Conformational polymorphism in a Schiff base macrocyclic organic ligand: an experimental and theoretical study

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SUPPLEMENTARY MATERIALS

Content

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Details of the X-ray data collection strategies and refinements. A three-circle Bruker AXS Smart Apex diffractometer equipped with an Apex II CCD detector was employed for the diffraction experiments. A graphite-monocromated normal focus X-ray source with Mo as emitting material was selected. All frames were collected with the ω-scan technique at 0.5 deg intervals in ω, with the sample-to-detector distance set at 50 mm. All the data collections were performed with the 2ϑ axis fixed at -30 deg. Due to small dimensions and low scattering power of the specimens, a quite high exposure time (45-50 s/frame) was used. For the sample corresponding to the crystal form IIº, a fast preliminary data collection with 2ϑ and ϕ axis fixed at 0 deg and exposure time of 15 s/frame was also performed; the obtained reflections were subsequently scaled and added together with the other data. In all experiments, a total of 180-183 deg in ω were explored at variable ϕ angles. In the case of polymorph IIº, 9 runs at steps of 40 deg in ϕ starting from ϕ = 0 deg were performed, whereas for the other two crystal forms a minor number of runs was judged to provide a sufficient number of data for the structure solution. More precisely, 4 runs at steps of 90 deg in ϕ, starting from ϕ = 0 deg, were employed for the other two samples.

The program Saint+ (Bruker, 1999) was used to process the diffraction images. Cell parameters for the three phases IIº, SOLV and I were determined from least-squares fitting on 2864, 1136 and 6041 indexed, intense reflections with Bragg angle between 4.0 and 39.0 deg, respectively. A small empirical correction for the beam anisotropy was applied by the program SADABS (Sheldrick, 2004). Due to the low values of the absorption coefficients μ's, the absorption correction was deemed not necessary for all the three crystal forms. Structure solutions and refinements were performed with the software Shelx97 (Sheldrick, 2008) available in the WinGX1.64.03a program package (Farrugia, 1999). A 0.65 Å^{-1} cut-off in $\sin\vartheta/\lambda$ (Cu-sphere limit) was applied throughout in the various refinements, as only reflections barely emerging from the background were available at higher resolution. All carbon-bonded hydrogen positions were idealized with a riding motion constraint in all the three forms. More precisely, an instruction AFIX *n*3 was used within the Shelx input stream to constrain the C-bonded hydrogen atoms, *n* being 1, 2 or 3 depending on the hybridization state of the carbon atom. The H3N atoms (those bonded to the N3 atoms), were on the

contrary left free to refine: we judged unnecessary further constraints as the final C-N-H geometries were perfectly sound and consistent to each other within the various DIEN crystal forms. As regards the thermal motion treatment, the U_{iso}'s of all the CH hydrogen atoms were estimated as 1.2 U_{iso} of the carbon atom to which they were bonded. On the contrary, the isotropic thermal parameter U_{iso} was left free for the amine hydrogen atoms within the unsolvated structures, whereas it was constrained to be equal among H3AN, H3BN and H3CN in SOLV. We judged that such choice for the solvated structure represented the best compromise among the attempt of reducing as much as possible the number of variable parameters (without loosing structural information) and the implementation of a final least-square model as similar as possible to that adopted in the other DIEN structures. Clearly, it should be noted that other refinement strategies equally feasible in terms of final statistics could be adopted. However, slightly different treatments of the hydrogen atoms are not expected to produce significant changes (in terms of estimated standard deviations) in the backbone geometries or in the overall agreement factors.

Anyhow, before performing any packing analysis and energy computation, the hydrogen positions within each independent molecule in the asymmetric unit were optimized in the gas-phase at the DFT B3LYP 6-311++G(p,d) theory level, with the coordinates of all the C and N atom having been kept frozen at their experimental values (see section 2.3 in the main text if the paper). In other words, the hydrogen positions obtained by the least-square refinements against the observed structure factors amplitudes were used just as starting point for the DFT partial optimizations, which in turn provided the H atom geometry used in the Hirshfeld surface fingerprint plot analysis and in all the calculations of the interaction energies.

An overall poorer fit was obtained when the data of the crystal form SOLV were examined because of the high number of weak and unobserved data. It should be noted that this phase crystallizes as very small thin plates and it contains disordered solvent. Data of better quality could be obtained by performing a diffraction experiment at very low temperature (T < 90 K). Anyhow, the disordered methyl group in the molecule of CH_3CN was modelled by refining the site occupation factor for the two accessible positions of the methyl carbon atom, with the thermal motion of the latter treated isotropically. Some attempts were also made to estimate anisotropic thermal parameters of the disordered carbon atom, but the results were unsatisfactory (the thermal ellipsoid of the acetonitrile methyl resulted enormously elongated, and the U_{ij} parameters were correlated with the site occupation factor). This was not surprising, as it is well-known that thermal motion may easily correlate with disorder: low-temperature experiments would be needed to deeply investigate the disorder in DIEN solvated structure, and to provide an unbiased (or, probably, less-biased) estimation of the solvent thermal motion. Considering more specifically the treatment of disorder, each of the two non-equivalent atoms was provided of three hydrogens at idealized positions,

according to the expected sp^3 geometry. At the end of the least-squares refinement, the refined occupation factors were as high as 0.54(3) and 0.46(3) for the two accessible methyl sites. Nevertheless, a quite high positive Fourier residue ($\Delta \rho \sim 1.0$ e·Å^{-3}) remained in another zone of the unit cell, more precisely ~2.6 Å apart from the atom H14C. The entire diffraction experiment was repeated on another sample of the same crystal form, giving identical results, so it appears to be unlikely that this observed electron density residue be due to uncorrected systematic errors still present in the data or to the poor sample quality. In the final model, it was attributed to the oxygen atom of a disordered water molecule. Its site occupation factor (s.o.f) was refined, giving 0.342(7) as final value. It was impossible to reliably locate the hydrogen atoms of such water molecule directly from the diffraction data. Anyhow, it is worth note that if water H atoms are positioned along the directions of the closest O-N neighbours, two reasonable hydrogen bonds are formed with atoms N3C (x, y, z) and N3A (1+x, -1+y, z) of two crystallographically independent macrocycle molecules, with H···N distances being as long as 2.83 and 1.71 Å, respectively (see also Table S4 below). Adopting this geometry, which is of course totally idealized, in the sense that it does not come at all from the experimental data except for the estimate of the oxygen atom position, the HOH angle results to be as large as 110.69 deg. Throughout the following discussion on intermolecular interactions and packing of the SOLV form, such idealized water hydrogen positions are adopted.

Eventually, the studies of crystal packing and molecular conformation were then carried out with Platon (Spek, 1990; Spek, 1998) and Diamond 3.2d (Brandenburg, 2010).

Theoretical calculations. The gas-phase calculations ran on a machine with 4 x 3065 MHz CPU with Linux 2.4.20-43.9.legacybigmem (x86) as operating system, whereas the solid-state ones were performed on a Dual Opteron QuadCore Server, with Linux v.2.6.26-2-amd64 (Debian 2.6.26-19) as operating system. Where possible, the same C_i symmetry as that found in the crystal was retained also in the gas-phase calculations. When molecular pairs made up by independent moieties were considered, however, this symmetry was retained for the pairs A-A, B-B and C-C, because only in such cases the two components of the pair are related by a crystallographic inversion centre.

No symmetry constraints were imposed at all during the optimization of the transition state between the immine endo- and immine eso- conformations, as there was no reason to believe that also the geometry of the transition state be centrosymmetric. The fully optimized gas-phase geometries of the molecules B and C of the form IIº have been used as starting (reactant) and ending (product) points, respectively, throughout such calculation. Firstly, a guess geometry was found on the potential energy hypersurface (PES) by the Linear Synchronous Transit (LST) procedure; it

corresponds to a new conformation, intermediate between the endo- and the eso geometries, with the two C5-C7 bonds rotated with respect to the phenyl rings such as the C7-H5 bonds, which lie originally almost in the phenyl planes, become roughly orthogonal to them. Subsequently, such starting geometry was optimized by searching for saddle points on the PES corresponding to possible transitions states. Anyway, some convergence problems were detected during the sequent optimization at the 6-311++G(p,d) B3LYP theory level. The procedure needed to be restarted and it eventually reached convergence after roughly four weeks of intensive calculations. Quite surprisingly, the geometry of the final, relaxed transition state appeared to be somewhat similar to the eso- product, with a lateral immine chain almost in the eso- arrangement. Such finding prompted us to consider the possibility of the existence of other true minima at higher energy, as interconversion process involves the rotations of both the lateral immine chains, which in turn can follow a conrotatory or disrotatory path, and other (meta)stable geometries may appear in this quite complex system. We therefore decided to explore more accurately the PES at a lower (6-31G(d)) theory level. We eventually succeeded in finding a new minimum corresponding to an intermediate endo- / eso- state (called "mixed" in the paper), with energy roughly at the midway between the conformers observed in the solid state (see Figure 8 in the paper). Interestingly, the planes of the aromatic ring within the molecule are not longer parallel in this intermediate form. With the same procedure above described (i.e. LST calculation starting from the optimized geometries of the endo- and the eso- conformers at the B3LYP 6-31G(d) level + further optimization of the transition state geometry) we found two possible transition states, one between the endo- and the mixed conformers and one between the latter and the eso- conformers. Vibrational frequencies have been evaluated for both the transition states TS1 and TS2, and for the newly found "mixed" true minimum, too, confirming that such stationary points all have the expected rank. It is worth note that both the transition states (named as TS1 and TS2 in Figure 8) are quite similar with respect to their nearest reagent (or product) along the reaction coordinate. As a matter of fact, in TS1 both the immine nitrogen atoms are still in the endo- arrangement, while in TS2 just the opposite is true, as both the immine N atoms share still the same eso- conformation. In both cases, however, one of the two chains appears to be somewhat distorted. As an example, the C5-C7=N1-C8 torsion angle is as large as -177.4 deg in the 6-31G(d) optimized endo- geometry, but changes to -173.3 deg in TS1 and to -177.8 deg in the mixed state. Then, it remains equal to -177.8 in TS2 and eventually becomes as large as -178.9 in the eso- form. It can be concluded that the main contribution to the activation barrier from the endo- conformer to the TS1 geometry is likely to be due to the loss of conjugation among the phenyl ring and the immine moiety, whereas the major changes on going from the eso- form to TS2 regard mainly the rotation of the phenyl group around the N2-C9 bond,

connecting the aromatic ring with the imidazolidine moiety.

It should be noted that, qualitatively, the 6-31G(d) interconversion energies are similar to those evaluated by the larger 6-311++G(p,d) basis set. As an example, the energy difference between the endo- and the eso- conformers in the gas phase comes out as large as 15.93 kJ·mol^{-1} when evaluated with the latter basis set, to be compared to the result of 12.13 kJ·mol^{-1} coming from the smaller 6-31G(d) one. As regards the transition states, as an example, the barrier associated to the eso- $\rightarrow$TS2 conversion was estimated as high as 22.37 kJ·mol^{-1} with the 6-311++G(p.d) basis set and as high as 22.23 kJ·mol^{-1} with the 6-31G(d) one. In other words, identical findings within 1 or 2 kcal·mol^{-1}are found using one of the above mentioned basis sets.

As regards the solid-state calculations, requirements tougher than the default ones provided by the CRYSTAL06 program were adopted in the evaluation of the Coulomb / Exchange integral series. More precisely, the truncation criteria (TOLINTEG keyword in the input stream) were set as low as 10^{-7}, 10^{-7}, 10^{-7}, 10^{-7}, 10^{-14} (Dovesi *et al*., 2006). Moreover, a 30 % eigenvalue mixing and a 4 hartree level shift were imposed to speed up convergence (Dovesi *et al.*, 2006). Eventually, a shrinking factor of 4 was employed to define both the Pack-Monkhorst and the Gilat nets to define the sampling in the reciprocal space.

The solid-state energies of the two polymorphs were corrected for the basis set superposition error (term E_{BSSE} in the summation (1): see the paper) by the counterpoise method (CP, Boys & Bernardi, 1970). CRYSTAL06 applies the CP method by supplementing the molecular basis set with the basis functions of an increasing number of "ghost" atoms, placed at the crystallographic atomic positions within a certain distance from the reference molecule. In this work, all the "ghosts" within 5.0 Å were considered, including up to 114 neighbours for both polymorphs. The amount of BSSE correction was evaluated for each independent molecule in the asymmetric unit.

$E_{rel}(i)$ in the summation (1) (see the paper) was computed with the Gaussian03 program by means of gas-phase calculations on each crystallographically independent molecule, starting from the solid state geometry of the C-N backbone, with the hydrogen atoms positions idealized in gas phase (see the paper). The 6-311++G(p,d) basis set, with the DFT-B3LYP hamiltonian, was adopted. The relaxation energy term is very important in the context of this work, as it allows to quantify the strain which is imposed globally on each molecular moiety by the crystalline environment. The greatest correction due to the relaxation energy was detected for one of the molecules in the crystal form IIº (more precisely, the "C" one: see the paper) and amounted to –34.11 kJ mol^{-1}.

Due to the large number of atoms and the low symmetry of the three systems, all the calculations here performed are quite demanding. The hydrogen optimizations in the gas phase took ~30 hours,

whereas the optimizations of the whole molecule was as long as ~35 hours on the machine above mentioned. The computational cost of the calculations on DIEN molecular pairs, on the other hand, was significantly higher (as an example, the molecular pair A-B of crystal form IIº took about 11 days on the machine above mentioned). Less CPU time was required for the single-point calculations in the solid state, which usually reached convergence of the SCF cycles within 24-48 hours.

Dispersion contribution to the total cohesive energies. By definition, the interaction energy of a certain reference molecule in a cluster or supramolecular assembly is given by the summation over all contributions among it and all the other surrounding moieties in the assembly. In particular, being $E_{\mathrm{int,AB}}$ the interaction energy between two molecules, A and B, the first composed by N α atoms and the second by M β atoms, it follows that the contribution coming from this pair can be expressed as:

$$E_{\mathrm{int},AB} = \sum_{\alpha \in A}^{N} \sum_{\beta \in B}^{M} E_{\alpha\beta} \qquad \text{(S-A)}$$

where $E_{\alpha\beta}$ is the interaction energy for the single atomic pair α ,β . On the other hand, when the cohesion energy $E_{\mathrm{coh,A}}$ of the molecule A in a surrounding cluster of molecules (symmetry-related or not) is desired, the $E_{\mathrm{int,AB}}$ contributions must be evaluated for all the molecular pairs within a certain distance and summed together:

$$E_{coh,A} = \sum_{B \neq A} E_{\mathrm{int},AB} \qquad \text{(S-B)}$$

It can be shown that this cohesive energy is just twice the intermolecular interaction energy of the molecule A. Obviously, the same considerations hold also for the dispersion contribution to the cohesive energy, E_{dis}, as the latter can be decomposed (as in the well-known Spackman's E_{cryst} model) in a summation such as

$$E_{coh,A} = E_{dis,A} + E_{rep,A} + E_{el,A} \qquad \text{(S-C)}$$

where $E_{\mathrm{rep,A}}$ and $E_{\mathrm{el,A}}$ are the exchange-repulsion term and the electrostatic part of the cohesive energy of the reference molecule A, respectively (not considered in this work).

In the context of the present study, we are interested in the dispersion energy of each crystallographically independent molecule within the crystal. When the asymmetric unit contains more than one molecule, i.e. $Z' > 1$ as in DIEN polymorphs, the contribution of each independent moiety must be computed separately, and eventually the mutual interaction terms among the symmetry independent units in the cell have to be added together. One of us (Lo Presti) wrote a simple code in FORTRAN 77, EDIS, to perform such calculation specifically for DIEN (the source code is provided in the Appendix of these notes, see below). Three choices are available for the

dispersion and repulsion potentials, controlled by the keywords "spack", "wilco" and "lenna", to use the parametrization by Spackman (Spackman, 1986), Williams & Cox (Williams & Cox, 1984) or 12,6 Lennard-Jones type (Lennard-Jones, 1931) with the same parametrization as that used in the AUTODOCK software (Morris *et al*., 1998), respectively. Moreover, EDIS requires information on the unit cell, atomic fractional coordinates, and symmetry operations. At the moment, EDIS is not able to reconstruct a molecule from its fragments, so the coordinates of all the atoms of all the whole molecules in the asymmetric unit have to be provided as input. For each independent molecule, it reconstructs a cluster within up to $\pm$ 5 unit translations along each cell axis and evaluates the molecular dispersion and repulsion contribution to the cohesion energies as a sum of atom-atom empirically derived potentials. Eventually, an instruction is present to correct for double-counting of molecular pair interactions due to symmetry redundancy[2]. All the calculations were performed in orthogonal cartesian coordinates, with Å, $kJ \cdot mol^{-1}$ as measure units.

Conformational analysis of the independent DIEN molecules. Our first task is to compare qualitatively and quantitatively, on geometrical grounds, the existing conformers in all the known DIEN crystal structures, included the two solvated forms previously reported in the Literature (Menif *et al*., 1990, Adams *et al*. 1991). For both forms IIº and SOLV, the asymmetric unit is composed by three half molecules, which are marked in the following discussion by the capital letters A, B and C according to their crystal environment. As the crystal packing is quite similar for molecules A and B, their labels have been unquestionably assigned considering also quantitative similarities in their conformations. We began marking as "A" the molecule closest to the origin in all the crystal forms, and "B" the independent moiety closest to "A". The centre of mass of "C" molecule, on the contrary, has fractional coordinates 1/2 1/2 1/2 both in SOLV and IIº and it is always easily recognized. If the root mean square deviations of backbone torsion angles (RMSD's) are considered between each possible molecular pair, it is easy to see that such values are considerably smaller when the A-A pairs are considered with respect to the A-B ones, no matter the crystal structure to which they belong.

In DIEN, where no charge transfer or other phenomena are expected which may affect the connectivity, conformational differences, if any, should concern mainly torsion angles and, to minor extent, bond angles, whereas the bond distances should remain unaffected by the crystal environment. This assertion has been verified by calculating the RMSD's of covalent bond distances and angles with respect to the corresponding weighted averages. All the 12 crystallographically

[2] In the case of DIEN, each molecule is composed by a symmetry independent part and a inversion-related one. Therefore, when the unit translations are applied to the *entire* molecule, no matter it was automatically generated, or it was provided as input, it is always possible to reconstruct the *same* molecule in each unit cell using combinations of unit translations and the identity (x, y, z) *or* the inversion (-x, -y, -z). As an example, the operations (x, y, -1+z) and (2-x, -y, 1-z) generate two fragment of the same A moiety, i.e. just the *same, whole* molecule A when they are applied to the reconstructed whole molecule. Accordingly, the program can correct the total energy estimates by dividing the total dispersion and repulsion contributions by an appropriate factor (2 in the present case).

independent molecules in the five known crystal forms (IIº, I, SOLV, KIGVEB and SOVJUI) were pairwise compared, considering only covalent bonds involving non-hydrogen atoms. Average results as low as $1.6 \cdot 10^{-2}$ Å and 1.1 deg were found for the RMSD on distances and angles, respectively. Anyhow, it is worth noting that excluding from the mean the two previously reported solvated forms, RMSD values become considerably smaller ($7 \cdot 10^{-3}$ Å and $7 \cdot 10^{-1}$ deg, respectively) due to the poorer-quality, on average, of both KIGVEB and SOVJUI structures with respect to the three newly reported crystal forms. In any case, it should be stressed that the RMSD outcomes are considerably greater for bond angles. In particular, the greatest RMSD values are found when the molecule C in the polymorph IIº come in comparison with each other molecule. As an example, the angle comparison between C IIº and B IIº independent units gives a RMSD estimate as large as 1.03 deg, whereas the same quantity becomes as low as 0.49 deg when the B IIº molecule is compared with the C SOLV one. As discussed in detail in the main text of the paper, the molecule C adopts a significantly different conformation in the crystal form IIº with respect to all the other independent units, no matter the crystal structure they belong. Such conformational change involves some bond angles, too: interestingly, as an example, the angle α (N3-C12-N2) in the crystal form IIº is about 3 deg higher for the molecule C with respect to both the molecules A and B in the same phase (see also the deposited cif files). This result is in agreement with the finding that one of the major changes involves just the imidazolidine fragment (see the discussion below). Such variability in bond angles is likely to be the consequence of the relative flexibility of the DIEN macrocycle.

Table S1 reports the puckering parameters (Cremer & Pople, 1975) of the imidazolidine ring of the independent molecules of DIEN in all the known crystal forms. It is worth note that the atom C12 of molecules A and B invariably lies about 0.5 Å far apart the average least-square plane passing through atoms C10, C11, N2 and N3. It can be seen that, apart from some unavoidable numerical differences, the eterocycle shares the same conformation (the so-called "twisted" one) for molecules A and B in all the polymorphs: the only exception is given by molecule B in the SOLV form, where the distortions above described force the five-membered ring to assume a conformation which is somewhat intermediate between the "twisted" and the "envelope" ones, being anyway closer to the latter in terms of its puckering phase (Table S1). Anyhow, with this only exception, it is possible to conclude that all the functional groups of molecule B adopt the same conformation in all the crystal forms, which is in turn very similar to that adopted by the molecule A, as the main differences in torsion angles regard the way by which the various chemically relevant moieties, by themselves essentially rigid, are interconnected to each other.

Considering the puckering coordinates of the third independent molecule C, other difference are evident with respect to both A and B and even between the phases IIº and SOLV. In IIº he q_2 amplitude is significantly smaller and the ϕ_2 phase about 40-60 deg higher in absolute value, when such parameters are compared among the independent molecules in all the three phases. The

conformation is then an "envelope", as in the case of the molecules B and C in SOLV. Anyhow, it is worth note that for molecule C in form IIº is the atom C11, not C12, which lies ~0.5 Å far apart the average least-square plane defined by the other four atoms. Therefore, the major conformational differences detected for C in the phase IIº (see the paper) involve the eterocycle ring also.

TABLE S1: Puckering coordinates of the 5-members imidazolidine rings in IIº, I and SOLV.

Molecule	A	B	C
Form IIº			
q_2	0.373 (2)	0.357 (2)	0.324 (3)
ϕ_2, deg	-10.9 (4)	-17.2 (4)	69.5 (4)
Conformation[a]	T	T	E
Form I			
q_2	0.369 (2)	0.361 (1)	
ϕ_2, deg	-13.3 (3)	-17.9 (3)	
Conformation[a]	T	T	
SOLV			
q_2	0.365 (2)	0.366 (4)	0.372 (2)
ϕ_2, deg	-20.6 (5)	-28.9 (4)	-32.5 (4)
Conformation[a]	T	E	E
KIGVEB			
q_2	0.388(8)	0.365(7)	
ϕ_2, deg	-15 (1)	-10 (1)	
Conformation[a]	T	T	
SOVJUI			
q_2	0.41(2)	0.35(2)	
ϕ_2, deg	-18(3)	-15(3)	
Conformation[a]	T	T	

[a] E: Envelope; T: Twisted. Atom sequence: N2-C10-C11-N3-C12. Conformation is assigned by considering to which pure arrangement (E or T) the X-ray derived puckering phase ϕ_2 is closest. More precisely, the five-membered ring always adopts a conformation intermediate between the pure E (which would involve a puckering phase ϕ_2 = 0, $\pm$ 36, $\pm$ 72... deg) and pure T (which would imply ϕ_2 = $\pm$ 18, $\pm$ 54, $\pm$ 90... deg) arrangements.

Intermolecular H···N contact geometry within the two DIEN polymorphs. Table S2 reports the geometry for the relevant C-H···N contacts in the two DIEN polymorphs, supplementing the information provided in Table 3 in the paper.

TABLE S2: N-H···N and C-H···N intermolecular contacts of the two DIEN polyorphs [a]

Reference Molecule	Contact	d_{D-H} / Å [b,c]	d_{D-N} / Å	$d_{H\cdots N}$ / Å [c]	$\alpha_{D-H\cdots N}$ / deg [c]	Symmetry [d]
Form IIº						
A	N3A-H3AN···N3B	1.013	3.581(3)	2.709	144.3	1-x, -y, 2-z
B	N3B-H3BN···N1A	1.014	3.411(3)	2.521	146.3	-1+x, y, z
C	N3C-H3CN···N3A	1.016	3.251(3)	2.264	163.6	x, y, -1+z
A	C8A-H7A···N1B	1.096	3.506(3)	2.478	155.5	1+x, y, z
A	C6A-H4A···N3B	1.084	3.508(3)	2.655	135.2	1+x, y, z
B	C11B-H13B···N2A	1.095	3.681(3)	2.972	122.8	1-x, -y, 2-z
B	C11B-H12B···N1A	1.093	3.614(3)	2.894	123.5	-1+x, y, z
C	C8C-H6C···N1B	1.097	3.631(4)	2.739	138.1	x, y, -1+z
C	C11C-H13C···N3C	1.094	3.608(4)	2.713	138.7	-1+x, 1+y, z
Form I						
A	N3A-H3AN···N3B	1.013	3.547(2)	2.706	140.5	x, y, z
B	N3B-H3BN···N1A	1.014	3.448(2)	2.549	147.6	x, y, z
A	C8A-H7A···N1B	1.097	3.573(2)	2.546	155.3	x, y, 1+z
A	C4A-H3A···N3A	1.086	3.801(3)	2.968	133.7	1+x, y, z
A	C6A-H4A···N3B	1.084	3.477(2)	2.653	132.4	x, y, z
B	C11B-H13B···N2A	1.094	3.606(3)	2.860	125.4	x, y, -1+z
B	C11B-H12B···N1A	1.093	3.696(3)	2.977	123.6	x, y, z

[a] All the H···N contacts with a CHN or NHN angle greater than 120 deg and a HN distance lower than 3.0 Å are displayed. [b] C-H and N-H covalent distances derived from a gas-phase optimization at the B3LYP 6-311++G(p,d) theory level of the hydrogen coordinates only. [c] Estimated standard deviations are derived only from the uncertainties of the carbon and nitrogen coordinates. [d] Symmetry operation generating the acceptor atom, with translations expressed in terms of unit cell axes as reported the deposited CIF file.

Relaxation of the independent molecules of the two polymorphs. Figure S1 displays the main geometry changes between the solid-state and the gas-phase optimized geometries. As described in the text, the relaxation involves relative rotations of the imidazolidine and the lateral immine chains and the most evident geometry changes regards the molecule C in the polymorph IIº. Anyhow, the main molecular immine endo- or immine eso- conformation is always retained.

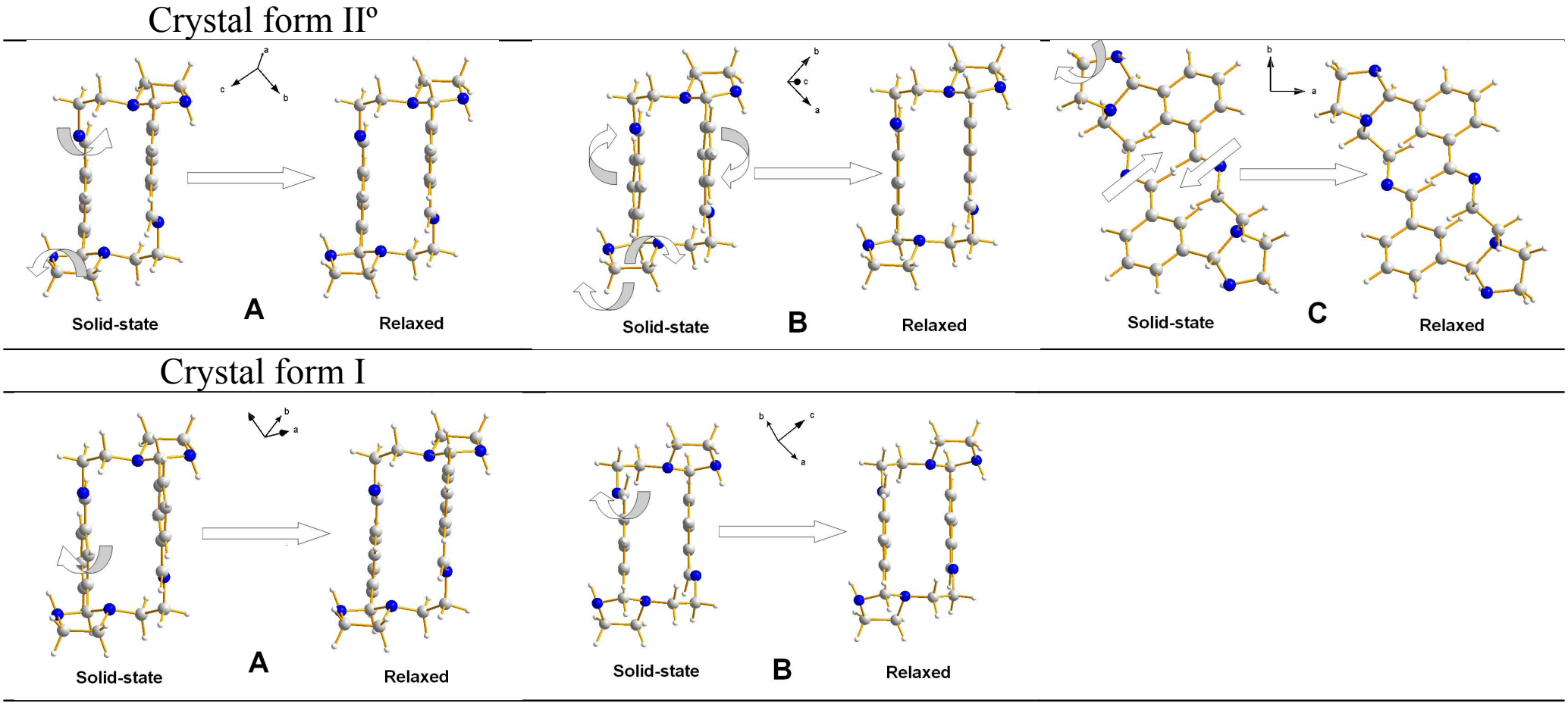
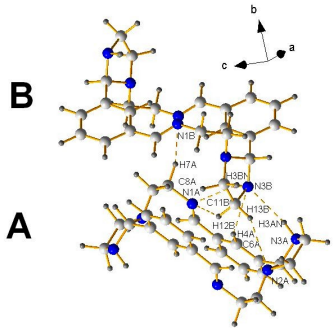
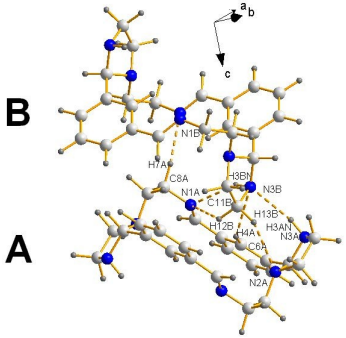
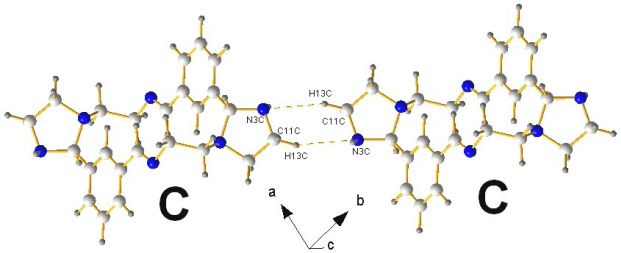


Figure S1. Colour online. Geometry changes of the crystallographic independent DIEN molecules upon relaxation for the two unsolvated crystal forms IIº and I.

Isolated molecular pairs of the two DIEN polymorphs.

Form IIº	Form I	Form IIº	Form I
			
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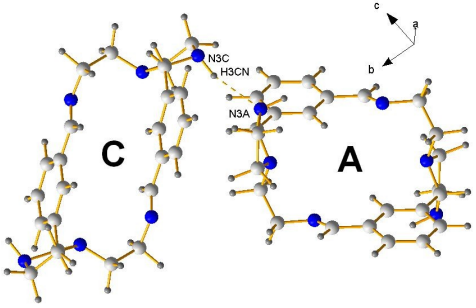		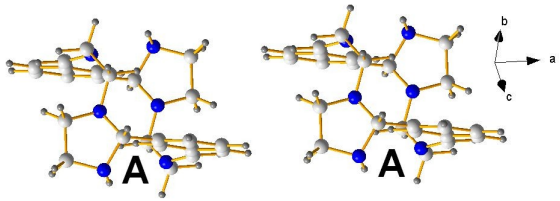	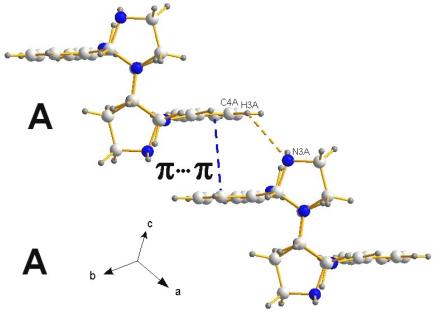
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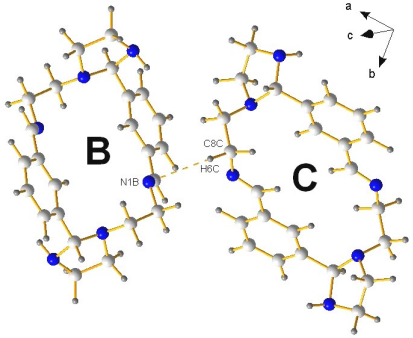
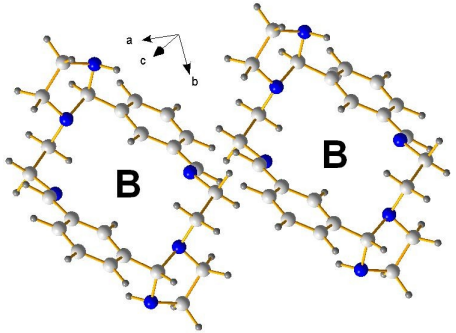
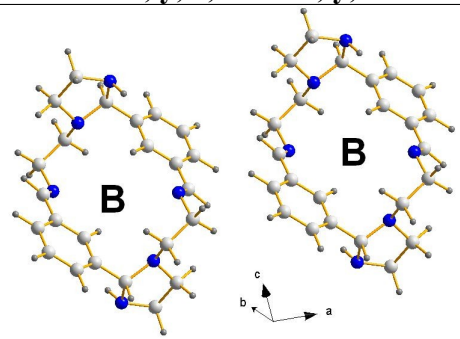
			
B: 1+x, y, z; C: x, y, z		B: x, y, z; B: 1+x, y, z	B: x, y, z; B: 1+x, y, z

Figure S2. Colour online. Isolated molecular pairs at the experimental X-ray geometries for the two DIEN polymorphs used for calculations of the total intermolecular interaction energies. The N-H···N, C-H···N and π ···π contacts elsewhere shown or discussed are also highlighted (see Table 3 and Table S2, respectively). For each pair, the symmetry operations used for generating the two molecules are also reported.

Solvated forms: crystal packing. Figure S3 reports the Hirshfeld surface fingerprint plots for all the known solvated forms of DIEN, KIGVEB (Menif *et al*., 1990), and SOVJUI (Adams *et al*., 1991) being reported in the Cambridge Structural Database (methanol and dichloromethane solvates, respectively) and SOLV being the newly discovered form reported in this paper for the first time (acetonitrile / water solvate). Some geometry manipulations have been applied on both the deposited and the SOLV geometry data before performing all the Hirshfeld surface analysis. In particular, (i) the covalent H-A distances (where "A" is C, N, O) were normalized to ideal values available from neutron data; (ii) misplaced or lacking hydrogen atoms in the Crystallographic Information Files retrieved from the Cambridge Structural Database were corrected, adding the appropriate H atoms in chemical sensible positions or erasing the hydrogen without sense, and (iii) no disorder at all was taken into account. In particular, as regards the SOLV and SOVJUI structures, the positions of disordered solvent groups have been averaged out between the two accessible sites of disorder and the attached hydrogen atoms have been accordingly relocated. In SOVJUI, the dichloromethane molecule lies near a crystallographic binary axis. It was treated as disordered in the original work with low (0.25) occupancy. We idealized this solvent to exact C_{2v} point symmetry and we placed it consequently on the C_2 axis. However, it should be noted that such solvent averaging implies only small shifts of the atomic positions, so it does not alter the main features of the fingerprint plots.

In the KIGVEB reported structure, on the other hand, a glide-related CH_3OH moiety (more precisely, at 1-x, y, 0.5-z) appears to be very near to the symmetry-independent one (the distance between symmetry-related "C25?" atoms of the adjacent methanol molecules is as large as 1.75 Å). In the original paper, a 50 % occupancy factor was assigned to the disordered methanol molecules near the glide, but when the disorder is artificially removed, the above mentioned short and unrealistic C-C contact results in equally unrealistic H-H distance when the methyl hydrogen atoms, which were missing in the deposited data, are added. We nevertheless performed the Hirshfeld surface analysis on the deposited KIGVEB geometry, without solvent averaging, as we judge that some uncertainty in the location of the solvent should not considerably alter the general appearance of the fingerprint plots and the sequent analysis of the overall macrocycle interactions in the unit cell.

Inspecting at Figure S3, the same features observed about the two DIEN polymorphs in the paper can again be evidenced. In particular, the following ones can be easily recognized: (i) quite large spikes along the main diagonal of the plots signalling the occurrence of several H···H contacts; (ii) lateral "wings" due to the C-H···π interactions, and (iii) long (or short, depending on the structure) lateral spikes due to intermolecular H bonds. Anyhow, it is worth note that some new features are also present in the plots reported in Figure S3. As an example, the large and quite long spike in the fingerprint plot of the molecule A in SOVJUI at minimum $d_i + d_e \sim 0.7+1.3$ Å is due to H···Cl contacts. Interestingly, at slightly higher d_i, just below the main spike, a sharper and shorter similar feature, due to N-H···N contacts, is clearly recognizable. Moreover, both SOVJUI and KIGVEB show a new common feature, which is missing in the other crystal forms studied in this work, i.e. a short and relatively large spike along the main diagonal, in the upper right part of the diagram. This is due to long C···C distances (above 3.8 Å) due to T-shaped phenyl-phenyl interactions among the extremity of the aromatic ring of the molecule A with the same group, almost perpendicularly oriented, of the molecule B at 0.5+x, 0.5+y, z (SOVJUI) or at -0.5+x, 0.5-y, 0.5+z (KIGVEB). Interestingly, some red points are visible in the fingerprints plot of the molecule A of both KIGVEB and SOVJUI structures at $d_i + d_e \sim 2.0 + 2.0$ Å, indicating some kind of eclipsed arrangement of the phenyl groups as already observed for the same molecule A in polymorph I, but in these solvated forms the least-squares planes through the aromatic rings belonging to symmetry related molecules are no longer parallel (the dihedral angles between such planes amount to 7.24 deg in KIGVEB and to 8.42 deg in SOVJUI respectively), indicating that the π ···π interaction, if any, should be definitely less important in these pairs. It is evident that, generally speaking, KIGVEB and SOVJUI have quite similar packing features, the greatest difference between them being, not surprisingly, the appearance of a significant amount of H···halogen interactions in the dichloromethane solvate SOVJUI form. The crystal packing of the SOLV form, on the contrary, appears to be quite different. As an example, in the plot relative to molecule A, a long and sharp spike in the hydrogen bond acceptor region appears due to the short contact between one water hydrogen and the imidazolidine N3A atom, which lie ~1.7 Å far away from each other (see also the discussion above). In molecule C, on the other hand, two short lateral spikes are visible in the upper left part of the diagram. Interestingly, the short blue spike at $d_i + d_e \sim 2.58$ Å is due to short H···C contacts, whereas that at $d_i + d_e \sim 2.63$ Å, which is green indicating a contact occurring with higher frequency, signal short H···O interactions involving the water molecule.

It can be concluded that in the DIEN solvated phases some packing features are common to all the three forms; moreover, in SOVJUI and KIGVEB a new feature appears signalling a T-shaped orientation of symmetry-independent phenyl fragments. Anyway, most of the above mentioned features are recognizable also in the two unsolvated forms, and really the fingerprint plots of SOLV

are quite similar to those of the two unsolvated polymorphs (compare the Figure 7 in the paper with the Figure S3). Interestingly, the molecule C in SOLV displays a greater number of H···H intermolecular contacts with respect to the same molecule in the form IIº (note the minor number of red points along the main diagonal of the latter): this is likely to be the consequence of the important conformational differences between such independent units, rather than of some direct effect of the solvent moieties. Moreover, the fingerprint plots of SOLV are quite similar to those of the two unsolvated ones (compare Fig. 7 in the paper and Fig. S4). Therefore, it can be said with some confidence that, at least in the present case, the inclusion of solvent molecules does not, by itself, alter dramatically the overall packing motifs in the solid phase; rather, some extra features are added in the fingerprint plots depending on the nature of the solvent molecules.

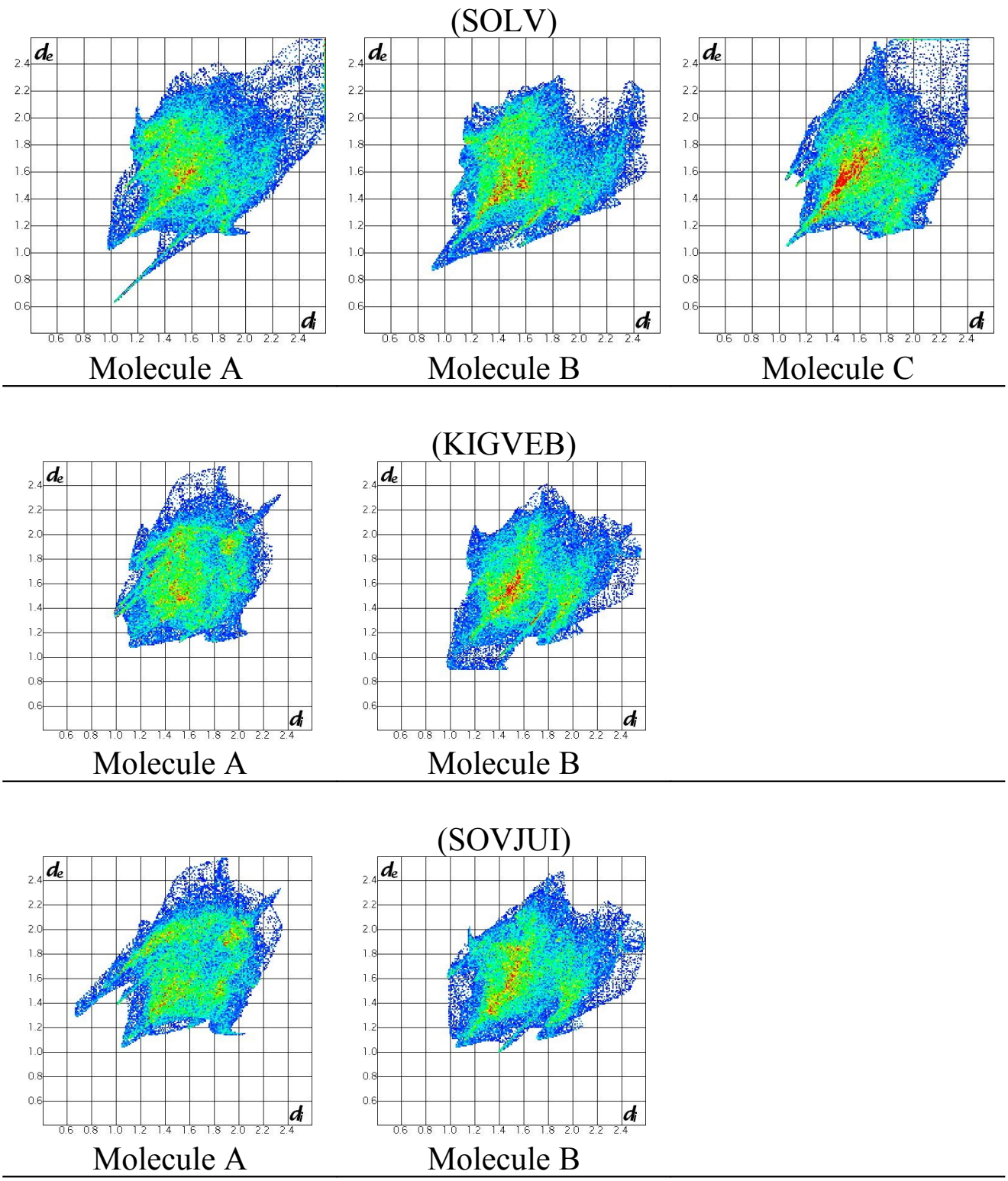


Figure S3. Colour online. Hirshfeld surface fingerprint plots of the nearest internal distance (d_i) vs. the nearest external distance (d_e) (Spackman & McKinnon, 2002) for each of the independent molecules in the two polymorphs of DIEN. The colours represent the number of points which share the same d_i, d_e coordinate (hot colours: many; cold colours: few). The graphics have been realized by the software Crystal Explorer 2.1 (Wolff *et al*., 2007).

Solvated forms: energetics. Table S3 reports the total quantum mechanical interaction energies, uncorrected for BSSE, for the same isolated molecular pairs discussed in Table 5 (see the paper) at the experimental solid-state geometries. The DFT B3LYP 6-311++G(p,d) theory level was adopted throughout. It should be noted that most of the interaction energies are repulsive or only weakly attractive, with the only remarkable exception of the C-C pair in the SOLV form. The presence of a third independent molecule, although in the endo- conformation in this case, provides again an important, favourable contribution to the overall crystal stability, as noted in the paper for the two unsolvated DIEN polymorphs. However, it should be remembered that all these energy estimates are to be considered as relative guidelines in individuating the most tightly bonded pairs in the crystal, as in a true lattice also the contributions provided by the surrounding moieties must be considered if more accurate energies are desired.

TABLE S3: Intermolecular interaction energies of relevant isolated DIEN molecular pairs at the experimental geometry they have in SOVJUI, KIGVEB and SOLV [a].

	A-B	A-C	B-C	C-C	A-A	B-B
SOVJUY	-2.84 6.10				+8.89 9.10	-0.31 12.46
KIGVEB	+0.59 6.05				+10.94 8.98	-0.27 12.34
SOLV	+0.78 6.28	+0.71 8.83	+8.42 6.50	-8.56 12.24	-2.40 12.24	+10.94 12.24

[a] First row: quantum mechanical total interaction energies. Second row: geometric distance between molecular centres of mass. All the quantities are given as $kJ \cdot mol^{-1}$ and Å.

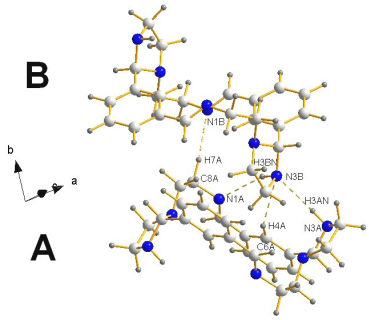
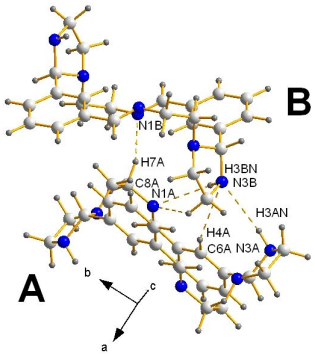
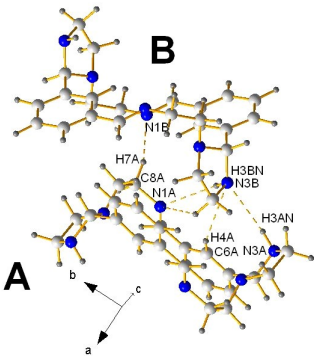
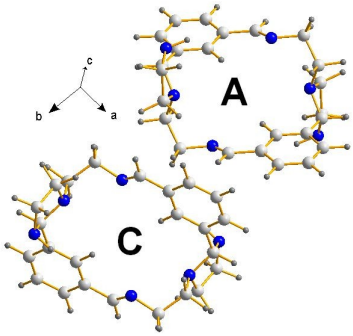
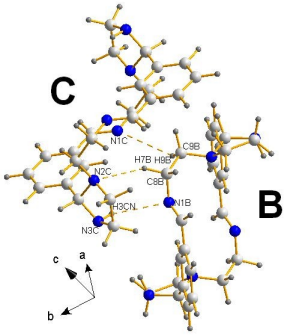
Intermolecular H···N contact geometry within the three DIEN solvated forms. Table S4 reports the geometry for the relevant H···N contacts in the three DIEN solvated forms, supplementing the information given in Table 6 of the paper. Accordingly, Figure S4 shows the relevant molecular pairs as in the Figure S2.

TABLE S4: D-H···A (D: donor, A: acceptor) intermolecular contacts in the three DIEN solvated forms [a]

Reference Molecule	Contact	d_{D-H} / Å [b]	d_{D-A} / Å	$d_{H\cdots A}$ / Å	$\alpha_{D-H\cdots A}$ / deg	Symmetry [c]
SOLV						
A	N3A-H3AN···N3B	1.014	3.494(4)	2.583	149.3	x, 1+y, z
B	N3B-H3BN···N1A	1.015	3.371(5)	2.475	146.9	-x, 1-y, -z
C	N3C-H3CN···N1B	1.015	3.608(4)	2.792	137.6	1+x, y, z
A	C8A-H7A···N1B	1.096	3.843(4)	2.827	154.2	x, y, z
A	C6A-H4A···N3B	1.084	3.465(4)	2.599	136.3	x, 1+y, z
B	C9B-H9B···N1C	1.093	3.778(5)	3.050	124.5	-1+x, y, z
B	C8B-H7B···N2C	1.096	3.861(3)	2.953	140.4	-1+x, y, z
A	C3A-H2A···N90 [d]	1.085	3.563(6)	2.762	130.5	x,y,-1+z
C	C7C-H5C···N90 [d]	1.101	3.658(7)	2.630	155.0	1+x,y,z
A	C11A-H13A···O1 [d]	1.092	3.372(13)	2.414	145.7	x, y, z
B	C2B-H1B···O1 [d]	1.085	3.433(12)	2.470	147.1	x, y, z
B	C12B-H14B···O1 [d]	1.107	3.422(12)	2.502	139.7	x, y, z
C	C2C-H1C···O1 [d]	1.086	3.402(9)	2.690	122.7	1+x, y, z
water [e]	O1-HO1···N3A	0.900	2.614(9)	1.713	180.0	1-x, 1-y, -z
water [e]	O1-HO2···N3B	0.900	3.725(3)	2.825	180.0	x, y, z
KIGVEB						
A	N3A-H3AN···N3B	1.009	3.798(8)	2.935	144.1	1-x, -y, -z
B	N3B-H3BN···N1A	1.009	3.624(7)	2.795	139.7	1+x, y, z
A	C8A-H7A···N1B	1.083	3.425(11)	2.413	154.9	0.5-x, 0.5-y, -z
A	C6A-H4A···N3B	1.083	3.735(8)	2.866	137.3	-1+x, y, z
B	C11B-H12B···N1A	1.083	3.710(7)	2.945	127.9	1+x, y, z
A	C11A-H13A···O1? [f]	1.083	3.413(14)	2.338	171.4	x, y, z
A	C2A-H1A···O1? [f]	1.083	3.360(14)	2.446	141.3	0.5-x, -0.5+y, 0.5-z
B	C4B-H3B···O1? [f]	1.083	3.820(18)	2.743	173.0	0.5+x,0.5-y,-0.5+z
B	C12B-H14B···O1? [f]	1.083	3.380(13)	2.683	121.7	0.5+x,0.5+y,z
SOVJUI						
A	N3A-H3AN···N3B	1.009	3.794(19)	2.928	144.4	1-x, y, 0.5-z
B	N3B-H3BN···N1A	1.009	3.648(16)	2.792	142.8	1-x, y, 0.5-z
A	C8A-H7A···N1B	1.083	3.424(25)	2.408	156	0.5-x, 0.5+y, 0.5-z
A	C6A-H4A···N3B	1.083	3.799(19)	2.934	137	1-x, y, 0.5-z
B	C11B-H12B···N1A	1.083	3.780(19)	3.034	126	1-x, y, 0.5-z
A	C11A-H13A···Cl1? [f]	1.083	3.735(32)	2.664	170	0.5-x, 0.5-y, -z
A	C2A-H1A···Cl2? [f]	1.083	3.489(39)	2.698	129	x, y, z
B	C4B-H3B···Cl1? [f]	1.083	3.677(42)	2.598	174	x, y, z
B	C12B-H14B···Cl1? [f]	1.083	3.417(32)	2.668	126	0.5-x, 0.5+y, 0.5-z

[a] All the D-H···A contacts with a DHN angle greater than 120 deg and a HN distance lower than 3.0 Å are displayed. [b] D-H distances derived from a gas-phase optimization at the B3LYP 6-311++G(p,d) theory level of the hydrogen coordinates only. [c] Symmetry operation generating the acceptor atom, with translations expressed in terms of unit cell axes as reported in the deposited CIF files. [d] N90 is the nitrogen atom of the acetonitrile molecule, while O1 is the water oxygen. [e] Water hydrogen atoms were manually located (not refined) around the oxygen atom such as reasonable hydrogen bond contacts could be set up (see paper). [f] Interaction with the disordered solvent. The atom O1? belongs to the methanol molecule, while Cl1? and Cl2? are chlorine atoms in the dichloromethane molecule. The "?" types were already present in the original CIF.

Isolated molecular pairs of the three DIEN solvated forms.

SOLV	KIGVEB	SOVJUI
 A: x, y, z; B: x, 1+y, z	 A: 1+x, y, z; B: x, y, z	 A: x, y, z; B: x, 1-y, -0.5+z
 A: x, y, z; C: -1+x, 1+y, -1+z		
 B: x, y, z; C: -1+x, y, z		

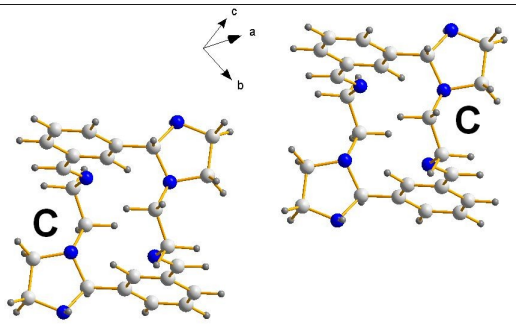
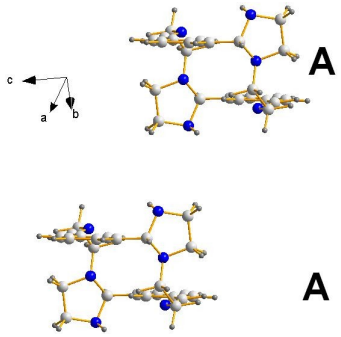
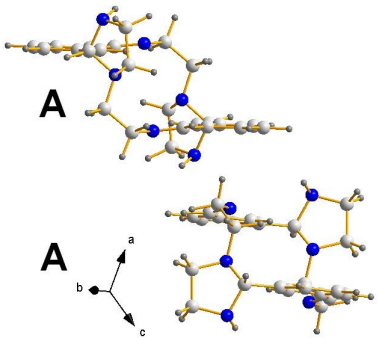
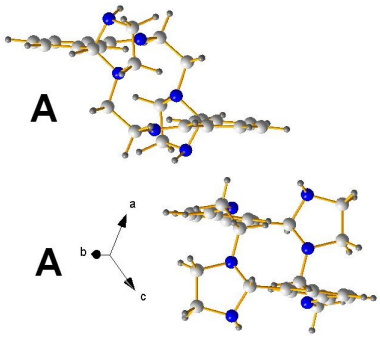
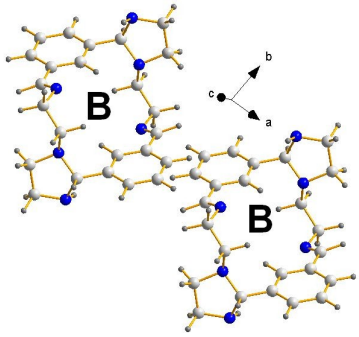
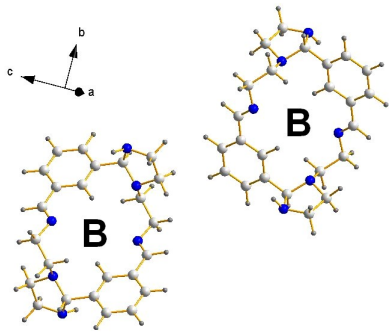
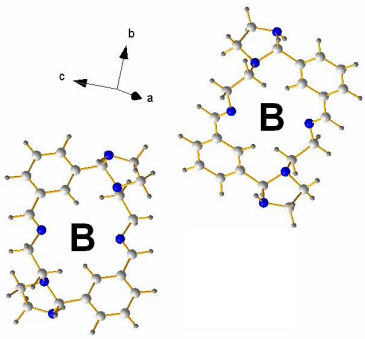
SOLV	KIGVEB	SOVJUI
 C: x, y, z; C: -1+x, y, z		
 A: x, y, z; A: 1+x, y, z	 A: 1+x, y, z; A: 1+x, -y, 0.5+z	 A: 0.5+x, 0.5-y, 0.5+z; A: 0.5+x, -0.5+y, z
 B: x, y, z; B: 1+x, y, z	 B: x, y, z; B: x, -y, 0.5+z	 B: 0.5+x, 0.5-y, -0.5+z; B: 0.5+x, -0.5+y, z

Figure S4. Colour online. Isolated molecular pairs at the experimental X-ray geometries for the three DIEN solvated forms used for calculations of the total intermolecular interaction energies. The N-H···N, C-H···N elsewhere shown or discussed are also highlighted (see Table S4). For each pair, the symmetry operations used for generating the two molecules are also reported.

References

Adams, H., Bailey, N. A., Fenton, D. E., Hempstead, P. D. & Westwood, G. P. (1991). *Journal of Inclusion Phenomena and Molecular Recognition in Chemistry* **11**, 63-69.

Boys, S. F. & Bernardi, F. (1970). *Mol. Phys*., **19**, 553-566.

Brandenburg, K. (2010) *Diamond (version 3.2d)- Crystal and Molecular Structure Visualization*, Crystal Impact GbR: Bonn, Germany. URL: http://www.crystalimpact.com/diamond/

Bruker (1999). *SAINT+. Version 6.01*. Bruker AXS Inc., Madison, Wisconsin, USA.

Buckingham, A. D. (1970) *Physical Chemistry: an Advanced Treatise*, Henderson D. Ed. Academic Press: New York, pp. 349-386.

Buckingham, A. D. (1978) *Intermolecular Interactions: From Diatomics to Biopolymers*, Pullmann, B. Ed. Wiley and Sons: Chichester, New York, pp. 1-67.

Cremer, D. & Pople, J. A. (1975) *J. Am. Chem. Soc.* **97**, 1354–1358.

Dovesi, R., Saunders, V. R., Roetti, C., Orlando, R., Zicovich-Wilson, C. M., Pascale, F., Civalleri, B., Doll, K., Harrison, N. M., Bush, I. J., D'Arco, Ph. & LLunell, M. (2006). *CRYSTAL06 User's Manual*. University of Torino, Torino, 2006.

Farrugia, L. J., (1999). *J. Appl. Cryst*. **32**, 837-838.

Lennard-Jones, J. E. (1931). *Proc. Phys. Soc*. **43**, 461-482.

Morris, G. M., Goodsell, D. S., Halliday, R. S., Huey, R., Hart, W. E., Belew, R. K. & Olson, A. J. (1998). *J. Comput. Chem*. **19**, 1639–1662. More information can be also found at the following url: http://www.csb.yale.edu/userguides/datamanip/autodock

Menif R., Martell, A. E., Squattritto, P. J. & Clearfield, A. (1990). *Inorg. Chem.* **29**, 4723-4729

Sheldrick, G. M. (2008). *Acta Cryst*. *A***64**, 112-122.

Sheldrick, G. M. (2004). *SADABS*. Institüt für Anorganische Chemie der Universität, Tammanstrasse 4, D-3400 Göttingen, Germany.

Spackman, M. A. (1986). *J. Chem. Phys*. **85**, 6587-6601.

Spackman, M. A. & McKinnon, J. K. (2002). *Crystal Growth & Design* **66**, 378–392.

Spek, A. L. (1990). *Acta Cryst*. *A***46**, C34.

Spek, A. L. (1998). *PLATON, A Multipurpose Crystallographic Tool*. Utrecht University, Utrecht, The Netherlands.

Williams, D. E. & Cox, S. R. (1984) *Acta Cryst*. B**40**, 404-417.

Wolff, S. K., Grimwood, D. J., McKinnon, J. J., Jayatilaka, D. & Spackman, M. A. (2007). *CrystalExplorer 2.1*. © 2005-2007 University of Western Australia. See also http://hirshfeldsurface.net/CrystalExplorer/.

Appendix. Source code (FORTRAN 77) of the program EDIS. The program was used on a Dual Opteron QuadCore platform, with Linux v.2.6.26-2-amd64 (Debian 2.6.26-19) as operating system. It was compiled with the FORTRAN 77 open source gfortran compiler, with the following string: "gfortran edis.f -o edis", and the executable was called with the following list of instructions:

```
#
ln -s edis.inp fort.1
ln -s debug.edis fort.2
ln -s cartesian.edis fort.3
ln -s energies.edis fort.4
/home/leo/bin/edis > out.edis
rm fort.1
rm fort.2
rm fort.3
rm fort.4
```

```
c
c                                          PROGRAM EDIS
c
c Calculation of empirical dispersion and repulsion contributions to the molecular interaction
c energy in the solid state. Source code in FORTRAN 77.
c
c Written by Dr. Leonardo Lo Presti, Università degli Studi di Milano, Dept. of Physical Chemistry
c and Electrochemistry, Via Golgi 19, 20133 Milano (MI), Italy, e-mail leonardo.lopresti@unimi.it
c Version 1.0, March, 2010.
c
c This code is supplied freely for non-commercial academic research purposes as an Appendix to the
c Supplementary Material of the following paper: Lo Presti, L., Soave, R., Longhi, M. & Ortoleva, E.
c (2010). Acta Cryst. 66, 527-543. Bug report or questions should be e-mailed to
c leonardo.lopresti@unimi.it. The code is provided "as is". The author cannot be considered responsible
c for any problem other user may experiment with his/her own operating systems, including system crash,
c data loss, etc. It would be kindly appreciated that the author be informed of any modification made
c on the source code. Moreover, the above mentioned paper should be cited whenever results obtained with
c this code on other chemical systems are published.
c
c WARNING: This program is currently able to handle symmetry only for triclinic, monoclinic and
c orthorhombic systems.
c
c Structure of the input file:
c
c FIRST ROW (6f10.0):cell parameters, in Angstroms and degrees: a, b, c, alpha, beta, gamma
c SECND ROW (4i5):   nat =   the number of atoms in the asymmetric unit. This quantity is currently not used
c                            in the program, as ENTIRE molecules (not fragments) in the asymmetric unit have
c                            to be input; the quantity "nat" is however here defined only for future improvements
```

```
c                          of the code (e.g. reconstruction of the molecules from its fragments).
c                    nsym =  total number of symmetry operations to be read. If the asymmetric unit contains
c                          only a fraction of a molecule, the symmetry operation(s) involved in the reconstruction
c                          of the whole molecule SHOULD NOT be read as input, as it is implicitly taken into
c                          account by providing the fractional coordinates of each ENTIRE molecule.
c                    nmol =  total number of molecules in the asymmetric unit.
c                    ncell = amount of unit cell translations to be accounted for when the molecular cluster is
c                          reconstructed around the asymmetric unit, taken as reference. Molecule-molecule
c                          interactions are calculated by recursively applying, for each of the nsym symmetry
c                          operations provided as input, unit translations within +/-ncell on the edges c, b, a,
c                          respectively.
c THIRD ROW (2a5):  potdis = keyword defining the parametrization to be used to compute the dispersion term (see infra).
c                    potrep = as above, for the repulsion term.
c                          At the moment, the following choices are available for the empirically derived
c                          dispersion and repulsion parameters:
c                          wilco = potential parameters by William & Cox, D.Williams & S.Cox, ActaB,40,404,1984.
c                          spack = potential parameters by Spackman, M.A.Spackman,J.Chem.Phys,85,6579,1986.
c                          lenna = 12,6 Lennard-Jones potential parameters taken from the parametrization used
c                                  in the program AUTODOCK (Morris et al.,J. Comput. Chem.1998,19,1639-1662; see
c                                  also http://www.csb.yale.edu/userguides/datamanip/autodock).
c ROWS FROM 4th TO 4th+nmol (2i5):
c                 natom(i) = number of atoms contained in the i-th molecule. Input first the molecules which contain the
c                          greatest number of atoms (i.e., in the case of, as just an example, hydrated glucose, input
c                          first the glucose molecule (24 atoms) and then the water molecule (3 atoms)).
C                  nasu(i) = number of effective molecular fragments contained in that molecular unit. This
C                          parameter serves to correct the energy for multiple-counting when the asymmetric unit
C                          contains only fractions of true molecules. As an example, in DIEN the asymmetric unit
C                          contains a certain number of half-molecules, so nasu=2 has to be input for the macrocycle
C                          molecules because each of them is in fact composed by TWO fragments. On the contrary,
C                          nasu=1 should be used for each solvent molecule, as they are composed by just ONE fragment.
C                          In practice, the program divides just by nasu(i) the individual contributions to both the
C                          dispersive and repulsive terms of the i-th molecule.
c ROWS FROM 4th+nmol+1 TO 4th+nmol+total number of atoms (a2,3f10.5):
c                   spec(n) = chemical symbol of the n-th atom. At the moment, the program recognizes only the following
c                          atomic species: C, H, N, O, CL.
c                 frac(n,j) = x, y, z fractional coordinates of the n-th atom.
c ROWS FROM 4th+nmol+total number of atoms+1 TO 4+nmol+total number of atoms+nsym (i5,f10.0,i5,f10.0,i5,f10.0):
c                 isign, at = the symmetry operations to reconstruct the cluster are input using a parameter, isign, which
c                          specifies the sign (+/-) to be applied to a certain fractional coordinate (in the usual order,
c                          i.e. X, Y, Z), and a parameter, at, which specifies the corresponding fraction translation along
c                          that coordinate (if any). As an example, the string '1   0.00000    1   0.00000    1  0.000000'
c                          is equivalent to the identity (X, Y, Z), while,e.g.,'1   0.00000   -1   0.50000    1  0.500000'
c                          corresponds to the symmetry operation X, 1/2-Y, 1/2+Z.
c
c The program reads the input file from the logical unit 1 and provides the following output files:
c
c -logical unit 2: for debug purposes, the following quantities are written in this order: cell edges, orthogonalizion matrix,
```

```
c                orthogonal coordinates of the molecules in the asymmetric unit, with a flag signalling the order number of the
c                i-th molecule, number of atoms and molecules generated in the cluster, partial energy sums.
c -logical unit 3: this is a quite large file (up to 16 MB for DIEN polymorphs) containing a list of the cartesian coordinates
c                  of all the atoms generated by the cluster construction routine, plus the corresponding symmetry operations.
c -logical unit 4: each molecule-molecule energy contribution, with the corresponding partial energy sums plus symmetry
c                  operations, is written in this file.
c -logical unit 6 (monitor): summary of the energy calculations, with the partial sums, the cohesive energy contribution, and
c                  the final interaction energy estimates.
c
c12345678901234567890123456789012345678901234567890123456789012345678901234567890
c Input example:
c     9.697   12.2426   13.9365    87.182    81.257    82.062
c  180    2    3    5
cwilcowilco
c   60    2
c   60    2
c   60    2
cC   1.24916  -0.13528   1.07705
cN   0.83907   0.18721   0.95126
cH  -0.02115   0.91268   0.51129
c             ...etc...
c    1   0.00000    1   0.00000    1  0.000000
c   -1   0.00000   -1   0.00000   -1  0.000000
c
c
c Current limitations: - up to 100 different symmetry operations.
c                      - up to 10 distinct molecules in the asymmetric unit.
c                      - up to a total of 500 rows of x,y,z fractional coordinates.
c                      - empirically derived potentials defined only for the following elements: C, H, N, O, Cl.
c                      - for Chlorine, only the Spackman's parametrization is available (the program prints a
c                        warning and switches to the latter if the 'wilco' or 'lenna' keywords are used).
c                      - no special parameters are provided for hydrogen, donor and acceptor atoms involved in
c                        hydrogen bonds.
c                      - the program is currently not able to reconstruct a whole molecule from a fragment,
c                        i.e. no connectivity search is performed. So, the coordinates of each WHOLE MOLECULE
c                        in the asymmetric unit have to be input. If more than a molecule is present in the
c                        asymmetric unit, the corresponding atom coordinates have to be grouped together, i.e. the
c                        input file must contain, in sequence, first all the atoms in the first molecule, then
c                        all the atoms in the second molecule, and so on. Different molecules are recognized on
c                        the basis of the above described parameters nmol and natom(i). If a molecule contains
c                        more than a fragment (in other words, if the entire molecule is generated by symmetry),
c                        take care of the parameter nasu(i) above described to correct for over-counting the
c                        same molecular pairs.
c
      program edisp
      character*1 ff
      character*2 spec(10,500)
```

```
      character*5 potdis,potrep
      integer z,zz
      dimension isign(100,3),at(100,3),frac(10,500,3),ortog(10,500,3)
      dimension O(3,3),anew(10,2000,3),natom(10),ivet2(3),vet2(3)
      dimension tx(11),ty(11),tz(11),anort(10,2000,3),vet(3)
      dimension dis(10,10),rep(10,10),ened(10),ener(10),nasu(10)
    1 format(6f10.0)
    2 format(4i5)
    3 format(a2,3f10.5)
    4 format(i5,f10.0,i5,f10.0,i5,f10.0)
    5 format(/,'Cell edges and angles:',6f10.5)
    6 format(3(3f10.5,/))
    7 format(2i5)
    8 format('Molecola:',i5,2x,a2,3f10.5)
    9 format(a2,3f10.5,i5)
   10 format(a2,6f10.5,i4,'X+',f5.2,2x,i4,'Y+',f5.2,2x,i4,'Z+',f5.2,2x)
   11 format('Molecular pair energy contributions:',5f15.5,i3,'X+',f5.2,
     !2x,i3,'Y+',f5.2,2x,i3,'Z+',f5.2,2x)
   12 format('Calculation of interactions for the species: ',2i5)
   13 format(30x,'Total:',2f15.5)
   15 format('Molecule:',i5,2x,'Dispersion contribution to the total int
     !eraction energy:',f10.2,2x,'kJ/mol',/,16x,'Repulsion contribution
     !to the total interaction energy:',1x,f10.2,2x,'kJ/mol',/)
   16 format('Total dispersion and repulsion contributions:',2f15.5,2x,'
     !kJ/mol; Total:',f15.5,2x,'kJ/mol')
   17 format('Molecules:',2i5,2x,'Dispersion contribution:',f10.2,2x,'kJ
     !/mol',2x,'Repulsion contribution:',f10.2,2x,'kJ/mol',2x,'Total:',f
     !10.2,2x,'kJ/mol')
   18 format(a2,6f10.5,i4,2x,f5.2,2x,i4,2x,f5.2,2x,i4,2x,f5.2)
   20 format(2a5)
   21 format('For the pairs involving molecule',i5,2x,'and',i5,', the fo
     !llowing number of atoms was generated:',i9,2x,/,'corresponding to
     !the following total number of molecules:',i5)
   22 format('Cohesive energy(disp), molecule',i5,2x,f10.2,2x,'kJ/mol')
   23 format('Cohesive energy (rep), molecule',i5,2x,f10.2,2x,'kJ/mol')
   24 format(/,'Partial total energy contributions divided by',i6,/)
c
      conv = 0.0174532925199433   !From degree to radians
      bohr = 0.5291772083         !From bohr to Angstroms, not used
      energy = 2625.5             !From au to kJ/mol, not used
c     sqen = sqrt(energy)
c     boh6 = bohr**6
      enum=2.718281828
c     write(6,*) 'Conversion factors:'
c     write(6,*) bohr,energy
c
      ff='N'
      do i=1,11
      tx(i)=0.0
      ty(i)=0.0
      tz(i)=0.0
      enddo
      do k=1,10
       nasu(k)=0
       ened(k)=0.0
       ener(k)=0.0
       do kk=1,10
       dis(k,kk)=0.0
       rep(k,kk)=0.0
       enddo
      enddo
      do i=1,3
      vet(i)=0.0
      ivet2(i)=0
      vet2(i)=0.0
      enddo
      do i=1,500
      spec(k,i)='  '
       do j=1,3
       frac(k,i,j)=0.0
       ortog(k,i,j)=0.0
       enddo
      enddo
      do i=1,100
```

```
       do j=1,3
       isign(i,j)=0
       at(i,j)=0.0
       enddo
      enddo
       do k=1,10
       do i=1,2000
        do j=1,3
        anew(k,i,j)=0.0
        anort(k,i,j)=0.0
        enddo
       enddo
       enddo
      edis=0.0
      erep=0.0
      atotdis=0.0
      atotrep=0.0
      atotsum=0.0
      distot=0.0
      dist=0.0
      reptot=0.0
      sumdis=0.0
      sumrep=0.0
c
      write(2,*) '                      Program EDIS'
      write(2,*) 'evaluation of dispersion and repulsive atom-atom cont
     *ributions'
      write(2,*) 'WARNING: to be used for systems from triclinic to ort
     *horhombic only'
      write(6,*) '                      Program EDIS'
      write(6,*) 'evaluation of dispersion and repulsive atom-atom cont
     *ributions'
      write(6,*) 'WARNING: to be used for systems from triclinic to ort
     *horhombic only'
c
      read(1,1) a,b,c,alpha,beta,gamma
      write(2,5) a,b,c,alpha,beta,gamma
      read(1,2) nat,nsym,nmol,ncell
      write(6,*) '         nat         nsym         nmol       ncell'
      write(6,*) nat,nsym,nmol,ncell
      if(ncell.gt.5) then
      write(6,*) 'Too many cells, increase ncell limit and the correspo
     !nding translation vectors tx,ty,tz in the program'
      goto 14
      endif
      acell=real(ncell)
      itc=ncell*2+1
c     write(6,*) acell,itc
      read(1,20) potdis,potrep
      if(potdis.ne.'wilco'.and.potdis.ne.'spack'.and.potdis.ne.'lenna')
     * then
      write(6,*) 'Dispersion potential unknown'
      goto 14
      endif
      if(potrep.ne.'wilco'.and.potrep.ne.'spack'.and.potrep.ne.'lenna')
     * then
      write(6,*) 'Repulsion potential unknown'
      goto 14
      endif
      write(4,*) 'Potentials and parameters used:'
      write(6,*) 'Potentials and parameters used:'
      if(potdis.eq.'wilco') write(4,*) 'Dispersion: D.Williams & S.Cox,
     ! ActaB,40,404,1984, Edis = -sqrt(a1*a2)/R^6.'
      if(potdis.eq.'spack') write(4,*) 'Dispersion: M.A.Spackman,J.Chem
     !.Phys,85,6579,1986, Edis = -a1*a2/R^6.'
      if(potdis.eq.'lenna') write(4,*) 'Dispersion: J.E. Lennard-Jones,
     ! Proc.Phys.Soc,43,461,1931, Edis = -4*epsilon*(sigma/R)^6.'
      if(potrep.eq.'wilco') write(4,*) 'Repulsion: D.Williams & S.Cox,
     !ActaB,40,404,1984, Erep = sqrt(b1*b2)*e^[(-c1*R-c2*R)/2.]'
      if(potrep.eq.'spack') write(4,*) 'Repulsion: M.A.Spackman,J.Chem.
     !Phys,85,6579,1986, Erep = b1*b2*e^[-c1*R-c2*R]'
      if(potrep.eq.'lenna') write(4,*) 'Repulsion: J.E. Lennard-Jones,
     !Proc.Phys.Soc,43,461,1931, Erep = 4*epsilon*(sigma/R)^12.'
c
```

```
      if(potdis.eq.'wilco') write(6,*) 'Dispersion: D.Williams & S.Cox,
     ! ActaB,40,404,1984, Edis = -sqrt(a1*a2)/R^6.'
      if(potdis.eq.'spack') write(6,*) 'Dispersion: M.A.Spackman,J.Chem
     !.Phys,85,6579,1986, Edis = -a1*a2/R^6.'
      if(potdis.eq.'lenna') write(6,*) 'Dispersion: J.E. Lennard-Jones,
     ! Proc.Phys.Soc,43,461,1931, Edis = -4*epsilon*(sigma/R)^6.'
      if(potrep.eq.'wilco') write(6,*) 'Repulsion: D.Williams & S.Cox,
     !ActaB,40,404,1984, Erep = sqrt(b1*b2)*e^[(-c1*R-c2*R)/2.]'
      if(potrep.eq.'spack') write(6,*) 'Repulsion: M.A.Spackman,J.Chem.
     !Phys,85,6579,1986, Erep = b1*b2*e^[-c1*R-c2*R]'
      if(potrep.eq.'lenna') write(6,*) 'Repulsion: J.E. Lennard-Jones,
     !Proc.Phys.Soc,43,461,1931, Erep = 4*epsilon*(sigma/R)^12'
      write(6,*)
c
      do i=1,nmol
      read(1,7) natom(i), nasu(i)
      enddo
      do k=1,nmol
      do i=1,natom(k)
      read(1,3) spec(k,i),(frac(k,i,j),j=1,3)
      if(spec(k,i).eq.'Cl') spec(k,i)='CL'
c     write(6,8) k,spec(k,i),(frac(k,i,j),j=1,3)
      if(spec(k,i).eq.'CL'.and.potdis.eq.'wilco') goto 700
      if(spec(k,i).eq.'CL'.and.potrep.eq.'wilco') goto 700
      if(spec(k,i).eq.'CL'.and.potdis.eq.'lenna') goto 700
      if(spec(k,i).eq.'CL'.and.potrep.eq.'lenna') goto 700
      goto 701
  700 continue
      if(ff.eq.'Y') goto 701
      ff='Y'
      write(4,*) 'WARNING: parameters for chlorine not defined within t
     !he Williams & Cox and Lennard-Jones potentials.'
      write(4,*) 'The program will switch to Spackman potentials'
      write(4,*) 'M.A.Spackman,J.Chem.Phys,85,6579,1986'
      write(6,*) 'WARNING: parameters for chlorine not defined within t
     !he Williams & Cox and Lennard-Jones potentials.'
      write(6,*) 'The program will switch to Spackman potentials'
      write(6,*) 'M.A.Spackman,J.Chem.Phys,85,6579,1986'
      potdis='spack'
      potrep='spack'
  701 continue
      enddo
      enddo
      do i=1,nsym
      read(1,4)isign(i,1),at(i,1),isign(i,2),at(i,2),isign(i,3),at(i,3)
      enddo
c
c Orthogonalization of coordinates
      rada=alpha*conv
      radb=beta*conv
      radg=gamma*conv
      cosa=cos(rada)
      cosb=cos(radb)
      cosg=cos(radg)
      sena=sin(rada)
      senb=sin(radb)
      seng=sin(radg)
      factor=sqrt(1.0-cosa**2.-cosb**2.-cosg**2.+2.*cosa*cosb*cosg)
      O(1,1)=a
      O(1,2)=b*cosg
      O(1,3)=c*cosb
      O(2,1)=0.00
      O(2,2)=b*seng
      O(2,3)=c*(cosa-cosb*cosg)/seng
      O(3,1)=0.0
      O(3,2)=0.0
      O(3,3)=c*factor/seng
      write(2,*) 'Orthoginalization matrix'
      do i =1,3
      write(2,6) (O(i,j),j=1,3)
      enddo
c
      do k=1,nmol
      do i=1,natom(k)
```

```
        do j=1,3
       ortog(k,i,1)=frac(k,i,1)*O(1,1)+frac(k,i,2)*O(1,2)+frac(k,i,3)*O
     *(1,3)
       ortog(k,i,2)=frac(k,i,1)*O(2,1)+frac(k,i,2)*O(2,2)+frac(k,i,3)*O
     *(2,3)
       ortog(k,i,3)=frac(k,i,1)*O(3,1)+frac(k,i,2)*O(3,2)+frac(k,i,3)*O
     *(3,3)
        enddo
      enddo
      enddo
      write(2,*) 'Orthogonal atom coordinates'
      do k=1,nmol
      do i=1,natom(k)
      write(2,9) spec(k,i), (ortog(k,i,j),j=1,3),k
      enddo
      enddo
      distot=0.0
      reptot=0.0
      sumdis=0.0
      sumrep=0.0
      dis1=0.0
      dis2=0.0
      dis3=0.0
      rep1=0.0
      rep2=0.0
      rep3=0.0
c
      tx(1)=-acell
      ty(1)=-acell
      tz(1)=-acell
      do ju=2,itc
      tx(ju)=tx(ju-1)+1.0
      ty(ju)=ty(ju-1)+1.0
      tz(ju)=tz(ju-1)+1.0
      enddo
c     write(6,*) (tx(ju),ju=1,itc)
c     write(6,*) (ty(ju),ju=1,itc)
c     write(6,*) (tz(ju),ju=1,itc)
c-----------------------------------------------------------------
c Calculation of the molecule-molecule interactions
c---------------------------------
      do z=1,nmol
        do zz=z,nmol
c---------------------------------
      write(4,12) zz,z
      n=0
c
      ktot=0
      do ih=1,nsym
      do i=1,itc
       do j=1,itc
        do k=1,itc
         do n=1,natom(z)
         anew(z,n,1)=frac(z,n,1)*isign(ih,1)+at(ih,1)+tx(i)
         anew(z,n,2)=frac(z,n,2)*isign(ih,2)+at(ih,2)+ty(j)
         anew(z,n,3)=frac(z,n,3)*isign(ih,3)+at(ih,3)+tz(k)
c
         anort(z,n,1)=anew(z,n,1)*O(1,1)+anew(z,n,2)*O(1,2)+anew(z,n,3)
     !*O(1,3)
         anort(z,n,2)=anew(z,n,1)*O(2,1)+anew(z,n,2)*O(2,2)+anew(z,n,3)
     !*O(2,3)
         anort(z,n,3)=anew(z,n,1)*O(3,1)+anew(z,n,2)*O(3,2)+anew(z,n,3)
     !*O(3,3)
c
         write(3,10) spec(z,n),(anort(z,n,jj),jj=1,3),tx(i),ty(j),tz(k),
     !isign(ih,1),at(ih,1),isign(ih,2),at(ih,2),isign(ih,3),at(ih,3)
         ktot=ktot+1
         enddo
        enddo
       enddo
      enddo
      enddo
      nmole=ktot/natom(1)
      write(2,21) z,zz,ktot,nmole
```

```
c
      rewind 3
      edis=0.0
      erep=0.0
      dist=0.0
      req=0.0
      req2=0.0
      epsi=0.0
      epsi2=0.0
      sumdis=0.0
      sumrep=0.0
      adiv=0.0
      do kj=1,nmole
      erep=0.0
c
      do i=1,natom(z)
      read(3,18)  spec(z,i),(anort(z,i,jj),jj=1,3),(vet(jj),jj=1,3),ivet
     !2(1),vet2(1),ivet2(2),vet2(2),ivet2(3),vet2(3)
c     if(z.eq.zz) then
c     if(vet(1).eq.0..and.vet(2).eq.0..and.vet(3).eq.0.) goto 151
c     endif
       if(spec(z,i).eq.'CL') then
       if(potrep.eq.'wilco') bb=1017.157957
       if(potrep.eq.'wilco') cc=1.731
       if(potrep.eq.'spack') bb=1017.157957
       if(potrep.eq.'spack') cc=1.731
       if(potdis.eq.'wilco') aa=73.355
       if(potdis.eq.'spack') aa=73.355
       endif
       if(spec(z,i).eq.'O ') then
       if(potrep.eq.'wilco') bb=230064.10
       if(potrep.eq.'wilco') cc=3.960
       if(potrep.eq.'spack') bb=504.04427078
       if(potrep.eq.'spack') cc=1.899175
       if(potdis.eq.'wilco') aa=1123.600
       if(potdis.eq.'spack') aa=31.9206783
       if(potrep.eq.'lenna'.or.potdis.eq.'lenna') then
       req=3.20
       epsi=0.8372
       endif
       endif
       if(spec(z,i).eq.'N ') then
       if(potrep.eq.'wilco') bb=254529.000
       if(potrep.eq.'wilco') cc=3.780
       if(potrep.eq.'spack') bb=471.86578120
       if(potrep.eq.'spack') cc=1.77445284
       if(potdis.eq.'wilco') aa=1378.400
       if(potdis.eq.'spack') aa=39.78695390
       if(potrep.eq.'lenna'.or.potdis.eq.'lenna') then
       req=3.50
       epsi=0.66976
       endif
       endif
       if(spec(z,i).eq.'C ') then
       if(potrep.eq.'wilco') bb=369743.000
       if(potrep.eq.'wilco') cc=3.6
       if(potrep.eq.'spack') bb=299.54689509
       if(potrep.eq.'spack') cc=1.49855282
       if(potdis.eq.'wilco') aa=2439.800
       if(potdis.eq.'spack') aa=53.37070592
       if(potrep.eq.'lenna'.or.potdis.eq.'lenna') then
       req=4.0
       epsi=0.6279
       endif
       endif
       if(spec(z,i).eq.'H ') then
       if(potrep.eq.'wilco') bb=11971.000
       if(potrep.eq.'wilco') cc=3.740
       if(potrep.eq.'spack') bb=85.10903058
       if(potrep.eq.'spack') cc=1.64595146
       if(potdis.eq.'wilco') aa=136.400
       if(potdis.eq.'spack') aa=10.15174759
       if(potrep.eq.'lenna'.or.potdis.eq.'lenna') then
       req=2.0
```

```
       epsi=0.08372
       endif
       endif
c
        do j=1,natom(zz)
c
        if(spec(zz,j).eq.'CL') then
        if(potrep.eq.'wilco') bbb=1017.157957
        if(potrep.eq.'wilco') ccc=1.731
        if(potrep.eq.'spack') bbb=1017.157957
        if(potrep.eq.'spack') ccc=1.731
        if(potdis.eq.'wilco') aaa=73.355
        if(potdis.eq.'spack') aaa=73.355
        endif
        if(spec(zz,j).eq.'O ') then
        if(potrep.eq.'wilco') bbb=230064.1
        if(potrep.eq.'wilco') ccc=3.960
        if(potrep.eq.'spack') bbb=504.04427078
        if(potrep.eq.'spack') ccc=1.899175
        if(potdis.eq.'wilco') aaa=1123.6
        if(potdis.eq.'spack') aaa=31.9206783
        if(potrep.eq.'lenna'.or.potdis.eq.'lenna') then
        req2=3.20
        epsi2=0.8372
        endif
        endif
        if(spec(zz,j).eq.'N ') then
        if(potrep.eq.'wilco') bbb=254529.000
        if(potrep.eq.'wilco') ccc=3.780
        if(potrep.eq.'spack') bbb=471.86578120
        if(potrep.eq.'spack') ccc=1.77445284
        if(potdis.eq.'wilco') aaa=1378.400
        if(potdis.eq.'spack') aaa=39.78695390
        if(potrep.eq.'lenna'.or.potdis.eq.'lenna') then
        req2=3.50
        epsi2=0.66976
        endif
        endif
        if(spec(zz,j).eq.'C ') then
        if(potrep.eq.'wilco') bbb=369743.000
        if(potrep.eq.'wilco') ccc=3.6
        if(potrep.eq.'spack') bbb=299.54689509
        if(potrep.eq.'spack') ccc=1.49855282
        if(potdis.eq.'wilco') aaa=2439.800
        if(potdis.eq.'spack') aaa=53.37070592
        if(potrep.eq.'lenna'.or.potdis.eq.'lenna') then
        req2=4.0
        epsi2=0.6279
        endif
        endif
        if(spec(zz,j).eq.'H ') then
        if(potrep.eq.'wilco') bbb=11971.000
        if(potrep.eq.'wilco') ccc=3.740
        if(potrep.eq.'spack') bbb=85.10903058
        if(potrep.eq.'spack') ccc=1.64595146
        if(potdis.eq.'wilco') aaa=136.400
        if(potdis.eq.'spack') aaa=10.15174759
        if(potrep.eq.'lenna'.or.potdis.eq.'lenna') then
        req2=2.0
        epsi2=0.08372
        endif
        endif
c
        dist=sqrt((ortog(zz,j,1)-anort(z,i,1))**2+(ortog(zz,j,2)-anort(
     !z,i,2))**2+(ortog(zz,j,3)-anort(z,i,3))**2)
        if(dist.le.0.5) goto 153
c
        if(potdis.eq.'wilco') then
        edis=-sqrt(aa*aaa)/dist**6.0+edis
        endif
        if(potdis.eq.'spack') then
        edis=-aa*aaa/dist**6.0+edis
        endif
        if(potdis.eq.'lenna') then
```

```
        reqt=0.5*(req+req2)
        epsit=sqrt(epsi*epsi2)
        sigma=reqt/(2.0**(1.0/6.0))
        edis=-4*epsit*(sigma/dist)**6.0+edis
        endif
c
        if(potrep.eq.'wilco') then
        erep=sqrt(bb*bbb)*enum**((-cc*dist-ccc*dist)/2.)+erep
        endif
        if(potrep.eq.'spack') then
        erep=bb*bbb*enum**(-cc*dist-ccc*dist)+erep
        endif
        if(potrep.eq.'lenna') then
        reqt=0.5*(req+req2)
        epsit=sqrt(epsi*epsi2)
        sigma=reqt/(2.0**(1.0/6.0))
        erep=4*epsit*(sigma/dist)**12.0+erep
        endif
c
        enddo
        goto 152
  152 continue
      if(erep.eq.NaN) erep=0.0
      if(edis.eq.NaN) edis=0.0
      goto 151
  151 continue
      enddo
c
      write(4,11) edis,erep,(vet(jk),jk=1,3),ivet2(1),vet2(1),ivet2(2),v
     !et2(2),ivet2(3),vet2(3)
c
C Here, before performing the partial summations, each molecular contribution is
C divided by the parameter nasu(z)
C
      adiv=real(nasu(z))
      if(adiv.gt.1.0) then
      edis=edis/adiv
      erep=erep/adiv
      endif
      sumdis=edis+sumdis
      sumrep=erep+sumrep
  153 continue
      edis=0.0
      erep=0.0
      enddo
      write(4,*) '---------------------------------'
c
c Sumdis and sumrep are the PARTIAL dispersive and repulsive contributions
c to the cohesive energy, respectively, i.e. the sum over all molecular contribution
c for each molecular pair (e.g. 1 and 2, 1 and 3, etc.). The total cohesive energy
c of, say, molecule 1, is given by the sum of all the interaction contributions involving
c the molecule 1: this is taken into account by the matrices dis(z,zz) and rep(z,zz).
c
      sumtot=sumdis+sumrep
      if(nasu(z).gt.1) write(4,24) nasu(z)
      write(4,13) sumdis,sumrep
      write(6,17) z,zz,sumdis,sumrep,sumtot
      write(2,17) z,zz,sumdis,sumrep,sumtot
      distot=sumdis+distot
      reptot=sumrep+reptot
      dis(z,zz)=sumdis+dis(z,zz)
      rep(z,zz)=sumrep+rep(z,zz)
  304 continue
      sumdis=0.0
      sumrep=0.0
      rewind 3
c------------------------
      enddo
      enddo
c------------------------
c
      do i=1,nmol
       do j=1,nmol
       dis(j,i)=dis(i,j)
```

```
        rep(j,i)=rep(i,j)
        enddo
       enddo
       write(6,*)
       do i=1,nmol
       do j=1,nmol
       write(2,22) i,dis(i,j)
       write(6,22) i,dis(i,j)
       enddo
       enddo
       write(6,*)
       do i=1,nmol
       do j=1,nmol
       write(2,23) i,rep(i,j)
       write(6,23) i,rep(i,j)
       enddo
       enddo
c
c Sum over rows in matrices dis and rep gives the total cohesive energy, which
c is just two times the interaction energy.
c
       do z=1,nmol
       do i=1,nmol
       ened(z)=dis(z,i)+ened(z)
       ener(z)=rep(z,i)+ener(z)
       enddo
c
c Calculation of the interaction energy of each molecule z.
c
       ened(z)=ened(z)/2.
       ener(z)=ener(z)/2.
       enddo
       write(6,*)
       do z=1,nmol
       write(4,15) z,ened(z),ener(z)
       write(6,15) z,ened(z),ener(z)
       enddo
c
       atotdis=0.0
       atotrep=0.0
       atotsum=0.0
       do z=1,nmol
       atotdis=atotdis+ened(z)
       atotrep=atotrep+ener(z)
       enddo
       atotsum=atotdis+atotrep
       write(4,*)
       write(4,16) atotdis,atotrep,atotsum
       write(6,16) atotdis,atotrep,atotsum
       write(6,*)
       atotdis=0.0
       atotrep=0.0
       atotsum=0.0
       distot=0.0
       reptot=0.0
       sumdis=0.0
       sumrep=0.0
       erep=0.0
c
   14 continue
c
       stop
       end
```