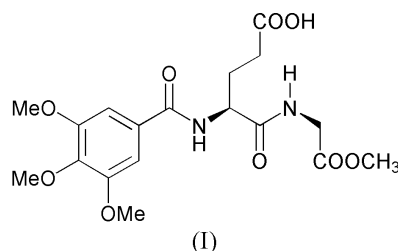


(4S)-4-(Methoxycarbonylmethylamino-carbonyl)-4-(3,4,5-trimethoxybenzamido)-butanoic acid**Xun Li,^{a*} Wen-Fang Xu,^a
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Shandong 250012, People's Republic of China,
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250002, People's Republic of ChinaCorrespondence e-mail:
tjulx2003@yahoo.com.cn**Key indicators**Single-crystal X-ray study
 $T = 298$ K
Mean $\sigma(\text{C}-\text{C}) = 0.004$ Å
 R factor = 0.061
 wR factor = 0.155
Data-to-parameter ratio = 13.6For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.

The title compound, $\text{C}_{18}\text{H}_{24}\text{N}_2\text{O}_9$, was synthesized by the condensation of *N*-(3,4,5-trimethoxybenzoyl)glutamic acid anhydride with L-glycine methyl ester hydrochloride in dichloromethane solution. The structure is stabilized by intermolecular hydrogen bonds.

Comment

Aminopeptidase N (APN) is a member of the membrane-bound zinc-dependent exopeptidase family, which is involved in the metabolism of angiotensin III in the brain and peripheral organs. The over-expression of APN is involved in several pathological conditions, including cancer (Yoneda *et al.*, 1992), leukemia, diabetic nephropathy (Bedir *et al.*, 1996), rheumatoid arthritis (Shimizu *et al.*, 2002), angiogenesis (Sato, 2004) and central nervous system diseases such as Alzheimer's disease (Sloane *et al.*, 2002). This has led to a search for APN inhibitors (APNIs) as potential therapeutic agents. Unfortunately, no such effective agents exist at the present time.



Antineoplaston A-10 (3-phenylacetyl-amino-2,6-piperidine-dione) is the first chemically identified APNI and has potential utility in breast cancer treatment (Badria, Mabed, El-Awadi *et al.*, 2000; Badria, Mabed, Khafagy & Abou-Zeid, 2000). A-10 and its metabolites have shown promising cytostatic responses when challenged on tumor tissue cultures or when administered to human patients with hepatocellular carcinoma (Abou-Zeid *et al.*, 2001).

Compound (I), one of the novel L-iso-glutamine derivatives synthesized in our laboratory, can serve as a potential anti-tumor agent (Wang *et al.*, 2003). It displays normal peptide geometry; the bond lengths and angles are unexceptional. The crystal structure is stabilized by intermolecular $\text{O}-\text{H}\cdots\text{O}$ and $\text{N}-\text{H}\cdots\text{O}$ hydrogen bonds; there are also weak $\text{C}-\text{H}\cdots\text{O}$ interactions (Table 1).

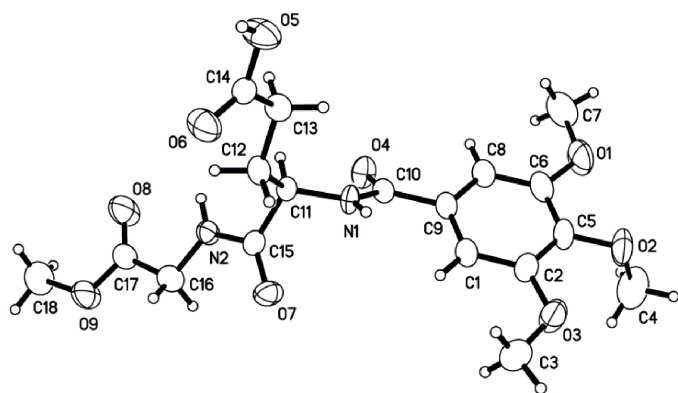
Experimental

Starting from 3,4,5-trihydroxybenzoic acid, *via* a three-step reaction, the key intermediate *N*-(3,4,5-trimethoxybenzoyl)glutamic acid anhydride was obtained according to the literature method (Fan,

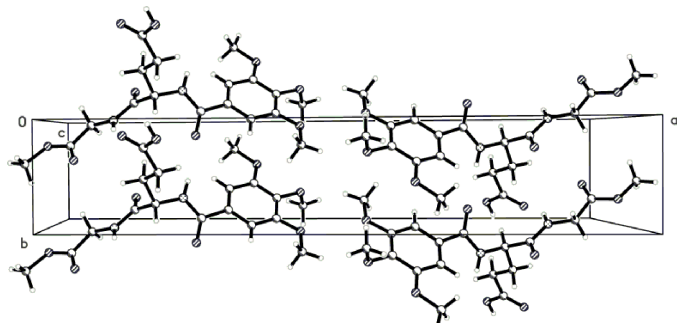
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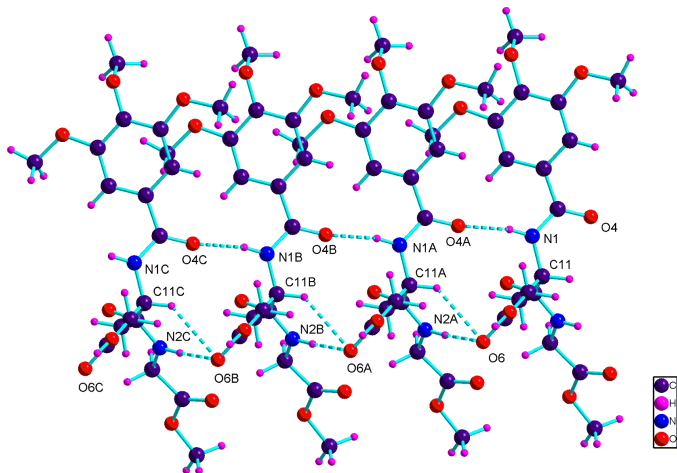
Online 22 January 2005


Figure 1

View of the molecule of (I), showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 30% probability level. H atoms are represented by small spheres of arbitrary radii.


Figure 2

The molecular packing of (I), viewed along the *c* axis.


Figure 3

Part of the crystal structure of (I), showing the formation of intermolecular hydrogen bonds (dashed lines). The molecule containing atom N1A is related to the molecule containing atom N1 by a unit-cell translation along *b*. Further unit-cell translations along *b* yield the molecules containing N1B and N1C.

1992) (m.p. 423–425 K, 55% yield). IR (KBr, ν cm^{-1}): 3310.0 (NH), 2945.1 (CH), 1777.0 and 1640.7 (O=C–O–C=O), 1504.2 (NH), 1239.6 and 1129.6 (C–O). ESI-MS (m/z): 323.8 [$M-H$]⁺. To a suspension of *N*-(3,4,5-trimethoxybenzoyl)glutamic acid anhydride (3.23 g, 10 mmol) and L-glycine methyl ester hydrochloride (2.5 g,

20 mmol) in dichloromethane (30 ml) was added triethylamine (5 ml). The resulting solution was stirred at room temperature for 2 h. The excess solvent was removed under reduced pressure. The residue was diluted with distilled water and acidified to pH 2 with 2M hydrochloric acid. After two days, colorless crystals of (I) were obtained (m.p. 442–445 K, 74% yield). Analysis found: C 52.60, H 5.96, N 6.69%; calculated for $\text{C}_{18}\text{H}_{24}\text{N}_2\text{O}_9$: C 52.42, H 5.87, N 6.79%. ¹H NMR (DMSO-*d*₆, p.p.m.): δ 8.45 (*d*, 1H, *J* = 7.5 Hz, NH), 8.38 (*t*, 1H, *J* = 5.4 Hz, NH), 7.23 (*s*, 2H, Ar–H), 4.47 (*m*, 1H, CH), 3.88 (*d*, 2H, *J* = 5.4 Hz, CH₂), 3.83 (*s*, 6H, 2-OCH₃), 3.69 (*s*, 3H, OCH₃), 3.62 (*s*, 3H, COOCH₃), 2.34 (*t*, 2H, *J* = 8.0 Hz, CH₂), 2.06, 1.92 (2 × *m*, 2H, CH₂). ESI-MS (m/z): 412.8 [$M-H$]⁺.

Crystal data

$\text{C}_{18}\text{H}_{24}\text{N}_2\text{O}_9$
 $M_r = 412.39$
 Monoclinic, $P2_1/c$
 $a = 27.665$ (9) Å
 $b = 5.1444$ (16) Å
 $c = 13.907$ (4) Å
 $\beta = 98.401$ (5)°
 $V = 1958.0$ (11) Å³
 $Z = 4$

$D_x = 1.399$ Mg m⁻³
 Mo $K\alpha$ radiation
 Cell parameters from 1522 reflections
 $\theta = 2.2$ – 22.0 °
 $\mu = 0.11$ mm⁻¹
 $T = 298$ (2) K
 Block, colorless
 0.25 × 0.15 × 0.10 mm

Data collection

Bruker SMART CCD area-detector diffractometer
 φ and ω scans
 9819 measured reflections
 3619 independent reflections
 2497 reflections with $I > 2\sigma(I)$

$R_{\text{int}} = 0.041$
 $\theta_{\text{max}} = 25.5$ °
 $h = -33 \rightarrow 26$
 $k = -6 \rightarrow 6$
 $l = -16 \rightarrow 16$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.061$
 $wR(F^2) = 0.155$
 $S = 1.04$
 3619 reflections
 267 parameters
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.0676P)^2 + 0.7151P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.33$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.20$ e Å⁻³

Table 1

Hydrogen-bond geometry (Å, °).

<i>D</i> –H... <i>A</i>	<i>D</i> –H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> –H... <i>A</i>
O5–H5...O7 ⁱ	0.82	1.85	2.667 (3)	174
N2–H2...O6 ⁱⁱ	0.86	2.38	3.193 (3)	157
N1–H1...O4 ⁱⁱⁱ	0.86	2.25	3.060 (3)	157
C11–H11...O6 ⁱⁱ	0.98	2.52	3.313 (3)	138
C18–H18B...O6 ^{iv}	0.96	2.47	3.014 (4)	116

Symmetry codes: (i) $x, -y + \frac{5}{2}, z - \frac{1}{2}$; (ii) $x, y - 1, z$; (iii) $x, y + 1, z$; (iv) $-x, y - \frac{3}{2}, -z + \frac{3}{2}$.

H atoms were positioned geometrically (with orientation to fit the observed electron density for the carboxylic O–H) and refined with a riding model [O–H = 0.82 Å, N–H = 0.86 Å, C–H = 0.93–0.98 Å, and $U_{\text{iso}}(\text{H}) = xU_{\text{eq}}(\text{carrier atom})$, where $x = 1.5$ for methyl H atoms and $x = 1.2$ for all other H atoms.

Data collection: SMART (Bruker, 1997); cell refinement: SAINT (Bruker, 1997); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Sheldrick, 2001); software used to prepare material for publication: SHELXTL.

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