

invivo[®]

The Human Microbiome Company

URINARY ECOLOGIX

TEST REPORTED: [REDACTED]
 TEST RECEIVED: [REDACTED]
 PATIENT NAME: [REDACTED]
 PATIENT DOB: [REDACTED]

CLINICIAN NAME: CLINICIAN
 SAMPLE TYPE: URINE
 SEX: FEMALE

Lab Director:
 Emma Beamish PhD



Lactobacillus	RESULTS:	RANGE:
<i>Lactobacillus crispatus</i>	12.2	<15.5
<i>Lactobacillus gasseri</i>	<DL	<9.9
<i>Lactobacillus iners</i>	5.8	<12.9

Pathobionts	RESULTS:	RANGE:
<i>Actinotignum schaalii</i>	18.8 HIGH	<6.0
<i>Aerococcus urinae</i>	5.0	<7.0
<i>Escherichia coli</i>	2.6	<7.7
<i>Staphylococcus saprophyticus</i>	<DL	<1.8
<i>Streptococcus agalactiae</i>	<DL	<5.0



Scan for more information and resources on Urinary EcologiX

Disclaimer: This test was developed, and its performance characteristics determined by Invivo Diagnostics. This test is not intended for use by consumers or physicians as a means to cure, treat, prevent, diagnose or mitigate any disease or other medical condition. The information contained in this document is in no way to be taken as prescriptive nor to replace the physicians duty of care and personalised care practices.

Pathogens

RESULTS:

RANGE:

Pathogen	Result	Category	Scale	Range
<i>Citrobacter freundii</i>	6.0	HIGH	0 4 5 8 9 12 13 16 17 20	<DL
<i>Enterococcus faecalis</i>	10.8	HIGH	0 4 5 8 9 12 13 16 17 20	<DL
<i>Klebsiella pneumoniae</i>	16.4	HIGH	0 4 5 8 9 12 13 16 17 20	<DL
<i>Proteus mirabilis</i>	18.9	HIGH	0 4 5 8 9 12 13 16 17 20	<DL
<i>Pseudomonas aeruginosa</i>	0.7	HIGH	0 4 5 8 9 12 13 16 17 20	<DL
<i>Serratia marcescens</i>	4.0	HIGH	0 4 5 8 9 12 13 16 17 20	<DL
<i>Uropathogenic E. coli (UPEC)</i>	1.3	HIGH	0 4 5 8 9 12 13 16 17 20	<DL

The Urinary EcologiX™ profile utilises the highly sensitive quantitative PCR (qPCR) TaqMan technology for analysis of the Urinary Tract microbiota. Microbial genes of interest are quantified within a sample and their abundances are normalised to an endogenous and highly conserved gene. The qPCR results are therefore reported as the relative abundance of a microorganism as proportional to the whole microbial community.



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