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Crystal structure and absolute configuration of (4*S*,5*R*,6*S*)-4,5,6-trihydroxy-3-methylcyclohex-2-enone (gabosine H)

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The molecule of the title keto carbasugar, $C_7H_{10}O_4$, is formed by a cyclohexene skeleton with an envelope conformation, substituted by carbonyl, methyl and hydroxyl groups. The crystal structure is controlled mainly by a combination of strong $O-H\cdots O$ and weak $C-H\cdots O$ hydrogen bonds, forming nearly perpendicular chains running parallel to the [110] and [110] directions. This perpendicularity is caused by a tetragonal pseudosymmetry influenced by the similarity between the *a* and *b* axes, the value of 90.9770 (10)° of the β angle and the action of a 2₁ screw axis, which transform each chain into its corresponding nearly orthogonal one.

1. Chemical context

Gabosines are regarded as secondary metabolites and were first isolated in 1974 from *Streptomyces strains* (Tsushiya *et al.*, 1974). These compounds are closely related to carbasugars and exhibit DNA binding properties (Tang *et al.*, 2000). To date, 15 gabosines have been isolated, of which 14 have been synthesized. Gabosine H is one of such kind, whose total synthesis has recently been achieved by our research group (Tibhe *et al.*, 2017), starting from a biotransformation of toluene that introduces chirality. A further sequence of reactions, including Mitsunobu and final removal of the acetyl protective group, led to the title compound.





2. Structural commentary

Fig. 1 shows the molecule of the title compound. The absolute configuration of gabosine H with the carbonyl, methyl and hydroxyl groups in equatorial positions, determined as 4S,5R,6S on the basis of synthetic pathway, was confirmed by X-ray diffraction on the basis of anomalous dispersion of light atoms only. The six-membered ring (C1–C6) in the molecule



Figure 1

The molecular structure of the title compound, showing the anisotropic displacement ellipsoids drawn at the 50% probability level.

adopts an envelope conformation with atom C5 as the flap [deviating from the plane through the other ring atoms by 0.639 (2) Å] and puckering parameters Q = 0.4653 (19) Å, $\theta = 129.5$ (2)° and $\varphi = 66.7$ (3)°.

Table 1Hydrogen-bond geometry (Å, °).

$D - H \cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$O4-H41\cdots O1^{i}$	0.94 (4)	1.96 (4)	2.873 (2)	163 (3)
$C6-H6\cdots O4^{ii}$	0.98	2.46	3.195 (2)	131
$C4-H4\cdots O6^{iii}$	0.98	2.36	3.345 (3)	179
$C6-H6\cdots O6^{iv}$	0.98	2.62	3.306 (2)	127
$O6-H61\cdots O5^{v}$	0.87 (4)	1.99 (4)	2.811 (2)	155 (3)
$O5-H51\cdots O4^{vi}$	0.85 (4)	2.45 (3)	3.050 (2)	128 (3)
$O5-H51\cdots O5^{vi}$	0.85 (4)	2.26 (4)	3.0402 (12)	152 (3)

Symmetry codes: (i) x - 1, y - 1, z; (ii) x + 1, y, z; (iii) x, y - 1, z; (iv) $-x + 1, y - \frac{1}{2}, -z + 1$; (v) $-x + 1, y + \frac{1}{2}, -z + 1$; (vi) $-x, y + \frac{1}{2}, -z + 1$.

3. Supramolecular features

In the crystal structure, hydrogen bonds $O4-H41\cdots O1^{i}$ [symmetry code: (i) x - 1, y - 1, z] link the molecules into chains that run along the [110] direction (Table 1). These chains are further connected by weaker C6-H6...O4ⁱⁱ and C4-H4···O6ⁱⁱⁱ [symmetry codes: (ii) x + 1, y, z; (iii) x, y - 1, z] hydrogen bonds along the $[\overline{1}10]$ direction, forming (001) sheets (Fig. 2). Considering that the chains run along the diagonal of the *ab* plane and the fact that $a \simeq b$, it is possible to observe that the 2_1 screw axis parallel to b transforms each chain into a nearly orthogonal one along $[\overline{110}]$ (Fig. 3). The orthogonal chains are connected by single C6-H6...O6^{iv}, O6-H61 \cdots O5^v and bifurcated O5-H51 \cdots O4^{vi} and O5-H51···O5^{vi} hydrogen bonds [symmetry codes: (iv) -x + 1, $y = \frac{1}{2}, -z = 1;$ (v) $-x = 1, y = \frac{1}{2};$ (vi) $-x, y = \frac{1}{2}, -z = 1$] to define a three-dimensional array along the [001] direction. These hydrogen bonds connect the orthogonal chains by pairs along



Figure 2

Partial crystal packing of the title compound showing the $C-H \cdots O$ and $O-H \cdots O$ hydrogen bonds (dotted lines) along [110] and [110], forming sheets parallel to the (001) plane.

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Partial crystal packing of the title compound connected into a nearly orthogonal assembly along [001] through $C-H\cdots O$ and $O-H\cdots O$ hydrogen bonds (dotted lines).

[001]. Between these neighboring [001] sheets, weak dipolar or van der Waals forces stabilize the assembly along the c-axis direction.

4. Database survey

A search of the Cambridge Structural Database (CSD Version 5.36 with one update; Groom *et al.*, 2016) was carried out considering molecular structures similar to gabosine and its derivatives. Among the natural compounds, only the structure of gabosine N, (4R,5R,6R)-4,5,6-trihydroxy-2-methylcyclohex-2-enone (Tang *et al.* 2000), has been reported. The remaining hits were mainly derivatives of other gabosines different from H or derivatives such as 5-hydroxy-4-methyl-7-oxabicyclo[4.1.0]hept-3-en-2-one (White *et al.*, 2010), which is an epoxide with different configuration of the asymmetric carbons compared with gabosine H.

5. Synthesis and crystallization

The synthesis of gabosine H was achieved by inversion of the allylic –OH group using Mitsunobu conditions followed by deprotection. (4R,5R,6S)-5-Acetoxy-4,5-dihydroxy-3-methyl-cyclohex-2-enone (**2**, Fig. 4; 0.149 mmol, 0.030 g) was dissolved in 1 ml of benzene and TPP (0.283 mmol, 0.078 g) was added along with *p*-nitrobenzoic acid (0.299 mmol, 0.050 g) and diisopropyl azodicarboxylate (DIAD; 0.297 mmol, 0.060 g). The reaction mixture was stirred at room temperature for 6 h. The solvent was evaporated and the crude mass was used for the next reaction without further purification. The crude

Experimental details.Crystal dataChemical formula $C_2H_{10}O_4$ M_r 158.15Crystal system, space groupMonoclinic, $P2_1$ Temperature (K)298 a, b, c (Å)5.4143 (2), 5.4176 (2), 11.9200 (5) β (°)90.977 (1) V (Å3)349.59 (2) Z 2Radiation typeCu K α μ (mm ⁻¹)1.06Crystal size (mm)0.37 × 0.34 × 0.10Data collectionDiffractometerDiffractometerBruker D8 Venture/Photon 100 CMOSAbsorption correctionMulti-scan (SADABS; Bruker, 2013) T_{min}, T_{max} 0.588, 0.754No. of measured, independent and observed $[I > 2\sigma(I)]$ reflections0.046 (4^{-1}) $Rint$ 0.046No. of reflections1492No. of reflections1492No. of restraints1H-atom treatmentH atoms treated by a mixture of independent and constrained refinement $\Delta \rho_{max}, \Delta \rho_{min}$ (e Å ⁻³)0.25, -0.18Absolute structureFlack x determined using 639 quotients $[(t^+)-(t^-)]/[(t^+)+(t^-)]$ <th>Table 2</th> <th></th>	Table 2	
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No. of restraints1H-atom treatmentH atoms treated by a mixture of independent and constrained refinement $\Delta \rho_{max}, \Delta \rho_{min}$ (e Å ⁻³)0.25, -0.18Absolute structureFlack x determined using 639 quotients $[(I^*)-(I^-)]/[(I^*)+(I^-)]$	No. of parameters	111
H-atom treatmentH atoms treated by a mixture of independent and constrained refinement $\Delta \rho_{max}, \Delta \rho_{min}$ (e Å ⁻³)0.25, -0.18Absolute structureFlack x determined using 639 quotients $[(I^+)-(I^-)]/[(I^+)+(I^-)]$	No. of restraints	1
$ \begin{array}{ll} \Delta \rho_{\max}, \Delta \rho_{\min} (e \ \text{\AA}^{-3}) & 0.25, -0.18 \\ \text{Absolute structure} & \text{Flack } x \ \text{determined using 639} \\ \text{quotients } [(I^+) - (I^-)]/[(I^+) + (I^-)] \end{array} $	H-atom treatment	H atoms treated by a mixture of independent and constrained refinement
Absolute structure Flack x determined using 639 quotients $[(I^+)-(I^-)]/[(I^+)+(I^-)]$	$\Delta \rho_{\rm max}, \Delta \rho_{\rm min} \ (e \ {\rm \AA}^{-3})$	0.25, -0.18
(Parsons <i>et al.</i> , 2013)	Absolute structure	Flack x determined using 639 quotients $[(I^+)-(I^-)]/[(I^+)+(I^-)]$ (Parsons <i>et al.</i> , 2013)
Absolute structure parameter0.09 (11)	Absolute structure parameter	0.09 (11)

Computer programs: SAINT (Bruker, 2013), SHELXS2014 (Sheldrick, 2008), SHELXL2014 (Sheldrick, 2015), Mercury (Macrae et al., 2008).

product was dissolved in MeOH (3.4 mL), a catalytic quantity of K₂CO₃ was added and the reaction mixture was stirred at room temperature for 5 min and filtered. Evaporation of the solvent from the filtrate afforded crude gabosine H, which was purified by column chromatography (CH₂Cl₂/MeOH, 9:1 ν/ν) to afford pure gabosine H as a white crystalline powder (yield: 7.2 mg, 30%; m.p. 390.6 K. Suitable crystals for X-ray analysis were obtained by dissolving the solid in a minimum amount of methanol and allowing it to evaporate at room temperature. IR (KBr): 3400, 2875, 1660 cm^{-1.} ¹H NMR (400 MHz, CD₃OD): δ = 2.07 (*s*, 3 H), 3.56 (*dd*, *J* = 10.8, 2.4 Hz, 1 H), 4.01 (*d*, *J* = 10.8 Hz, 1 H), 4.23 (*d*, *J* = 8.4 Hz, 1 H), 5.92 (*s*, 1 H).





6. Refinement

Crystal data, data collection and structure refinement details are summarized in Table 2. H atoms bonded to C were placed in calculated positions (C–H = 0.93–0.98 Å) and included as riding contributions with isotropic displacement parameters set to 1.2–1.5 times the U_{eq} of the parent atom. Hydroxy H atoms were located in difference density maps and were refined with $U_{iso}(H) = 1.5 U_{eq}(O)$. The absolute structure parameter y was calculated using *PLATON* (Spek, 2009). The resulting value of 0.07 (7) indicates that the absolute structure was determined correctly (Hooft *et al.*, 2008).

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supporting information

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Crystal structure and absolute configuration of (4*S*,5*R*,6*S*)-4,5,6-trihydroxy-3methylcyclohex-2-enone (gabosine H)

Gaurao D. Tibhe, Mario A. Macías, Enrique Pandolfi, Valeria Schapiro and Leopoldo Suescun

Computing details

Data collection: *SAINT* (Bruker, 2013); cell refinement: *SAINT* (Bruker, 2013); data reduction: *SAINT* (Bruker, 2013); program(s) used to solve structure: *SHELXS2014* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL2014* (Sheldrick, 2015); molecular graphics: *Mercury* (Macrae *et al.*, 2008); software used to prepare material for publication: *SHELXL2014* (Sheldrick, 2015).

F(000) = 168

 $\theta = 3.7 - 78.8^{\circ}$

 $\mu = 1.06 \text{ mm}^{-1}$

T = 298 K

 $D_{\rm x} = 1.502 {\rm Mg} {\rm m}^{-3}$

Parallelepiped, colorless

 $0.37 \times 0.34 \times 0.10 \text{ mm}$

Cu *K* α radiation, $\lambda = 1.54178$ Å

Cell parameters from 9784 reflections

(4S,5R,6S)-4,5,6-Trihydroxy-3-methylcyclohex-2-enone

Crystal data

 $C_{7}H_{10}O_{4}$ $M_{r} = 158.15$ Monoclinic, $P2_{1}$ a = 5.4143 (2) Å b = 5.4176 (2) Å c = 11.9200 (5) Å $\beta = 90.977$ (1)° V = 349.59 (2) Å³ Z = 2

Data collection

Bruker D8 Venture/Photon 100 CMOS	12187 measured reflections
diffractometer	1492 independent reflections
Radiation source: Cu Incoatec microsource	1472 reflections with $I > 2\sigma(I)$
Detector resolution: 10.4167 pixels mm ⁻¹	$R_{\rm int} = 0.046$
j and ω scans	$\theta_{\text{max}} = 79.1^{\circ}, \ \theta_{\text{min}} = 3.7^{\circ}$
Absorption correction: multi-scan	$h = -6 \rightarrow 6$
(SADABS; Bruker, 2013)	$k = -6 \rightarrow 6$
$T_{\min} = 0.588, \ T_{\max} = 0.754$	$l = -15 \rightarrow 14$

Refinement

Refinement on F^2 Secondary atom site location: difference Fourier Least-squares matrix: full map $R[F^2 > 2\sigma(F^2)] = 0.033$ Hydrogen site location: mixed $wR(F^2) = 0.088$ H atoms treated by a mixture of independent *S* = 1.08 and constrained refinement 1492 reflections $w = 1/[\sigma^2(F_o^2) + (0.0546P)^2 + 0.0518P]$ 111 parameters where $P = (F_0^2 + 2F_c^2)/3$ 1 restraint $(\Delta/\sigma)_{\rm max} < 0.001$ $\Delta \rho_{\rm max} = 0.25 \text{ e} \text{ Å}^{-3}$ Primary atom site location: structure-invariant direct methods $\Delta \rho_{\rm min} = -0.18 \ {\rm e} \ {\rm \AA}^{-3}$

Extinction correction: SHELXL2014 (Sheldrick, 2015), $Fc^*=kFc[1+0.001xFc^2\lambda^3/sin(2\theta)]^{-1/4}$ Extinction coefficient: 0.161 (15) Absolute structure: Flack *x* determined using 639 quotients $[(I^+)-(I^-)]/[(I^+)+(I^-)]$ (Parsons *et al.*, 2013) Absolute structure parameter: 0.09 (11)

Special details

Geometry. All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

	<i>x</i>	у	Ζ	$U_{\rm iso}$ */ $U_{\rm eq}$
C1	0.4992 (3)	0.2954 (4)	0.22586 (16)	0.0293 (4)
C2	0.3815 (4)	0.1293 (4)	0.14457 (16)	0.0313 (5)
H2	0.4304	0.1373	0.0702	0.038*
C3	0.2068 (3)	-0.0338 (3)	0.17173 (15)	0.0262 (4)
C31	0.0921 (4)	-0.2029 (5)	0.08715 (17)	0.0374 (5)
H31A	0.1711	-0.1813	0.0163	0.056*
H31B	-0.0807	-0.1656	0.0790	0.056*
H31C	0.1119	-0.3706	0.1116	0.056*
C4	0.1234 (3)	-0.0631 (3)	0.29155 (15)	0.0249 (4)
H4	0.2190	-0.1965	0.3269	0.030*
C5	0.1658 (3)	0.1719 (4)	0.35829 (15)	0.0237 (4)
Н5	0.0534	0.3005	0.3302	0.028*
C6	0.4314 (3)	0.2607 (3)	0.34819 (14)	0.0258 (4)
H6	0.5418	0.1368	0.3818	0.031*
01	0.6472 (3)	0.4524 (3)	0.19769 (14)	0.0453 (5)
O4	-0.1316 (3)	-0.1192 (3)	0.29994 (14)	0.0398 (4)
H41	-0.172 (6)	-0.273 (8)	0.269 (3)	0.060*
O5	0.1120 (3)	0.1206 (3)	0.47319 (11)	0.0336 (4)
H51	0.096 (5)	0.263 (7)	0.502 (3)	0.050*
O6	0.4549 (3)	0.4821 (3)	0.40965 (13)	0.0374 (4)
H61	0.606 (7)	0.485 (7)	0.437 (3)	0.056*

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters $(Å^2)$

Atomic displacement parameters $(Å^2)$

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}	
C1	0.0252 (8)	0.0305 (10)	0.0322 (9)	-0.0046 (8)	0.0038 (7)	0.0021 (8)	
C2	0.0322 (9)	0.0360 (11)	0.0257 (8)	-0.0051 (8)	0.0055 (7)	-0.0002 (8)	
C3	0.0251 (8)	0.0263 (9)	0.0274 (8)	0.0013 (7)	0.0018 (6)	-0.0011 (7)	
C31	0.0429 (11)	0.0358 (11)	0.0335 (10)	-0.0084 (10)	0.0007 (8)	-0.0050 (9)	
C4	0.0241 (8)	0.0219 (9)	0.0289 (9)	0.0001 (7)	0.0061 (6)	0.0011 (7)	
C5	0.0227 (8)	0.0242 (9)	0.0243 (8)	0.0024 (6)	0.0037 (6)	0.0007 (6)	
C6	0.0240 (8)	0.0267 (10)	0.0267 (8)	0.0011 (7)	0.0004 (6)	-0.0019 (7)	
01	0.0464 (9)	0.0459 (10)	0.0440 (8)	-0.0236 (8)	0.0080(7)	-0.0002 (7)	
O4	0.0287 (8)	0.0363 (9)	0.0548 (9)	-0.0099 (6)	0.0152 (6)	-0.0124 (7)	
O5	0.0363 (7)	0.0388 (8)	0.0260 (7)	-0.0005 (6)	0.0091 (5)	-0.0016 (6)	

06	0.0329 (7)	0.0364 (9)	0.0429 (8)	-0.0016 (6)	-0.0044 (6)	-0.0125 (7)
Geome	tric parameters (A	ľ, °)				
C1-0	01	1.220 (3)	C4—C5	1.:	517 (2)
C1—C	2	1.461 (3)	C4—H4	0.9	9800
C1—C	6	1.521 (2)	C5—O5	1.4	432 (2)
С2—С	3	1.338 (3)	C5—C6	1.:	523 (2)
С2—Н	2	0.9300		С5—Н5	0.9	9800
С3—С	31	1.490 (3)	C6—O6	1.4	410 (2)
С3—С	4	1.514 (2)	С6—Н6	0.9	9800
C31—	H31A	0.9600		O4—H41	0.9	94 (4)
C31—	H31B	0.9600		O5—H51	0.3	35 (4)
C31—1	H31C	0.9600		O6—H61	0.3	87 (4)
C4—0	94	1.419 (2)			
01—C	C1—C2	121.89	(18)	O4—C4—H4	10	8.6
O1—C	C1—C6	121.36	(18)	С3—С4—Н4	10	8.6
С2—С	1—C6	116.75	(16)	С5—С4—Н4	10	8.6
С3—С	2—C1	123.26	(17)	O5—C5—C4	10	7.89 (15)
С3—С	2—Н2	118.4		O5—C5—C6	11	0.15 (14)
C1C	2—Н2	118.4		C4—C5—C6	11	0.99 (14)
С2—С	3—C31	122.04	(17)	O5—C5—H5	10	9.3
С2—С	3—C4	121.40	(16)	С4—С5—Н5	10	9.3
C31—C3—C4 116.52 (16)		(16)	С6—С5—Н5	10	9.3	
С3—С	31—H31A	109.5		O6—C6—C1	11	1.83 (16)
C3—C31—H31B		109.5		O6—C6—C5	107.72 (14)	
H31A—C31—H31B		109.5		C1—C6—C5	110.99 (14)	
С3—С	31—H31C	109.5		Об—Сб—Нб	10	8.7
H31A-	—С31—Н31С	109.5		С1—С6—Н6	10	8.7
H31B-	—С31—Н31С	109.5		С5—С6—Н6	10	8.7
O4—C	24—C3	113.27	(15)	C4—O4—H41	11	3 (2)
O4—C	24—C5	106.33	(14)	С5—О5—Н51	10	3 (2)
С3—С	4—C5	111.22	(14)	С6—О6—Н61	10	6 (2)
01—C	C1—C2—C3	-175.5	(2)	O4—C4—C5—C6	-1	75.86 (15)
С6—С	1—C2—C3	5.4 (3)		C3—C4—C5—C6	-52.12 (19)	
C1—C	2—C3—C31	-179.2	9 (19)	01—C1—C6—O6	28	.4 (3)
C1—C	2—C3—C4	-1.9 (3)	C2—C1—C6—O6	-1	52.56 (18)
С2—С	3—C4—O4	145.37	(18)	01—C1—C6—C5	14	8.7 (2)
C31—	C3—C4—O4	-37.2 ((2)	C2—C1—C6—C5	-3	2.2 (2)
С2—С	3—C4—C5	25.7 (2)	05-C5-C6-06	-6	52.1 (2)
C31—	C3—C4—C5	-156.8	5 (17)	C4—C5—C6—O6	17	8.49 (14)
04—C	24—C5—O5	63.37 (19)	O5—C5—C6—C1	17	5.17 (16)
С3—С	4—C5—O5	-172.8	9 (14)	C4—C5—C6—C1	55	.8 (2)

supporting information

D—H···A	<i>D</i> —Н	$H \cdots A$	$D \cdots A$	D—H··· A	
04—H41…O1 ⁱ	0.94 (4)	1.96 (4)	2.873 (2)	163 (3)	
C6—H6····O4 ⁱⁱ	0.98	2.46	3.195 (2)	131	
C4—H4···O6 ⁱⁱⁱ	0.98	2.36	3.345 (3)	179	
C6—H6···O6 ^{iv}	0.98	2.62	3.306 (2)	127	
O6—H61···O5 ^v	0.87 (4)	1.99 (4)	2.811 (2)	155 (3)	
O5—H51···O4 ^{vi}	0.85 (4)	2.45 (3)	3.050 (2)	128 (3)	
O5—H51…O5 ^{vi}	0.85 (4)	2.26 (4)	3.0402 (12)	152 (3)	

Hydrogen-bond geometry (Å, °)

Symmetry codes: (i) *x*-1, *y*-1, *z*; (ii) *x*+1, *y*, *z*; (iii) *x*, *y*-1, *z*; (iv) -*x*+1, *y*-1/2, -*z*+1; (v) -*x*+1, *y*+1/2, -*z*+1; (vi) -*x*, *y*+1/2, -*z*+1.