

N-(*tert*-Butoxycarbonyl)-*O*-(hydroxyethyl)tyrosine methyl esterChun-Yan Liu^{a,b*} and Hui Li^a^aSchool of Pharmaceutical Science and Technology, Tianjin University, Tianjin 300072, People's Republic of China, and ^bNorth China Coal Medical University, Tangshan 063000, People's Republic of China

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Key indicators

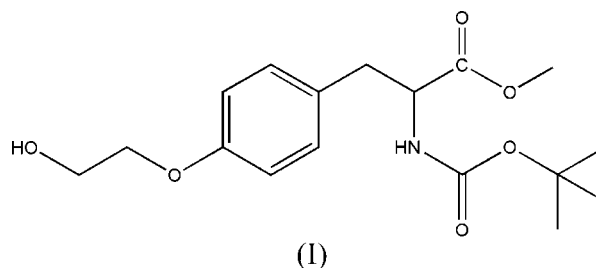
Single-crystal X-ray study
T = 294 K
Mean $\sigma(\text{C}-\text{C}) = 0.005 \text{ \AA}$
R factor = 0.060
wR factor = 0.168
Data-to-parameter ratio = 14.0For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

In the title compound (systematic name: *tert*-butyl *N*-{2-[4-(2-hydroxyethoxy)phenyl]-1-(methoxycarbonyl)ethyl}carbamate), $\text{C}_{17}\text{H}_{25}\text{N}_1\text{O}_6$, the crystal structure is stabilized by $\text{O}-\text{H}\cdots\text{O}$ and $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds.

Comment

The positron-labeled *L*-tyrosine analog *O*-(2-[18*F*]fluoroethyl)-*L*-tyrosine (FET) is becoming increasingly important as an amino acid positron emission tomography (PET) tracer for the detection and localization of tumors with a higher specificity than other available tracers, especially for brain tumors (Kaim *et al.*, 2002).

The structure of the title compound, (I), an intermediate in the synthesis of FET, is reported here (Fig. 1). A combination of intermolecular $\text{O}-\text{H}\cdots\text{O}$ and $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds (Table 1) helps to establish the crystal packing (Fig. 2).



Experimental

A solution of *N*-(*tert*-butoxycarbonyl)tyrosine methyl ester (1 g, 3.4 mmol) in dimethylformamide (25 ml) was added, with stirring, to potassium carbonate (1.17 g, 8.5 mmol), Bu_4NI (0.13 g, 0.34 mmol) and 18-C-6 crown ether (0.18 g, 0.68 mmol). The reaction mixture was heated at 398 K for 12 h, after which water (20 ml) was added and the layers were separated. The aqueous phase was extracted with dichloromethane, the combined organic layers were dried (Na_2SO_4) and the solvent evaporated. The residue was chromatographed on silica, with light petroleum–ethyl acetate (3:2 *v/v*) as eluant, to give the product (yield 0.47 g, 40.5%). Single crystals of (I) (m.p. 362–363 K) were obtained by slow evaporation of a light petroleum–ethyl acetate (1:2 *v/v*) solution.

Crystal data

$\text{C}_{17}\text{H}_{25}\text{NO}_6$	$V = 3584.7 (14) \text{ \AA}^3$
$M_r = 339.38$	$Z = 8$
Monoclinic, $C2/c$	Mo $K\alpha$ radiation
$a = 26.379 (6) \text{ \AA}$	$\mu = 0.10 \text{ mm}^{-1}$
$b = 9.706 (2) \text{ \AA}$	$T = 294 (2) \text{ K}$
$c = 14.150 (3) \text{ \AA}$	$0.30 \times 0.28 \times 0.24 \text{ mm}$
$\beta = 98.327 (4)^\circ$	

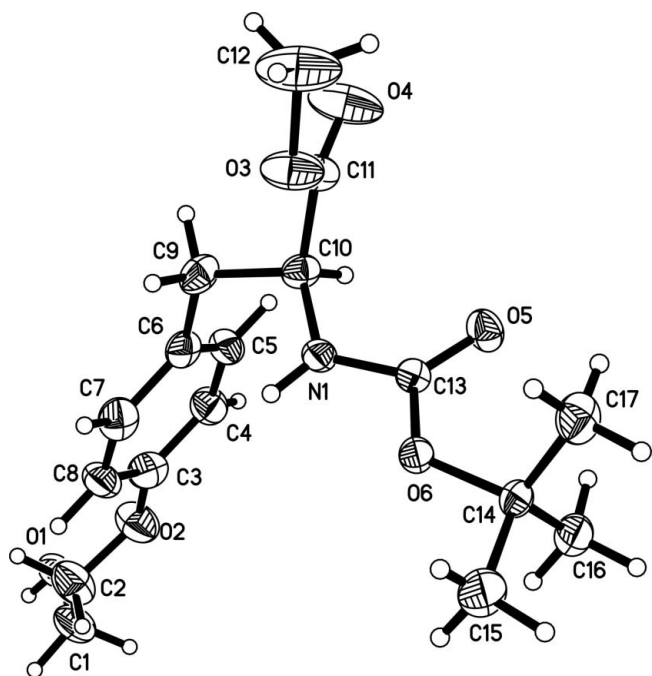


Figure 1
The molecular structure of (I) showing displacement ellipsoids drawn at the 30% probability level (arbitrary spheres for the H atoms).

Data collection

Bruker SMART 1000 CCD diffractometer	8980 measured reflections
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	3172 independent reflections
$T_{\min} = 0.972, T_{\max} = 0.978$	1846 reflections with $I > 2\sigma(I)$
	$R_{\text{int}} = 0.044$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.060$	H atoms treated by a mixture of independent and constrained refinement
$wR(F^2) = 0.168$	$\Delta\rho_{\text{max}} = 0.89 \text{ e } \text{\AA}^{-3}$
$S = 1.02$	$\Delta\rho_{\text{min}} = -0.34 \text{ e } \text{\AA}^{-3}$
3172 reflections	
227 parameters	
13 restraints	

Table 1
Hydrogen-bond geometry ($\text{\AA}, ^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N1-H1A\cdots O1^i$	0.83 (3)	2.28 (3)	3.113 (4)	178 (3)
$O1-H1\cdots O5^{ii}$	0.814 (10)	2.052 (14)	2.852 (3)	167 (4)

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

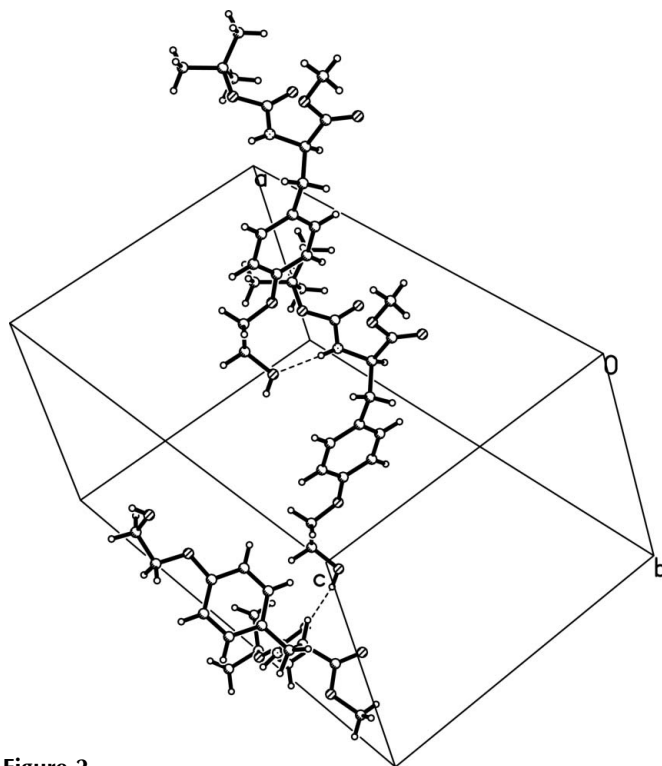


Figure 2
Part of the extended structure of (I). Dashed lines represent the hydrogen bonds

The O- and N-bound H atoms were located in a difference map and their positions were freely refined with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{N})$ or $1.5U_{\text{eq}}(\text{O})$. The C-bound H atoms were geometrically placed ($C-H = 0.93-0.98 \text{ \AA}$) and refined as riding with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ or $1.5U_{\text{eq}}(\text{methyl C})$.

Data collection: SMART (Bruker, 1997); cell refinement: SAINT (Bruker, 1997); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Bruker, 1997); software used to prepare material for publication: SHELXTL.

References

Bruker (1997). SMART (Version 5.611), SAINT (Version 6.10) and SHELXTL (Version 6.10). Bruker AXS Inc., Madison, Wisconsin, USA.
Kaim, A. H., Weber, B., Kurrer, M. O., Westera, G., Schweitzer, A., Gottschalk, J., von Schulthess, G. K. & Buck, A. (2002). *Eur. J. Nucl. Med.* **29**, 648–654.
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