

**sclt 0203-11-01**

Sample ID: BIA240729S0009  
Strain: sour chem

Produced:  
Collected:  
Received: 07/29/2024  
Completed: 08/02/2024  
Batch#:

Client  
**cloud 9**  
Lic. # sclt0203  
4082 Noyestar Rd  
East Hardwick, VT 05836

Matrix: Plant  
Type: Flower - Cured  
Sample Size: 6.23 g  
Lot#:



**Summary**

Test	Date Tested	Result
Sample		Complete
Cannabinoids	07/30/2024	Complete
Moisture	07/30/2024	11.40% - Complete
Water Activity	07/30/2024	0.571 aw - Complete
Terpenes	07/31/2024	Complete
Microbials	08/01/2024	Complete

**Cannabinoids**

Completed

<b>28.21%</b> Total THC	<b>0.06%</b> Total CBD	<b>33.59%</b> Total Cannabinoids
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Analyte	LOQ	Results	Results	Mass
	mg/g	%	mg/g	mg/serving
CBDVa	0.0005	<LOQ	<LOQ	
CBDV	0.0012	<LOQ	<LOQ	
CBDa	0.0008	0.07	0.7	
CBGa	0.0008	1.38	13.8	
CBG	0.0019	0.10	1.0	
CBD	0.0019	<LOQ	<LOQ	
THCV	0.0021	<LOQ	<LOQ	
CBN	0.0013	<LOQ	<LOQ	
Δ9-THC	0.0020	0.87	8.7	
Δ8-THC	0.0019	<LOQ	<LOQ	
Δ10-THC	0.0002	<LOQ	<LOQ	
CBC	0.0024	<LOQ	<LOQ	
THCa	0.0034	31.17	311.7	
<b>Total THC</b>		<b>28.21</b>	<b>282.07</b>	
<b>Total CBD</b>		<b>0.06</b>	<b>0.62</b>	
<b>Total</b>		<b>33.59</b>	<b>335.90</b>	<b>0.00</b>

Analyst: 056

Cannabinoids Methodology: High Performance Liquid Chromatography (HPLC) using PerkinElmer FLEXAR™ with Photo Diode Array Detector (PDA)

Total CBD and total THC are calculated values, to account for assumed decarboxylation from the acid form (THCA or CBDA) to the neutral form, causing weight loss of the acid group. These values are calculated as follows:

Total THC = (THCA x 0.877) + Δ9-THC

Total CBD = (CBDA x 0.877) + CBD Reagent

Blanks: < LOQs for all analytes

LOQ = The lowest quantity that this method can reliably detect. Any cannabinoid that was not detected is assumed to be less than the stated LOQ (<LOQ).

All results reflect dry weight of material, based on % moisture of the sample.

Measurement of Uncertainty (MU): the parameter, associated with the result of a measurement, that characterizes the dispersion of the values that could reasonably be attributed to the particular quantity subject to measurement. Δ9-THC MU = ±0.005% Total THC MU = ±0.007%

All other cannabinoid MU values are available upon request.

All moisture analysis is determined by loss-on-drying measurement using OHAUS Model MB90 Moisture Content Readers.




Luke Emerson-Mason  
Laboratory Director  
08/02/2024

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(866) 506-5866  
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**Terpenes**
**Completed**

Analyte	LOQ	Results	Results
	mg/g	mg/g	%
β-Myrcene	0.010	23.505	2.351
α-Pinene	0.010	7.382	0.738
β-Pinene	0.010	4.061	0.406
β-Caryophyllene	0.010	2.944	0.294
Limonene	0.010	2.828	0.283
α-Humulene	0.010	1.004	0.100
Camphene	0.010	0.097	0.010
Terpinolene	0.010	0.077	0.008
α-Bisabolol	0.010	0.042	0.004
Linalool	0.010	0.032	0.003
γ-Terpinene	0.010	0.022	0.002
Caryophyllene Oxide	0.010	0.015	0.002
Eucalyptol	0.010	0.014	0.001
α-Terpinene	0.010	0.013	0.001
3-Carene	0.010	<LOQ	<LOQ
cis-Nerolidol	0.010	<LOQ	<LOQ
Geraniol	0.010	<LOQ	<LOQ
Guaiol	0.010	<LOQ	<LOQ
Isopulegol	0.010	<LOQ	<LOQ
Ocimene	0.010	<LOQ	<LOQ
p-Cymene	0.010	<LOQ	<LOQ
trans-Nerolidol	0.010	<LOQ	<LOQ
<b>Total</b>		<b>42.037</b>	<b>4.204</b>

**Primary Aromas**


Analyst: 045

LOQ = The lowest quantity this method can reliably detect. Any terpene that was not detected is assumed to be less than the stated LOQ (&lt;LOQ).

Terpene Methodology: Headspace Sampler, Gas Chromatography-Mass Spectrometry (GC-MS), using Perkin Elmer Clarus® SQ8 GC MS

Reagent Blanks: &lt; LOQs for all analytes

All results reflect dry weight of material, based on % moisture of the sample.

All moisture analysis is determined by loss-on-drying measurement using OHAUS Model MB90 Moisture Content Readers.




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**Pathogens**

Completed

Pathogens	LOD	Results
	CFU/g	CFU/g
Aspergillus	5	Not Detected
Shiga Toxin E. Coli	5	Not Detected
Salmonella SPP	5	Not Detected

Analyst: 018

Test Methodology: Bio-Rad IQ-Check PCR Kits

cfu/g = colony forming units per gram

LOD = The lowest quantity that this method can reliably detect. Any microbial growth that was not detected is assumed to be less than the stated LOD (<LOD).

Reagent Blanks: <LOD for all analytes




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