Dipole Parallel Alignment in the Crystal Structure of a Polar Biphenyl: 4′-Acetyl-4-Methoxybiphenyl (AMB)†

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Ⓦ **This paper contains enhanced objects available on the Internet at http://pubs.acs.org/crystal.**

ABSTRACT: 4′-Acetyl-4-methoxybiphenyl (AMB) was synthesized via a catalytic Suzuki cross-coupling reaction, and the crystal structure was determined. The crystals of AMB feature an orthorhombic unit cell with $a = 7.900(6)$ Å, $b = 5.429(4)$ Å, and $c = 26.80(2)$ Å, and the crystals are noncentrosymmetric, space group $Pna2_1$. The crystal structure of AMB features parallel alignment of essentially planar molecules in the *syn* conformation with molecular dipole moments of about 5.4 D and affords about 53% of maximal polar alignment. The polar crystal structure of *syn*-AMB contrasts with the nonpolar crystal structure of the homologue 4-methoxyacetophenone (*syn*-MAP). The fundamental difference between the packing motives of AMB and MAP is explained on the basis of lateral arene−arene interactions. The lattice architecture of AMB is compared to the motives realized in the only two other parallel-aligned polar biphenyls, 4′-*n*-butoxy-4-cyanobiphenyl (nBCB) and 4′-(dimethylamino)-4-cyanobiphenyl (DMACB). The analysis provides conceptual insights to guide the rational design of polar materials, and several resulting hypotheses are stated explicitly and can be tested.

Introduction

We have accomplished high anisotropy and near-perfect polar order[1] in molecular organic crystals of unsymmetrically 4,4′-disubstituted acetophenone azines using a rational design.[2] The crystal structures of the (MeO,I)-azine,[3] the (MeO,Br)-azine,[4,5] and the (MeO,Cl)-azine,[6] respectively, are similar but differ in subtle details because of the occurrence of one, two, and four independent molecules, respectively. Deep analysis of these prototypes[7,8] has led to improved designs of spacer-connected diarenes as well as to new designs without spacers. Here we apply the lessons learned from these earlier studies to the problem of engineering parallel-aligned polar molecules bearing biphenyl spacers.

We are aware of only two reports of crystal structures of parallel-aligned unsymmetrical diphenyls. In 1987, Haase et al.[9] reported the crystal structure of 4′-*n*-butoxy-4-cyanobiphenyl (nBCB), and in 1991, Zyss et al.[10] reported the crystal structure of 4′-(dimethylamino)-4-cyanobiphenyl (DMACB). In 1997, Desiraju et al.[11] employed halogen bonding[12−15] between iodine and nitro groups in an attempt to achieve parallel alignment in crystals of 4-iodo-4′-nitrobiphenyl (INB). The crystal structure analysis could not be refined completely, but the reasonable claim of parallel alignment was based on crystal structure simulations. The proposed structure was consistent with the measured X-ray powder pattern and the occurrence of second harmonic generation. Masciocchi, Bergamo, and Sironi later suggested that these crystals of 4-iodo-4′-nitrobiphenyl contained admixtures of 4,4′-dinitrobiphenyl (DNB).[16] Hulliger and Langley argued that preferred intrinsic defects in INB as well as substitutions by DNB admixtures cause faulted chains and the presence of parallel and antiparallel aligned twisted biphenyl chains.[17]

In this context, we report here the realization of parallel alignment in crystals of *syn*-4′-acetyl-4-methoxybiphenyl (*syn*-

Chart 1. Conformations of 4′-Acetyl-4-Methoxybiphenyl (AMB) and Definition of the Dihedral Angles μ, τ, and α

syn-AMB   *anti*-AMB
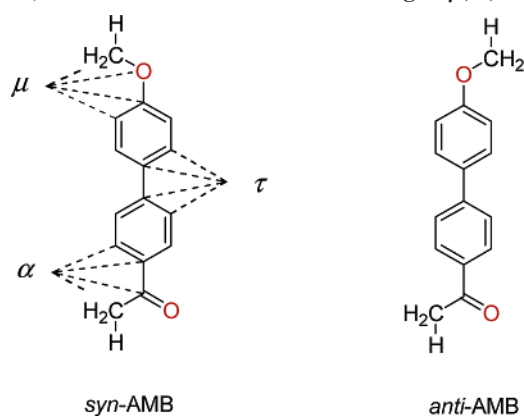
AMB; Chart 1) and an analysis of the crystal structure to gain conceptual insights into the causes for parallel alignment. AMB was synthesized by catalytic Suzuki cross-coupling of methoxyphenylboronic acid and bromoacetophenone, employing the conditions by Fu et al.[18] The crystal structure was determined and analyzed. The analysis employed ab initio pair energies to assess the strengths of intermolecular interactions and to compute the effective dipole moment of each molecule. These data are contrasted with the (nonpolar) crystal structure[19] of the analogous "(MeO,Acetyl)-monophenyl", the 4-methoxyacetophenone (*syn*-MAP), which is nonpolar. We conclude with a description of the differences in the crystal architectures of AMB as compared to nBCB and DMACB.

Experimental and Theoretical Section

Synthesis of 4′-Acetyl-4-Methoxybiphenyl (AMB). The synthesis was carried out in a glovebox under nitrogen. All chemicals were bought from Aldrich. Tris(dibenzylideneacetone)dipalladium (Pd₂(dba)₃, 0.068 g, 0.074 mmol), potassium fluoride (2.74 g, 47.2 mmol), and methoxyphenylboronic acid (2.38 g, 15.7 mmol) were combined in a reaction flask and stirred magnetically. To the mixture were added bromoacetophenone (2.82 g, 14.2 mmol) in 15 mL of dry THF and 0.75 mL

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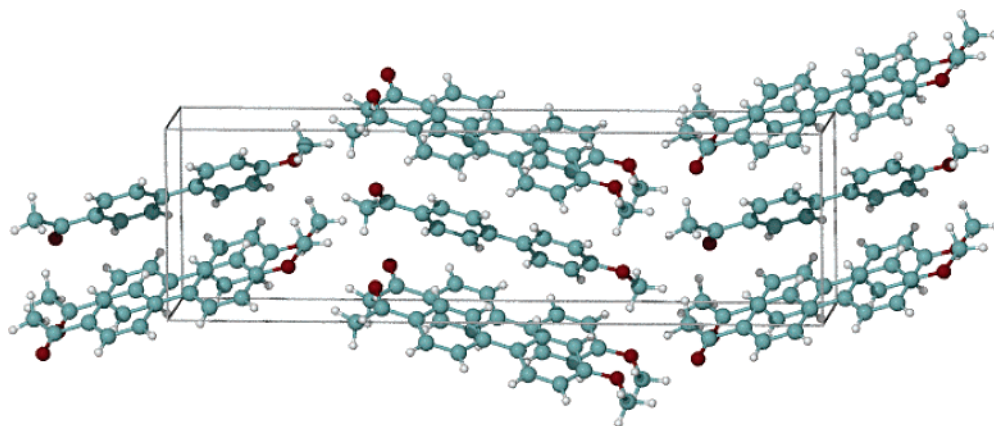† Solid-state dipole moment calculations by Z.W. Crystal structure determination by C.L.B.

Figure 1. Crystal of *syn*-(MeO,acetyl)-biphenyl (*syn*-AMB), featuring perfect dipole-parallel alignment along the long axis within two-dimensional layers and near-perfect dipole-parallel alignment in the stacking direction. In contrast, the crystal structure of the analogous "(MeO,acetyl)-phenyl" aka 4-methoxyacetophenone (*syn*-MAP) is not polar.

Ⓦ Web versions of the crystal structure of *syn*-AMB (in Ⓦ html and Ⓦ pdb formats) and *syn*-MAP (in Ⓦ html and Ⓦ pdb formats) are available. Note that the free CHIME plugin is required for the display of the pdb files.
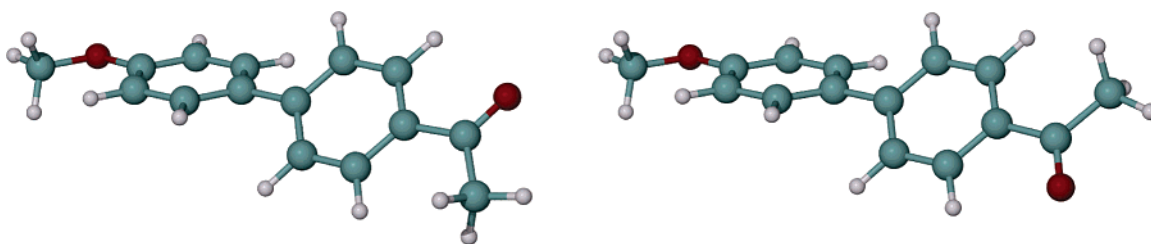

Figure 2. MP2(full)/6-31G* optimized conformers *syn*-AMB (left, $\tau = 42.9°$, $\mu = -0.3°$, $\alpha = 0.3°$) and *anti*-AMB (right, $\tau = 42.9°$, $\mu = -0.5°$, $\alpha = 0.0°$).

Ⓦ Web versions of the optimized structures of AMB, with syn conformation, planar (in Ⓦ html and Ⓦ pdb formats) and twisted (in Ⓦ html and Ⓦ pdb formats), and anti conformation, planar (in Ⓦ html and Ⓦ pdb formats) and twisted (in Ⓦ html and Ⓦ pdb formats) are available.

of a 0.20 M solution of tris-*tert*-butylphosphine in THF. The reaction mixture was stirred at room temperature for 6−8 h. The reaction mixture was diluted with ether, cleaned first by pouring it through a silica gel pad, and the product was isolated by silica gel column chromatography using a 40:60 mixture of hexane and chloroform as eluent. ^{1}H NMR (250 MHz, CDCl$_3$): δ 8.01 (d, $J = 8.42$, 2H), 7.64 (d, $J = 8.46$, 2H), 7.58 (d, $J = 8.81$, 2H), 7.00 (d, $J = 8.81$, 2H), 3.86 (s, 3H), 2.63 (s, 3H). ^{13}C NMR (250 MHz, CDCl$_3$): δ 197.7, 159.9, 145.4, 135.3, 132.3, 128.9, 128.4, 126.6, 114.4, 55.4, 26.6.

Crystallography. Crystals of AMB were grown by slow evaporation from a chloroform solution. AMB crystallizes in the orthorhombic crystal system in the space group *Pna*2$_1$, and experimental and structural details are given as Supporting Information.

Computed Structures and Binding Energies. Ab initio electronic structure theoretical methods were employed.[20,21] Geometry optimizations of the monomer were performed with second-order Møller−Plesset theory[22] employing the 6-31G* basis set MP2(full)/6-31G*. All binding energies were determined with the same theoretical method and were based on the X-ray structure, MP2(full)/6-31G*//X-ray. Total energies and Cartesian coordinates of the optimized structures are provided in the Supporting Information.

The fastest way for the computation of the binding energy of a dimer is by way of eq 1. The better alternative involves the calculation of

$$BE_1 = E(\text{dimer}) - 2E(\text{monomer}) \qquad (1)$$

$$BE_2 = E(\text{dimer}) - E(\text{molecule 1}) - E(\text{molecule 2}) \qquad (2)$$

both molecules in the dimer and the determination of the binding energy via eq 2. The difference between the two methods reflects on the quality of the software employed to compute the Cartesian coordinates of the dimer on the basis of the X-ray unit cell data. Equation 2 will always provide a binding energy that is essentially free of variations due to

numerical variations of atom positioning, because the same errors are made in the calculation of the dimer and each of the two molecules.

Results and Discussion

Molecular Parallel Alignment. In the crystal structure of AMB there is one unique molecule and the unit cell contains four molecules (Figure 1). The biphenyls are parallel aligned and oriented approximately along the *c* direction in layers that extend in the *a* and *b* directions. Successive layers are rotated by 180° about the *c* direction, and the unit cell is thus rather long in that direction; $a = 7.900(6)$ Å, $b = 5.429(4)$ Å, and $c = 26.80(2)$ Å.

Molecular Structure. The structure of AMB in the solid state features the *syn* conformation, and it is almost C_s symmetric with $\tau = 2.6°$, $\mu = 2.4°$, and $\alpha = 0.8°$. We designate the *syn* and *anti* conformations via the relative position if the methyl groups are as shown in Chart 1 (τ for *t*orsion, μ for *m*ethoxy, and α for *a*cetyl).

syn- and *anti*-AMB were first optimized with the constraint to C_s symmetry and then optimized again without any symmetry constraint and beginning with a chiral structure (Figure 2). The relaxation of the planar structures ($\tau = \mu = \alpha = 0°$) leads to structures with $\alpha \approx 0°$ and $\mu \approx 0°$, and the only significant twist angle is $\tau \approx 43°$. The *syn* and *anti* structures are isoenergetic, and both prefer the twisted structure over the planar structure by 3.5 kcal/mol. This situation is similar to the case of biphenyl itself. Biphenyl famously favors the twisted structure with $\tau \approx 43°$ in the gas phase,[23,24] while biphenyl appears planar in the crystals at room temperature[25] and down to 110 K.[26] At very
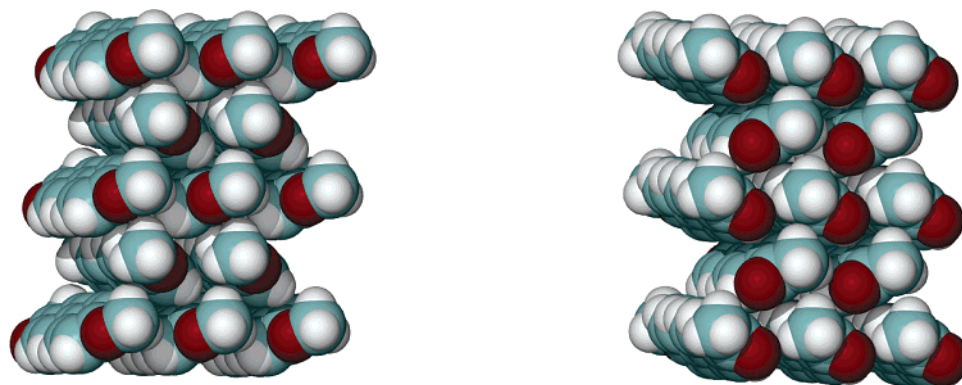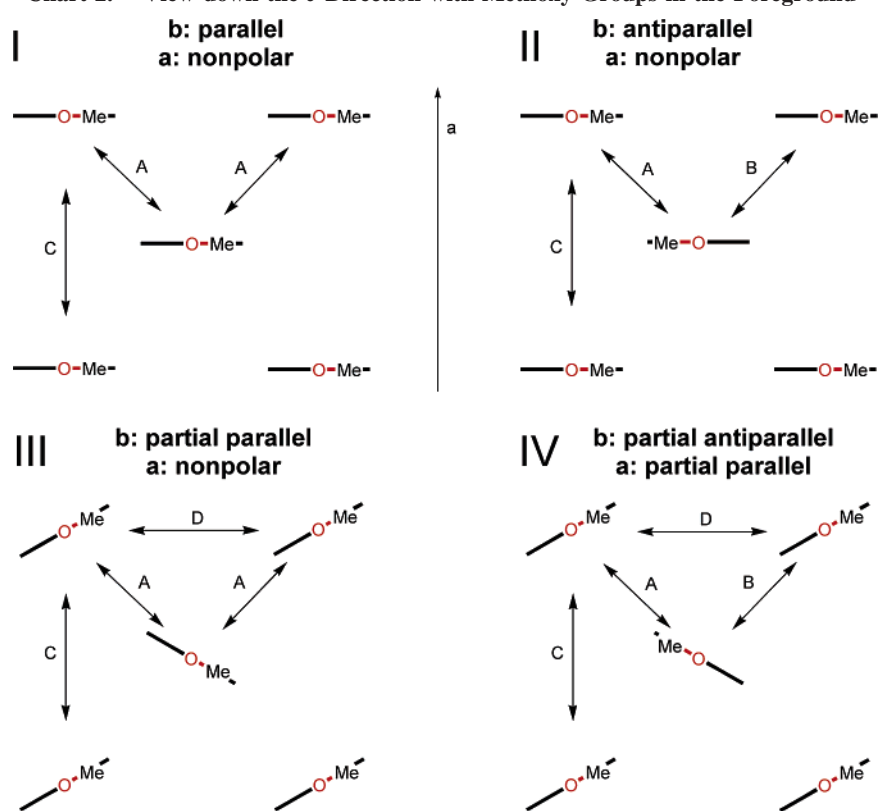
Figure 3. Space-filling models of a 2d layer viewed down the *c* direction. Methoxy and acetyl groups, respectively, are in the foreground on the left and right, respectively.

Ⓦ Web versions of the models with methoxy (in Ⓦ html and Ⓦ pdb formats) and acetyl (in Ⓦ html and Ⓦ pdb formats) groups are available.

Chart 2.   View down the *c* Direction with Methoxy Groups in the Foreground[a]

[a] Situation **IV** is realized in the crystal of **1**.

low temperatures (20 K), another phase has been characterized that contains twisted biphenyl with $\tau \approx 10°$.[27]

Molecular Parallel Alignment in Layers. The long axis of *syn*-AMB is aligned approximately with the *c* direction, and all molecules within each 2d layer are parallel aligned in this *c* direction (Figure 3). Chart 2 illustrates the alignment within the layers.

The molecules are packed face centered, and this packing may occur with parallel (left) or antiparallel (right) alignment in the *b* direction. The latter is favored by the dipole–dipole interactions between the substituents. The lateral interaction involves double arene–arene interactions: that is, interactions in which both arenes of one biphenyl interact with both arenes of a neighboring biphenyl.[28,29] Abbreviating "f" for face and "e" for edge, a double arene–arene interaction can be specified

by a term (12|34) where 1 and 2 are the arenes in one molecule and 3 and 4 in the other and where 1 interacts with 3 and 2 interacts with 4. The antiparallel alignment gives rise to two offset (ff|ff) interactions **A** and **B**, and this mode of packing occurs.

There is no polarity in the *a* direction so long as the planes of all molecules are parallel (top). The situations shown at the bottom of Chart 2 are created by rotating the molecules in the corners and in the center by the same amount but in opposite directions. The change from **II** to **IV** causes polarity in the *a* and *b* directions and is beneficial, as it changes the (ff|ff) contacts **A** and **B** into double-T (ff|ee) contacts **A** and **B**. In addition, the weak (ff|ff) contact **C** becomes offset and the additional (ff|ff) contact **D** emerges. The (ff|ee) contacts **A** and
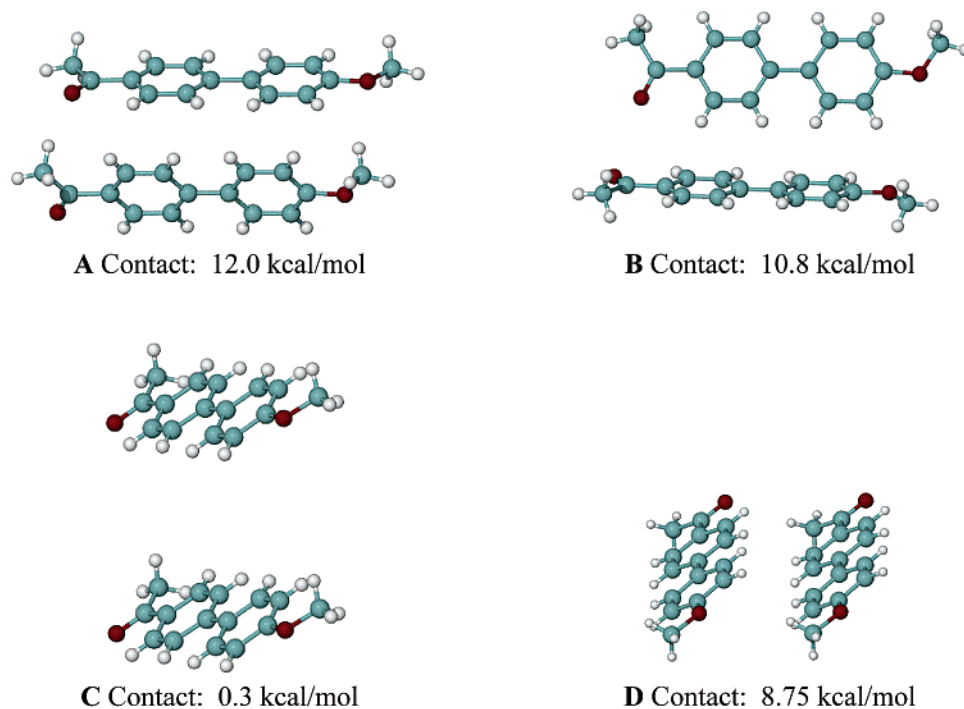
A Contact: 12.0 kcal/mol

B Contact: 10.8 kcal/mol

C Contact: 0.3 kcal/mol

D Contact: 8.75 kcal/mol

Figure 4. Each AMB molecule engages in two (ff|ee) contacts **A** and two (ff|ee) contacts **B** as well as two (ff|ff) contacts **C** and two (ff|ff) contacts **D**. For comparison, the crystal structure of biphenyl (RT, BIPHEN) also contains planar biphenyls with (ff|ee) and (ff|ff) contacts.

Ⓦ Web versions of the following structures are available: contacts A (in Ⓦ html and Ⓦ pdb formats), B (in Ⓦ html and Ⓦ pdb formats), C (in Ⓦ html and Ⓦ pdb formats), D (in Ⓦ html and Ⓦ pdb formats), and biphenyl (in Ⓦ html and Ⓦ pdb formats) with ff|ee (in Ⓦ html and Ⓦ pdb formats) and ff|ff (in Ⓦ html and Ⓦ pdb formats) contacts.
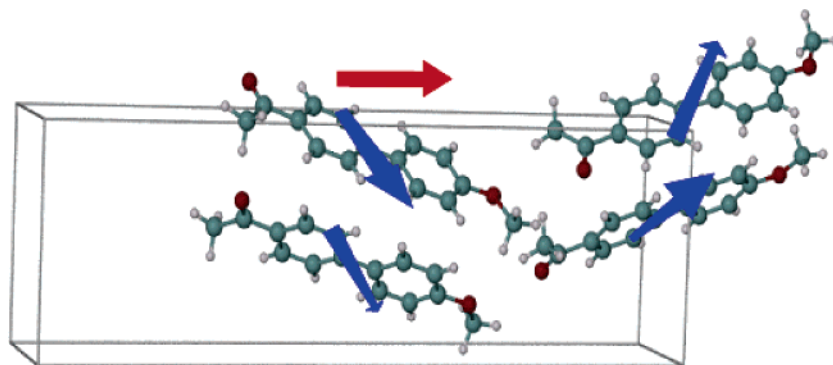
Figure 5. The dipole moments of the AMB molecules are additive in the *c* direction. Dipoles are directed from "minus" to "plus".

B and the (ff|ff) contacts **C** and **D** are shown in Figure 4, along with the computed binding energies.

The arene−arene attractions result from van der Waals and quadrupole−quadrupole forces. These interactions are supplemented by dipole−dipole attractions between the substituents and van der Waals attractions between the methyl groups. Figure 3 illustrates well that the surfaces of the 2d layer are not "filled", and the MeO and MeCO surfaces both feature ridges of closely packed methyl groups.

Effective Molecular Dipole Moment. The computed dipole moment of AMB is $\mu = 5.40$ D. The direction of the dipole moment does not coincide with the long axis of AMB. Instead, the dipole direction greatly depends on the direction of the carbonyl bond. Figure 5 illustrates the dipole moments superimposed on all four molecular orientations. Since successive layers are rotated by 180° about the *c* direction, only the dipole moment component along the *c* direction contributes to the crystal polarity. On the basis of the crystal structure and computed molecular dipole moment, we computed $\mu_c = 2.88$

D. Hence, the degree of dipole alignment is about 53% of the maximal polar alignment (MPA). This corresponds to an angle of 58.1° between the directions of the molecular dipole moment and the overall crystal dipole moment.

Interlayer Interactions. Each 2d layer is *polar*, with the resulting dipole moment perpendicular to the layer surface, and there is thus a natural tendency to stack these layers *with polar order*. Aside from this electrostatic force, additional interlayer interactions occur and help to stabilize the stacking mode. Figure 6 provides another view of the ridges formed by rows of methyl groups on both layer surfaces, and the illustration at the top of Figure 6 shows how these ridges interlock. Dashed lines are drawn between methoxy O atoms and acetyl methyl hydrogens and also between the acetyl O atoms and the methoxy methyl hydrogens. The C−H bonds are mildly polar, because of their connection to electronegative atoms or positively charged atoms. While not hydrogen bonds in the strong sense, these interactions contribute to the stabilization of the intersurface interaction.[30]
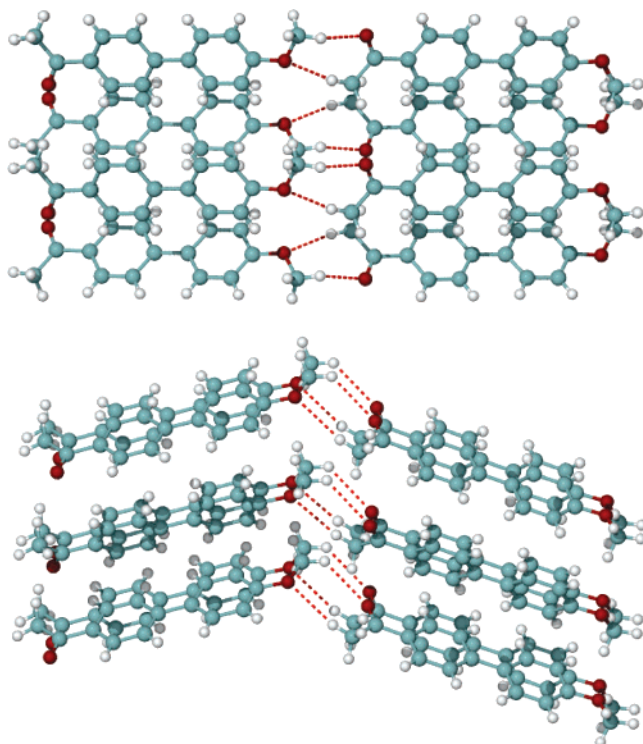
Figure 6. Across the layer interface, each AMB molecule engages in two EN−CH₂−H···O contacts with another molecule AMB. These interactions are responsible for the *syn* conformation and the directionality of the layer stacking.

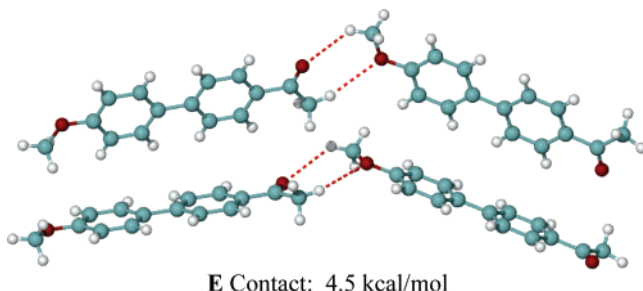Ⓦ Web versions of the crystal structure in Ⓦ html and Ⓦ pdb formats are available.

E Contact: 4.5 kcal/mol

Figure 7. Perspectives of the EN−CH₂−H···O contacts that contribute to interlayer bonding; d(OCH₂−H···O=C) = 2.672 Å and d(COCH₂−H···O) = 2.715 Å.

Ⓦ Web versions of contact E (in Ⓦ html and Ⓦ pdb formats) are available.

Figure 7 shows a small piece of the crystal structure comprised of two pairs of biphenyls engaged in such an interaction.

It is these weak interactions that cause the *syn* conformation of AMB so that infinite chains can be formed. Moreover, the C−H···O contacts are contained in seven-membered rings, and this arrangement causes the kink between the long axes of molecules in successive layers (Chart 3). The analysis of the crystal architecture suggests that one strategy to achieving perfect parallel alignment in the c direction entails the disruption of these directional bonding interactions.

With the recognition of the C−H···O contacts between the layers, one wonders about an alternative stacking of the 2d layers in such as way as to provide for C−H···O contacts between pairs of acetyl groups, as shown at the bottom of Chart 3. The disadvantages of such an arrangement, however, lie with the

Chart 3.   C−H···O Contacts Causing *Syn* Conformation and the Directional Interlayer Bonding
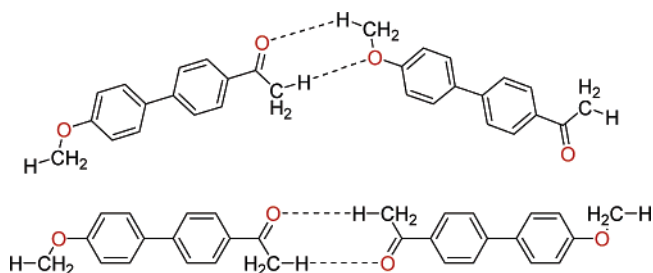
stacking of successive polar layers in opposite directions and with the weakness of the interlayer interaction between surfaces decorated with methoxy groups.

Conclusion

The unsymmetrical donor−acceptor substituted biphenyl 4′-acetyl-4-methoxybiphenyl (AMB) crystallizes in the noncentrosymmetric space group *Pna*2₁. The crystal structure of AMB features parallel alignment of essentially planar molecules in the *syn* conformation with molecular dipole moments of about 5.4 D and affords dipole alignment of about 53% of the maximal polarity.

Within the parallel-aligned layers of AMB, each molecule engages in double T-contacts and double face-to-face contacts, much like in the crystal structure of the parent biphenyl. It is this mode of lateral arene−arene interaction that differentiates AMB from nBCB and DMACP. nBCB and DMACP feature twisted biphenyls and different degrees of longitudinal slippage between neighboring biphenyls. In DMCAP, every Ph−CN moiety of one molecule aligns with the Ph−Ph moiety of another, and there are no double arene−arene contacts at all. nBCB features some slipped Ph−CN/Ph−Ph interaction as well as some double arene−arene interactions. Hence, *AMB is the first representative of a class of polar organic molecular materials that are based on the lateral double arene−arene interaction mode of the parent biphenyl*.

The quantum-mechanical calculations of the pair binding energies show strong lateral intermolecular bonding of 8.5−12 kcal/mol (contacts **A**, **B**, and **D**; Figure 4) and much weaker pair binding along the long axis (contact **E**; Figure 7). Since the intermolecular acetyl−methoxy interactions should be very similar for *syn*-AMB and *syn*-MAP, we consider the high lateral binding to cause the fundamental structural difference between *syn*-AMB and *syn*-MAP. Parallel alignment can only be preferred over antiparallel alignment if the arene−arene interactions are so much better in the parallel-aligned form that they can overcompensate for the disadvantage associated with dipole−dipole repulsion in the antiparallel form. The probability for this condition increases with an increase of the overall arene−arene interaction. This argument suggests that 4′-acetyl-4-methoxy*triphenyl* also might prefer parallel alignment in the solid state, and this hypothesis can be tested.

The formation of acetyl-*O* methoxy-*H* contacts has been identified as the most likely reason for the adoption of the *syn* conformation, and these contacts contribute to *directional* interlayer attraction. Hence, the analysis suggests that a reasonable and rational strategy to achieve a higher degree of parallel alignment in the c direction entails the disruption of these directional bonding interactions. This hypothesis also can be tested by suitable choices of donors and acceptors.

Supporting Information Available: Tables giving crystallographic details, computed total energies, and Cartesian coordinates of optimized structures; crystal data are also given as a CIF file. This material is available free of charge via the Internet at http://pubs.acs.org.

References

(1) *Anisotropic Organic Materials−Approaches to Polar Order*; Glaser, R., Kaszynski, P., Eds.; ACS Symposium Series 798; American Chemical Society: Washington, DC, 2001.

(2) Glaser, R.; Knotts, N.; Wu, H. *ChemTracts Org. Chem.* **2003**, *16*, 443.

(3) Lewis, M.; Barnes, C.; Glaser, R. *J. Chem. Crystallogr.* **2000**, *30*, 489.

(4) Glaser, R. E.; Chen, G. S. Dipole Aligned Molecular Materials with Nonlinear Optical Properties. U.S. Patent 6 229 047, May 8, 2001.

(5) Chen, G. S.; Wilbur, J. K.; Barnes, C. L.; Glaser, R. *J. Chem. Soc., Perkin Trans. 2* **1995**, 2311.

(6) Lewis, M.; Barnes, C.; Glaser, R. *Acta Crystallogr., Sect. C* **2000**, *56*, 393.

(7) (a) Glaser, R.; Chen, G. S. *J. Comput. Chem.* **1998**, *19*, 1130. (b) Glaser, R.; Lewis, M.; Wu, Z. *J. Mol. Model.* **2000**, *6*, 86.

(8) Lewis, M.; Glaser, R. *J. Org. Chem.* **2002**, *67*, 1441.

(9) Walz, L.; Paulus, H.; Haase, W. *Z. Kristallogr.* **1987**, *180*, 97.

(10) Zyss, J.; Ledoux, I.; Bertault, M.; Toupet, E. *Chem. Phys.* **1991**, *150*, 125.

(11) Jagarlapudi, A. R. P. S.; Allen, F. H.; Allen, F. H.; Hoy, V. J.; Howard, J. A. K.; Thaimattam, R.; Biradha, K.; Desiraju, G. R. *Chem. Commun.* **1997**, 101.

(12) Bent, H. A. *Chem. Rev.* **1968**, *68*, 587.

(13) Metrangolo, P.; Resnati, G. *Chem. Eur. J.* **2001**, *7*, 2511.

(14) Crihfield, A.; Hartwell, J.; Phelps, D.; Walsh, R. B.; Harris, J. L.; Payne, J. F.; Pennington, W. T.; Hanks, T. W. *Cryst. Growth Des.* **2003**, *3*, 313.

(15) Glaser, R.; Chen, N.; Wu, W.; Knotts, N.; Kaupp, M. *J. Am. Chem. Soc.* **2004**, *126*, 4412.

(16) Masciocchi, N.; Bergamo, M.; Sironi, A. *Chem. Commun.* **1998**, 1347.

(17) Hulliger, J.; Langley, P. J. *Chem. Commun.* **1998**, 2557.

(18) Littke, A. F.; Dai, C.; Fu, G. C. *J. Am. Chem. Soc.* **2000**, *122*, 4020.

(19) Ruhl, S.; Bolte, M. *Z. Kristallogr.* **2000**, *215*, 499.

(20) Cramer, C. J. *Essentials of Computational Chemistry*; Wiley: Chichester, U.K., 2002.

(21) Frisch, M. J. et al. *Gaussian 98, Revision A.9*; Gaussian, Inc., Pittsburgh, PA, 1998.

(22) Head-Gordon, M.; Pople, J. A.; Frisch, M. J. *Chem. Phys. Lett.* **1988**, *153*, 503.

(23) Almenningen, A.; Bastainsen, O.; Fernholt, L.; Cycin, B. N.; Cycin, S. J.; Samdal, S. *J. Mol. Struct. (THEOCHEM)* **1985**, *128*, 59.

(24) Grein, F. *J. Phys. Chem.* **2002**, *106*, 3823.

(25) Crystal structures of biphenyl at 295 K are as follows. (a) BIPHEN ($R = 14.8$): Trotter, J. *Acta Crystallogr.* **1961**, *14*, 1135. (b) BIPHEN01 ($R = 8.9$): Hargreaves, A.; Rizvi, S. H. *Acta Crystallogr.* **1962**, *15*, 365. (c) BIPHEN02 ($P2_1/c$, $R = 3.8$, no coordinates reported): Robertson, G. B. *Nature (London)* **1961**, *191*, 593. (d) BIPHEN04 ($R = 6.3$): Charbonneau, G.-P.; Delugeard, Y. *Acta Crystallogr., Sect. B* **1977**, *33*, 1586.

(26) At 110 K, BIPHEN03 ($R = 6.6$): Charbonneau, G.-P.; Delugeard, Y. *Acta Crystallogr., Sect. B* **1976**, *32*, 1420.

(27) At 20 K, BIPHEN05 ($R = 8.8$, no coordinates reported): Baudour, J. L. *Methods Struct. Anal. Modulated Struct. Quasicryst.* **1991**, 383.

(28) Lewis, M.; Wu, Z.; Glaser, R. Arene-Arene Double T-Contacts: Lateral Synthons in the Engineering of Highly Anisotropic Organic Molecular Crystals; Chapter 7 in ref 1.

(29) Glaser, R.; Dendi, L. R.; Knotts, N.; Barnes, C. L. *Cryst. Growth Des.* **2003**, *3*, 291.

(30) Desiraju, G. R. *Acc. Chem. Res.* **2002**, *35*, 565.

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