

# Lisa Bennett

|                |  |                        |             |                    |                                |
|----------------|--|------------------------|-------------|--------------------|--------------------------------|
| Date of Birth: | 28 Jan, 1959   | Practitioner:          | Leigh Gibbs | Report ID:         | R225100000446                  |
| Sex:           | FEMALE   | Practice phone number: | -           | Primary Sample ID: | BCL7400                        |
| Phone number:  | +61428160197   | Practice:              | -           | Report released:   | 10:30 pm on 15 Oct 2025 (AEST) |
| Location:      | Unit 2 35 Horizon Drive WEST<br>BALLINA NSW 2478 Australia | Practice Address:      | -           |                    |                                |

## Overview

### Pathologist Notes

Submitted sample was assayed at >48 hours after collection which may result in reduced reported Secretory IgA concentrations. In such cases, we recommend to also consider clinical symptoms and other diagnostic tests for the final diagnosis and/or to request another patient sample. Submitted sample recorded exposure between 25-30 degrees after collection which may result in reduced reported Zonulin concentrations. In such cases, we recommend to also consider clinical symptoms and other diagnostic tests for the final diagnosis and/or to request another patient sample. Diagnostic assays (exclusive of expert summary): Approved by Prof. Paul Griffin, FRCPA Clinical Microbiologist.



Accreditation No. 20563  
Site No. 24651

Specimen processed by Microba Laboratories.  
MetaXplore™ reports are generated based on the testing of faecal samples.  
The faecal occult blood, polymerase chain reaction (PCR) and enzyme-linked immunosorbent assays (ELISA) used in the MetaXplore™ range are diagnostic and are approved for clinical use.  
NATA/RCPA accreditation does not cover the performance of services with \* indicated.

For assistance, contact  
1300 974 621

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Targeted Pathogen Panel

Parasitic

| Status       | Name                    |
|--------------|-------------------------|
| Not Detected | Cryptosporidium spp.    |
| Not Detected | Cyclospora cayetanensis |
| Not Detected | Dientamoeba fragilis    |
| Not Detected | Entamoeba histolytica   |
| Not Detected | Giardia lamblia         |

Bacterial

| Status       | Name                                |
|--------------|-------------------------------------|
| Not Detected | Aeromonas spp.                      |
| Not Detected | Campylobacter spp.                  |
| Not Detected | Clostridium difficile toxin B       |
| Not Detected | E. coli O157                        |
| Not Detected | Enteroaggregative E. coli (EAEC)    |
| Not Detected | Enteropathogenic E. coli (EPEC)     |
| Not Detected | Enterotoxigenic E. coli (ETEC)      |
| Not Detected | Hypervirulent Clostridium difficile |

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| Status       | Name                    |
|--------------|-------------------------|
| Not Detected | Salmonella spp.         |
| Not Detected | Shiga Toxin             |
| Not Detected | Shigella spp./EIEC      |
| Not Detected | Vibrio spp.             |
| Not Detected | Yersinia enterocolitica |

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Gastrointestinal (GI) Markers

|              | Marker                | Result       | Reference Range            |
|--------------|-----------------------|--------------|----------------------------|
| Optimal      | Calprotectin *        | 34.51 µg/g   | ≤ 50.00 µg/g               |
| Optimal      | Lactoferrin *         | 0.58 µg/g    | ≤ 7.20 µg/g                |
| Optimal      | Pancreatic Elastase * | 677.42 µg/mL | ≥ 200.00 µg/mL             |
| Optimal      | Secretory IgA *       | 1338.43 µg/g | 500.00 µg/g - 2000.00 µg/g |
| Optimal      | Zonulin *             | 83.20 ng/mL  | ≤ 100.00 ng/mL             |
| Not Detected | Faecal Occult Blood   | -            | -                          |

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## Microbiome Health Report

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Microbiome Markers

|                 | Marker                                      | Relative Abundance | Compared to Healthy Cohort |                   |
|-----------------|---|--------------------|----------------------------|-------------------|
| High            | Propionate producing microbes               | 16.41 %            | +2.31                      | RESEARCH USE ONLY |
| High            | Trimethylamine producing microbes           | 6.30 %             | +1.76                      | RESEARCH USE ONLY |
| Low             | IPA producing microbes                      | 0.03 %             | -1.96                      | RESEARCH USE ONLY |
| Borderline High | Hydrogen sulphide producing microbes        | 8.72 %             | +0.86                      | RESEARCH USE ONLY |
| Borderline Low  | Butyrate producing microbes                 | 14.71 %            | -0.71                      | RESEARCH USE ONLY |
| Optimal         | Acetate producing microbes                  | 73.16 %            | +0.59                      | RESEARCH USE ONLY |
| Optimal         | BCAA producing microbes                     | 53.58 %            | -0.29                      | RESEARCH USE ONLY |
| Optimal         | Beta-glucuronidase producing microbes       | 17.72 %            | -0.02                      | RESEARCH USE ONLY |
| Optimal         | Oxalate consuming microbes                  | 1.00 %             | -0.41                      | RESEARCH USE ONLY |
| Not Detected    | <i>B. fragilis</i> toxin producing microbes | 0.00 %             | -                          | RESEARCH USE ONLY |
| Not Detected    | Hexa-LPS producing microbes                 | 0.00 %             | -                          | RESEARCH USE ONLY |
| Not Detected    | Methane producing archaea                   | 0.00 %             | -                          | RESEARCH USE ONLY |

|                | Marker              | Result | Compared to Healthy Cohort |                   |
|----------------|---------------------|--------|----------------------------|-------------------|
| Low            | Microbial Richness  | 106    | -2.00                      | RESEARCH USE ONLY |
| Borderline Low | Microbial Diversity | 3.52   | -1.24                      | RESEARCH USE ONLY |
| Optimal        | Mucin Degradation   | 530.04 | -0.74                      | RESEARCH USE ONLY |

Gastrointestinal (GI) Markers

|         | Marker    | Result | Reference Range |                   |
|---------|-----------|--------|-----------------|-------------------|
| Optimal | Faecal pH | 6.09   | 5.70 - 7.30     | RESEARCH USE ONLY |

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Emerging Metabolites

|                 | Marker                              | Relative Abundance | Compared to Healthy Cohort |                   |
|-----------------|-------------------------------------|--------------------|----------------------------|-------------------|
| High            | Ammonia (urease) producing microbes | 19.58 %            | +2.41                      | RESEARCH USE ONLY |
| High            | Histamine producing microbes        | 4.29 %             | +1.74                      | RESEARCH USE ONLY |
| High            | Lactate producing microbes          | 79.48 %            | +1.29                      | RESEARCH USE ONLY |
| Low             | Vitamin K producing microbes        | 7.86 %             | -1.51                      | RESEARCH USE ONLY |
| Borderline High | Human DNA                           | 0.77 %             | +0.86                      | RESEARCH USE ONLY |
| Borderline Low  | GABA producing microbes             | 10.22 %            | -0.77                      | RESEARCH USE ONLY |
| Optimal         | GABA consuming microbes             | 8.49 %             | +0.38                      | RESEARCH USE ONLY |