclopedia of Supramolecular Chemistry*, Marcel Dekker, New York, in press.
28. W. D. S. Motherwell, H. L. Ammon, J. D. Dunitz, A. Dzyabchenko, P. Erk, S. L. Price, H. Scheraga, B. Schweizer, M. U. Schmidt, B. P. van Eijck, P. Verwer, and D. E. Williams, *Acta Crystallogr., Sect. B* **58** (2002) 647–661.
29. S. Coe, J. J. Kane, T. L. Nguyen, L. M. Toledo, E. Winiger, F. W. Fowler, and J. W. Lauher, *J. Am. Chem. Soc.* **119** (1997) 86–93.
30. J. Makarević, M. Jokić, Z. Raza, V. Čaplar, D. Katalenić, Z. Štefanić, B. Kojić-Prodić, and M. Žinić, *Croat. Chem. Acta* **77** (2004) 403–414.
31. Y.-L. Chang, M.-A. West, F. W. Fowler, J. W. Lauher, *J. Am. Chem. Soc.* **115** (1993), 5991–6000.
32. D. S. Goodsell, *Bionanotechnology: Lessons from Nature* Wiley & Sons, New York, 2003.
33. D. S. Goodsell, *The Machinery of Life*, Springer, Heidelberg, 1993.
34. S. Li, C. P. Hill, W. I. Sundquist, and J. Finch, *Nature*, **407** (2000) 409–413.

## SAŽETAK

## Vodikove veze i molekularno udruživanje

Biserka Kojić-Prodić, Zoran Štefanić i Mladen Žinić

Stara koncepcija komplementarnosti povezana s procesom molekularnoga prepoznavanja predstavlja jednostavan pristup razumijevanju molekularnoga udruživanja. Nevalentne interakcije koje upravljaju (samo)-udruživanjem temeljne su u supramolekularnoj kemiji i kristalnome inženjerstvu. Među nevalentnim interakcijama koje su odgovorne za molekularno udruživanje, vodikove veze imaju vodeću ulogu. Nekoliko primjera molekularnoga udruživanja bitnih u životnim procesima i (bio)nano materijalima ukazuju na važnost ove pojave. Sustavna analiza motiva vodikovih veza, kao funkcija donorskih i akceptorskih svojstava protona i stereokemijskih parametara, uključujući kiralnost, predstavljena je za velik broj derivata di(aminokiselina) i di(aminoalkohola) s oksalilnim, ftaloilnim i fumarilnim mostovima. U svjetlu kristalnoga inženjerstva posebna je pozornost posvećena molekularnoj topologiji takovih molekularnih skupina vezanih pomoću vodikovih veza.