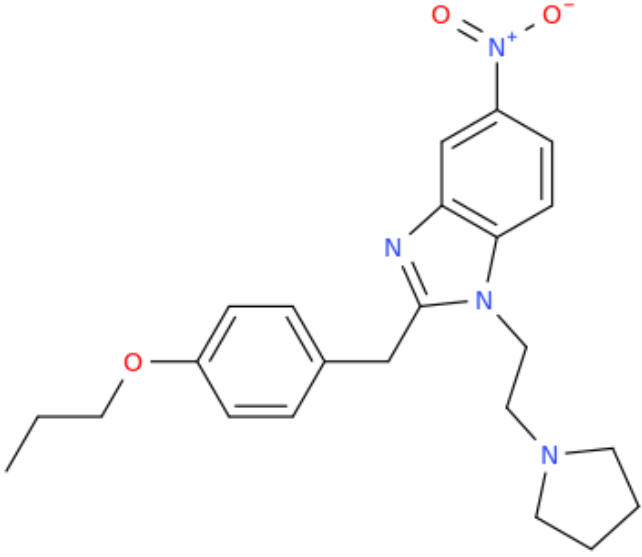


ANALYTICAL REPORT<sup>1</sup>N-Pyrrolidino Protonitazene (C<sub>23</sub>H<sub>28</sub>N<sub>4</sub>O<sub>3</sub>)

## 5-nitro-2-[(4-propoxyphenyl)methyl]-1-[2-(pyrrolidin-1-yl)ethyl]-1H-1,3-benzodiazole

Remark – other active cpd. detected: none

Sample ID:	3220-22
Sample description:	powder - yellow
Sample type:	RM-reference material
Comments:	CAY Lot#0654417-6,
Date of entry (DD/MM/YYYY):	23/02/2023
web link	<a href="http://www.policija.si/apps/nfl_response_web/seznam.php">http://www.policija.si/apps/nfl_response_web/seznam.php</a>

Substance identified-structure <sup>2</sup> (base form)	
Systematic name:	5-nitro-2-[(4-propoxyphenyl)methyl]-1-[2-(pyrrolidin-1-yl)ethyl]-1H-1,3-benzodiazole
Other names:	5-nitro-2-(4-propoxybenzyl)-1-(2-(pyrrolidin-1-yl)ethyl)-1H-benzo[d]imidazole; Protonitazepyne
Formula (per base form)	C <sub>23</sub> H <sub>28</sub> N <sub>4</sub> O <sub>3</sub>
M <sub>w</sub> (g/mol)	408,5
Salt form:	base
StdInChIKey (per base form)	KCRWXNIIIXGBPID-UHFFFAOYSA-N
Other active cpd. detected	none
Add.info (purity..)	≥98%

<sup>1</sup> Approved by: Dr. Sonja Klemenc<sup>2</sup> Created by OPSIN free tool: <http://opsin.ch.cam.ac.uk/> DOI: 10.1021/ci100384d

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## Report updates

date	comments (explanation)

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## Supporting information

Analytical technique:	applied	remarks
GC-MS (EI ionization)	+	NFL GC-RT (min): 19,37 BP(1): 84; BP(2): 107,BP(3) :85,
FTIR-ATR	+	direct measurement
GC-IR (solid phase)	+	always as base form
HPLC-TOF	+	exact mass theoretical: 408,2161 / measured $\Delta$ ppm: -1,89

**1. GC-MS (Agilent):** GC-method is RT locked to tetracosane (9.258 min). Injection volume 1  $\mu$ l and split mode (1:50). Injector temperature: 280 °C. Chromatographic separation: on column HP1-MS (100% dimethylpolysiloxane), length 30 m, internal diameter 0.25 mm, film thickness 0.25  $\mu$ m. Carrier gas He: flow-rate 1.2 ml/min. GC oven program: 170 °C for 1 min, followed by heating up to 190 °C at rate 8 °C/min, then heating up to 293 °C at a rate of 18 °C/min, hold for 6.1 min, then heating at 50 °C/min up to 325 °C and finally 9.1 min isothermal. MSD source EI = 70 eV. GC-MS transfer line T= 235°C, source and quadropole temperatures 280°C and 180°C, respectively. Scan range m/z scan range: from 50 (30 until 6 min.) to 550 (300 until 6 min) amu.

**2. FTIR-ATR (Perkin Elmer):** scan range 4000-400  $\text{cm}^{-1}$ ; resolution 4 $\text{cm}^{-1}$

**3. GC- (MS)-IR solid phase (GC-MS (Agilent) & IR (Spectra analyses-Danny)**

GC-method: Injection volume 1  $\mu$ l and split mode (1:5). Injector temperature 280 °C. Chromatographic separation as above (1). Split MS: IR = 1 : 9.

MSD source EI = 70 eV. GC-MS transfer line T= 235°C, source and quadropole temperatures 280°C and 180°C, respectively. Scan range m/z scan range: from 50 (30 until 6 min.) to 550 (300) amu.

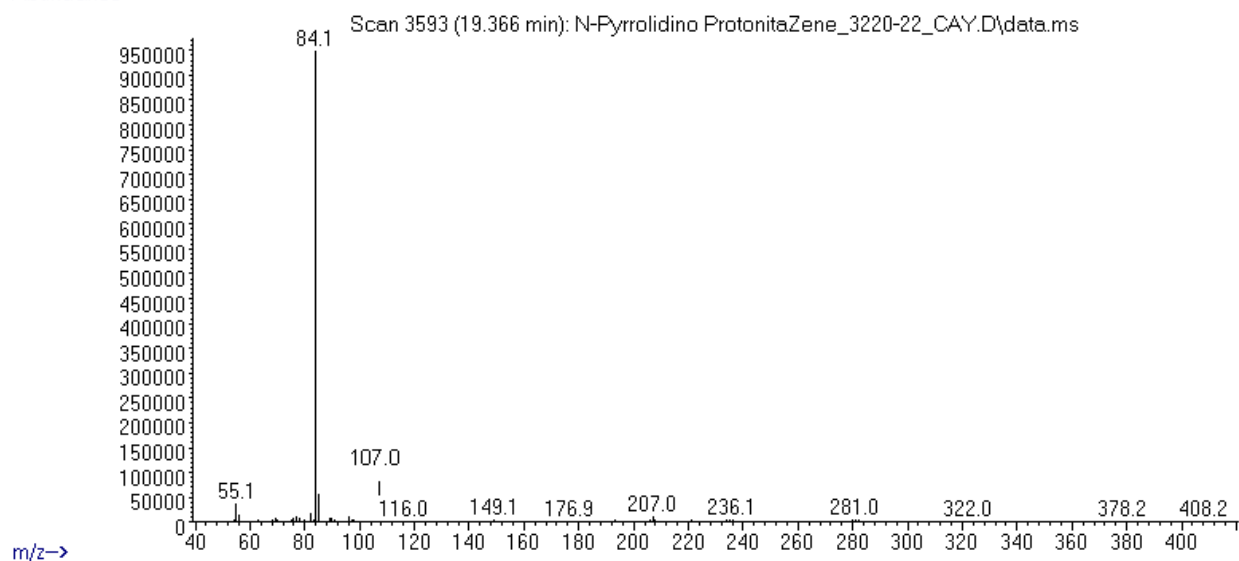
IR (condensed (solid) phase): IR scan range 4000 to 650, resolution 4  $\text{cm}^{-1}$ .

**4. HPLC-TOF (Agilent):** 6230B TOF with Agilent 1260 Infinity HPLC with binary pump, column: Zorbax Eclipse XDB-C18, 50 x 4.6 mm, 1.8 micron. Mobile phases (A) 0.1% formic acid and 1mM ammonium formate in water; (B) 0.1% formic acid in methanol (B). Gradient: starting at 5% B, changing to 40% B over 4 min, then to 70% over 2 min and in 5 min to 100%, hold 1 min and back to 5%, equilibration for 1.7 min. The flow rate: 1.0 ml/min; Injection volume 1  $\mu$ l. MS parameters: 2GHz, Extended Dynamic range mode to a maximum of 1700 amu, acquisition rate 1.30 spectra/sec. Sample ionisation: by Agilent Jet Stream technology (Dual AJS ESI). Ion source: positive ion scan mode with mass scanning from 82 to 1000 amu. Other TOF parameters: drying gas (N<sub>2</sub>) and sheath temperature 325 °C; drying gas flow rate 6 l/min; sheath gas flow rate 8 l/min; nebulizer 25 psig; Vcap. 4000 V; nozzle 2000 V; skimmer 65 V; fragmentor 175 V and Octopole RF 750 V.

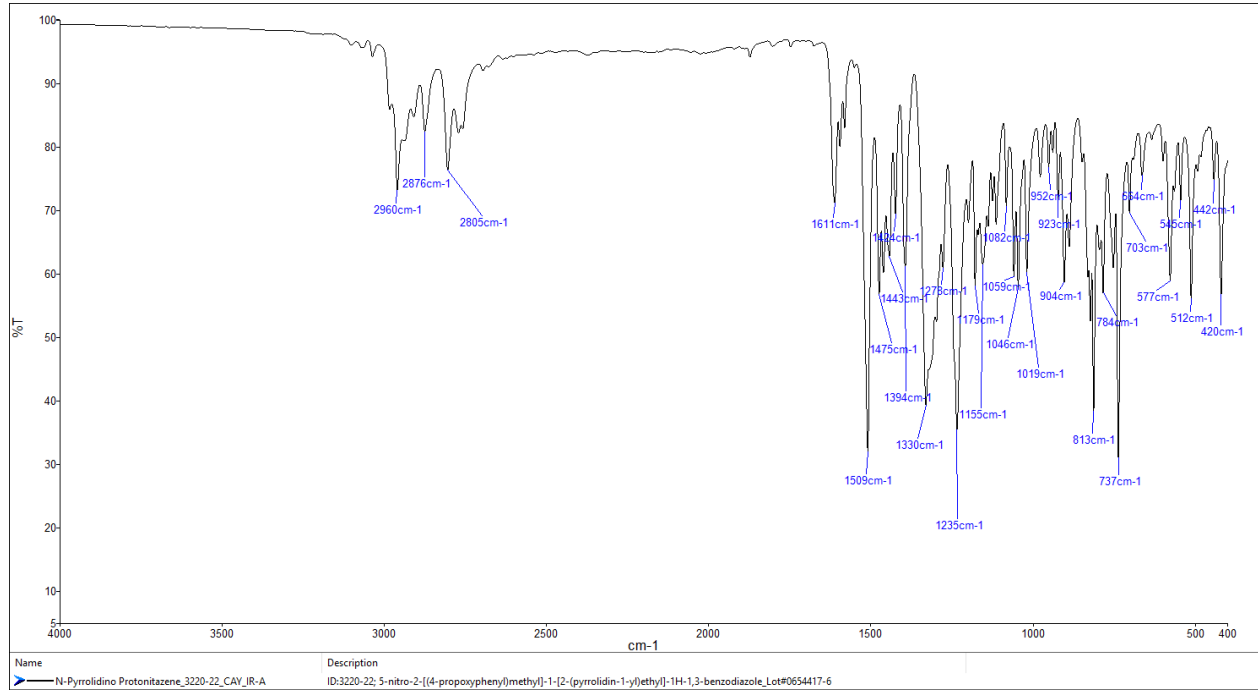
# ANALYTICAL RESULTS

MS (EI)

Abundance



FTIR-ATR (direct measurement – sample as received)



IR- (solid phase – after chromatographic separation) - spectrum per base form

