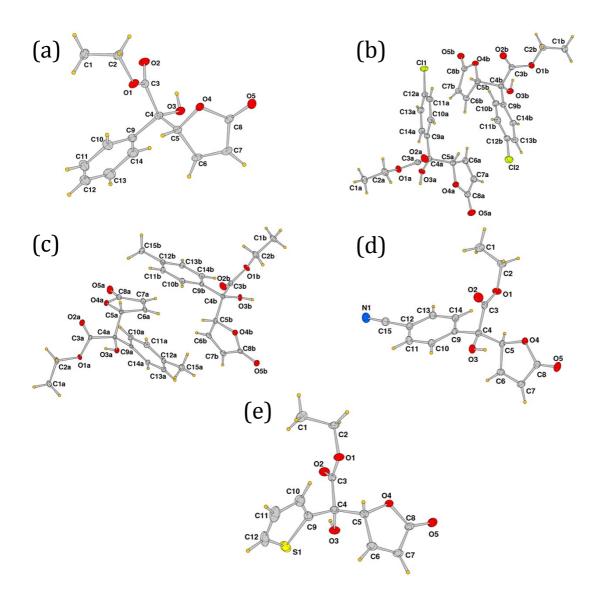
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## Supramolecular Synthons in the Gamma-Hydroxybutenolides

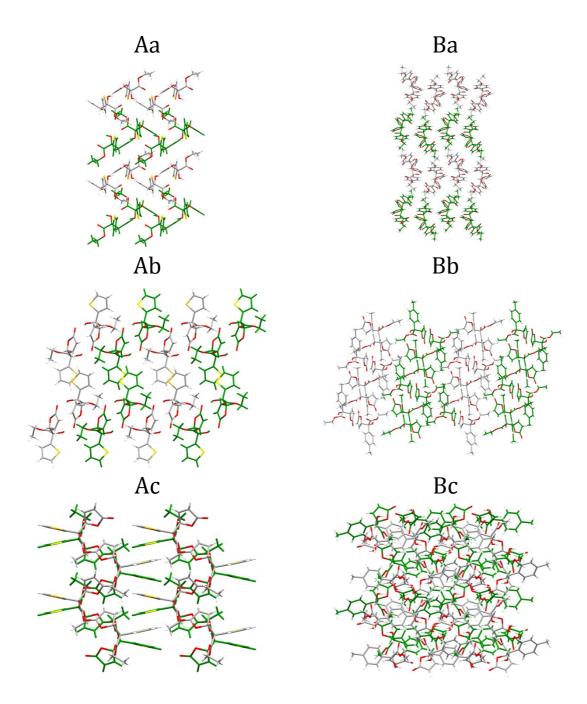
Margherita De Rosa,<sup>a,\*</sup> Pellegrino La Manna,<sup>a</sup> Annunziata Soriente,<sup>a</sup> Carmine Gaeta,<sup>a</sup> Carmen Talotta,<sup>a</sup> Neal Hickey,<sup>b,\*</sup> Silvano Geremia,<sup>b</sup> and Placido Neri <sup>a</sup>

<sup>a</sup>Dipartimento di Chimica e Biologia "A. Zambelli", Università degli Studi di Salerno, Via Giovanni Paolo II 132, I-84084 Fisciano (Salerno), Italy.

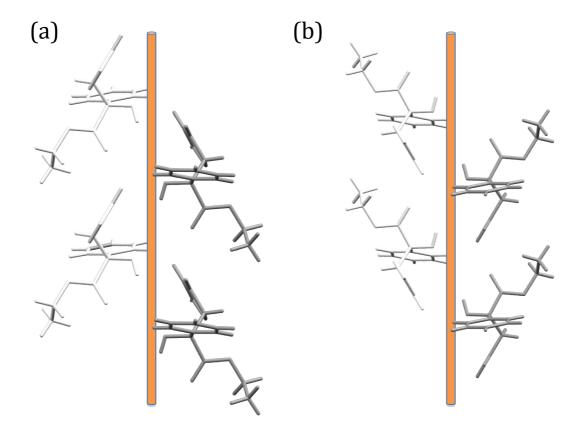
<sup>b</sup>Centro di Eccellenza in Biocristallografia, Dipartimento di Scienze Chimiche e Farmaceutiche, Università di Trieste, via L. Giorgieri 1, 34127 Trieste, Italy.



**Figure S1**. Ellipsoid plots at 50% probability for  $\gamma$ -hydroxybutenolides **3a** (a),**3b** (b), **3c** (c), **3d**(d) and **3e** (e).

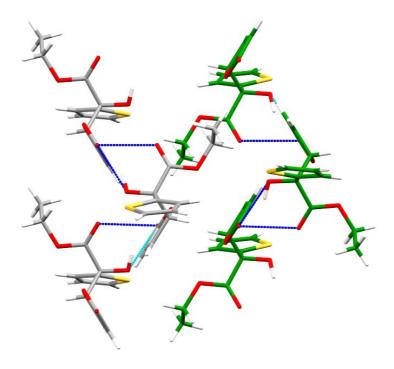


**Figure S2**. The packing arrangements of syn- $\gamma$ -hydroxybutenolide **3e** (A) and syn- $\gamma$ -hydroxybutenolide **3c** (B), as viewed along the a-axis (a), b-axis (b) and c-axis (c). Carbon atoms are represented in different colours (grey and green) to distinguish between the enantiomers.

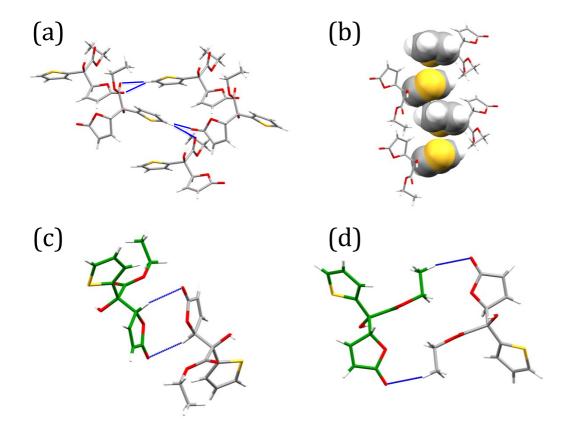


**Figure S3**. Handedness of  $2_1$  helices, on the basis of supramolecular-tilt-chirality (STC) proposed by Miyata and co-workers. For clarity, molecules in front of the  $2_1$  screw axis (orange cylinder) are depicted entirely in a darker shade of grey with respect to those behind the axis. The handedness of the helix is determined by the direction the tilt of the molecule in front of the  $2_1$ axis. Thus, (a) represents a left-handed helix and (b) a right-handed helix.

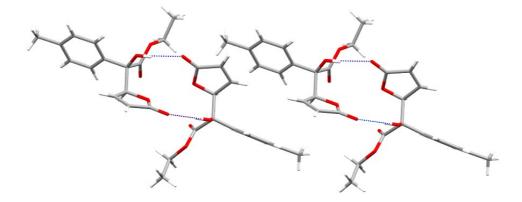
<sup>1</sup>I. Hisaki, T. Sasaki, N. Tohnai, M. Miyata, Chemistry - A European Journal, 2012, 18, 10066



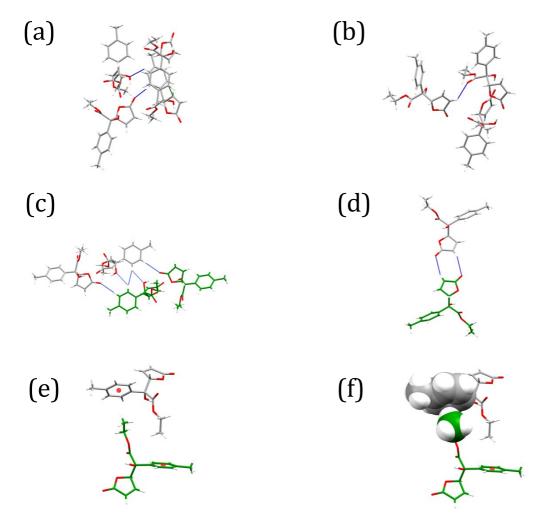
**Figure S4**. Helical arrangement, viewed down the a-axis, of the enantiomers around the  $2_1$  screw axis for syn- $\gamma$ -hydroxybutenolide **3e**. 3 molecules, representing a full turn, are shown for each enantiomer. The carbon atoms are depicted in grey and green to distinguish between the two enantiomorphic helices.



**Figure S5**. Overview of the weak non-covalent packing contacts in syn- $\gamma$ -hydroxybutenolide **3e**. (a) bridged C12H12···O2 / C12H12···O5 interactions between adjacent helical strands of molecules with the same chirality; (b) interlocking, zipper-like stacking of the phenyl rings which arises between adjacent helical strands of molecules with the same chirality; (c) reciprocal C7H7···O5 interactions between helical strands of different enantiomers; (d) reciprocal C1H1C···O5 interactions between helical strands of different enantiomers. The carbon atoms are depicted in grey and green to distinguish between the enantiomers.



**Figure S6**. Homochiral dimers of syn—hydroxybutenolide **3c**.



**Figure S7.** Overview of the weak, non-covalent packing contacts in syn- $\gamma$ -hydroxybutenolide **3c**. (a) network of interactions between the hydrogen bond oxygen atoms (O3A, O5B) of one dimer with aromatic hydrogens on two adjacent dimers; (b) interaction between the H7 butenolide hydrogen and the O2 carbonyl oxygen atom of an adjacent molecule; (c) reciprocal interactions between the hydrogen bond oxygen atoms (O3B, O5A) of one dimer with phenyl hydrogens on an adjacent molecule; (d) reciprocal interactions between a vinylic hydrogen and the carbonyl oxygen of two facing butenolide rings; (e) CH- $\pi$  interaction between a methyl hydrogen and a phenyl ring, with reciprocal CH···O interactions between a methyl hydrogen of the phenyl acceptor molecule and the O1 oxygen atom of the methyl donor molecule; (f) as in (e), with the CH- $\pi$  interaction shown as a space fill model. The carbon atoms are depicted in grey and green to distinguish between the enantiomers.

Table S1. Crystallographic data for compound 3d

CCDC code	CCDC 1523707
Formula	$C_{15} H_{13} N O_5$
Formula weight	287.26
Temperature (K)	100
Wavelength (Å)	0.7
Crystal system	Orthorhombico
Space group	Pn2 <sub>1</sub> a
a (Å)	10.2780 (3)
b (Å)	10.4130 (16)
c (Å)	12.405 0 (11)
α (°)	90
β (°)	90
γ (°)	90
V (Å <sup>3</sup> )	1327.6 (2)
$Z$ , $\rho_{calc}$ (g.mm <sup>-3</sup> )	4, 1.437
μ (mm <sup>-1</sup> )	0.104
F (000)	600
Data collection $\theta$ range	2.515 - 29.983
Refl. Collected / unique	24594 / 3912
R <sub>int</sub>	0.0269
Completeness (%)	96.3
Refinement methoda	FMLS on F <sup>2</sup>
Data/Restraints/Parameters	3912 /0 / 193
GooF	1.056
$R_1$ , w $R_2$ [I>2 $\sigma$ (I)]	0.0277, 0.0764
R <sub>1</sub> , wR <sub>2</sub> all data	0.0278, 0.0764
ls shift su max/mean	0.001 / 0
Largest. Diff. peak/hole (e. Å <sup>3</sup> )	0.043 / -0.19
Absoulte structure parameter	0.03 (9)
_(Flack)	

<sup>a</sup>Full-matrix least-squares (FMLS) on F<sup>2</sup>