

# Elissa Zarzour

Date of Birth **16 Aug 2005**

Sex **Female**

Location **4 Tyrone Terrace, BANORA POINT NSW 2486  
Australia**

Referred by **Leigh Gibbs**

Report ID **R125080018732**

Primary Sample ID **BCH2201**

Sampling -

Report Released on **11:58am on 11 August 2025 (AEST)**



# Targeted Pathogen Panel

Elissa Zarzour

METAXPLORE™ GI PLUS

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PARASITIC

MARKER	RESULT	DESCRIPTION
<i>Cryptosporidium</i> spp.	NOT DETECTED	
<i>Cyclospora cayetanensis</i>	NOT DETECTED	
<i>Dientamoeba fragilis</i>	NOT DETECTED	
<i>Entamoeba histolytica</i>	NOT DETECTED	
<i>Giardia lamblia</i>	NOT DETECTED	

\*NATA/RCPA accreditation does not cover the performance of services with this symbol.



Accreditation No. **20563**  
Site No. **24651**

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**1300 974 621**

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BACTERIAL

MARKER	RESULT	DESCRIPTION
<i>Aeromonas</i> spp.	NOT DETECTED	
<i>Campylobacter</i> spp.	NOT DETECTED	
<i>Clostridium difficile</i> toxin B	NOT DETECTED	
<i>E. coli</i> O157	NOT DETECTED	
Enteraggregative <i>E. coli</i> (EAEC)	NOT DETECTED	
Enteropathogenic <i>E. coli</i> (EPEC)	NOT DETECTED	
Enterotoxigenic <i>E. coli</i> (ETEC)	NOT DETECTED	
Hypervirulent <i>Clostridium difficile</i>	NOT DETECTED	
<i>Salmonella</i> spp.	NOT DETECTED	
Shiga Toxin	NOT DETECTED	
<i>Shigella</i> spp./EIEC	NOT DETECTED	
<i>Vibrio</i> spp.	NOT DETECTED	
<i>Yersinia enterocolitica</i>	NOT DETECTED	

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Primary Sample ID **BCH2201**

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# Diversity

INSIGHTS 7

Login at [practitioner.co-biome.com](https://practitioner.co-biome.com) to view

## Microbial Markers

RESEARCH USE ONLY  
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Marker	Relative Abundance	Distance from Average
Microbial Diversity	<div><div>ND</div><div><div></div><div>3.28</div></div></div>	-1.78
Microbial Richness	<div><div>ND</div><div><div></div><div>99.00</div></div></div>	-2.22



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# Intestinal Motility

INSIGHTS 12

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## Gastrointestinal Health Markers

Marker Name		Range
Faecal pH	<div><div></div><div></div><div></div></div>	5.70 - 7.30
	<div>RESEARCH USE ONLY NOT FOR DIAGNOSTIC USE</div> <div>6.02</div>	

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## Microbial Markers

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Marker	Relative Abundance	Distance from Average
Methane producing archaea -	<div><div></div><div>0.00%</div></div>	0.00
Microbial Diversity	<div><div>ND</div><div>3.28</div></div>	-1.78
Propionate producing microbes +	<div><div>ND</div><div>1.79%</div></div>	-1.03



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# Intestinal Inflammation

INSIGHTS 32

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## Microbial Markers

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Marker	Relative Abundance	Distance from Average
IPA producing microbes +	<div><div>ND</div><div>0.02%</div></div>	-2.50
Acetate producing microbes +	<div><div>ND</div><div>73.44%</div></div>	+0.63
Butyrate producing microbes +	<div><div>ND</div><div>12.13%</div></div>	-1.41
Hexa-LPS producing microbes -	<div><div>ND</div><div>0.99%</div></div>	+1.20
Mucin Degradation	<div><div>ND</div><div>806.96</div></div>	+0.92
Propionate producing microbes +	<div><div>ND</div><div>1.79%</div></div>	-1.03



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# Intestinal Barrier

INSIGHTS 14

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## Microbial Markers

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Marker	Relative Abundance	Distance from Average
IPA producing microbes +	ND 0.02%	-2.50
<i>B. fragilis</i> toxin producing microbes -	0.00%	0.00
Butyrate producing microbes +	ND 12.13%	-1.41
Hexa-LPS producing microbes -	ND 0.99%	+1.20
Hydrogen sulphide producing microbes +	ND 4.91%	-0.53



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# Systemic Inflammation

INSIGHTS 27

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## Microbial Markers

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Marker	Relative Abundance	Distance from Average
IPA producing microbes +	<div><div>ND</div><div><div></div><div>0.02%</div></div></div>	-2.50
BCAA producing microbes -	<div><div>ND</div><div><div></div><div>67.69%</div></div></div>	+1.06
Butyrate producing microbes +	<div><div>ND</div><div><div></div><div>12.13%</div></div></div>	-1.41
Hexa-LPS producing microbes -	<div><div>ND</div><div><div></div><div>0.99%</div></div></div>	+1.20
Microbial Diversity	<div><div>ND</div><div><div></div><div>3.28</div></div></div>	-1.78
Trimethylamine producing microbes -	<div><div>ND</div><div><div></div><div>1.43%</div></div></div>	-1.32



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# Detox / Retox

INSIGHTS 5

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Marker	Relative Abundance	Distance from Average
Beta-glucuronidase producing microbes -	<div><div>ND</div><div><div></div></div><div>26.92%</div></div>	+1.01
Oxalate consuming microbes +	<div><div>ND</div><div><div></div></div><div>2.58%</div></div>	+0.64

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# Emerging Metabolites

INSIGHTS 0

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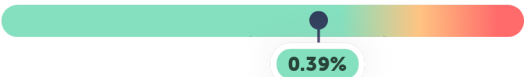


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## Microbial Markers

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Marker	Relative Abundance	Distance from Average
Ammonia (urease) producing microbes	ND  19.96%	+2.45
GABA consuming microbes	ND  3.58%	-1.26
GABA producing microbes	ND  6.67%	-1.43
Histamine producing microbes	ND  0.46%	+0.12
Human DNA	ND  0.39%	+0.47
Lactate producing microbes	ND  78.20%	+1.14
Vitamin K producing microbes	ND  22.43%	+0.68



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