In the title compound, C₁₈H₂₁NO₃, the oxazolidine ring adopts an envelope conformation with the N atom at the flap position. The two benzene rings make dihedral angles of 74.27 (14) and 73.26 (15)° with the mean plane through the oxazolidine ring. In the crystal structure, O—H⋯O and C—H⋯O hydrogen bonds connect adjacent molecules into chains along [010] incorporating R₂(8) loops and further stabilization is provided by weak intermolecular C—H⋯π interactions.

Related literature

For general background to and applications of the title oxazolidine compound, see: Fitzgerald et al. (2004); Kamat et al. (2000); Kumar et al. (2004); Walton et al. (2003). For graph-set descriptions of hydrogen-bond ring motifs, see: Bernstein et al. (1995). For a related structure, see: Duffy et al. (2004). For bond-length data, see: Allen et al. (1987). For the stability of the temperature controller used for the data collection, see: Cosier & Glazer (1986).

Experimental

Crystal data

C₁₈H₂₁NO₃

M_r = 299.36

Orthorhombic, P₂₁₂₁₂₁

a = 7.8893 (6) Å

b = 11.7697 (9) Å

c = 17.4392 (13) Å

V = 1619.3 (2) Å³

Z = 4

Mo Kα radiation

μ = 0.08 mm⁻¹

T = 120 K

0.31 × 0.15 × 0.15 mm

Data collection

Bruker SMART APEXII CCD diffractometer

9140 measured reflections

2131 independent reflections

1622 reflections with I > 2σ(I)

R_{int} = 0.067

Refinement

R[F²] = 0.043

wR(F²) = 0.096

S = 1.07

2131 reflections

206 parameters

H atoms treated by a mixture of independent and constrained refinement

Δρ_{max} = 0.19 e Å⁻³

Δρ_{min} = −0.21 e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

Cg₁ is the centroid of the C10–C15 phenyl ring.

<table>
<thead>
<tr>
<th>D—H⋯A</th>
<th>D—H</th>
<th>H⋯A</th>
<th>D⋯A</th>
<th>D—H⋯A</th>
</tr>
</thead>
<tbody>
<tr>
<td>O1—H1O1⋯O3'</td>
<td>0.92 (4)</td>
<td>2.08 (3)</td>
<td>2.90 (3)</td>
<td>148 (3)</td>
</tr>
<tr>
<td>C5—H5A⋯O1''</td>
<td>0.93</td>
<td>2.42</td>
<td>3.24 (3)</td>
<td>148</td>
</tr>
<tr>
<td>C16—H16A⋯Cg1'</td>
<td>0.96</td>
<td>2.91</td>
<td>3.62 (3)</td>
<td>133</td>
</tr>
</tbody>
</table>

Symmetry codes: (i) −x+1, y+1, z (ii) −x+1, y+1, −z+1 (iii) −x+1, y−1, z

Data collection: APEX2 (Bruker, 2009); cell refinement: SAINT (Bruker, 2009); data reduction: SAINT; program(s) used to solve structure: SHELXTL (Sheldrick, 2008); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL and PLATON (Spek, 2009).

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