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L-2-Aminobutyric acid: two fully ordered polymorphs with $Z' = 4$

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The crystal structure of L-2-aminobutyric acid, an L-alanine analogue with an ethyl rather than a methyl side chain, has proved elusive owing to problems growing diffraction quality crystals. Good diffraction data have now been obtained for two polymorphs, in space groups $P2_1$ and $I2$, revealing surprisingly complex, yet fully ordered crystalline arrangements with $Z' = 4$. The closely related structures are divided into hydrophilic and hydrophobic layers, the latter being the thinnest ever found for an amino acid (other than α-glycine). The hydrophobic layers furthermore contain conspicuous pseudo-centers-of-symmetry, leading to overall centrosymmetric intensity statistics. Uniquely, the four molecules in the asymmetric unit can be divided into two pairs that each forms an independent hydrogen-bond network.

1. Introduction

The crystal structures of amino acids with side chains devoid of hydrogen-bond donating and/or accepting groups (hydrophobic amino acids) represent an interesting group for studies of the interplay between the formation of favourable hydrogen bonds and proper aggregation of hydrophobic groups. In a recent survey Fábián *et al.* (2008) analysed the hydrogen-bonding patterns in such crystals and identified a series of hydrogen-bonded chain and ring motifs. Usually these structures are divided into hydrophilic and hydrophobic layers, where a hydrophilic layer can be regarded as being composed of two individual, hydrogen-bonded sheets. Görbitz *et al.* (2009) identified five types of sheets, one that contains both L- and D-amino acids, called LD, and four that are constructed from amino acids of one hand only, called L1, L2, L3 and L*x*, when the chirality is L. These sheets in turn generate six types of layers: LD–LD and L1–D1 for racemates or complexes between L- and D-amino acids (pseudo-racemates), as well as L1–L1, L2–L2, L3–L3 and L*x*–L*x* (or corresponding combination of D sheets) for enantiopure compounds. The L2–L2 layer, with $Z' = 2$, was shown to have the most favourable hydrogen-bonding pattern. Some relevant crystal packing arrangements are depicted in Fig. 1.

For any type of hydrophilic layer the thickness (as well as in-layer periodicity) is virtually constant, while for the hydrophobic layers the thickness covers a substantial range as a result of the variable side chains. This is seen in Figs. 1(*a*) and (*b*), which display L2–L2 structures with almost identical hydrophilic layers, but radically different hydrophobic layers. In principle, there is no upper limit to the width of hydrophobic layers, but the lower limit is determined by the ability of the side chains to form a reasonably close-packed

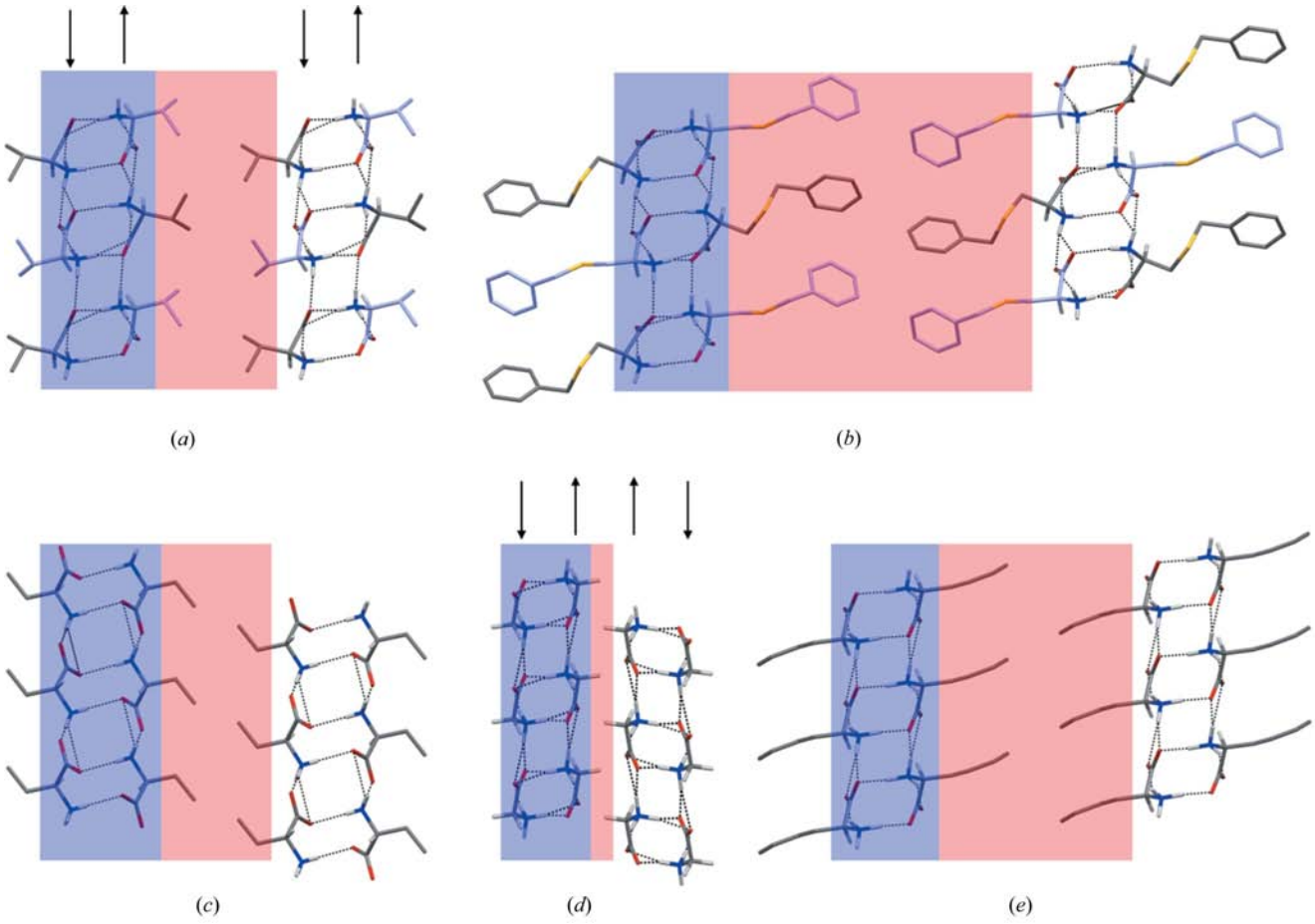
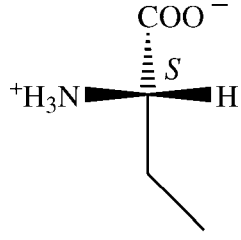


Figure 1
Crystal structures of selected amino acids (same scale). Blue and red rectangles highlight hydrophilic and hydrophobic regions within the crystals. The structures (with layer type in parentheses) are: (*a*) L-Val (=L2–L2; Dalhus & Görbitz, 1996), (*b*) *S*-benzyl-L-Cys (L2–L2; Troup *et al.*, 2001), (*c*) DL-Abu (*A* form) (LD–LD; Voogd & Derissen, 1980), (*d*) α-Gly (L1–D1; Langan *et al.*, 2002), (*e*) L-Nle (L*x*–L*x*; Torii & Iitaka, 1973). H atoms bonded to C have been left out for clarity. When there are two molecules in the asymmetric unit, as for (*a*) and (*b*), C atoms of one molecule are coloured in light blue. Arrows in (*a*) and (*d*) indicate the directions of head-to-tail hydrogen-bonded chains involving the amino and carboxylate groups.

arrangement without sizeable voids. This can evidently be achieved by the isopropyl side chain of L-Val (Fig. 1*a*), while the methyl side chain of alanine, in the racemate (Subha Nandhini *et al.*, 2001) as well as the pure enantiomer (Destro *et al.*, 1988), prefers the formation of one-dimensional hydrophobic columns surrounded by a three-dimensional hydrogen-bonding pattern. The efficiency of the molecular packing is reflected by crystal density; for the experimental $P2_12_12_1$ structure of L-Ala values in the range 1.378–1.405 g cm^{-3} were obtained for temperatures between 298 (Lehmann *et al.*, 1972) and 23 K (Destro *et al.*, 1988), while the density of a predicted, higher-energy layered polymorph of L-Ala is only 1.205 g cm^{-3} (Cooper *et al.*, 2007; Day, 2009).

How about 2-aminobutyric acid (Abu) with an ethyl side chain? The racemate, DL-Abu, has a tetragonal polymorph (*B*) with hydrophobic columns (Voogd & Hulscher, 1980) as well as three known monoclinic polymorphs *A*, Fig. 1(*c*) (Voogd & Derissen, 1980), *C* (Akimoto & Iitaka, 1972) and *D* (Nakata *et al.*, 1980) that are all divided into layers. The hydrophobic layers in these structures are among the thinnest found for amino acid structures.



(I)

The crystal structure of L-Abu (I) has conspicuously been missing from the series of known amino acid structures because of obstacles in obtaining suitable single crystals. This, together with the known disorder problems for the racemate, suggests that L-Abu could be a borderline case for the formation of hydrophobic layers. The solid-state structure of L-Abu is the focus of the present investigation.

Table 1
Experimental details.

For all structures: $C_4H_9NO_2$, M_r = 103.12. Experiments were carried out at 110 K with Mo $K\alpha$ radiation using a Bruker Apex II CCD diffractometer. Absorption was corrected for by multi-scan methods, *SADABS* (Bruker, 2007*c*). Refinement was on 261 parameters with 1 restraint. H-atom parameters were constrained.

	α form	β form
Crystal data		
Crystal system, space group	Monoclinic, $P2_1$	Monoclinic, $I2$
a, b, c (Å)	9.614 (6), 5.227 (3), 21.385 (13)	9.646 (2), 5.2145 (12), 42.885 (10)
β (°)	100.326 (7)	100.295 (3)
V (Å^3)	1057.1 (11)	2122.5 (8)
Z	8	16
μ (mm^{-1})	0.10	0.10
Crystal size (mm)	1.10 × 0.34 × 0.10	0.40 × 0.32 × 0.18
Data collection		
T_{min}, T_{max}	0.749, 0.990	0.791, 0.982
No. of measured, independent and observed [$I > 2\sigma(I)$] reflections	6460, 2700, 2468	7238, 2083, 1852
R_{int}	0.042	0.031
Refinement		
$R[F^2 > 2\sigma(F^2)]$, $wR(F^2)$, S	0.058, 0.165, 1.12	0.044, 0.120, 1.05
No. of reflections	2700	2083
$\Delta\rho_{max}$, $\Delta\rho_{min}$ (e Å^{-3})	0.37, −0.26	0.26, −0.25

Computer programs used: *APEX*2 (Bruker, 2007*a*), *SAINT-Plus* (Bruker, 2007*b*), *SHELXTL* (Sheldrick, 2008).

2. Experimental

2.1. Crystal preparation and structure determination

Crystals in the shape of blocks or plates were grown by several methods, including slow evaporation and equilibration of an aqueous solution against acetonitrile by vapour diffusion. Although many crystals looked good in a polarizing microscope, the diffraction properties were generally poor resulting in broad and partly overlapping reflections. A data set was collected for one specimen and yielded a unit cell with dimensions a = 42.241 (10), b = 5.2145 (12), c = 9.690 (2) Å and β = 92.690 (3)°. Systematic absences indicated that the space group was monoclinic $C2$, and the structure was apparently solved without problems by the *XS* module of *SHELXTL* (Sheldrick, 2008), but subsequent refinement led to a badly disordered structure with R = 0.138. Continued crystallization efforts employed a mixture of 80% water and 20% tetramethoxysilane (TMS; total volume 1.0 ml) rather than pure water as the solvent. After vigorous stirring for ∼1 min, the mixture was left to polymerize into a gel (1 h), whereupon equilibration against acetonitrile proceeded as before. A crystal obtained this way, visually not different from other ones in the same tube, was shown to have a $P2_1$ unit cell, from now on referred to as the α form, with half the volume of the $C2$ cell. This crystal was incidentally the only one tested with this symmetry. Afterwards, the crystal structure of the original $C2$ polymorph (β form) was solved again, this time by the *XM* module of *SHELXTL*, which produced a fully ordered structure on refinement. The $C2$ unit cell was later abandoned in favour of the more unconventional $I2$ setting in order to facilitate direct comparison between the two polymorphs. Below, when data are given for both the α form and the β form, a slash (/) is used to separate the two with α first.

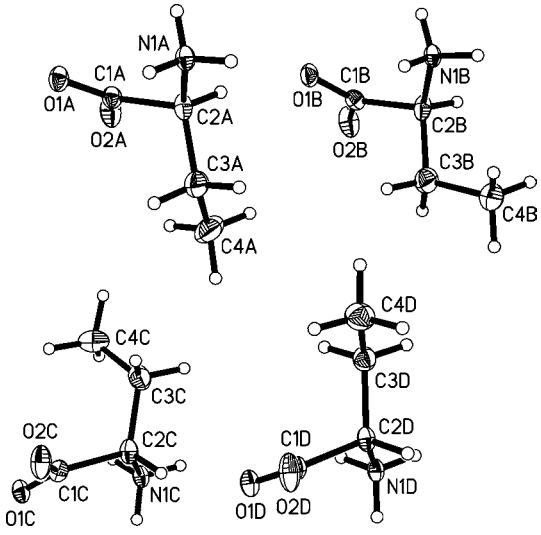


Figure 2
The asymmetric unit of L-Abu (α form) with atomic numbering. Displacement ellipsoids have been drawn at the 50% probability level and H atoms are shown as spheres of arbitrary size. The asymmetric unit of the β form is almost indistinguishable from that of the α form (drawing available as supplementary material).

2.2. Data collection and structure refinement

Data were collected by measuring three sets of exposures at 110 K with the detector set at 2θ = 29°. The exposure time was 30 s and the crystal-to-detector distance 6.00 cm. Both structures, with Z' = 4, were refined without constraints or restraints on C, N or O positions. H atoms were positioned with idealized geometry with fixed N—H = 0.91 Å and C—H = 0.98 (methyl), 0.99 (methylene) or 1.00 Å (methine), while permitting free rotation of methyl and amino groups. U_{iso} values were set to $1.2U_{eq}$ of the carrier atom, or $1.5U_{eq}$ for amino and methyl groups. In the absence of significant anomalous scattering effects, 1473/1532 (α/β) Friedel pairs were merged. Experimental details are given in Table 1.

3. Results and discussion

3.1. Molecular and crystal structure

Fig. 2 shows the highly variable side-chain orientations of the four independent molecules in the asymmetric unit; N1—C2—C3—C4 is *gauche*+ for molecule C [64.2 (4)/64.4 (4)°], *trans* for molecules A [−168.6 (3)/−173.1 (3)°] and D

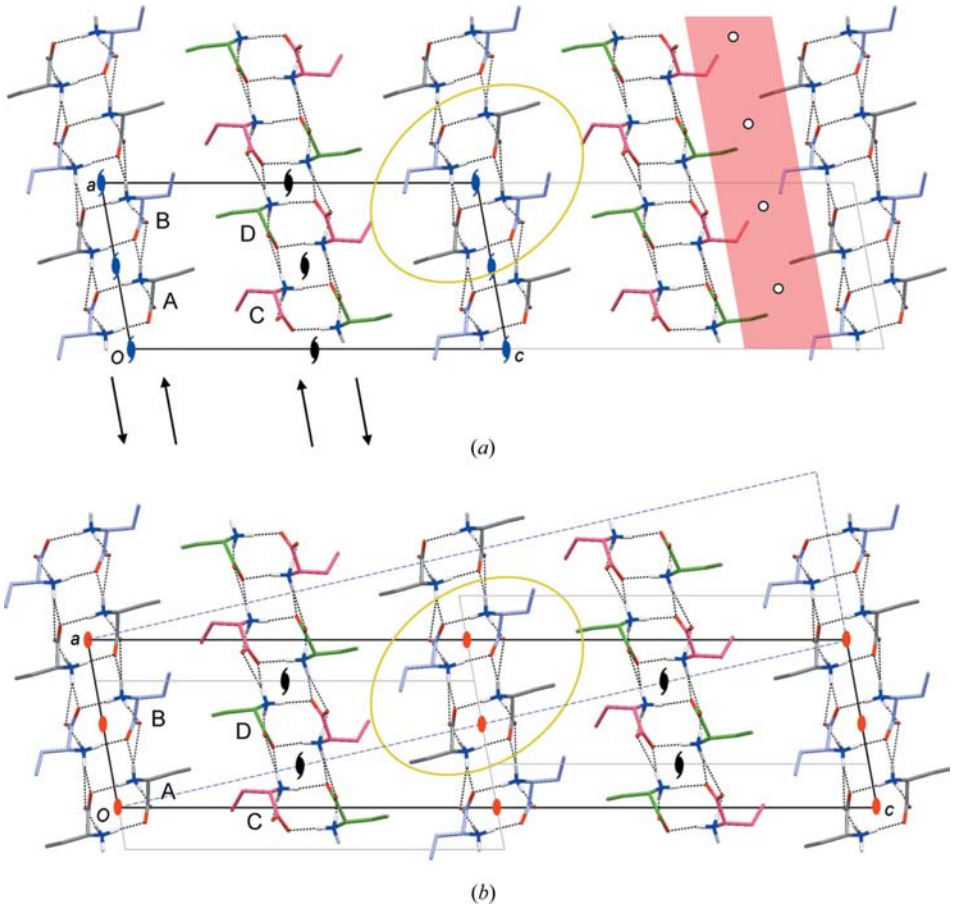


Figure 3
L-Abu unit cell and crystal-packing arrangements for (*a*) the $P2_1$ α form and (*b*) the $I2$ β form, both viewed along the *b* axis. Side-chain H atoms have been left out for clarity, C atoms are coloured according to molecule: *A* = grey, *B* = light blue, *C* = pink, *D* = green. As in Fig. 1, a hydrophobic layer has been coloured in red in (*a*), the small circles indicate pseudo-centers-of-symmetry. One additional unit cell is shown in light grey in (*a*), in (*b*) the unit-cell content of the α form is indicated twice in a similar manner. The dashed, violet unit cell in (*b*) shows the conventional *C*2 setting of this polymorph with a 42.241 (10) Å *a* axis (see above). Symbols for symmetry elements are depicted in black when common to both polymorphs, or in blue or red when present only in the α form or β form, respectively. Orange ellipses highlight hydrogen-bonded heterodimers in (*a*) and homodimers in (*b*). Arrows in (*a*) are used as in Fig. 1.

[−175.6 (3)/−173.7 (3)°] and *gauche*− for molecule *B* [−55.5 (4)/−55.7 (4)°]. The main effect of this unusual combination of torsion angles is the introduction of remarkable pseudo-centers-of-symmetry in the hydrophobic layers. One such center can be seen in Fig. 2, but they become very obvious in the packing diagrams in Fig. 3. This pseudo-symmetry is extensive; only the carboxylate groups do not obey it. As a result, the intensity statistics suggest centrosymmetric space groups (observed $|E^2 - 1|$ = 0.917/0.930, theoretical centrosymmetric = 0.968, non-centrosymmetric = 0.736). Additionally, similar molecular geometries (except *C*4) within the asymmetric unit means that both unit cells are pseudo-*C*-centered (see supplementary material[1]). In the experimental data for the α form, this is manifested by reflections with $h + k$ = even having, on average, 7.3 times higher intensity than reflections with $h + k$ = odd.

Any disorder in side-chain orientation between molecule *A* and *B* or between *C* and *D* for either polymorph in Fig. 3 would blur the difference between them, and given how similar they are it is in fact surprising that no signs of side-chain disorder could be detected.

Conceptually, the structure of the α form may be converted to the β form, as shown in Fig. 4, where every second stack of unit cells along the *c* axis slides one half of a unit-cell length along the *a* axis. The full unit-cell content of the α polymorph is thus retained in the β polymorph, and the Materials module of *Mercury* (Macrae *et al.*, 2008), which quantifies the similarity in molecular packing between crystal structures, yields an r.m.s. deviation of 0.066 Å for the comparison of two clusters of 15 molecules, with a remarkable similarity of 0.998 between the calculated powder X-ray diagrams (p.x.r.d.; see supplementary material). Under normal circumstances, such figures would indicate the two structures to be identical.

The effect on crystallographic symmetry upon transition from the α to the β polymorph is also seen in Fig. 4; one half of the twofold screw axes of the α form is undisturbed, while the second half is lost. Instead a corresponding series of regular twofold rotation axes are generated, in nearly the same positions, but shifted $\frac{1}{4}$ of a unit-cell length along the *a* axis. A series of CSD searches (Allen, 2002) did not reveal any other pairs of polymorphs with Z' = 4 incorporating this type of relationship. Both crystal forms appear to be stable indefinitely at ambient conditions, so there is no indication that this sliding process actually takes place in true crystals.

An additional peculiarity of L-Abu becomes evident from a comparison between Fig. 3 and Fig. 1: while other structures have just one type of hydrophilic layer with hydrogen bonds, both L-Abu polymorphs have two (but only one type of hydrophobic layer, as the others). For compounds with only a very limited number of hydrogen-bond donating and accepting groups, the formation of crystal structures with one-dimensional hydrogen-bonded *chains* is generally quite common (in addition to dimers), and when $Z' \geq 2$ the inde-

[1] Supplementary data for this paper are available from the IUCr electronic archives (Reference: PS5004). Services for accessing these data are described at the back of the journal.

Table 2
Hydrogen-bonding patterns and thickness d (Å) of hydrophilic and hydrophobic layers in amino-acid crystal structures.

Compound	Refcode†	Hydrogen bonding‡	d(h.phil)	d(h.phob)	Ref.
L-Abu (α form)	–	Lx–Lx	5.62, 5.40§	5.01	This work
L-Abu (β form)	–	Lx–Lx	5.63, 5.41§	5.03	This work
L-Nle	LNLEUC10	Lx–Lx	5.49	9.82	(*a*)
L-Cys (mon)	LCYSTN04	L2–L2	5.50	5.22	(*b*)
L-Val	LVALIN01	L2–L2	5.61	6.32	(*c*)
S-Benzyl-L-Cys	ICAMOO	L2–L2	5.71	15.62	(*d*)
DL-Abu (A)	DLABUT05	LD–LD	6.07	5.61	(*e*)
DL-Abu (C)	DLABUT02	LD–LD	5.92	5.60	(*f*)
DL-Abu (D)	DLABUT03	LD–LD	6.10	5.72	(*g*)
DL-Cys	BOQCUF	LD–LD	6.17	5.76	(*h*)
Gly (α form)	GLYCIN21	L1–D1	4.98	1.00¶	(*i*)
DL-Val (mon)	VALIDL	L1–D1	5.00	6.05	(*j*)
DL-Val (tri)	VALIDL03	L1–D1	4.95	5.87	(*k*)

References: (*a*) Torii & Iitaka (1973); (*b*) Görbitz & Dalhus (1996); (*c*) Dalhus & Görbitz (1996); (*d*) Troup *et al.* (2001); (*e*) Voogd & Derissen (1980); (*f*) Akimoto & Iitaka (1972); (*g*) Nakata *et al.* (1980); (*h*) Luger & Weber (1999); (*i*) Langan *et al.* (2002); (*j*) Mallikarjunan & Rao (1969); (*k*) Flaig *et al.* (2002). † Cambridge Structural Database, Version 6.31 of November 2009 (Allen, 2002). ‡ Pattern according to classification by Görbitz *et al.* (2009). § *AB* and *CD* layer, respectively. ¶ Calculated by replacing the side-chain H atom with a C atom and using the midpoint of the new 1.541 Å Cα—Cβ bond as the region border.

pendent molecules may occasionally also form independent chains. A typical example with $Z' = 3$ is found for 2-isopropyl-5-methyl-cyclohexanol (CSD: BAVLOZ, Bombicz *et al.*, 1999) with homomeric $\cdots A\cdots A\cdots$, $\cdots B\cdots B\cdots$ and $\cdots C\cdots C\cdots$ chains. Structures with two (or more) independent two-dimensional hydrogen-bonded *layers* appear, however, to be very rare, but 4-((*E*)-2-(4-chlorophenyl)ethenyl)-(1,3,5)triazino(1,2-*a*)benzimidazol-2-amine is another example (also with $Z' = 4$; CSD: EFOMUI, Suvorova *et al.*, 2007).[2] Among amino acid and peptides with $Z' > 1$ L-Abu is probably the first compound with two such layers.

3.2. Hydrophobic layers

Using the midpoints of the Cα—Cβ bonds as reference points and borders between hydrophobic and hydrophilic regions in the crystals, it is easy to compute the thickness of hydrophilic and hydrophobic layers in various amino acid structures as shown in Fig. 1. Selected results are given in Table 2.

Calculating molecular volumes from V/Z, a much smaller value is obtained for DL-Val (143.9 Å^3) than for L-Val (151.1 Å^3), which translates into a corresponding difference in crystal density (1.352 *versus* 1.284 g cm^{-3}). In contrast, L-Abu has a significantly higher density than its racemate, 1.296/1.291 *versus* 1.247 g cm^{-3} (*A* form), and consequently occupies a smaller average molecular volume, 132.1/132.7 *versus* 137.3 Å^3. This is a direct result of the very efficient stacking of L-Abu side chains within 5.01/5.03 Å hydrophobic layers (Table 2), the smallest values ever recorded for crystal structures of enantiomeric amino acids, racemates or pseudo-racemic 1:1 complexes between L- and D-amino acids (Dalhus & Görbitz, 1999*a*,*b*).[3]

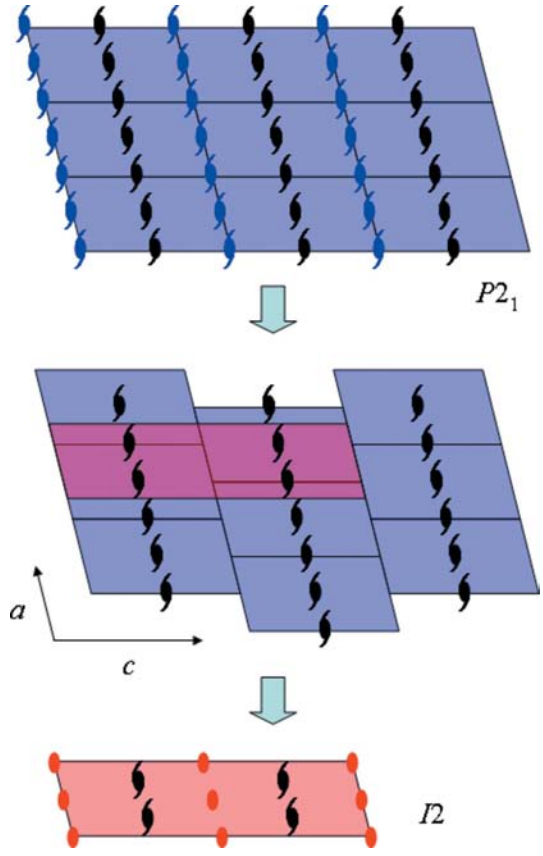


Figure 4
Schematic illustration of a hypothetical conversion of the $P2_1$ α form to the $I2$ β form by sliding every second stack of molecules along the c axis half a unit cell along the a axis. Symmetry elements are displayed as in Fig. 3.

Values for the three LD–LD layered polymorphs of DL-Abu are in the range 5.60–5.72 Å, with slightly thicker 5.92–6.10 Å hydrophilic layers. After L-Abu, the thinnest hydrophobic layers, 5.22 Å, are found for the monoclinic L2–L2 polymorph of L-Cys, which can be regarded as an analogue of L-Abu with terminal —SH rather than —CH$_3$. A full hydrophobic layer is generated from two identical half-layers in the case of L-Cys, while for L-Abu a half-layer is joined with its approximate mirror image, giving the pseudo-centers-of-symmetry as discussed above. An illustration showing the similarity between side-chain stacking in these two structures together with L-Val is available as supplementary material.

3.3. Hydrogen bonds

The two molecules in the asymmetric unit of L2–L2 structures not only have different side-chain orientations, but also slightly different hydrogen-bonding interactions, as shown for L-Val (Dalhus & Görbitz, 1996) in Fig. 5(*a*).

[2] Computer programs for automated search for hydrogen-bond motifs in crystal structures have been developed and may be useful for locating such systems (Fábián *et al.*, 2008).

[3] The predicted *C*2 polymorph of L-Ala with Lx–Lx layers and $Z' = 1$ (Cooper *et al.*, 2007; Day, 2009) in comparison has 4.221 Å hydrophobic layers.

Table 3
Hydrogen-bond distances (Å) and angles (°) in the L*x*–L*x* structures of L-Abu (*α* form) and L-Nle (Torii & Iitaka, 1973), Fig. 1(*d*).

Data for the *β* form of L-Abu, available as supplementary material, are very similar, except that the acceptors for H1*A* and H1*B* are O1*A* and O1*B*.

	H···O	N···O	N—H···O
N1*A*—H1*A*···O1*B*^{i}	1.88	2.754 (4)	160
N1*A*—H2*A*···O1*B*^{ii}	1.92	2.796 (4)	160
N1*A*—H3*A*···O2*A*^{ii}	1.86	2.747 (4)	165
N1*B*—H1*B*···O1*A*^{iii}	1.92	2.814 (4)	165
N1*B*—H2*B*···O1*A*^{iv}	1.92	2.803 (3)	164
N1*B*—H3*B*···O2*B*^{ii}	1.89	2.781 (4)	168
N1*C*—H1*C*···O1*D*^{v}	1.93	2.815 (4)	163
N1*C*—H2*C*···O2*C*^{v}	1.91	2.799 (4)	163
N1*C*—H3*C*···O1*D*^{vi}	1.97	2.819 (4)	154
N1*D*—H1*D*···O1*C*^{iv}	1.95	2.813 (3)	159
N1*D*—H2*D*···O2*D*^{v}	1.87	2.762 (4)	165
N1*D*—H3*D*···O1*C*^{vii}	1.90	2.771 (4)	161
N1—H1···O1^{viii}†	1.93	2.792 (6)	159
N1—H2···O1^{ix}	1.92	2.813 (5)	165
N1—H3···O2^{v}	1.92	2.799 (6)	163

Symmetry codes: (i) $1-x, y+\frac{1}{2}, -z$; (ii) $x, y+1, z$; (iii) $1-x, y-\frac{1}{2}, -z$; (iv) $x+1, y, z$; (v) $x, y-1, z$; (vi) $1-x, y-\frac{1}{2}, 1-z$; (vii) $1-x, y+\frac{1}{2}, 1-z$; (viii) $1-x, y, 1-z$; (ix) $\frac{1}{2}+x, y-\frac{1}{2}, z$. † L-Nle: Atom names modified to be compatible with the present investigation, N—H distances normalized to 0.91 Å.

The four independent molecules of L-Abu also have different side-chain rotamers, but their involvements in hydrogen bonds are almost indistinguishable, Fig. 5(*b*) and Table 3. Essentially, the interactions of each molecule can be regarded as an average between the two molecules in the L2 sheet (Görbitz *et al.*, 2009), with a particularly short interaction to the *anti* lone pair of carboxylate atom O2, 1.885 and 1.858 Å in Fig. 5(*a*). This is what characterizes an L*x* sheet, and the hydrogen-bonding energy of the resulting L*x*–L*x* layers has been calculated to be almost on the same level as the L2–L2 layers of L-Val and other acids (Görbitz *et al.*, 2009). The L*x*–L*x* layers are, however, sterically incompatible with any side-chain branching at C$^{\beta}$ or C$^{\gamma}$, and they have previously been found only for L-norleucine (L-Nle; Torii & Iitaka, 1973), Fig. 1(*e*), and the dimeric amino acids L-cystine (—CH_2—S—S—CH_2— link; Dahaoui *et al.*, 1999) and L-lanthionine (—CH_2—S—CH_2— link; Desiraju & Rao, 1990), all with Z' = 1. The hydrogen-bond parameters of these four structures are very similar (only L-Nle is included in Table 3). The only other amino acid structure with two different molecules sharing the same set of hydrogen bonds is L-4-fluoro-Phe (In *et al.*, 2003). As for L-Phe (Weissbuch *et al.*, 1990), its aromatic side chain is incompatible not only with the L*x*–L*x* pattern but, due to excessive steric conflict, also with the common L2–L2 pattern. These compounds instead use the alternative higher energy L1–L1 hydrogen-bonding pattern (Görbitz *et al.*, 2009).

A characteristic property observed for regular layered structures of chiral amino acids is the persistent formation of hydrogen-bonded dimers. In structures with Z' = 2 such dimers are always formed between different molecules, *e.g.* the *A*–*B* dimers seen for L-Val in Fig. 1(*a*). Such heterodimers are also found in the *α* form of L-Abu, Fig. 2(*a*). The *β* form, on the other hand, contains not only *C*–*D* heterodimers, but also *A*–*A* and *B*–*B* homodimers, as highlighted in Fig. 2(*b*). These are the first homodimers found in a structure with $Z' > 1$.

Finally, in all crystal structures of amino acids with a layered structure type, the N—H···O(*syn*) head-to-tail hydrogen-bonded chains of partner sheets within a hydrophilic layer have an antiparallel arrangement; Fig. 1 gives five examples. Less obvious is the antiparallel arrangement of such chains on opposite sides of a hydrophobic layer, as indicated for L-Val in Fig. 1(*a*). Among more than 70 previously investigated layered amino acid structures, only two have parallel chains, *α*-Gly shown in Fig. 1(*d*) (Langan *et al.*, 2002) and a complex between L-Val and L-Met (Dalhus & Görbitz, 1999*b*). The structures of L-Abu shown in Fig. 3 are thus rare examples of packing arrangements with parallel neighbour chains across a hydrophobic layer.

3.4. Conclusion

In conclusion, the two polymorphs of L-Abu distinguish this amino acid in many ways from other hydrophobic amino acid structures. The crystal-packing arrangements, both with Z' = 4, uniquely involve two independent hydrogen-bonded layers, as well as very slim hydrophobic layers with remarkable pseudo-centers-of-symmetry. In a rare fashion, the hydrophobic layers

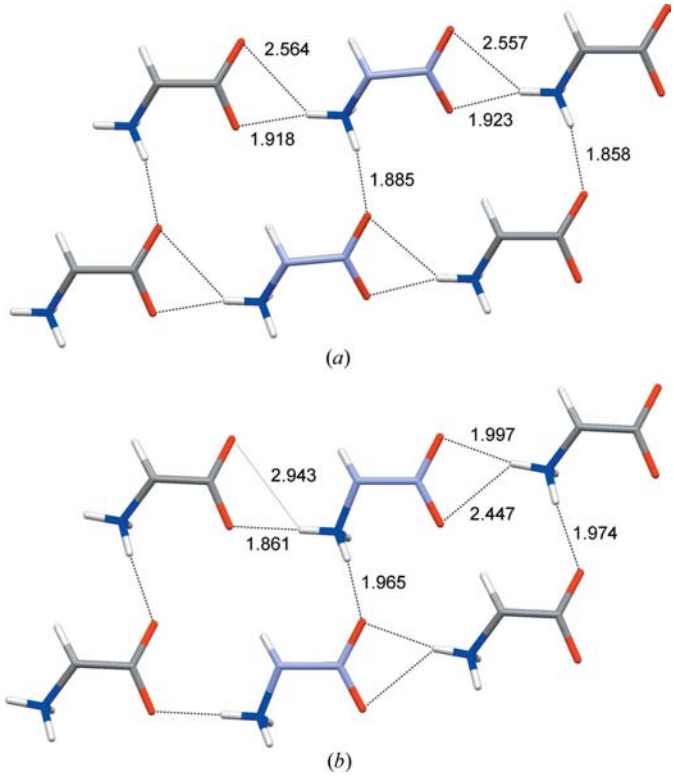


Figure 5
Hydrogen bonding in (*a*) an L*x* sheet of L-Abu (*A* and *B* molecules of the *α* form, the corresponding L*x* sheets generated by *C* and *D* molecules in the same structure are virtually identical as are both types of sheets in the *β* form) and (*b*) in the L2 sheet of L-Val (Dalhus & Görbitz, 1996). Side chains have been removed for clarity. Hydrogen-bond distances are indicated. For L-Val N—H distances were adjusted to 0.91 Å (as used in both refinements of L-Abu) to make values in (*a*) and (*b*) directly comparable.

are bordered by parallel rather than antiparallel head-to-tail hydrogen-bonded chains involving the charged amino and carboxylate groups. The hydrogen-bonding patterns within hydrophilic layers all belong to the L*x*–L*x* class (Görbitz *et al.*, 2009), found previously only for three other amino acids with unbranched side chains. The special relationship between the $P2_1$ and $I2$ polymorphs (described as the sliding of every second stack of molecules along the *c* axis of the former half a unit cell along the *a* axis to obtain the latter) is probably observed here for the first time for organic molecules with $Z' = 4$.

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