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Key indicators

Single-crystal X-ray study
 $T = 100$ K
Mean $\sigma(C-C) = 0.004$ Å
 R factor = 0.046
 wR factor = 0.113
Data-to-parameter ratio = 11.8For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.**(+)-14 β a-3-Oxoglycyrrhetic acid: catemeric
hydrogen bonding in a non-racemic triterpenoid
diketo acid**

The title compound, (+)-10,13-dioxo-2 α ,4 α β ,6 $\alpha\alpha$,6 β β ,9,9,12 α β -heptamethyl-1,2,3,4,4a,5,6,6a,6b,7,8,8 $\alpha\alpha$,9,10,11,12,12a,12 $\beta\alpha$,-13,14 $\beta\alpha$ -eicosahydricene-2 β -carboxylic acid, $C_{30}H_{44}O_4$, aggregates as carboxyl-to-ketone hydrogen-bonding catemers. Hydrogen bonds progress from the carboxyl group of one molecule to the remote-ring ketone group of a translationally related neighbor in an adjoining cell connected by a common a cell-edge [$O \cdots O = 2.766(3)$ Å and $O-H \cdots O = 163^\circ$], yielding chains that extend in the [011] direction. In the crystal structure, there are also four $C-H \cdots O$ close contacts.

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Comment

Our study of hydrogen bonding in ketocarboxylic acids encompasses crystalline compounds as small as C_6 and as large as C_{30} . The title compound, (I), is a picenoid triterpene derived from the aglycone portion of glycyrrhizic acid, isolated from licorice root (*Glycyrrhiza glabra* L.). It is a rigid, chiral, nonracemic ζ,λ -diketo acid, and we report here that (I) adopts the carboxyl-to-ketone catemeric hydrogen-bonding mode in the solid.

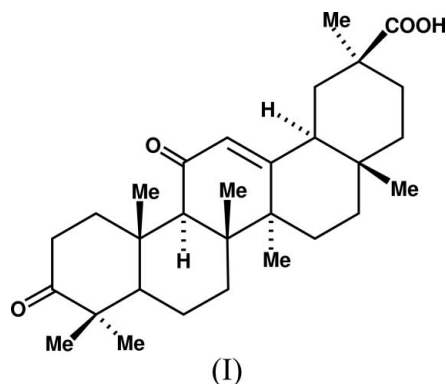


Fig. 1 shows the molecular structure of (I), with numbering based on the pentacyclic aromatic, plicene. All the rings adopt chair conformations except the enone ring, which is necessarily flattened to a half-chair, and all the ring junctures are *trans* except that involving the enone. The conformation of the carboxyl-substituted ring places its carboxyl group equatorial, with both its methyl groups axial. The carboxyl group is rotated as shown in Fig. 1, so that the C1–C2–C15–O3 torsion angle is 6.8 (5)°.

The catemeric hydrogen-bonding geometry in (I) precludes the averaging mechanisms that underlie the disordering of C–O bond lengths and C–C–O angles in carboxyl dimers.

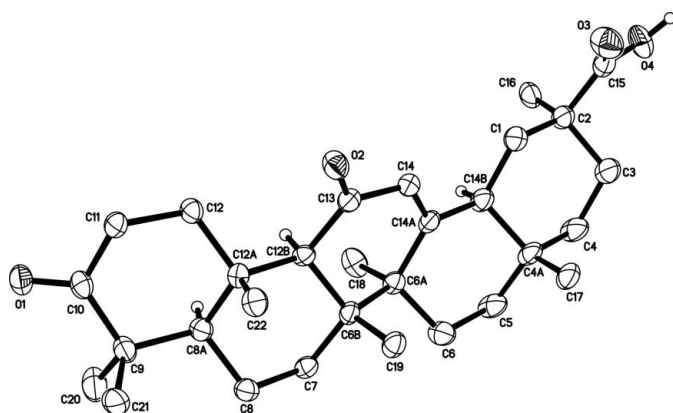


Figure 1

The molecular structure of (I). Displacement ellipsoids are shown at the 40% probability level. For clarity, all methyl and methylene H atoms have been omitted, but methine H atoms are retained to show the stereochemistry.

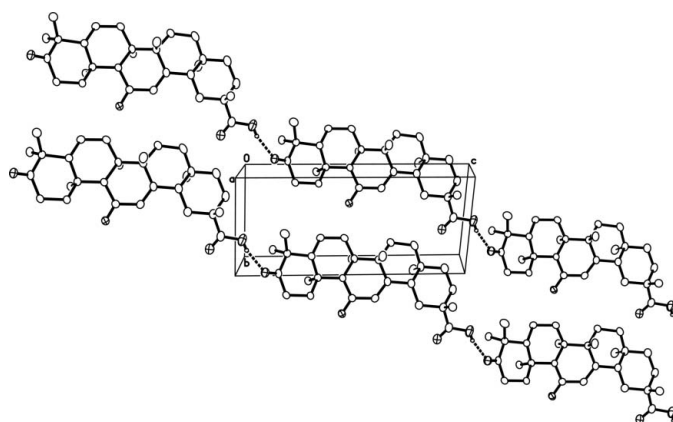


Figure 2

A partial packing diagram for (I), illustrating the catemeric hydrogen bonding. For clarity, all carbon-bound H atoms have been omitted. Displacement ellipsoids are shown at the 40% probability level. Hydrogen bonds are shown as dashed lines.

Hence, in (I) these values (Table 1) resemble those in other highly ordered carboxylic acids (Borthwick, 1980).

Fig. 2 shows the packing arrangement. Carboxyl-to-ketone hydrogen bonds among translationally related molecules produce chains that extend in the [011] direction. We characterize the geometry of this hydrogen bonding using a combination of the $\text{H}\cdots\text{O}=\text{C}$ angle and the $\text{H}\cdots\text{O}=\text{C}-\text{C}$ torsion angle. These describe the approach of the H atom to the receptor O in terms of its deviation from, respectively, $\text{C}=\text{O}$ axiality (ideal = 120°) and planarity with the carbonyl group (ideal = 0°). In (I), these angles are $\text{H4}-\text{O1A}-\text{C10A} = 139^\circ$ and $\text{H4}-\text{O1A}-\text{C10A}-\text{C9A} = 7^\circ$. By contrast, the isomer of (I) we have previously described (Brunskill *et al.*, 1999) has β (*cis*) stereochemistry at C14B, which produces a marked molecular curvature and an axial carboxyl group, leading to hydrogen bonding seriously distorted from coplanarity, described by approach angles of 127 and -52° . This distortion from ideal angles in the case of the *cis* epimer is not

reflected in the packing efficiencies of the two compounds, whose densities are 1.233 Mg m^{-3} at 298 K for the *cis* epimer versus 1.238 Mg m^{-3} at 100 K for (I).

In the crystal structure, there are four intermolecular $\text{C}-\text{H}\cdots\text{O}$ close contacts (Table 2), with distances within the 2.4–2.7 Å range which we routinely survey for such packing interactions (Steiner, 1997).

Experimental

Commercial 18β -glycyrrhetic acid, of known absolute configuration (Klyne & Buckingham, 1978), was obtained from ICN Pharmaceuticals, Costa Mesa, CA, USA. Jones oxidation provided the C14b β material (Brunskill *et al.*, 1999), which was then epimerized by refluxing with acetic acid/HCl to yield (I), of known positive rotation (Logemann *et al.*, 1957), crystallized from acetic acid (m.p. 598 K). The solid-state (KBr) IR spectrum of (I) has $\text{C}=\text{O}$ absorptions at 1721 and 1686 cm^{-1} conforming to shifts typical of catemers and due, respectively, to removal of hydrogen bonding from carboxyl $\text{C}=\text{O}$ and addition of hydrogen bonding to the saturated ketone. In CHCl_3 solution these coalesce to a single peak centered at 1699 cm^{-1} , consistent with a dimerically hydrogen-bonded carboxyl. The enone system appears normally at 1655 and 1638 cm^{-1} in KBr and 1658 and 1621 cm^{-1} in CHCl_3 .

Crystal data

$\text{C}_{30}\text{H}_{44}\text{O}_4$	$V = 628.39 (3) \text{ \AA}^3$
$M_r = 468.65$	$Z = 1$
Triclinic, $P1$	$D_x = 1.238 \text{ Mg m}^{-3}$
$a = 6.6054 (2) \text{ \AA}$	Cu $K\alpha$ radiation
$b = 7.2228 (2) \text{ \AA}$	$\mu = 0.63 \text{ mm}^{-1}$
$c = 14.5495 (3) \text{ \AA}$	$T = 100 (2) \text{ K}$
$\alpha = 90.085 (2)^\circ$	Parallelepiped, colorless
$\beta = 96.287 (2)^\circ$	$0.28 \times 0.14 \times 0.09 \text{ mm}$
$\gamma = 114.225 (2)^\circ$	

Data collection

Bruker SMART CCD APEX-II	8622 measured reflections
area-detector diffractometer	3702 independent reflections
φ and ω scans	3345 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan	$R_{\text{int}} = 0.026$
(SADABS; Sheldrick, 2001)	$\theta_{\text{max}} = 67.7^\circ$
$T_{\text{min}} = 0.843$, $T_{\text{max}} = 0.945$	

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0454P)^2 + 0.3681P]$
$R[F^2 > 2\sigma(F^2)] = 0.046$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.113$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.04$	$\Delta\rho_{\text{max}} = 0.29 \text{ e \AA}^{-3}$
3702 reflections	$\Delta\rho_{\text{min}} = -0.20 \text{ e \AA}^{-3}$
315 parameters	Absolute structure: Flack (1983),
H-atom parameters constrained	1651 Friedel pairs
	Flack parameter: 0.2 (3)

Table 1

Selected geometric parameters (\AA , $^\circ$).

O3–C15	1.206 (4)	O4–C15	1.334 (4)
O3–C15–C2	126.4 (3)	O4–C15–C2	111.5 (3)

Table 2

Hydrogen-bond and close-contact geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
O4—H4 \cdots O1 ⁱ	0.84	1.95	2.766 (3)	163
C7—H7A \cdots O2 ⁱⁱ	0.99	2.66	3.579 (4)	155
C17—H17C \cdots O3 ⁱⁱⁱ	0.98	2.64	3.575 (4)	159
C20—H20A \cdots O4 ^{iv}	0.98	2.46	3.304 (4)	144
C21—H21B \cdots O4 ^v	0.98	2.69	3.225 (4)	115

Symmetry codes: (i) $x, y + 1, z + 1$; (ii) $x, y - 1, z$; (iii) $x - 1, y - 1, z$; (iv) $x, y - 1, z - 1$; (v) $x - 1, y - 1, z - 1$.

All H atoms for (I) were found in electron density difference maps. The O-bound H atom was constrained to an idealized position with O—H distance fixed at 0.84 Å and $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{O})$. The methyl H atoms were placed in ideally staggered positions with C—H distances of 0.98 Å and $U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$. The methylene and methine H atoms were placed in geometrically idealized positions and constrained to ride on their parent C atoms with C—H distances of 0.99 and 1.00 Å, respectively, and $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$. The absolute configuration is known by reference to the known chirality of the enantiopure acid employed and is consistent with the rather imprecise experimental Flack (1983) parameter.

Data collection: *SMART* (Bruker, 2000); cell refinement: *SAINT-Plus* (Bruker, 2000); data reduction: *SAINT-Plus*; program(s) used to

solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 2000); software used to prepare material for publication: *SHELXTL*.

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