

ANALYTICAL REPORT¹

N-Cyclohexylmethyline (C17H23NO3)

1-(2H-1,3-benzodioxol-5-yl)-2-[cyclohexyl(methyl)amino]propan-1-one

Remark – other active cpd. detected

| | |
|-----------------------------|---|
| Sample ID: | 3168-22 |
| Sample description: | powder - white off |
| Sample type: | RM-reference material |
| Comments: | CAY Lot#0638414-3, |
| Date of entry (DD/MM/YYYY): | 15/06/2022 |
| web link | http://www.policija.si/apps/nfl_response_web/seznam.php |

| | |
|---|---|
| Substance identified-structure ² (base form) | |
| Systematic name: | 1-(2H-1,3-benzodioxol-5-yl)-2-[cyclohexyl(methyl)amino]propan-1-one |
| Other names: | 1-(benzo[d][1,3]dioxol-5-yl)-2-(cyclohexyl(methyl)amino)propan-1-one; 3,4-Methylenedioxy-N,N-Cyclohexylmethcathinone; 3,4-Methylenedioxy-α-Cyclohexylmethylcathinone; 3,4-Methylenedioxy-α-Methylcyclohexylaminopropiophenone; 3,4-Methylenedioxy-N-cyclohexy |
| Formula (per base form) | C17H23NO3 |
| M _w (g/mol) | 289,38 |
| Salt form: | HCl |
| StdInChIKey (per base form) | YKIOVTWPVRMUPN-UHFFFAOYSA-N |
| Other active cpd. detected | |
| Add.info (purity..) | ≥98% |

¹ Approved by: Dr. Sonja Klemenc² Created by OPSIN free tool: <http://opsin.ch.cam.ac.uk/> DOI: 10.1021/ci100384d

Report updates

| date | comments (explanation) |
|------|------------------------|
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| | |
| | |

Supporting information

| Analytical technique: | applied | remarks |
|-------------------------|---------|---|
| GC-MS (EI ionization) | + | NFL GC-RT (min): 8,66 BP(1): 140; BP(2): 58,BP(3) :55, |
| FTIR-ATR | + | direct measurement |
| GC-IR (condensed phase) | + | always as base form |
| HPLC-TOF | + | exact mass theoretical: 289,1678 / measured Δppm: -1,86 |

1. GC-MS (Agilent): GC-method is RT locked to tetracosane (9.258 min). Injection volume 1 µl 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 µm. 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 cm⁻¹; resolution 4cm⁻¹

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

GC-method: Injection volume 1 µl 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.

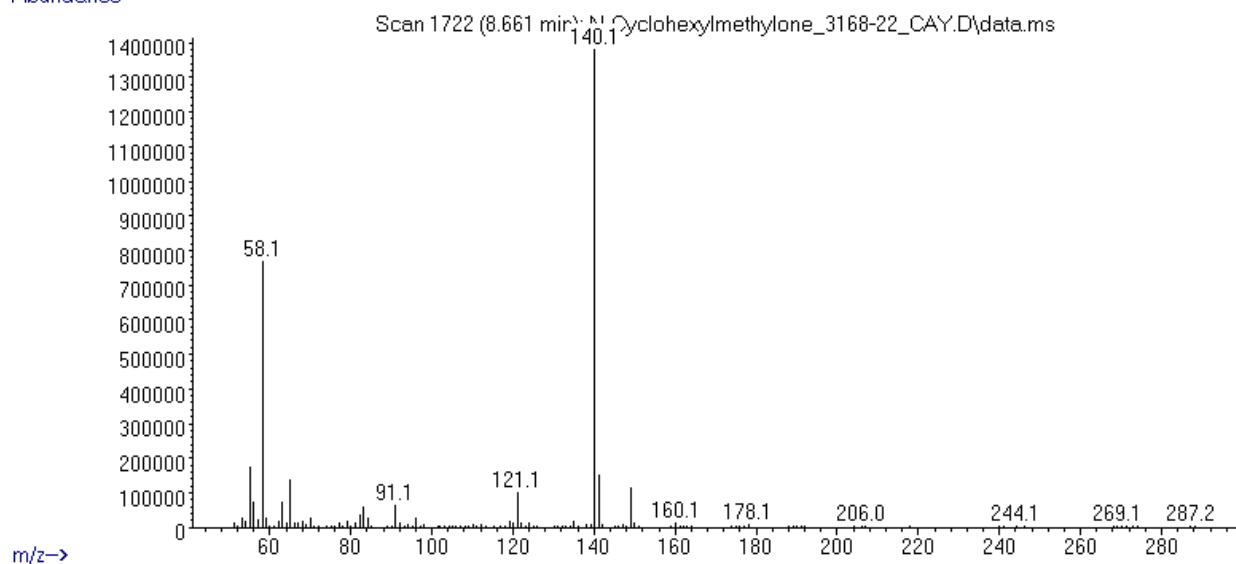
IR (condensed (solid) phase): IR scan range 4000 to 650, resolution 4 cm⁻¹.

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 µl. 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 (N2) 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.

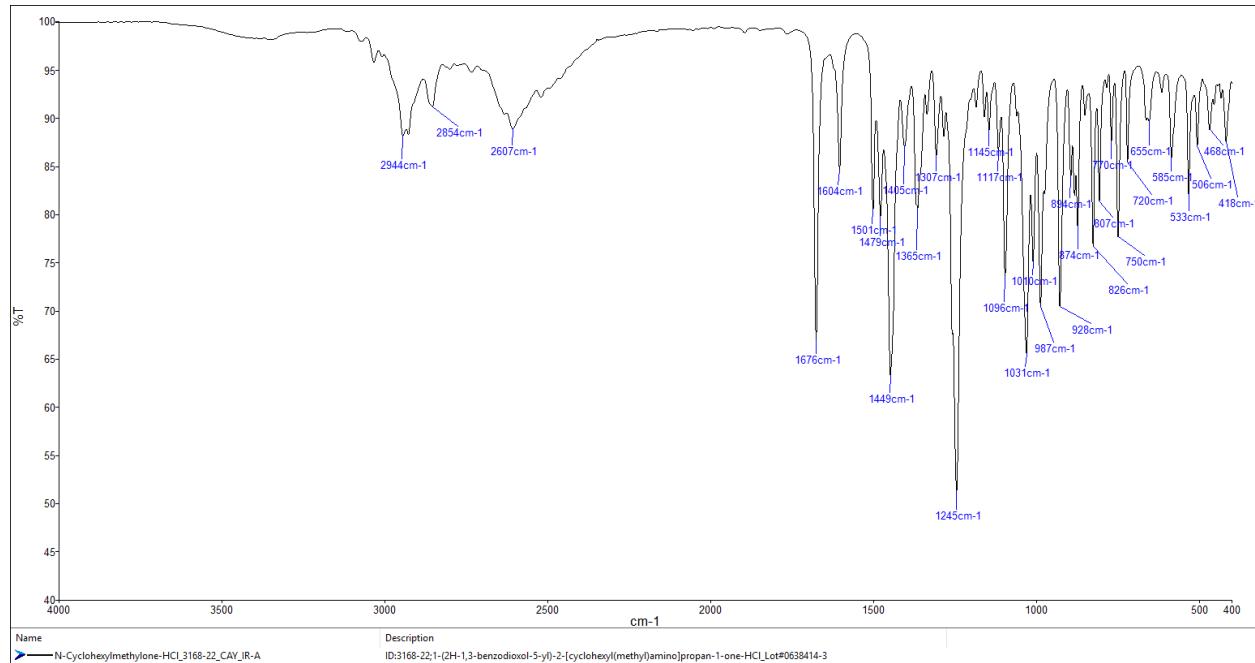
ANALYTICAL RESULTS

MS (EI)

Abundance



FTIR-ATR (direct measurement – sample as received)



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

