April 18, 2025

Luminex Corporation
Sheri Calderon
Senior Regulatory Affairs Associate
4088 Commercial Avenue
Northbrook, Illinois 60062

Re: K243013
Trade/Device Name: LIAISON PLEX Gram-Negative Blood Culture Assay
Regulation Number: 21 CFR 866.3365
Regulation Name: Multiplex Nucleic Acid Assay For Identification Of Microorganisms And Resistance Markers From Positive Blood Cultures
Regulatory Class: Class II
Product Code: PEN, NSU
Dated: March 21, 2025
Received: March 21, 2025

Dear Sheri Calderon:

We have reviewed your section 510(k) premarket notification of intent to market the device referenced above and have determined the device is substantially equivalent (for the indications for use stated in the enclosure) to legally marketed predicate devices marketed in interstate commerce prior to May 28, 1976, the enactment date of the Medical Device Amendments, or to devices that have been reclassified in accordance with the provisions of the Federal Food, Drug, and Cosmetic Act (the Act) that do not require approval of a premarket approval application (PMA). You may, therefore, market the device, subject to the general controls provisions of the Act. Although this letter refers to your product as a device, please be aware that some cleared products may instead be combination products. The 510(k) Premarket Notification Database available at https://www.accessdata.fda.gov/scripts/cdrh/cfdocs/cfpmn/pmn.cfm identifies combination product submissions. The general controls provisions of the Act include requirements for annual registration, listing of devices, good manufacturing practice, labeling, and prohibitions against misbranding and adulteration. Please note: CDRH does not evaluate information related to contract liability warranties. We remind you, however, that device labeling must be truthful and not misleading.

If your device is classified (see above) into either class II (Special Controls) or class III (PMA), it may be subject to additional controls. Existing major regulations affecting your device can be found in the Code of Federal Regulations, Title 21, Parts 800 to 898. In addition, FDA may publish further announcements concerning your device in the Federal Register.

Additional information about changes that may require a new premarket notification are provided in the FDA guidance documents entitled "Deciding When to Submit a 510(k) for a Change to an Existing Device" (https://www.fda.gov/media/99812/download) and "Deciding When to Submit a 510(k) for a Software Change to an Existing Device" (https://www.fda.gov/media/99785/download).

Your device is also subject to, among other requirements, the Quality System (QS) regulation (21 CFR Part 820), which includes, but is not limited to, 21 CFR 820.30, Design controls; 21 CFR 820.90, Nonconforming product; and 21 CFR 820.100, Corrective and preventive action. Please note that regardless of whether a change requires premarket review, the QS regulation requires device manufacturers to review and approve changes to device design and production (21 CFR 820.30 and 21 CFR 820.70) and document changes and approvals in the device master record (21 CFR 820.181).

Please be advised that FDA's issuance of a substantial equivalence determination does not mean that FDA has made a determination that your device complies with other requirements of the Act or any Federal statutes and regulations administered by other Federal agencies. You must comply with all the Act's requirements, including, but not limited to: registration and listing (21 CFR Part 807); labeling (21 CFR Part 801 and Part 809); medical device reporting (reporting of medical device-related adverse events) (21 CFR Part 803) for devices or postmarketing safety reporting (21 CFR Part 4, Subpart B) for combination products (see https://www.fda.gov/combination-products/guidance-regulatory-information/postmarketing-safety-reporting-combination-products); good manufacturing practice requirements as set forth in the quality systems (QS) regulation (21 CFR Part 820) for devices or current good manufacturing practices (21 CFR Part 4, Subpart A) for combination products; and, if applicable, the electronic product radiation control provisions (Sections 531-542 of the Act); 21 CFR Parts 1000-1050.

All medical devices, including Class I and unclassified devices and combination product device constituent parts are required to be in compliance with the final Unique Device Identification System rule ("UDI Rule"). The UDI Rule requires, among other things, that a device bear a unique device identifier (UDI) on its label and package (21 CFR 801.20(a)) unless an exception or alternative applies (21 CFR 801.20(b)) and that the dates on the device label be formatted in accordance with 21 CFR 801.18. The UDI Rule (21 CFR 830.300(a) and 830.320(b)) also requires that certain information be submitted to the Global Unique Device Identification Database (GUDID) (21 CFR Part 830 Subpart E). For additional information on these requirements, please see the UDI System webpage at https://www.fda.gov/medical-devices/device-advice-comprehensive-regulatory-assistance/unique-device-identification-system-udi-system.

Also, please note the regulation entitled, "Misbranding by reference to premarket notification" (21 CFR 807.97). For questions regarding the reporting of adverse events under the MDR regulation (21 CFR Part 803), please go to https://www.fda.gov/medical-devices/medical-device-safety/medical-device-reporting-mdr-how-report-medical-device-problems.

For comprehensive regulatory information about medical devices and radiation-emitting products, including information about labeling regulations, please see Device Advice (https://www.fda.gov/medical-devices/device-advice-comprehensive-regulatory-assistance) and CDRH Learn (https://www.fda.gov/training-and-continuing-education/cdrh-learn). Additionally, you may contact the Division of Industry and Consumer Education (DICE) to ask a question about a specific regulatory topic. See the DICE website (https://www.fda.gov/medical-devices/device-advice-comprehensive-regulatory-

assistance/contact-us-division-industry-and-consumer-education-dice) for more information or contact DICE by email (DICE@fda.hhs.gov) or phone (1-800-638-2041 or 301-796-7100).

Sincerely,

Noel J. Gerald -S

Noel J. Gerald, Ph.D.
Deputy Division Director
Division of Microbiology Devices
OHT7: Office of In Vitro Diagnostics
Office of Product Evaluation and Quality
Center for Devices and Radiological Health

Enclosure

DEPARTMENT OF HEALTH AND HUMAN SERVICES
Food and Drug Administration

Indications for Use

Form Approved: OMB No. 0910-0120
Expiration Date: 07/31/2026
See PRA Statement below.

510(k) Number *(if known)*
K243013

Device Name
LIAISON PLEX® Gram-Negative Blood Culture Assay

Indications for Use *(Describe)*
The LIAISON PLEX® Gram-Negative Blood Culture (BCN) Assay, performed using the automated, sample-to-result LIAISON PLEX® System, is a qualitative multiplexed in vitro diagnostic test for the simultaneous detection and identification of selected gram-negative pathogens and/or selected genetic determinants associated with antimicrobial resistance in positive blood culture bottles. LIAISON PLEX® BCN Assay is performed directly on blood culture media using blood culture bottles identified as positive by a continuous monitoring blood culture system which contain gram-negative bacteria as determined by Gram stain.

The LIAISON PLEX® BCN Assay detects and identifies the following:
Resistance Markers:
CTX-M (blaCTX-M)
IMP (blaIMP)
KPC (blaKPC)
NDM (blaNDM)
OXA (blaOXA)
VIM (blaVIM)
MCR
SME (blaSME)

Gram Negative Genera and Species:
Enterobacteriaceae / Morganellaceae
Acinetobacter baumannii
Acinetobacter spp.
Citrobacter spp.
Enterobacter spp. (1)
Escherichia coli (2)
Haemophilus influenzae
Klebsiella oxytoca
Klebsiella pneumoniae
Klebsiella variicola
Morganella morganii
Neisseria meningitidis
Proteus spp.
Pseudomonas aeruginosa
Pseudomonas spp.
Salmonella spp.
Serratia marcescens
Stenotrophomonas maltophilia

(1) Due to reclassification, Klebsiella aerogenes will be reported Enterobacter spp.
(2) LIAISON PLEX® BCN Assay will not distinguish between Escherichia coli and Shigella spp. (S. dysenteriae, S. boydii, S. flexneri and S. sonnei)

LIAISON PLEX® BCN Assay contains targets for the detection of genetic determinants associated with resistance to

carbapenems (blaCTX-M, blaIMP, blaKPC, blaNDM, blaOXA48-like, blaVIM, blaSME) to aid in the identification of potentially antimicrobial-resistant organisms in positive blood culture samples. In addition, the panel includes an assay for the detection of the mobilized genetic determinant MCR, an emerging marker of public health importance. The antimicrobial resistance gene or marker detected may or may not be associated with the agent responsible for disease. Negative results for these select antimicrobial resistance gene and marker assays do not indicate susceptibility, as multiple mechanisms of resistance to ß-lactams and colistin exist.

LIAISON PLEX® BCN Assay is indicated for use in conjunction with other clinical and laboratory findings to aid in the diagnosis of bacterial bloodstream infections (BSI). LIAISON PLEX® BCN Assay is not intended to monitor treatment of these infections. Sub-culturing of positive blood cultures is necessary to recover organisms for antimicrobial susceptibility testing (AST), for identification of organisms not detected by LIAISON PLEX® BCN Assay, to detect mixed infections that may not be detected by LIAISON PLEX® BCN Assay, for association of antimicrobial resistance marker genes to a specific organism, or for epidemiological typing.

Type of Use *(Select one or both, as applicable)*

☒ Prescription Use (Part 21 CFR 801 Subpart D) ☐ Over-The-Counter Use (21 CFR 801 Subpart C)

CONTINUE ON A SEPARATE PAGE IF NEEDED.

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510(k) Summary

This Summary of 510(k) safety and effectiveness information is being submitted in accordance with the requirements of 21 CFR 807.92.

Preparation date: 16 April 2025

A. 510(k) Number:

K243013

B. Purpose for Submission:

Traditional 510(k), New Device

C. Measurand:

Nucleic acid sequences for the following organisms: *Enterobacteriaceae / Morganellaceae, Acinetobacter baumannii, Acinetobacter* spp., *Citrobacter* spp., *Enterobacter* spp., *Escherichia coli, Haemophilus influenzae, Klebsiella oxytoca, Klebsiella pneumoniae, Klebsiella variicola, Morganella morganii, Neisseria meningitidis, Proteus* spp., *Pseudomonas aeruginosa, Pseudomonas* spp., *Salmonella* spp., *Serratia marcescens,* and *Stenotrophomonas maltophilia.* Nucleic acid sequences for the following resistance markers: CTX-M (*bla*CTX-M), IMP (*bla*IMP), KPC (*bla*KPC), NDM (*bla*NDM), OXA (*bla*OXA), VIM (*bla*VIM), MCR, and SME (*bla*SME).

D. Type of Test:

Qualitative Multiplexed Direct Detection Hybridization Assay

E. Applicant:

Sheri Calderon, Luminex Corporation
4088 Commercial Avenue
Northbrook, IL 60062
(847) 400-9000

F. Proprietary and Established Names:

LIAISON PLEX® Gram-Negative Blood Culture Assay

G. Regulatory Information:

Product Code	Classification	Regulation Section	Panel
PEN	II	21 CFR 866.3365 – Multiplex Nucleic Acid Assay for Identification of Microorganisms and Resistance Markers from Positive Blood Cultures	83 (Microbiology)

H. Intended Use:

1. Intended use(s):

The LIAISON PLEX® Gram-Negative Blood Culture (BCN) Assay, performed using the automated, sample-to-result LIAISON PLEX® System, is a qualitative multiplexed in vitro diagnostic test for the simultaneous detection and identification of selected gram-negative pathogens and/or selected genetic determinants associated with antimicrobial resistance in positive blood culture bottles. LIAISON PLEX® BCN Assay is performed directly on blood culture media using blood culture bottles identified as positive by a continuous monitoring blood culture system which contain gram-negative bacteria as determined by Gram stain.

The LIAISON PLEX® BCN Assay detects and identifies the following:

Resistance Markers	Gram Negative *Genera* and *Species*
CTX-M (*bla*CTX-M)	*Enterobacteriaceae / Morganellaceae*
IMP (*bla*IMP)	*Acinetobacter baumannii*
KPC (*bla*KPC)	*Acinetobacter* spp.
NDM (*bla*NDM)	*Citrobacter* spp.
OXA (*bla*OXA)	*Enterobacter* spp.[1]
VIM (*bla*VIM)	*Escherichia coli* [2]
MCR	*Haemophilus influenzae*
SME (*bla*SME)	*Klebsiella oxytoca*
	Klebsiella pneumoniae
	Klebsiella variicola
	Morganella morganii
	Neisseria meningitidis
	Proteus spp.
	Pseudomonas aeruginosa
	Pseudomonas spp.
	Salmonella spp.
	Serratia marcescens
	Stenotrophomonas maltophilia

[1] Due to reclassification, *Klebsiella aerogenes* will be reported *Enterobacter* spp.
[2] LIAISON PLEX BCN Assay will not distinguish between *Escherichia coli* and *Shigella* spp. (*S. dysenteriae, S. boydii, S. flexneri* and *S. sonnei*)

LIAISON PLEX® BCN Assay contains targets for the detection of genetic determinants associated with resistance to carbapenems ($bla_{\text{CTX-M}}$, bla_{IMP}, bla_{KPC}, bla_{NDM}, $bla_{\text{OXA48-like}}$, bla_{VIM}, bla_{SME}) to aid in the identification of potentially antimicrobial-resistant organisms in positive blood culture samples. In addition, the panel includes an assay for the detection of the mobilized genetic determinant MCR, an emerging marker of public health importance. The antimicrobial resistance gene or marker detected may or may not be associated with the agent responsible for disease. Negative results for these select antimicrobial resistance gene and marker assays do not indicate susceptibility, as multiple mechanisms of resistance to ß-lactams and colistin exist.

LIAISON PLEX® BCN Assay is indicated for use in conjunction with other clinical and laboratory

findings to aid in the diagnosis of bacterial bloodstream infections (BSI). LIAISON PLEX® BCN Assay is not intended to monitor treatment of these infections. Sub-culturing of positive blood cultures is necessary to recover organisms for antimicrobial susceptibility testing (AST), for identification of organisms not detected by LIAISON PLEX® BCN Assay, to detect mixed infections that may not be detected by LIAISON PLEX® BCN Assay, for association of antimicrobial resistance marker genes to a specific organism, or for epidemiological typing.

2. Indication(s) for use:
   Same as intended use.

3. Special conditions for use statement(s):
   For prescription use only.
   For *in vitro* diagnostic use only.

4. Special instrument requirements:
   For use with LIAISON PLEX® Systems.

I. Device Description:

The LIAISON PLEX® Gram-Negative Blood Culture (BCN) Assay is an automated test for the detection and identification of nucleic acid from gram-negative bacteria in a positive blood culture media sample. The BCN Assay is performed directly on blood culture media using blood culture bottles identified as positive by a continuous monitoring blood culture system, and which contain gram-negative bacteria, as determined by a Gram stain.

The LIAISON PLEX® System is a fully automated, bench-top "sample-to-answer" device that performs sample preparation, polymerase chain reaction (PCR) and microarray-based hybridization for the detection of target-specific nucleic acids. The test reagents are supplied as a single, disposable test cartridge. PCR is not performed on the LIAISON PLEX® BCN Assay, as it is a non-amplified, direct detection test performed on the LIAISON PLEX® System.

J. Substantial Equivalence Information:

1. Predicate device name(s):
   VERIGENE Blood Culture Gram-Negative (BC-GN) Nucleic Acid Test

2. Predicate 510(k) number(s):
   K132843

3. Comparison with predicate:
   The following tables compare the LIAISON PLEX® Gram-Negative Blood Culture Assay to the VERIGENE Gram-Negative Blood Culture (BC-GN) Nucleic Acid Test.

Comparison to Predicate Device	Predicate Device: K132843 VERIGENE Gram-Negative Blood Culture (BC-GN) Nucleic Acid Test, K132843	Candidate Device: K243013 LIAISON PLEX® Gram-Negative Blood Culture Assay
Product Code	PEN	PEN
Regulation Number	21 CFR 866.3365	21 CFR 866.3365
Organism Detected	Organisms: *Acinetobacter* spp., *Citrobacter* spp., *Enterobacter* spp., *Proteus* spp., *Escherichia coli, Klebsiella pneumoniae, Klebsiella oxytoca, and Pseudomonas aeruginosa* Resistance Markers: CTX-M (*bla*CTX-M), KPC (*bla*KPC), NDM (*bla*NDM), VIM (*bla*VIM), IMP (*bla*IMP), and OXA (*bla*OXA)	Organisms: *Enterobacteriaceae / Morganellaceae, Acinetobacter baumannii, Acinetobacter* spp., *Citrobacter* spp., *Enterobacter* spp., *Escherichia coli, Haemophilus influenzae, Klebsiella oxytoca, Klebsiella pneumoniae, Klebsiella variicola, Morganella morganii, Neisseria meningitidis, Proteus* spp., *Pseudomonas aeruginosa, Pseudomonas* spp., *Salmonella* spp., *Serratia marcescens,* and *Stenotrophomonas maltophilia* Resistance markers: CTX-M (*bla*CTX-M), IMP (*bla*IMP), KPC (*bla*KPC), NDM (*bla*NDM), OXA (*bla*OXA), VIM (*bla*VIM), MCR, and SME (*bla*SME).
Measurand	Nucleic acid from Organisms detected	Same
Intended Use	The Verigene® Gram Negative Blood Culture Nucleic Acid Test (BC-GN), performed using the sample-to-result Verigene System, is a qualitative multiplexed in vitro diagnostic test for the simultaneous detection and identification of selected gram-negative bacteria and resistance markers. BC-GN is performed directly on blood culture media using blood culture bottles identified as positive by a continuous monitoring blood culture system and which contain gram-negative bacteria as determined by gram stain. BC-GN detects and identifies the following: **Bacterial Genera and Species** *Acinetobacter* spp. *Citrobacter* spp. *Enterobacter* spp. *Proteus* spp. *Escherichia coli*[1] *Klebsiella pneumoniae* *Klebsiella oxytoca* *Pseudomonas aeruginosa* **Resistance Markers** CTX-M (*bla*CTX-M) KPC (*bla*KPC) NDM (*bla*NDM) VIM (*bla*VIM) IMP (*bla*IMP)	The LIAISON PLEX® Gram-Negative Blood Culture (BCN) Assay, performed using the automated, sample-to-result LIAISON PLEX® System, is a qualitative multiplexed *in vitro* diagnostic test for the simultaneous detection and identification of selected gram-negative pathogens and/or selected genetic determinants associated with antimicrobial resistance in positive blood culture bottles. BCN is performed directly on blood culture media using blood culture bottles identified as positive by a continuous monitoring blood culture system and which contain gram-negative bacteria as determined by Gram stain. The BCN Assay detects and identifies the following: **Gram Negative Genera and Species** *Enterobacteriaceae / Morganellaceae* *Acinetobacter baumannii* *Acinetobacter* spp. *Citrobacter* spp. *Enterobacter* spp.[1] *Escherichia coli*[2] *Haemophilus influenzae* *Klebsiella oxytoca* *Klebsiella pneumoniae* *Klebsiella variicola*

Comparison to Predicate Device	Predicate Device: K132843 VERIGENE Gram-Negative Blood Culture (BC-GN) Nucleic Acid Test, K132843	Candidate Device: K243013 LIAISON PLEX® Gram-Negative Blood Culture Assay
	OXA (*bla*OXA) [1]BC-GN will not distinguish *Escherichia coli* from *Shigella* spp. (*S. dysenteriae*, *S. flexneri*, *S. boydii*, and *S. sonnei)* BC-GN is indicated for use in conjunction with other clinical and laboratory findings to aid in the diagnosis of bacterial bloodstream infections; however, it is not used to monitor these infections. Sub-culturing of positive blood cultures is necessary to recover organisms for antimicrobial susceptibility testing (AST), for identification of organisms not detected by BC-GN, to detect mixed infections that may not be detected by BC-GN, for association of antimicrobial resistance marker genes to a specific organism, or for epidemiological typing.	*Morganella morganii* *Neisseria meningitidis* *Proteus* spp. *Pseudomonas aeruginosa* *Pseudomonas* spp. *Salmonella* spp. *Serratia marcescens* *Stenotrophomonas maltophilia* **Resistance Markers** CTX-M (*bla*CTX-M) IMP (*bla*IMP) KPC (*bla*KPC) NDM (*bla*NDM) OXA (*bla*OXA) VIM (*bla*VIM) MCR SME (*bla*SME) [1] Due to reclassification, Klebsiella aerogenes will be reported Enterobacter spp. [2] LIAISON PLEX BCN will not distinguish between *Escherichia coli* and *Shigella* spp. (*S. dysenteriae, S. boydii, S. flexneri* and *S. sonnei*) LIAISON PLEX® BCN Assay contains targets for the detection of genetic determinants associated with resistance to carbapenems (blaCTX-M, blaIMP, blaKPC, blaNDM, blaOXA48-like, blaVIM, blaSME) to aid in the identification of potentially antimicrobial-resistant organisms in positive blood culture samples. In addition, the panel includes an assay for the detection of the mobilized genetic determinant MCR, an emerging marker of public health importance. The antimicrobial resistance gene or marker detected may or may not be associated with the agent responsible for disease. Negative results for these select antimicrobial resistance gene and marker assays do not indicate susceptibility, as multiple mechanisms of resistance to ß-lactams and colistin exist. LIAISON PLEX® BCN Assay is indicated for use in conjunction with other clinical and laboratory findings to aid in the diagnosis of bacterial bloodstream infections (BSI). LIAISON PLEX® BCN Assay is not intended to monitor treatment of these infections.

Comparison to Predicate Device	Predicate Device: K132843 VERIGENE Gram-Negative Blood Culture (BC-GN) Nucleic Acid Test, K132843	Candidate Device: K243013 LIAISON PLEX® Gram-Negative Blood Culture Assay
		Sub-culturing of positive blood cultures is necessary to recover organisms for antimicrobial susceptibility testing (AST), for identification of organisms not detected by LIAISON PLEX® BCN Assay, to detect mixed infections that may not be detected by LIAISON PLEX® BCN Assay, for association of antimicrobial resistance marker genes to a specific organism, or for epidemiological typing.
Automated System (Sample to Answer)	Automated	Same
Instrumentation	VERIGENE	LIAISON PLEX
Sample Types	Positive Blood Culture	Same

K. Standards/Guidance Documents Referenced:

- Class II Special Controls Guideline: Multiplex Nucleic Acid Assay for Identification of Microorganisms and Resistance Markers from Positive Blood Cultures (May 2015)
- Electronic Submission Template for Medical Device 510(k) Submissions - Guidance for Industry and Food and Drug Administration Staff (October 2, 2023).
- Content of Premarket Submissions for Device Software Functions - Guidance for Industry and Food and Drug Administration Staff (June 14, 2023).
- Cybersecurity in Medical Devices: Quality System Considerations and Content of Premarket Submissions - Guidance for Industry and Food and Drug Administration Staff (September 23, 2023).
- Statistical Guidance on Reporting Results from Studies Evaluating Diagnostic Tests - Guidance for Industry and FDA Staff (March 13, 2007).
- CLSI. User Protocol for Evaluation of Qualitative Test Performance; Approved Guideline - Second Edition. CLSI document EP12-A2. Wayne, PA: Clinical and Laboratory Standards Institute; 2008.
- CLSI. Evaluation of Stability of In Vitro Diagnostic Reagents; Approved Guideline. CLSI document EP25-A. Wayne, PA: Clinical and Laboratory Standards Institute; 2009.
- ISO 14971:2019 Medical devices - Application of risk management to medical devices
- IEC 62366-1:2015 +A1:2020 Medical devices - Part 1: Application of usability engineering to medical devices
- ISO 62304:2006 Medical device software - Software life-cycle processes
- ISO 15223-1:2021: Medical Devices - Symbols to be used with medical device labels, labeling and information to be supplied - Part 1: General requirements
- IEC 61010-1 Ed. 3.1 2017-01: Safety requirements for electrical equipment for measurement, control, and laboratory use - Part 1: General requirements
- EN 61010-2-101:2002/IEC 61010-2-101:2015: Safety requirements for electrical equipment for measurement, control and laboratory use - Part 2-101: Particular requirements for in vitro diagnostic (IVD) medical equipment.
- IEC 60601-1-2:2014 (Edition 4.0): Medical electrical equipment - Part 1-2: General requirements for basic safety and essential performance - Collateral Standard: Electromagnetic disturbances - Requirements and tests
- ISO 13485:2016/EN ISO 13485:2016; Medical devices - Quality Management System - Requirements for regulatory purposes
- ISO 20916:2019; In vitro diagnostic medical devices. Clinical performance studies using specimens from human subjects. Good study practice
- EN ISO 18113-1:2011; In vitro diagnostic medical devices - Information supplied by the manufacturer (labeling). Terms, definition and general requirements
- EN ISO 18113-2:2011; In vitro diagnostic medical devices - Information supplied by the manufacturer (labeling) – Part 2: In vitro diagnostic reagents for professional use

- EN ISO 18113-3:2011; In vitro diagnostic medical devices - Information supplied by the manufacturer (labeling) – Part 3: In vitro diagnostic instruments for professional use
- EN ISO 23640:2015; In vitro diagnostic medical devices - Evaluation of stability of in vitro diagnostic reagents
- IEC 61326-1:2012; Electrical equipment for measurement control and laboratory use - EMC requirements - Part 1: General requirements
- EN 61326-2-6:2006/IEC 61326-2-6:2012; Electrical equipment for measurement control and laboratory use - EMC requirements - Part 2-6: Particular requirements - In vitro diagnostic (IVD) medical equipment

L. Test Principle:

The LIAISON PLEX® Gram-Negative Blood Culture (BCN) Assay is performed directly on blood culture media using blood culture bottles identified as positive by a continuous monitoring blood culture system, and which contain gram-negative bacteria, as determined by a Gram stain. The system consists of an instrument and a single-use, disposable test cartridge. The user loads an aliquot of the sample into the sample port of the LIAISON PLEX® Gram-Negative Blood Culture Assay Cartridge. Next, the user sets up the sample order on the LIAISON PLEX® System by first entering the sample information or scanning the barcode ID located on the sample tube, then scanning the barcode ID located on the test cartridge. Last, the user inserts the test cartridge into the processing module to initiate the test. The LIAISON PLEX® System identifies the assay being run and automatically initiates the proper testing protocol to process the sample, analyze the data, and generate test results.

The LIAISON PLEX® System automates the LIAISON PLEX® BCN Assay sample analysis through the following steps: a) Sample Preparation: Nucleic acid extraction via mechanical and chemical cell lysis and magnetic bead-based nucleic acid isolation; b) Hybridization: Extracted nucleic acid hybridize to target-specific capture DNA on a microarray format, and target-specific mediator and gold nanoparticle probe hybridize to captured nucleic acids; c) Signal Analysis: Gold nanoparticle probes bound specifically to target-containing spots in the microarray are silver-enhanced, and light scatter from the spots is measured and further analyzed to determine the presence (Detected) or absence (Not Detected) of a target.

M. Performance Characteristics:

1. Analytical performance:

   a. *Precision/Reproducibility:*

   Site-to-site Reproducibility

   Site-to-site reproducibility of the LIAISON PLEX® BCN Assay was evaluated by testing LIAISON PLEX® BCN Assay cartridges with a reproducibility panel, blinded to operators, consisting of eight blood culture samples; six representative on-panel organisms

(*Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Haemophilus influenzae*, *Neisseria meningitidis*, *Escherichia coli*, and *Serratia marcescens*) individually cultured at ring positivity and eight hours after ring positivity, one negative sample contrived with an off-panel organism (*Staphylococcus aureus*), and one negative blood culture matrix (NBM) sample. Each sample of the blinded reproducibility panel was tested in triplicate for each sample type by two operators at three sites, two external and one internal, for five non-consecutive testing days. The call agreement results (%) are presented in Table 1, which demonstrated 100% call accuracy for ring positive, ring positive plus 8 hours, and negative blood matrix samples, and 99.4% call accuracy for the contrived negative sample (*Staphylococcus aureus*). Overall, results of site-to-site reproducibility evaluation demonstrated 99.9% reproducibility of the LIAISON PLEX® BCN Assay.

Table 1. LIAISON PLEX® Gram-Negative Blood Culture Assay Site-to-Site Reproducibility Results Summary

Organism ID	Reportable Targets	Sample Type	Call Agreement (%) with Expected Results				Overall 95% C.I.
			Site 1	Site 2	Site 3	Overall (All Sites)	
Acinetobacter baumannii	*Acinetobacter baumannii* | *Acinetobacter* spp.	Ring Positive	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
		Ring Positive + 8 HR	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
Klebsiella pneumoniae	*Enterobacteriaceae / Morganellaceae | Klebsiella pneumoniae*	Ring Positive	100% (30/30)	100% (31/31)	100% (30/30)	100% (91/91)	95.9% - 100%
		Ring Positive + 8 HR	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
Haemophilus influenzae	*Haemophilus influenzae*	Ring Positive	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
		Ring Positive + 8 HR	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
Neisseria meningitidis	*Neisseria meningitidis*	Ring Positive	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
		Ring Positive + 8 HR	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
Escherichia coli	*Enterobacteriaceae / Morganellaceae | Escherichia coli*	Ring Positive	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
		Ring Positive + 8 HR	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
Serratia marcescens	*Enterobacteriaceae / Morganellaceae |Serratia marcescens*	Ring Positive	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
		Ring Positive + 8 HR	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%

Organism ID	Reportable Targets	Sample Type	Call Agreement (%) with Expected Results				Overall 95% C.I.
			Site 1	Site 2	Site 3	Overall (All Sites)	
Staphylococcus aureus	None	Ring Positive + 8 HR	98.3% (59/60)	100% (60/60)	100% (60/60)	99.4% (179/180)	96.9% - 99.9%
No Target (Negative Blood Matrix)	None	Ring Negative	100% (60/60)	100% (60/60)	100% (60/60)	100% (180/180)	97.9% - 100%
Resistance Markers							
Acinetobacter baumannii	OXA	Ring Positive	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
		Ring Positive + 8 HR	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
Klebsiella pneumoniae	KPC	Ring Positive	100% (30/30)	100% (31/31)	100% (30/30)	100% (91/91)	95.9% - 100%
		Ring Positive + 8 HR	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
Escherichia coli	MCR	Ring Positive	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
		Ring Positive + 8 HR	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
Serratia marcescens	SME	Ring Positive	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
		Ring Positive + 8 HR	100% (30/30)	100% (30/30)	100% (30/30)	100% (90/90)	95.9% - 100%
Overall Agreement (All Targets / Sample Types)			99.8% (479/480)	100% (481/481)	100% (480/480)	99.9% (1440/1441)	
Overall (All Sites) 95% Confidence Interval							99.6% - 100%

Precision/Repeatability

Within laboratory (operator-to-operator) precision/repeatability of the LIAISON PLEX® BCN Assay was evaluated based on the results generated by two operators testing site-to-site reproducibility samples at ring positivity and at 8 hours plus ring positivity, contrived negative, and negative blood culture samples. Within laboratory precision/repeatability of the LIAISON PLEX® BCN Assay was 99.8%, and results are summarized in **Table 2**.

Table 2. LIAISON PLEX® Gram-Negative Blood Culture Assay Within-Laboratory Precision/Repeatability Results Summary

Organism	Target Type	Agreement with Expected Results	
		Operator 1	Operator 2
Acinetobacter baumannii	Ring Positive	100% 15/15	100% 15/15
	Ring Positive +8 Hours	100% 15/15	100% 15/15
Klebsiella pneumoniae	Ring Positive	100% 15/15	100% 15/15
	Ring Positive +8 Hours	100% 15/15	100% 15/15
Haemophilus influenzae	Ring Positive	100% 15/15	100% 15/15
	Ring Positive +8 Hours	100% 15/15	100% 15/15
Neisseria meningitidis	Ring Positive	100% 15/15	100% 15/15
	Ring Positive +8 Hours	100% 15/15	100% 15/15
Escherichia coli	Ring Positive	100% 15/15	100% 15/15
	Ring Positive +8 Hours	100% 15/15	100% 15/15
Serratia marcescens	Ring Positive	100% 15/15	100% 15/15
	Ring Positive +8 Hours	100% 15/15	100% 15/15
Staphylococcus aureus	Off-panel Negative	100% 30/30	96.7% 29/30
No Target (Negative Blood Matrix)	Off-panel Negative	100% 30/30	100% 30/30

b. *Linearity/assay reportable range:*

Not applicable. The LIAISON® PLEX Gram-Negative Blood Culture Assay is a qualitative assay.

c. *Traceability, Stability, Expected values (controls, calibrators, or methods):*

<u>Controls</u>

Several controls are built into the assay and system to ensure identification of processing

errors and to establish validity of test results.

Internal Controls

Each LIAISON PLEX® Gram-Negative Blood Culture Assay cartridge includes internal controls to ensure performance of sample preparation and detection. The internal extraction control is present in the lysis tube when the sample is added. Sample preparation is initiated and the extraction control assesses extraction, nucleic acid recovery, and detection. Finally, addition of a post-extraction hybridization control serves as an indicator of successful hybridization. Internal control results are reported as Pass or Fail on the printed reports (see **Table 3** for detailed explanations of each control result). Internal controls must generate a signal above threshold in each internal reaction for the system to report a valid test result.

Table 3. Interpretation of Controls on the LIAISON PLEX® Gram-Negative Blood Culture Assay Report

Internal Control Result	Explanation	Suggested Action
Pass	Test was completed and internal controls were successful, indicating that valid results were generated.	Review and report results
Fail	One or more internal control failed.	Repeat test with a new cartridge

External Controls

Positive and negative external controls should be tested with each new lot or shipment of reagents, or monthly, (whichever occurs first), or in accordance with updated local, regional, state, and/or federal guidelines. Verified negative blood matrix can be used as the negative control. Previously characterized positive samples or verified negative blood matrix spiked with well characterized organisms may be used as the external positive control. External controls should be used in accordance with laboratory protocols and in accordance with local, state, and federal accrediting organizations, as applicable.

Stability

Specimen Stability

Performance of the LIAISON PLEX® Gram-Negative Blood Culture (BCN) Assay was assessed using specimens tested in a fresh state (at bottle/ring positive and at bottle/ring positive + 8 hours) and after exposure to various storage conditions. Conditions tested included refrigerated storage (2° to 8°C) and room temperature storage (15°C to 30°C) to span the typical “fresh specimen” storage conditions across multiple time points. Positive specimens containing four target organisms representing a total of eight gram-negative targets and select resistance markers were tested as well as negative blood matrix control specimen containing no target organisms. All positives tested yielded 100% positivity across all time-points and storage conditions tested. The negative sample demonstrated 0% positivity across all time-points and storage conditions tested. The results demonstrated that specimens may be stored under the following temperature conditions

without impacting the performance of the LIAISON PLEX® BCN cartridge:

- Up to 72 hours (3 days) at Refrigerated (2-8°C) or Room Temperature (15-30°C) storage conditions.

Device Stability

A shelf-life study was conducted to evaluate the real-time stability of the LIAISON PLEX® BCN Assay at the recommended storage conditions of room temperature (15°C – 30°C). Real-time stability was assessed using seven Positive Control panels which interrogate all reportable targets in the assay, and one Negative Control which consisted of negative blood matrix. Results of real-time stability demonstrated the LIAISON PLEX BCN® Assay is stable for at least 3 months when stored at 15°C – 30°C. Shelf-life will be extended based upon results of on-going stability testing.

An open box stability study was performed to evaluate the stability of the LIAISON PLEX® BCN Assay cartridges at room temperature once removed from their foil pouch. Testing was performed shortly after kits were manufactured and will be repeated at the end of the product shelf-life. Non-aged ($T_{initial}$) cartridges were tested at 0 hours (T0), 2 hours (T2), and 9 hours (T9) after removal from their pouch. Each time point included testing of seven Positive Control panels which interrogate all reportable targets in the assay, and one Negative Control which consisted of negative blood matrix. Results of open-box stability indicate the cartridges are stable for up to eight hours after cartridges are removed from their foil pouches and stored at room temperature.

Fresh vs. Frozen Specimen Stability

A fresh vs. frozen specimen stability study was performed to evaluate the performance of the LIAISON PLEX® Blood Culture Negative (BCN) Assay across specimens that have been prepared “fresh” (at two growth durations referred to as Bottle/Ring Positive and Bottle/Ring Positive + 8 hours) and subjected to a range of freeze/thaw (F/T) cycles as well as those experiencing a prolonged storage in frozen conditions. The study was performed using four representative organisms detected by the LIAISON PLEX® BCN Assay cultured in blood culture bottles. Performance testing using negative blood matrix served as a control test during the study. Material was tested under 5 different conditions – Initial Testing: Fresh, 1st Freeze-thaw, 2nd Freeze-thaw; 1-Month Testing: 1st Freeze-thaw and 2nd Freeze-thaw. Material was frozen for a minimum of 8 hours in between each freeze-thaw cycle. In the 1-Month testing, material was frozen for at least 34 days prior to the 1st freeze-thaw. A total of 455 replicates were included in this study. The results demonstrated 100% positivity for target positive samples at both growth durations and all freeze-thaw conditions. The negative blood demonstrated 0% positivity of all reportable targets for the assay at all freeze-thaw conditions.

d. Growth and Detection Study

The Growth and Detection study was performed to evaluate detection of species / targets listed in **Table 4** in blood cultures. For the evaluation, 15 organisms representing all 26 reportable targets were tested at Ring Positive and Ring Positive + 8 hours. Concentrations

for both conditions are outlined in **Table 4**. One negative blood bottle was also grown for at least five days in an automated blood culture system until it was flagged as "negative" and was also tested on the LIAISON PLEX® BCN Assay.

A minimum of three Bottle/Ring Positive and three Bottle/Ring Positive +8 Hour bottles from each BCN organism were tested in triplicate and one negative blood bottle was tested in triplicate on the LIAISON PLEX® BCN Assay. The LIAISON PLEX® BCN Assay results, presented in **Table 4** and **Table 5**, demonstrated 100% positivity for target positive samples and 0% positivity when tested with negative blood.

Table 4 – Growth and Detection Summary – Positive Samples

Positive Samples							
Species Tested	Targets Tested	At Positivity			8 Hours After Positivity		
		Per Bottle (CFU/mL)	Mean (CFU/mL)	Positive Agreement /Total (% Detected)	Per Bottle (CFU/mL)	Mean (CFU/mL)	Positive Agreement /Total (% Detected)
Acinetobacter baumannii [OXA] IHMA 128307	*Acinetobacter baumannii* / *Acinetobacter* spp. / OXA	2.13E+08 2.18E+08 1.86E+08	2.06E+08	9/9 (100%)	2.09E+08 1.06E+08 1.75E+08	1.63E+08	9/9 (100%)
Citrobacter freundii [VIM] IHMA 549813	*Citrobacter* spp. / *Enterobacteriaceae / Morganellaceae* / VIM	9.63E+08 1.49E+09 1.39E+09	1.28E+09	9/9 (100%)	1.76E+09 2.16E+09 1.68E+09	1.87E+09	9/9 (100%)
Enterobacter cloacae ATCC 35030	*Enterobacter* spp. / *Enterobacteriaceae / Morganellaceae*	1.46E+09 1.61E+09 1.68E+09	1.58E+09	9/9 (100%)	1.68E+09 2.07E+09 2.36E+09	2.04E+09	9/9 (100%)
Escherichia coli [MCR] NCTC 13846	*Enterobacteriaceae / Morganellaceae* / *Escherichia coli* / MCR	1.70E+09 1.96E+09 1.95E+09	1.87E+09	9/9 (100%)	1.45E+09 1.83E+09 1.66E+09	1.65E+09	9/9 (100%)
Klebsiella oxytoca [CTX-M] IHMA 683079	CTX-M / *Enterobacteriaceae / Morganellaceae* / *Klebsiella oxytoca*	4.53E+08 1.48E+09 9.73E+08	9.69E+08	9/9 (100%)	5.3E+08 2.9E+08 2.04E+08	3.41E+08	9/9 (100%)
Klebsiella pneumoniae [KPC] IHMA 629630	*Enterobacteriaceae / Morganellaceae* / KPC / *Klebsiella pneumoniae*	1.33E+09 1.66E+09 1.69E+09	1.56E+09	9/9 (100%)	1.55E+09 1.61E+09 1.59E+09	1.58E+09	9/9 (100%)
Klebsiella variicola ATCC BAA-830	*Enterobacteriaceae / Morganellaceae* / *Klebsiella variicola*	1.66E+09 1.82E+09 1.78E+09	1.75E+09	9/9 (100%)	2.00E+09 2.13E+09 2.05E+09	2.06E+09	9/9 (100%)
Salmonella ent ent Enteritidis ATCC 13076	*Enterobacteriaceae / Morganellaceae* / *Salmonella* spp.	4.90E+07 1.38E+08 5.80E+08	2.56E+08	9/9 (100%)	1.88E+09 2.06E+09 1.61E+09	1.85E+09	9/9 (100%)
Serratia	*Enterobacteriaceae /*	1.55E+08	2.38E+08	9/9	1.82E+09	1.47E+09	12/12[1]

Positive Samples							
Species Tested	Targets Tested	At Positivity			8 Hours After Positivity		
		Per Bottle (CFU/mL)	Mean (CFU/mL)	Positive Agreement /Total (% Detected)	Per Bottle (CFU/mL)	Mean (CFU/mL)	Positive Agreement /Total (% Detected)
marcescens [SME] NCTC 13920	*Morganellaceae* | SME | *Serratia marcescens*	3.27E+08 2.32E+08		(100%)	1.39E+09 1.19E+09		(100%)
Morganella morganii [NDM] IHMA 605873	*Enterobacteriaceae / Morganellaceae* | *Morganella morganii* | NDM	1.77E+09 1.76E+09 1.52E+09	1.68E+09	9/9 (100%)	2.75E+09 2.65E+09 2.74E+09	2.71E+09	9/9 (100%)
Pseudomonas aeruginosa [IMP] IHMA 576602	IMP | *Pseudomonas aeruginosa* | *Pseudomonas* spp.	8.97E+08 7.30E+08 7.70E+08	7.99E+08	9/9 (100%)	1.33E+09 1.14E+09 1.30E+09	1.26E+09	9/9 (100%)
Stenotrophomonas maltophilia ATCC 13636	*Stenotrophomonas maltophilia*	3.83E+08 5.23E+08 4.37E+08	4.48E+08	9/9 (100%)	1.23E+09 9.47E+08 8.27E+08	1.00E+09	9/9 (100%)
Proteus mirabilis ATCC 12453	*Enterobacteriaceae / Morganellaceae* | *Proteus* spp.	2.14E+09 2.35E+09 2.30E+09	2.26E+09	9/9 (100%)	2.28E+09 1.80E+09 2.28E+09	2.12E+09	9/9 (100%)
Haemophilus influenzae ATCC 9007	*Haemophilus influenzae*	2.12E+09 2.32E+09 1.96E+09	2.13E+09	9/9 (100%)	1.37E+09 2.42E+09 1.32E+09	1.70E+09	9/9 (100%)
Neisseria meningitidis ATCC 43744	*Neisseria meningitidis*	2.39E+08 2.36E+08 8.93E+07	1.88E+08	9/9 (100%)	1.43E+08 4.10E+08 3.07E+08	2.87E+08	9/9 (100%)

[1]One OXA false positive was observed in initial testing. An additional set of replicates was tested resulting in 12 total replicates.

Table 5 – Growth and Detection Summary – Negative Samples

Negative Samples				
Species Tested	Targets Tested	Per Bottle (CFU/mL)	Mean (CFU/mL)	Targets Detected/Total (% Detected)
Negative Blood	None	0.00E+00	0.00E+00	0/3 (0%)

e. Analytical Reactivity (Inclusivity)

The analytical reactivity study was performed to evaluate the inclusivity of the LIAISON PLEX® BCN Assay through laboratory testing of multiple strains representing "on-panel" reportable target bacteria or bacterial species. All on-panel organisms (n = 246) were

tested in triplicate. One hundred percent (100%) positivity was noted for all targets including expected resistance marker calls for 245 of the 246 on-panel organisms. A summary of organism results is listed in **Table 6** and a summary of resistance marker results is listed in **Table 7**. Of the 246 on-panel organisms tested, 17 organisms generated additional target calls that align with known cross-reactivity based on *in silico* analysis, or design features. Additionally, one on-panel organism (*S. proteamaculans*) only generated the known cross-reactivity target call, not the expected target call. The 18 cross-reactive organisms are highlighted in **Table 8**.

Table 6: LIAISON PLEX® BCN Assay Analytical Reactivity (Inclusivity) Summary by Organism

Reportable Target (Family)	Reportable Target (Genus)	Reportable Target (Species)	Organism	Number of strains	Positivity
N/A	*Acinetobacter* spp.	N/A	*Acinetobacter guillouiae*	1	100%
			Acinetobacter radioresistens	2	100%
			Acinetobacter baylyi	1	100%
			Acinetobacter bereziniae	1	100%
			Acinetobacter calcoaceticus	1	100%
			Acinetobacter haemolyticus	1	100%
			Acinetobacter indicus	1	100%
			Acinetobacter johnsonii	1	100%
			Acinetobacter junii	1	100%
			Acinetobacter lwoffii	1	100%
			Acinetobacter nosocomialis	1	100%
			Acinetobacter pittii	1	100%
			Acinetobacter schindleri	1	100%
			Acinetobacter ursingii	1	100%
	Acinetobacter spp.	*Acinetobacter baumannii*	*Acinetobacter baumannii*	5	100%
Enterobacteriaceae / Morganellaceae	*Citrobacter* spp.	N/A	*Citrobacter amalonaticus*	2	100%
			Citrobacter braakii	2	100%
			Citrobacter farmeri	1	100%
			Citrobacter freundii	4	100%
			Citrobacter gillenii	1	100%
			Citrobacter koseri	5	100%
			Citrobacter murliniae	1	100%
			Citrobacter rodentium	1	100%
			Citrobacter sedlakii	1	100%
			Citrobacter werkmanii	1	100%
			Citrobacter youngae	1	100%
Enterobacteriaceae	*Enterobacter*	N/A	*Enterobacter cloacae*	10	100%

Reportable Target (Family)	Reportable Target (Genus)	Reportable Target (Species)	Organism	Number of strains	Positivity
/ *Morganellaceae*	spp.		*Enterobacter aerogenes*	5	100%
			Enterobacter amnigenus	1	100%
			Enterobacter asburiae	1	100%
			Enterobacter bugandensis	1	100%
			Enterobacter cancerogenus	1	100%
			Enterobacter hormaechei	2	100%
			Enterobacter ludwigii	1	100%
Enterobacteriaceae / *Morganellaceae*	N/A	*Escherichia coli*	*Escherichia coli*	21	100%
			Shigella boydii	2	100%
			Shigella dysenteriae	2	100%
			Shigella flexneri	2	100%
			Shigella sonnei	2	100%
Enterobacteriaceae / *Morganellaceae*	N/A	*Klebsiella oxytoca*	*Klebsiella oxytoca*	5	100%
Enterobacteriaceae / *Morganellaceae*	N/A	*Klebsiella pneumoniae*	*Klebsiella pneumoniae*	26	100%
Enterobacteriaceae / *Morganellaceae*	N/A	*Klebsiella variicola*	*Klebsiella variicola*	5	100%
N/A	N/A	*Haemophilus influenzae*	*Haemophilus influenzae*	6	100%
Enterobacteriaceae / *Morganellaceae*	N/A	*Morganella morganii*	*Morganella morganii*	5	100%
N/A	N/A	*Neisseria meningitidis*	*Neisseria meningitidis*	10	100%
Enterobacteriaceae / *Morganellaceae*	*Proteus* spp.	N/A	*Proteus hauseri*	1	100%
			Proteus mirabilis	5	100%
			Proteus myxofaciens	1	100%
			Proteus penneri	1	100%
			Proteus vulgaris	2	100%
N/A	*Pseudomonas* spp.	N/A	*Pseudomonas alcaligenes*	1	100%
			Pseudomonas chlororaphis	1	100%
			Pseudomonas fluorescens	1	100%
			Pseudomonas luteola	1	100%
			Pseudomonas mendocina	1	100%
			Pseudomonas monteilii	1	100%
			Pseudomonas mosselii	1	100%
			Pseudomonas	1	100%

Reportable Target (Family)	Reportable Target (Genus)	Reportable Target (Species)	Organism	Number of strains	Positivity
			mucidolens		
			Pseudomonas oryzihabitans	1	100%
			Pseudomonas pseudoalcaligenes	1	100%
			Pseudomonas putida	1	100%
			Pseudomonas resinovorans	1	100%
			Pseudomonas stutzeri	1	100%
			Pseudomonas veronii	1	100%
		Pseudomonas aeruginosa	*Pseudomonas aeruginosa*	4	100%
Enterobacteriaceae / Morganellaceae	*Salmonella* spp.	N/A	*Salmonella bongori*	1	100%
			Salmonella enterica	12	100%
			Salmonella enterica subsp. arizonae	1	100%
			Salmonella enterica subsp. diarizonae	1	100%
			Salmonella enterica subsp. houtenae	1	100%
			Salmonella enterica subsp. indica	1	100%
N/A	N/A	*Stenotrophomonas maltophilia*	*Stenotrophomonas maltophilia*	5	100%
Enterobacteriaceae / Morganellaceae	N/A	*Serratia marcescens*	*Serratia marcescens*	6	100%
Enterobacteriaceae / Morganellaceae	N/A	N/A	*Cedecea davisae*	2	100%^
			Cedecea lapagei	1	100%^
			Cedecea neteri	1	100%
			Cronobacter muytjensii	1	100%
			Cronobacter sakazakii	2	100%
			Enteric group 137	1	100%
			Escherichia albertii	1	100%^
			Escherichia fergusonii	1	100%
			Escherichia hermanii	1	100%
			Edwardsiella tarda	1	100%
			Hafnia alvei	1	100%
			Kluyvera ascorbata	1	100%^
			Kluyvera cryocrescens	1	100%
			Kluyvera georgiana	1	100%
			Kluyvera intermedia	1	100%
			Leclercia adecarboxylata	1	100%^

Reportable Target (Family)	Reportable Target (Genus)	Reportable Target (Species)	Organism	Number of strains	Positivity
			Lelliottia nimipressuralis	1	100%^
			Pantoea agglomerans	1	100%
			Plesiomonas shigelloides	1	100%
			Pluralibacter gergoviae	1	100%
			Providencia acalifaciens	1	100%
			Providencia heimbachae	1	100%
			Providencia rettigeri	1	100%^
			Providencia stuartii	1	100%^
			Rahnella aquatillis	1	100%
			Raoultella ornithinolytica	1	100%^
			Raoultella planticola	1	100%^
			Raoultella terrigena	1	100%^
			Serratia plymuthica	1	100%
			Serratia grimesii	1	100%^
			Xenorhabdus bovienii	1	100%^
			Xenorhabdus poinarii	1	100%
			Yersinia enterocolitica	1	100%
			Yokenella regensburgei	1	100%
			Serratia ficaria	1	100%^
			Serratia fonticola	1	100%^
			Serratia liquefaciens	1	100%^
			Serratia proteamaculans	1	0%^
			Serratia rubidaea	1	100%^

^ See Table 8. Known Cross-Reactive Organisms

Table 7: LIAISON PLEX BCN Assay Analytical Reactivity (Inclusivity) Resistance Marker Summary

Reportable Target (Resistance Marker)	Organism	# of strains	% Detected
CTX-M	*Citrobacter freundii*	1	100%
	Enterobacter cloacae	5	100%
	Escherichia coli	14	100%
	Klebsiella oxytoca	2	100%
	Klebsiella pneumoniae	16	100%
	Kluyvera ascorbata	1	100%
	Kluyvera georgiana	1	100%
	Morganella morganii	1	100%
	Salmonella enterica	1	100%
IMP	*Escherichia coli*	1	100%
	Klebsiella pneumoniae	2	100%
	Proteus mirabilis	1	100%
	Pseudomonas aeruginosa	1	100%

Reportable Target (Resistance Marker)	Organism	# of strains	% Detected
KPC	*Citrobacter freundii*	2	100%
	Enterobacter cloacae	1	100%
	Enterobacter hormaechei	1	100%
	Klebsiella pneumoniae	3	100%
	Morganella morganii	1	100%
MCR	*Enterobacter cloacae*	2	100%
	Escherichia coli	5	100%
	Klebsiella pneumoniae	4	100%
	Salmonella enterica	2	100%
NDM	*Enterobacter cloacae*	1	100%
	Escherichia coli	4	100%
	Klebsiella pneumoniae	1	100%
	Morganella morganii	1	100%
OXA	*Acinetobacter baumannii*	5	100%
	Acinetobacter radioresistens	2	100%
	Acinetobacter indicus	1	100%
	Escherichia coli	2	100%
	Klebsiella pneumoniae	5	100%
SME	*Serratia marcescens*	6	100%
VIM	*Enterobacter cloacae*	1	100%
	Klebsiella pneumoniae	2	100%
	Pseudomonas aeruginosa	3	100%

Table 8: LIAISON PLEX® BCN Assay Known Analytical Reactivity (Inclusivity) Cross Reactive Organisms

Cross-Reactive Organism	Strain ID	Expected Target	Additional Target DETECTED	Number Detected
Cedecea davisae	ATCC 33431	*Enterobacteriaceae / Morganellaceae*	*Klebsiella oxytoca*	1/3
Cedecea lapagei	ATCC 43028	*Enterobacteriaceae / Morganellaceae*	*Klebsiella oxytoca*	1/3
Escherichia albertii	ATCC 46494	*Enterobacteriaceae / Morganellaceae*	*Escherichia coli*	2/3
Kluyvera ascorbata	ATCC 33433	*Enterobacteriaceae / Morganellaceae* | CTX-M	*Klebsiella oxytoca*	3/3
Leclercia adecarboxylata	ATCC 23216	*Enterobacteriaceae / Morganellaceae*	*Enterobacter* spp.	3/3
Lelliottia nimipressuralis	ATCC 9912	*Enterobacteriaceae / Morganellaceae*	*Enterobacter* spp.	3/3
Providencia rettigeri	ATCC 9250	*Enterobacteriaceae / Morganellaceae*	*Proteus* spp.	1/3
Providencia stuartii	UTMB GN-403	*Enterobacteriaceae / Morganellaceae*	*Proteus* spp.	1/3

Cross-Reactive Organism	Strain ID	Expected Target	Additional Target DETECTED	Number Detected
Raoultella ornithinolytica	ATCC 31898	*Enterobacteriaceae / Morganellaceae*	*Klebsiella oxytoca*	3/3
Raoultella planticola	ATCC 33531	*Enterobacteriaceae / Morganellaceae*	*Klebsiella oxytoca*	3/3
Raoultella terrigena	ATCC 33257	*Enterobacteriaceae / Morganellaceae*	*Citrobacter* spp.	3/3
Serratia ficaria	ATCC 33105	*Enterobacteriaceae / Morganellaceae*	*Serratia marcescens*	3/3
Serratia fonticola	ATCC 29844	*Enterobacteriaceae / Morganellaceae*	*Serratia marcescens*	3/3
Serratia grimesii	ATCC 14461	*Enterobacteriaceae / Morganellaceae*	*Proteus* spp.	2/3
Serratia liquefaciens	ATCC 27592	*Enterobacteriaceae / Morganellaceae*	*Serratia marcescens*	3/3
Serratia proteamaculans	ATCC 35475	*Enterobacteriaceae / Morganellaceae*[#]	*Serratia marcescens*	3/3
Serratia rubidaea	ATCC 27593	*Enterobacteriaceae / Morganellaceae*	*Serratia marcescens*	3/3
Xenorhabdus bovienii	ATCC 35271	*Enterobacteriaceae / Morganellaceae*	*Proteus* spp.	2/3

Expected Target not detected.

Predicted (in silico) Reactivity (Inclusivity) Results

For all targets, *in silico* inclusivity analysis was performed using sequences available in the GenBank and WGS (whole genome shotgun) databases from February to April 2024. Alignments of the signal fragment for each target were generated using MAFFT (version 7.490). For all targets, the inclusivity analysis involved assessing the percent homology of each oligo sequence to its binding region on each target sequence retrieved from the public databases. The predicted inclusivity based on sequence homology is the percentage of sequences with at least 90% oligo identity. In determining oligo identity, the highest percent identity of each oligo in the same component was assessed and then the lowest percent identity of the two components (capture and mediator probes) is used to characterize the inclusivity of the sequence. *In silico* analysis results are summarized below in **Table 9**.

Table 9 – *In silico* Analysis Results

Reportable Target	Inclusive Organism/Target	Total # Sequences in Alignment	# Sequences with Percent Oligo Identity ≥ 90%	Predicted Inclusivity Percentage (%)
Acinetobacter baumannii	*Acinetobacter baumannii*	1456	1450	100
Acinetobacter spp. [a]	*Acinetobacter* spp.	4451	4445	100
Citrobacter spp. [b]	*Citrobacter freundii*	440	440	100
	Citrobacter koseri	425	422	99
	other *Citrobacter* species	1065	1065	100

Reportable Target	Inclusive Organism/Target	Total # Sequences in Alignment	# Sequences with Percent Oligo Identity ≥ 90%	Predicted Inclusivity Percentage (%)
Enterobacter spp. [c]	*Enterobacter cloacae*	266	266	100
	Klebsiella / Enterobacter aerogenes	1083	1083	100
	other *Enterobacter* species	3795	3777	100
Enterobacteriaceae / Morganellaceae	*Enterobacteriaceae*	28524	28442	100
	Morganellaceae	3829	3715	97
Escherichia coli	*Escherichia coli*	5083	5067	100
	Shigella boydii	711	711	100
	Shigella dysenteriae	277	277	100
	Shigella flexneri	246	246	100
	Shigella sonnei	1061	1061	100
Haemophilus influenzae	*Haemophilus influenzae*	236	236	100
Klebsiella oxytoca [d]	*Klebsiella oxytoca* species complex	2117	2105	99
Klebsiella pneumoniae	*Klebsiella pneumoniae*	6163	6131	99
Klebsiella variicola	*Klebsiella variicola*	106	105	99
Morganella morganii	*Morganella morganii*	728	728	100
Neisseria meningitidis	*Neisseria meningitidis*	179	179	100
Proteus spp. [e]	*Proteus* spp.	484	481	99
Pseudomonas aeruginosa	*Pseudomonas aeruginosa*	1341	1341	100
Pseudomonas spp. [f]	*Pseudomonas* spp.	6480	6473	100
Salmonella spp.	*Salmonella bongori*	122	122	100
	Salmonella enterica	420	420	100
	Salmonella enterica subsp. *arizonae*	14	14	100
	Salmonella enterica subsp. *diarizonae*	21	21	100
	Salmonella enterica subsp. *enterica*	2164	2162	100
	Salmonella enterica subsp. *houtenae*	7	7	100
	Salmonella enterica subsp. *salamae*	26	26	100
	Salmonella enterica subsp. *VII*	2	2	100
Serratia marcescens	*Serratia marcescens*	262	262	100
Stenotrophomonas maltophilia	*Stenotrophomonas maltophilia*	410	408	100
CTX-M [g]	CTX-M	12187	12146	100
IMP [h]	IMP	1448	1441	100
KPC [i]	KPC	4032	4031	100
MCR [j]	MCR-1	1695	1695	100
	MCR-2	32	32	100
	MCR-3	211	210	100
NDM [k]	NDM	5426	5420	100
OXA [l]	OXA-23 family	1721	1718	100
	OXA-24/40/143 family	403	403	100
	OXA-48 family	1968	1962	100
	OXA-58 family	425	425	100

Reportable Target	Inclusive Organism/Target	Total # Sequences in Alignment	# Sequences with Percent Oligo Identity ≥ 90%	Predicted Inclusivity Percentage (%)
SME [m]	SME	189	188	99
VIM [n]	VIM	1438	1438	100

[a] Includes sequences for 86 *Acinetobacter* species.

[b] Includes sequences for 17 *Citrobacter* species.

[c] Includes sequences for 22 *Enterobacter* species.

[d] Includes sequences for 6 members of the *Klebsiella oxytoca* species complex (KoSC).

[e] Includes sequences for 11 *Proteus* species.

[f] Includes sequences for 282 *Pseudomonas* species.

[g] Includes sequences for CTX-M-1 to CTX-M-269; not all types have sequences available.

[h] Includes sequences for IMP-1 to IMP-102; not all types have sequences available.

[i] Includes sequences for KPC-1 to KPC-208; not all types have sequences available.

[j] Includes sequences for MCR-1.1 to MCR1.37, MCR-2.1 and MCR-2.8, and MCR-3.1 to MCR-3.42; not all types have sequences available.

[k] Includes sequences for NDM-1 to NDM-61; not all types have sequences available.

[l] Includes sequences for OXA-23 family, OXA-24/40/143 family, OXA-48 family and OXA-58 family; not all types have sequences available.

[m] Includes sequences for SME-1 to SME-5; not all types have sequences available.

[n] Includes sequences for VIM-1 to VIM-86; not all types have sequences available.

f. Analytical Specificity (Exclusivity)

Cross-Reactivity

The analytical specificity study was performed to evaluate cross-reactivity of the LIAISON PLEX® BCN Assay through testing "off-panel" organisms, including both those phylogenetically related to the on-panel organisms and organisms likely to be present in typical blood culture samples. Out of the 113 off-panel species tested in triplicate, 17 species generated positive results. Summary results for all 113 species are listed in **Table 10a**. Of those 17 species that generated positive results, 11 species were cross-reactive and those cross-reactive calls are listed in **Table 10b**.

Table 10a: LIAISON PLEX® BCN Assay Analytical Specificity (Cross-Reactivity) Summary

Organism	Positivity	Organism	Positivity
Gram Positive			
Abitrophia defectiva	0%	*Leuconostoc carnosum*	0%
Aerococcus viridans	0%	*Leuconostoc mesenteroids*	0%
Arcanobacterium bernardiae	0%	*Listeria grayi*	0%
Arcanobacterium haemolyticum	0%	*Listeria innocua*	0%
Bacillus cereus	0%	*Listeria ivanovii*	0%
Bacillus licheniformins	0%	*Listeria welshimeri*	0%
Bacillus subtilis	0%	*Micrococcus luteus*	0%
Bacillus thuringiensis	0%	*Micrococcus lylae*	0%
Corynebacterium amycolatum	0%	*Pediococcus acidilactici*	0%
Corynebacterium diphtheriae	0%	*Pediococcus pentosaceus*	0%

Organism	Positivity	Organism	Positivity
Corynebacterium pseudodiptheriticum	0%	*Peptostreptococcus anaerobius*	0%
Corynebacterium striatum	0%	*Planococcus citreus*	0%
Cutibacterium acnes	0%	*Planococcus kocurii*	0%
Cutibacterium avidum	0%	*Rothia dentocariosa*	0%
Propionibacterium freudenreichii	0%	*Rothia (Stomatococcus) mucilaginosa*	0%
Enterococcus avium	0%	*Staphylococcus capitis*	0%
Enterococcus casseliflavis, VRE, vanC	0%	*Staphylococcus caprae*	0%
Enterococcococcus dispar	0%	*Staphylococcus cohnii*	0%
Enterococcus durans	0%	*Staphylococcus haemolyticus*	0%
Enterococcus flavescens	0%	*Staphylococcus hominis*	0%
Enterococcus gallinarum, vanC	0%	*Staphylococcus intermedius*	0%
Enterococcus hirae	0%	*Staphylococcus lugdunensis*	0%
Enterococcus mundtii	0%	*Streptococcus agalactiae*	0%
Enterococcus raffinosus	0%	*Streptococcus anginosus*	0%
Erysipelothrix rhusiopathiae	0%	*Streptococcus bovis*	0%
Kocuria kristinae	0%	*Streptococcus constellatus*	0%
Kytococcus sedentarius, Met R	0%	*Streptococcus equinus*	0%
Lactobacillus acidophilus	0%	*Streptococcus mitis*	0%
Lactobacillus crispatus	0%	*Streptococcus pneumoniae*	0%
Lactobacillus rhamnosus	0%	*Streptococcus pyogenes*	0%
Corynebacterium frankenforstense	0%		
Gram Negative			
Aggregatibacter aphrophilus	0%	*Fusobacterium nucleatum*	0%
Bacteroides fragilis	0%	*Haemophilus haemolyticus*	0%
Brevundimonas diminuta	0%	*Herbaspirillum huttiense*	0%
Burkholderia cepacia	0%	*Kingella kingae*	0%
Capnocytophaga ochracea	0%	*Moraxella catarrhalis*	0%
Cardiobacterium hominis	0%	*Neisseria lactamica*	0%
Comamonas testosteroni	0%	*Neisseria mucosa*	0%
Delftia acidovorans	0%	*Neisseria sicca*	0%
Eikenella corrodens	0%	*Parabacteroides distasonis*	0%
Elizabethkingia meningoseptica	0%	*Pasteurella aerogenes*	0%
Fusobacterium necrophorum	0%	*Prevotella bivia*	0%
Aeromonas hydrophila	0%	*Klebsiella quasivariicola*	100%
Haemophilus parainfluenzae	0%	*Providencia rustigiani*	100%
Haemophilus parahaemolyticus	33%	*Providencia vermicola*	100%
Enterobacter kobei	100%	*Pseudomonas paraeruginosa*	100%
Haemophilus aegyptius	100%	*Serratia entomophila*	100%
Klebsiella grimontii	100%	*Serratia nevei*	100%
Klebsiella huaxiensis	100%	*Serratia odorifera*	100%
Klebsiella michiganensis	100%	*Serratia quinivorans*	100%
Klebsiella quasipneumoniae	100%	*Serratia ureilytica*	100%
Lelliottia amnigena	100%		

Organism	Positivity	Organism	Positivity
Yeast/Fungi			
Aspergillus fumigatus	0%	*Candida tropicalis*	0%
Candida albicans	0%	*Cryptococcus neoformans*	0%
Candida famata	0%	*Kluyveromyces lactis*	0%
Candida glabrata	0%	*Saccharomyces cerevisiae*	0%
Candida krusei	0%	*Schizosaccharomyces pombe*	0%
Candida parapsilosis	0%		

Table 10b: LIAISON PLEX® BCN Assay Cross-Reactive Organisms Summary

Organism	Positivity	Results	
Not Reported to Cause Bloodstream Infections			
		Inclusive	**Cross-reacting**
Lelliottia amnigena	100%	*Enterobacteriaceae / Morganellaceae*	*Enterobacter* spp.
Pseudomonas paraeruginosa	100%	*Pseudomonas* spp.	*Pseudomonas aeruginosa*
Serratia nevei	100%	*Enterobacteriaceae / Morganellaceae*	*Serratia marcescens*
Serratia entomophila	100%	*Enterobacteriaceae / Morganellaceae*	*Serratia marcescens*
Serratia ureilytica	100%	*Enterobacteriaceae / Morganellaceae*	*Serratia marcescens*
Klebsiella quasivariicola	100%	*Enterobacteriaceae / Morganellaceae*	*Klebsiella pneumoniae*
Rare/Not Primarily Associated with Bloodstream Infections			
		Inclusive	**Cross-reacting**
Haemophilus aegyptius	100%	None	*Haemophilus influenzae*
Klebsiella michiganensis	100%	*Enterobacteriaceae / Morganellaceae*	*Klebsiella oxytoca*
Rare/Opportunistic with Some Documented Bloodstream Infection Cases			
		Inclusive	**Cross-reacting**
Klebsiella grimontii	100%	*Enterobacteriaceae / Morganellaceae*	*Klebsiella oxytoca*
Klebsiella quasipneumoniae	100%	*Enterobacteriaceae / Morganellaceae*	*Klebsiella pneumoniae*
Haemophilus parahaemolyticus	33%	None	*Enterobacteriaceae / Morganellaceae*

In Silico Cross-Reactivity

In silico exclusivity assessment of the oligo sequences incorporated in the assay designs was performed against on-panel and off-panel organisms listed in **Table 11**. Based on the analysis of sequences available in the GenBank nucleotide database as of June 7, 2024, the following potential cross-reactivity is predicted:

- *Acinetobacter baumannii* oligo designs are predicted to detect some strains of *Acinetobacter pittii* and *Klebsiella pneumoniae*.
- Some strains of *Escherichia* species (*E. albertii, E. coli, E. fergusonii, E. marmotae*), *Raoultella terrigena* and *Shigella* species (*S. boydii, S. dysenteriae, S. flexneri, S. sonnei*) are predicted to produce false positive *Citrobacter* spp. results.
- *Enterobacter* spp. oligo designs are predicted to detect some strains of *Klebsiella huaxiensis, Leclercia adecarboxylata* and *Lelliottia* species (*Lelliottia amnigena, Lelliottia nimipressuralis*).
- Some strains of *Aeromonas hydrophila*, *Aggregatibacter aphrophilus*, *Corynebacterium frankenforstense*, *Haemophilus parahaemolyticus*, *Haemophilus parainfluenzae* and

Pseudomonas wenzhouensis are predicted to produce false positive *Enterobacteriaceae / Morganellaceae* results.

- *Escherichia coli* oligo designs are predicted to detect some strains of *Escherichia albertii* and *Escherichia marmotae*.
- *Haemophilus influenzae* oligo designs are predicted to detect some strains of *Haemophilus aegyptius*.
- Some strains of *Cedecea* species (*C. davisae, C. lapagei, C. neteri*), *Enterobacter* species (*E. kobei, E. mori*), *Escherichia coli*, *Klebsiella* species (*K. aerogenes, K. electrica, K. grimontii, K. huaxiensis, K. michiganensis, K. pasteurii, K. pneumoniae, K. variicola*), *Kluyvera* species (*K. ascorbate, K. cryocrescens*), *Raoultella* species (*R. ornithinolytica, R. planticola*) and unspecified *Superficieibacter* species are predicted to produce false positive *Klebsiella oxytoca* results.
- *Klebsiella pneumoniae* oligo designs are predicted to detect some strains of *Enterobacteriaceae bacterium* and *Klebsiella* species (*K. africana, K. grimontii, K. quasipneumoniae, K. quasivariicola, K. variicola*).
- Some strains of *Cronobacter muytjensii*, *Klebsiella pneumoniae* and *Klebsiella quasipneumoniae* are predicted to produce false positive *Klebsiella variicola* results.
- Some strains of *Arsenophonus* species (*A. apicola, A. endosymbiont, A. nasoniae*), *Haemophilus parahaemolyticus, Leclercia adecarboxylata*, *Morganella psychrotolerans*, *Providencia* species (*P. hangzhouensis, P. heimbachae, P. huaxiensis, P. manganoxydans, P. rettgeri, P. rustigianii, P. stuartii, P. vermicola*), *Serratia* species (*S. grimesii, S. proteamaculans, S. quinivorans*) and *Xenorhabdus* species (*X. bovienii, X. budapestensis, X. griffiniae, X. hominickii, X. poinarii*) are predicted to produce false positive *Proteus* spp. results.
- *Pseudomonas aeruginosa* oligo designs are predicted to detect some strains of *Pseudomonas paraeruginosa* and *Pseudomonas fluorescens*.
- *Salmonella* spp. oligo designs are predicted to detect one strain of *Enterobacteriaceae bacterium*.
- Some strains of *Serratia* species (*S. bockelmannii, S. entomophila, S. ficaria, S. fonticola, S. grimesii, S. inhibens, S. liquefaciens, S. nematodiphila, S. nevei, S. odorifera, S. proteamaculans, S. quinivorans, S. rhizosphaerae, S. rubidaea, S. surfactantfaciens, S. symbiotica, S. ureilytica*) are predicted to produce false positive *Serratia marcescens* results.
- *Stenotrophomonas maltophilia* oligo designs are predicted to detect some strains of *Enterobacter cloacae* and other *Stenotrophomonas* species (*S. acidaminiphila, S. nitritireducens, S. rhizophila*).
- Some strains of *Serratia liquefaciens* are predicted to produce false positive *Serratia marcescens* and CTX-M results.
- Some strains of *Serratia liquefaciens* and *Serratia nevei* are predicted to produce false positive *Serratia marcescens* and IMP results.
- Some strains of *Serratia nevei* are predicted to produce false positive *Serratia marcescens* and OXA results.

Table 11. Potential Cross-Reactive Organisms assessed in the *In Silico* Exclusivity Analysis

On-Panel Organisms	Off-Panel Organisms			
	Gram-Positive Bacteria	Gram-Negative Bacteria	Resistance Markers	Yeasts / Viruses / Parasites
Acinetobacter baumannii	*Actinomyces israelii*	*Actinobacillus hominis*	AmpC	*Aspergillus flavus*
Acinetobacter spp.	*Actinomyces naeslundii*	*Actinobacillus ureae*	CMY	*Aspergillus fumigatus*
Citrobacter spp.	*Actinomyces odontolyticus*	*Aeromonas caviae*	*mecA*	*Aspergillus niger*
Enterobacter spp.	*Aerococcus sanguinicola*	*Aeromonas hydrophila*	*mecC*	*Aspergillus terreus*

On-Panel Organisms	Off-Panel Organisms			
	Gram-Positive Bacteria	Gram-Negative Bacteria	Resistance Markers	Yeasts / Viruses / Parasites
Enterobacteriaceae	*Aerococcus urinae*	*Aeromonas sobria*	*ompK36*	*Blastomyces dermatitidis*
Escherichia coli / Shigella spp.	*Aerococcus viridans*	*Aggregatibacter actinomycetemcomitans*	RAHN	*Candida albicans*
Haemophilus influenzae	*Arcanobacterium bernardiae*	*Aggregatibacter aphrophilus*	SHV	*Candida auris*
Klebsiella oxytoca	*Arcanobacterium haemolyticum*	*Bacteroides caccae*	SPM	*Candida dubliniensis*
Klebsiella pneumoniae	*Arthrobacter psychrolactophilus*	*Bacteroides fragilis*	TEM	*Candida duobushaemulonii*
Klebsiella variicola	*Bacillus* spp.	*Bacteroides ovatus*	*vanA*	*Candida famata*
Morganella morganii	*Brochothrix thermosphacta*	*Bacteroides thetaiotaomicron*	*vanB*	*Candida glabrata*
Morganellaceae	*Carnobacterium divergens*	*Bacteroides uniformis*	*vanC*	*Candida guilliermondii*
Neisseria meningitidis	*Carnobacterium maltaromaticum*	*Bacteroides vulgatus*	*vanD*	*Candida haemulonii*
Proteus spp.	*Cellulomonas turbata*	*Bacteroides xylanisolvens*	*vanM*	*Candida inconspicua*
Pseudomonas aeruginosa	*Cellulosimicrobium cellulans*	*Bordetella bronchiseptica*		*Candida kefyr*
Pseudomonas spp.	*Clostridioides difficile*	*Bordetella parapertussis*		*Candida krusei*
Salmonella spp.	*Clostridium bifermentans*	*Bordetella pertussis*		*Candida lipolytica*
Serratia marcescens	*Clostridium clostridioforme*	*Brevundimonas diminuta*		*Candida lusitaniae*
Stenotrophomonas maltophilia	*Clostridium perfringens*	*Brevundimonas vesicularis*		*Candida metapsilosis*
CTX-M	*Clostridium ramosum (Thomasclavelia ramosa)*	*Burkholderia cepacia*		*Candida multis-gemmis*
IMP	*Clostridium septicum*	*Burkholderia mallei*		*Candida nivariensis*
KPC	*Clostridium tertium*	*Burkholderia multivorans*		*Candida norvegensis*
MCR (MCR-1, MCR-2, MCR-3)	*Clostridium tetani*	*Burkholderia pseudomallei*		*Candida orthopsilosis*
NDM	*Corynebacterium* spp.	*Campylobacter hominis*		*Candida parapsilosis*
OXA	*Cutibacterium acnes*	*Capnocytophaga ochracea*		*Candida sojae*
SME	*Cutibacterium avidum*	*Cardiobacterium hominis*		*Candida tropicalis*
VIM	*Cutibacterium granulosum*	*Chlamydia trachomatis*		*Candida viswanathii*
	Enterococcus avium	*Chlamydophila pneumoniae*		*Coccidioides immitis*
	Enterococcus casseliflavus	*Chromobacterium violaceum*		*Coccidioides posadasii*

On-Panel Organisms	Off-Panel Organisms			
	Gram-Positive Bacteria	**Gram-Negative Bacteria**	**Resistance Markers**	**Yeasts / Viruses / Parasites**
	Enterococcus cecorum	*Comamonas testosteroni*		*Cryptococcus amylolentus*
	Enterococcus dispar	*Delftia acidovorans*		*Cryptococcus gattii*
	Enterococcus durans	*Eikenella corrodens*		*Cryptococcus neoformans*
	Enterococcus faecalis	*Elizabethkingia meningoseptica*		*Cryptococcus uniguttulatus*
	Enterococcus faecium	*Fusobacterium necrophorum*		*Cutaneotrichosporon curvatum*
	Enterococcus flavescens	*Fusobacterium nucleatum*		*Cyberlindnera fabianii*
	Enterococcus gallinarum	*Haemophilus aegyptius*		*Geotrichum capitatum (Magnusiomyces capitatus)*
	Enterococcus hirae	*Haemophilus ducreyi*		*Histoplasma capsulatum*
	Enterococcus mundtii	*Haemophilus haemolyticus*		*Kluyveromyces lactis*
	Enterococcus raffinosus	*Haemophilus parahaemolyticus*		*Kodamaea ohmeri*
	Erysipelothrix rhusiopathiae	*Haemophilus parainfluenzae*		*Lodderomyces elongisporus*
	Finegoldia magna	*Haemophilus parasuis*		*Magnusiomyces capitatus*
	Gemella haemolysans	*Haemophilus quentini*		*Millerozyma farinosa*
	Gemella morbillorum	*Haemophilus sputorum*		*Naganishia albida*
	Granulicatella adiacens	*Herbaspirillum huttiense*		*Papiliotrema laurentii*
	Granulicatella elegans	*Kingella denitrificans*		*Penicillium chrysogenum*
	Kocuria kristinae	*Kingella kingae*		*Rhodotorula mucilaginosa*
	Kocuria rhizophila	*Kingella negevensis*		*Saccharomyces cerevisiae*
	Kytococcus sedentarius	*Kingella oralis*		*Schizosaccharomyces pombe*
	Lactobacillus acidophilus	*Legionella pneumophila*		*Talaromyces marneffei*
	Lactobacillus crispatus	*Leptospira interrogans*		*Trichosporon asahii*
	Lactobacillus rhamnosus	*Moraxella catarrhalis*		*Wickerhamomyces anomalus*
	Lactococcus garvieae	*Moraxella osloensis*		BK Virus
	Lactococcus lactis	*Mycobacterium tuberculosis*		Chikungunya Virus

On-Panel Organisms	Off-Panel Organisms			
	Gram-Positive Bacteria	**Gram-Negative Bacteria**	**Resistance Markers**	**Yeasts / Viruses / Parasites**
	Leuconostoc carnosum	*Neisseria gonorrhoeae*		Cytomegalovirus
	Leuconostoc citreum	*Neisseria lactamica*		Dengue Virus
	Leuconostoc mesenteroides	*Neisseria mucosa*		Enterovirus
	Listeria spp.	*Neisseria sicca*		Epstein Barr Virus
	Macrococcus caseolyticus	*Parabacteroides distasonis*		Hepatitis A virus
	Micrococcus luteus	*Parabacteroides merdae*		Hepatitis B virus
	Mycobacterium avium complex (MAC)	*Pasteurella aerogenes*		Hepatitis C virus
	Mycobacterium fortuitum	*Pasteurella canis*		Human alphaherpesvirus 1
	Mycobacterium mucogenicum	*Pasteurella multocida*		Human alphaherpesvirus 2
	Mycoplasma hominis	*Pasteurella stomatis*		Human betaherpesvirus 6
	Mycoplasma pneumoniae	*Prevotella bivia*		Human betaherpesvirus 7
	Nocardia farcinica	*Prevotella buccae*		Human Immunodeficiency Virus
	Parvimonas micra	*Prevotella denticola*		JC Virus
	Pediococcus acidilactici	*Prevotella melaninogenica*		Measles Virus
	Pediococcus pentosaceus	*Prevotella oralis*		Mumps Virus
	Peptostreptococcus anaerobius	*Psychrobacter cryohalolentis*		Parvovirus B19
	Planococcus citreus	*Psychrobacter immobilis*		Rubella Virus
	Planococcus kocurii	*Ralstonia mannitolilytica*		Varicella Zoster Virus
	Propionibacterium freudenreichii	*Ralstonia pickettii*		West Nile Virus
	Propionibacterium propionicum (Arachnia propionica)	*Serratia* spp.		Zika Virus
	Rhodococcus equi	*Stenotrophomonas acidaminiphila*		*Plasmodium falciparum*
	Rothia dentocariosa	*Stenotrophomonas nitritireducens*		*Trypanosoma cruzi*
	Rothia mucilaginosa	*Stenotrophomonas rhizophila*		
	Sarcina ventriculi	*Treponema pallidum*		
	Solibacillus silvestris	*Veillonella parvula*		
	Staphylococcus spp.	*Vibrio alginolyticus*		

On-Panel Organisms	Off-Panel Organisms			
	Gram-Positive Bacteria	Gram-Negative Bacteria	Resistance Markers	Yeasts / Viruses / Parasites
	Streptococcus spp. *Ureaplasma parvum* *Ureaplasma urealyticum* *Vagococcus fluvialis* *Weissella paramesenteroides*	*Vibrio parahaemolyticus* *Vibrio vulnificus*		

g. Interference

Competitive Inhibition / Co-Infection and Microbial Interference

The competitive inhibition and microbial interference study was executed to evaluate the performance of the LIAISON PLEX® BCN Assay detection of on-panel organisms in the presence of highly concentrated, potentially interfering microbes (off-panel) and potential co-infections with highly concentrated on-panel organisms.

To evaluate competitive inhibition, a set of ten representative on-panel strains were tested to assess dual target detection when combined in a pair-wise fashion with the same on-panel strains, as listed in **Table 12**. The ten on-panel pair-wise strain mixtures were each tested in triplicate as a low concentration (ring positive) – high concentration (ring positive + 8 hours) combination. The on-panel organisms were chosen to be representative of clinically relevant poly-microbial infections in blood stream pathogens.

To assess microbial interference, seven off-panel microbes were combined in pairs with the same ten representative on-panel strains for assay evaluation, as listed in **Table 13**. These specific organisms were chosen as they are potentially interfering micro-organisms that are commonly found in sites of blood stream infections that may be present in positive blood culture samples but are not expected to be detected by the LIAISON PLEX® BCN Assay. Off-panel microbe pair testing with on-panel strains was performed in triplicate in high-low concentration combinations, respectively.

As can be observed in **Tables 12** and **13**, 100% target detection was achieved for all ten on-panel organisms, both in the presence of on-panel strains and in the presence of off-panel microbes.

Table 12: LIAISON PLEX® BCN Assay Competitive Inhibition Summary

On-Panel High Concentration Target	Positivity	On-Panel Low Concentration Target	Positivity
Acinetobacter baumannii	100%	*Citrobacter freundii*	100%
	100%	*Enterobacter cloacae*	100%
	100%	*Escherichia coli*	100%
	100%	*Haemophilus influenzae*	100%
	100%	*Klebsiella oxytoca*	100%

On-Panel High Concentration Target	Positivity	On-Panel Low Concentration Target	Positivity
	100%	*Klebsiella pneumoniae*	100%
	100%	*Neisseria meningitidis*	100%
	100%	*Proteus mirabilis*	100%
	100%	*Pseudomonas aeruginosa*	100%
Citrobacter freundii	100%	*Acinetobacter baumannii*	100%
	100%	*Enterobacter cloacae*	100%
	100%	*Escherichia coli*	100%
	100%	*Haemophilus influenzae*	100%
	100%	*Klebsiella oxytoca*	100%
	100%	*Klebsiella pneumoniae*	100%
	100%	*Neisseria meningitidis*	100%
	100%	*Proteus mirabilis*	100%
	100%	*Pseudomonas aeruginosa*	100%
Enterobacter cloacae	100%	*Acinetobacter baumannii*	100%
	100%	*Citrobacter freundii*	100%
	100%	*Escherichia coli*	100%
	100%	*Haemophilus influenzae*	100%
	100%	*Klebsiella oxytoca*	100%
	100%	*Klebsiella pneumoniae*	100%
	100%	*Neisseria meningitidis*	100%
	100%	*Proteus mirabilis*	100%
	100%	*Pseudomonas aeruginosa*	100%
Escherichia coli	100%	*Acinetobacter baumannii*	100%
	100%	*Citrobacter freundii*	100%
	100%	*Enterobacter cloacae*	100%
	100%	*Haemophilus influenzae*	100%
	100%	*Klebsiella oxytoca*	100%
	100%	*Klebsiella pneumoniae*	100%
	100%	*Neisseria meningitidis*	100%
	100%	*Proteus mirabilis*	100%
	100%	*Pseudomonas aeruginosa*	100%
Haemophilus influenzae	100%	*Acinetobacter baumannii*	100%
	100%	*Citrobacter freundii*	100%
	100%	*Enterobacter cloacae*	100%
	100%	*Escherichia coli*	100%
	100%	*Klebsiella oxytoca*	100%
	100%	*Klebsiella pneumoniae*	100%
	100%	*Neisseria meningitidis*	100%
	100%	*Proteus mirabilis*	100%
	100%	*Pseudomonas aeruginosa*	100%
Klebsiella oxytoca	100%	*Acinetobacter baumannii*	100%
	100%	*Citrobacter freundii*	100%

On-Panel High Concentration Target	Positivity	On-Panel Low Concentration Target	Positivity
	100%	*Enterobacter cloacae*	100%
	100%	*Escherichia coli*	100%
	100%	*Haemophilus influenzae*	100%
	100%	*Klebsiella pneumoniae*	100%
	100%	*Neisseria meningitidis*	100%
	100%	*Proteus mirabilis*	100%
	100%	*Pseudomonas aeruginosa*	100%
Klebsiella pneumoniae	100%	*Acinetobacter baumannii*	100%
	100%	*Citrobacter freundii*	100%
	100%	*Enterobacter cloacae*	100%
	100%	*Escherichia coli*	100%
	100%	*Haemophilus influenzae*	100%
	100%	*Klebsiella oxytoca*	100%
	100%	*Neisseria meningitidis*	100%
	100%	*Proteus mirabilis*	100%
	100%	*Pseudomonas aeruginosa*	100%
Neisseria meningitidis	100%	*Acinetobacter baumannii*	100%
	100%	*Citrobacter freundii*	100%
	100%	*Enterobacter cloacae*	100%
	100%	*Escherichia coli*	100%
	100%	*Haemophilus influenzae*	100%
	100%	*Klebsiella oxytoca*	100%
	100%	*Klebsiella pneumoniae*	100%
	100%	*Proteus mirabilis*	100%
	100%	*Pseudomonas aeruginosa*	100%
Proteus mirabilis	100%	*Acinetobacter baumannii*	100%
	100%	*Citrobacter freundii*	100%
	100%	*Enterobacter cloacae*	100%
	100%	*Escherichia coli*	100%
	100%	*Haemophilus influenzae*	100%
	100%	*Klebsiella oxytoca*	100%
	100%	*Klebsiella pneumoniae*	100%
	100%	*Neisseria meningitidis*	100%
	100%	*Pseudomonas aeruginosa*	100%
Pseudomonas aeruginosa	100%	*Acinetobacter baumannii*	100%
	100%	*Citrobacter freundii*	100%
	100%	*Enterobacter cloacae*	100%
	100%	*Escherichia coli*	100%
	100%	*Haemophilus influenzae*	100%
	100%	*Klebsiella oxytoca*	100%
	100%	*Klebsiella pneumoniae*	100%
	100%	*Neisseria meningitidis*	100%

On-Panel High Concentration Target	Positivity	On-Panel Low Concentration Target	Positivity
	100%	*Proteus mirabilis*	100%

Table 13: LIAISON PLEX® BCN Assay Microbial Interference Summary

On-Panel Low Concentration Target	Positivity	Off-Panel High Concentration Target	Positivity
Acinetobacter baumannii	100%	*Bacillus cereus*	0%
	100%	*Clostridium perfringens*	0%
	100%	*Corynebacterium striatum*	0%
	100%	*Cutibacterium (Propionibacterium) acnes*	0%
	100%	*Staphylococcus aureus*	0%
	100%	*Staphylococcus epidermidis*	0%
	100%	*Streptococcus mitis*	0%
Citrobacter freundii	100%	*Bacillus cereus*	0%
	100%	*Clostridium perfringens*	0%
	100%	*Corynebacterium striatum*	0%
	100%	*Cutibacterium (Propionibacterium) acnes*	0%
	100%	*Staphylococcus aureus*	0%
	100%	*Staphylococcus epidermidis*	0%
	100%	*Streptococcus mitis*	0%
Enterobacter cloacae	100%	*Bacillus cereus*	0%
	100%	*Clostridium perfringens*	0%
	100%	*Corynebacterium striatum*	0%
	100%	*Cutibacterium (Propionibacterium) acnes*	0%
	100%	*Staphylococcus aureus*	0%
	100%	*Staphylococcus epidermidis*	0%
	100%	*Streptococcus mitis*	0%
Escherichia coli	100%	*Bacillus cereus*	0%
	100%	*Clostridium perfringens*	0%
	100%	*Corynebacterium striatum*	0%
	100%	*Cutibacterium (Propionibacterium) acnes*	0%
	100%	*Staphylococcus aureus*	0%
	100%	*Staphylococcus epidermidis*	0%
	100%	*Streptococcus mitis*	0%
Haemophilus influenzae	100%	*Bacillus cereus*	0%
	100%	*Clostridium perfringens*	0%
	100%	*Corynebacterium striatum*	0%
	100%	*Cutibacterium (Propionibacterium) acnes*	0%
	100%	*Staphylococcus aureus*	0%

On-Panel Low Concentration Target	Positivity	Off-Panel High Concentration Target	Positivity
	100%	*Staphylococcus epidermidis*	0%
	100%	*Streptococcus mitis*	0%
Klebsiella oxytoca	100%	*Bacillus cereus*	0%
	100%	*Clostridium perfringens*	0%
	100%	*Corynebacterium striatum*	0%
	100%	*Cutibacterium (Propionibacterium) acnes*	0%
	100%	*Staphylococcus aureus*	0%
	100%	*Staphylococcus epidermidis*	0%
	100%	*Streptococcus mitis*	0%
Klebsiella pneumoniae	100%	*Bacillus cereus*	0%
	100%	*Clostridium perfringens*	0%
	100%	*Corynebacterium striatum*	0%
	100%	*Cutibacterium (Propionibacterium) acnes*	0%
	100%	*Staphylococcus aureus*	0%
	100%	*Staphylococcus epidermidis*	0%
	100%	*Streptococcus mitis*	0%
Neisseria meningitidis	100%	*Bacillus cereus*	0%
	100%	*Clostridium perfringens*	0%
	100%	*Corynebacterium striatum*	0%
	100%	*Cutibacterium (Propionibacterium) acnes*	0%
	100%	*Staphylococcus aureus*	0%
	100%	*Staphylococcus epidermidis*	0%
	100%	*Streptococcus mitis*	0%
Proteus mirabilis	100%	*Bacillus cereus*	0%
	100%	*Clostridium perfringens*	0%
	100%	*Corynebacterium striatum*	0%
	100%	*Cutibacterium (Propionibacterium) acnes*	0%
	100%	*Staphylococcus aureus*	0%
	100%	*Staphylococcus epidermidis*	0%
	100%	*Streptococcus mitis*	0%
Pseudomonas aeruginosa	100%	*Bacillus cereus*	0%
	100%	*Clostridium perfringens*	0%
	100%	*Corynebacterium striatum*	0%
	100%	*Cutibacterium (Propionibacterium) acnes*	0%
	100%	*Staphylococcus aureus*	0%
	100%	*Staphylococcus epidermidis*	0%
	100%	*Streptococcus mitis*	0%

Interfering Substances

The interfering substances study was performed to evaluate the performance of the LIAISON PLEX® BCN Assay in the presence of non-microbial (endogenous and exogenous) interfering substances which may be present in blood culture specimens. A set of four representative "on-panel" organisms were tested to assess effectiveness of target detection in the presence of six interfering substances. Each interfering substance was tested across five replicates. In addition, a negative control (five replicates) was tested alongside the positive specimens to assess impact of the same interfering agents in specimens containing no target; additionally, a positive control (specimen without interfering substances) for all four targets was also tested to assess for detection capabilities.

All four targets demonstrated 100% positivity in the presence of all six interfering substances, and 0% target detection was observed in the negative control sample in the presence of the same interfering substances (**Table 14**). Additionally, 100% target detection was observed for the positive control for each target.

Table 14: LIAISON PLEX® BCN Assay Interfering Substances Summary

Interfering Substance	Interfering Substance Concentration	Target	Positivity
N/A	N/A	*Acinetobacter baumannii*	100%
		Escherichia coli	100%
		Haemophilus influenzae	100%
		Neisseria meningitidis	100%
Unconjugated Bilirubin	20 mg/dL	*Acinetobacter baumannii*	100%
		Escherichia coli	100%
		Haemophilus influenzae	100%
		Neisseria meningitidis	100%
		Negative Control	0%
Conjugated Bilirubin	20 mg/dL	*Acinetobacter baumannii*	100%
		Escherichia coli	100%
		Haemophilus influenzae	100%
		Neisseria meningitidis	100%
		Negative Control	0%
Hemoglobin	14 g/L	*Acinetobacter baumannii*	100%
		Escherichia coli	100%
		Haemophilus influenzae	100%
		Neisseria meningitidis	100%
		Negative Control	0%
Intralipid	3000 mg/dL	*Acinetobacter baumannii*	100%
		Escherichia coli	100%
		Haemophilus influenzae	100%
		Neisseria meningitidis	100%
		Negative Control	0%

Interfering Substance	Interfering Substance Concentration	Target	Positivity
γ-globulin	6 g/dL	*Acinetobacter baumannii*	100%
		Escherichia coli	100%
		Haemophilus influenzae	100%
		Neisseria meningitidis	100%
		Negative Control	0%
Sodium polyanetholsulfonate (SPS)	0.25% w/v	*Acinetobacter baumannii*	100%
		Escherichia coli	100%
		Haemophilus influenzae	100%
		Neisseria meningitidis	100%
		Negative Control	0%

Carry-Over/Cross Contamination

This study was performed to evaluate the risk of carry-over and cross contamination occurring during normal use of the device when highly concentrated positive specimens are processed alongside negative specimens. Two operators tested 30 high concentration positive samples consisting of *Morganella morganii* at a final concentration of 2.74E+09 CFU/mL and 30 negative samples consisting of Negative Blood Matrix. This concentration of *Morganella morganii* was selected as the representative analyte for the high positive control since it was the highest concentration material from the LIAISON PLEX® Growth and Detection study Ring Positive + 8 hours growths, thus representing the most challenging scenario for potential cross contamination. Testing was performed on one LIAISON PLEX® instrument containing 6 blades/modules over the course of four days. The samples were loaded into cartridges alternating between positive and negative samples (checkerboard fashion), six specimens at a time using sample prep trays. The results, presented in **Table 15**, demonstrate 100% agreement between expected and observed results, indicating that no cross contamination occurred within runs and no carry-over was observed across runs.

Table 15. Overall Results

Overall Percent Agreement between Expected and Observed Results	100%
***Morganella morganii* Positivity in High Positive Control Replicates**	100%
***Morganella morganii* Positivity in Negative Control Replicates**	0%

h. Assay Cut-off

The specific assay parameters for the LIAISON PLEX® BCN Assay are considered confidential and proprietary.

2. Comparison Studies:

a. Method comparison with predicate device:

Refer to Section 3 Clinical Performance.

b. Matrix Comparison: Testing of Blood Culture Bottle Types / Matrix Equivalency

The performance of LIAISON PLEX® Gram-Negative Blood Culture (BCN) Assay was evaluated across 12 different types of commercially available blood culture media bottles using representative on-panel BCN targets with resistance markers, off-panel (gram-positive) LIAISON PLEX® BCN Assay targets, and negative blood matrix (NBM). The results, presented in **Table 16**, demonstrate that all 12 bottle types are compatible with the LIAISON PLEX® Gram-Negative Blood Culture (BCN) Assay. A total of 650 independent blood culture bottles were evaluated, which included 506 gram-negative bottle cultures, 120 gram-positive bottle cultures, and 24 negative blood matrix bottles; see **Table 16**, final row. The effectiveness of bioMerieux BACT/ALERT® FA Plus blood culture bottle – was established through blood culture growth required for all other analytical studies, such as growth and detection and analytical reactivity/inclusivity verification testing, and was not included in testing performed for the media equivalency study.

Table 16: LIAISON PLEX® Gram-Negative Blood Culture (BCN) Assay Media Equivalency/ Universal Blood Culture Bottle Result Summary

Manufacturer System	Blood Culture Bottle Manufacturer	Blood Culture Bottle Type	Number of Inoculated Bottles		Negative Blood Matrix[b] (Negative Detection)
			Gram-Negative Bacteria (Positive Detection)	Gram-positive Bacteria (Negative Detection)	
Biomerieux BACT/ALERT® 3D System	**Biomerieux BACT/ALERT®**	BACT/ALERT® SA (Aerobic)	21/21	10/10	2/2
		BACT/ALERT® SN (Anaerobic)	58/58	10/10	2/2
		BACT/ALERT® FN Plus (Anaerobic)	21/21	10/10	2/2
		BACT/ALERT® PF Plus (Pediatric)	63/63	10/10	2/2
N/A[a]	**Becton Dickinson[a] BACTEC™**	BACTEC™ Standard	21/21	10/10	2/2
		BACTEC™ Plus (Aerobic)	21/21	10/10	2/2
		BACTEC™ Standard (Anaerobic)	50/50	10/10	2/2
		BACTEC™ Plus (Anaerobic)	58/58	10/10	2/2
		BACTEC™ Peds Plus (Pediatric)	63/63	10/10	2/2
		BACTEC™ Lytic (Anaerobic)	20/20	10/10	2/2
N/A[a]	**Thermo Scientific[a] VersaTREK™**	REDOX™ 1 EZ Draw™ (Aerobic)	60/60	10/10	2/2

Manufacturer System	Blood Culture Bottle Manufacturer	Blood Culture Bottle Type	Number of Inoculated Bottles		Negative Blood Matrix[b] (Negative Detection)
			Gram-Negative Bacteria (Positive Detection)	Gram-positive Bacteria (Negative Detection)	
		REDOX™ 2 EZ Draw™ (Anaerobic)	50/50	10/10	2/2
Number of Expected Calls/Total Number of Independent Blood Bottles			**506/506 (100%)**	**120/120 (100%)**	**24/24 (100%)**
			650/650 (100%)		

[a] For gram-negative blood culture preparation, BACTEC™ and VersaTREK™ systems were not available and corresponding media bottles were placed in a standard laboratory incubator with a shaker for growth. For gram-positive blood culture growth, only VersaTREK™ bottles needed to be placed in a standard laboratory incubator with a shaker in lieu of VersaTREK™ system; BACT/ALERT ® and BACTEC™ blood bottles were grown using corresponding automated blood culture systems up to bottle ring positivity.

[b] Negative Blood Matrix (NBM) was tested using two independent blood inoculations per bottle type and each NBM sample was tested in replicates of three (total six replicates per bottle type) per study design; 72 total runs from 24 total bottle inoculations.

The average concentrations of each organism grown in 12 different types of media bottles are shown in **Table 17**; representing the approximate concentrations obtained from a mono-bacterial blood culture used in this testing.

Table 17: Concentration of Blood Cultures in Different Media Bottles Used in Testing

Gram-Negative (On-panel) Organism*	Expected Result	Strain ID	Average Positive Blood Culture Concentration (CFU/mL)
Acinetobacter baumannii	*Acinetobacter* spp., *Acinetobacter baumanii*, OXA	IHMA 128307	3.03E+08
Acinetobacter lwoffii	*Acinetobacter* spp.	ATCC 15309	2.05E+08
Citrobacter freundii	*Enterobacteriaceae/Morganellaceae, Citrobacter* spp., VIM	IHMA 549813	1.03E+09
Citrobacter amalonaticus	*Enterobacteriaceae/Morganellaceae, Citrobacter* spp.	ATCC 25405	9.87E+09
Enterobacter cloacae	*Enterobacteriaceae/Morganellaceae, Enterobacter* spp.	ATCC 35030	1.16E+09
Enterobacter aerogenes	*Enterobacteriaceae/Morganellaceae, Enterobacter* spp.	ATCC 35029	9.50E+09
Proteus mirabilis	*Enterobacteriaceae/Morganellaceae, Proteus* spp.	ATCC 12453	6.64E+08
Proteus vulgaris	*Enterobacteriaceae/Morganellaceae, Proteus* spp.	ATCC 29905	4.54E+08
Salmonella bongori	*Enterobacteriaceae/Morganellaceae, Salmonella* spp.	ATCC 43975	1.42E+09

Gram-Negative (On-panel) Organism*	Expected Result	Strain ID	Average Positive Blood Culture Concentration (CFU/mL)
Salmonella enterica subsp. *arizonae*	*Enterobacteriaceae/Morganellaceae*, *Salmonella* spp.	ATCC 13314	1.67E+09
Pseudomonas aeruginosa	*Pseudomonas* spp., *Pseudomonas aeruginosa*, IMP	IHMA 576602	4.88E+08
Pseudomonas mendocina	*Pseudomonas* spp.	ATCC 25411	5.24E+08
Klebsiella oxytoca	*Enterobacteriaceae/Morganellaceae*, *Klebsiella oxytoca*, CTX-M	IHMA 683079	7.29E+08
Klebsiella pneumoniae	*Enterobacteriaceae/Morganellaceae*, *Klebsiella pneumoniae*, KPC	IHMA 629630	6.61E+08
Klebsiella variicola	*Enterobacteriaceae/Morganellaceae*, *Klebsiella variicola*	Clinical Isolate V0512	1.28E+09
Escherichia coli	*Enterobacteriaceae/Morganellaceae*, *Escherichia coli*, MCR	NCTC 13846	1.17E+09
Serratia marcescens	*Enterobacteriaceae/Morganellaceae*, *Serratia marcescens*, SME	IHMA 1642209	1.34E+09
Morganella morganii	*Enterobacteriaceae/Morganellaceae*, *Morganella morganii*, NDM	IHMA 605873	1.28E+09
Haemophilus influenzae	*Haemophilus influenzae*	ATCC 9007	6.70E+08
Neisseria meningitidis	*Neisseria meningitidis*	ATCC 43744	3.07E+08
Stenotrophomonas maltophilia	*Stenotrophomonas maltophilia*	ATCC 700269	4.18E+08
Gram-Positive (Off-panel) Organism*	**Expected Result**	**Strain ID**	**Average Positive Blood Culture Concentration (CFU/mL)**
Enterococcus faecalis	No Target Detected	ATCC 51575	7.51E+08
Enterococcus faecium	No Target Detected	ATCC 700221	4.12E+08
Staphylococcus aureus (MRSA)	No Target Detected	ATCC BAA-2312	2.07E+08
Staphylococcus epidermidis (MRSE)	No Target Detected	ATCC 35984	2.26E+08
Streptococcus agalactiae	No Target Detected	ATCC 12386	7.50E+08
Streptococcus constellatus	No Target Detected	ATCC 27823	5.25E+08
Bacillus subtilis	No Target Detected	ATCC 19659	8.50E+07
Bacillus cereus[a]	No Target Detected	ATCC 10702	4.4E+08
Corynebacterium diphtheriae	No Target Detected	ATCC 27010	3.74E+08
Corynebacterium striatum	No Target Detected	ATCC 43735	3.48E+08
Listeria monocytogenes	No Target Detected	ATCC 15313	7.58E+08

[a] Concentration of Bacillus cereus representing single blood bottle culture in VersaTREK™ REDOX™2 EZ Draw™ Media.

*Genus and species taxonomies are ever evolving based on the latest research. The strain ID is a unique identifier that will not be changed by the supplier. Therefore, the strain ID assigned by the supplier should be the reference

used for that material. The genus and species should be for reference purposes only.

3. Clinical Performance:

A multi-site clinical study established the diagnostic accuracy of the LIAISON PLEX® Gram-Negative Blood Culture (BCN) Assay for the detection and identification of pathogenic gram-negative organisms in positive blood culture. The clinical performance of the LIAISON® PLEX BCN Assay was evaluated using clinical specimens prospectively collected between March 2024 and July 2024 from four geographically diverse clinical sites within the United States. The clinical study utilized remnant, de-identified blood culture specimens collected from patients exhibiting clinical signs and symptoms of bloodstream infection, evidenced by positive identification by a continuous monitoring blood culture system.

A total of 381 unique prospectively collected specimens that met the pre-determined inclusion criteria were enrolled in the study. Clinical runs and re-runs using the LIAISON PLEX® BCN Assay were tested on the LIAISON PLEX® System by trained operators at four clinical sites. For targets that exhibited low prevalence rates in the prospective study, the prospective specimen set was supplemented with 231 pre-selected left-over, de-identified specimens sourced from seven vendors in the United States and one site in Italy. The pre-selected specimens were identified by Standard of Care (SoC) testing and confirmed as positive by VITEK 2 and/or PCR followed by bi-directional sequencing (BDS) according to the reference method algorithm prior to enrollment in the study. To minimize bias, pre-selected specimens were tested across the five sites in a randomized, blinded manner along with negative specimens.

Out of the 381 specimens enrolled in the prospective arm of the study, 30 prospective specimens were excluded from the analysis (one (1) duplicate patient enrollment, and 29 with incomplete reference testing results due to mixed growth, insufficient growth, or no growth).

Contrived specimens were tested to supplement the positive clinical specimens in the prospective and pre-selected study cohorts for all targets. A total of 746 specimens were contrived, blinded, randomized, and tested along with negative specimens at four testing sites during April 2024– August 2024.

Table 18 provides a summary of the general demographic information of the 351 prospectively collected and 231 pre-selected specimens that were included in the study analysis.

Table 18: LIAISON PLEX® BCN Assay Summary of the General Demographic Information

	Prospective (N =351)	**Pre-selected (N=231)**
	# Specimens (%)	**# Specimens (%)**
Gender		
Male	181 (51.6%)	136 (58.9%)
Female	170 (48.4%)	91 (39.4%)
Gender Unknown	0 (0.0%)	4 (1.7%)
Total	351 (100.0%)	231 (100.0%)
Age (years)		
0-1	10 (2.8%)	13 (5.6%)
>1-5	3 (0.9%)	2 (0.9%)
>5-21	10 (2.8%)	4 (1.7%)

	Prospective (N =351)	Pre-selected (N=231)
	# Specimens (%)	# Specimens (%)
>21-65	142 (40.5%)	90 (39.0%)
>65	181 (51.6%)	107 (46.3%)
Age Unknown	5 (1.4%)	15 (6.5%)
Total	351 (100.0%)	351 (100.0%)
Subject Status		
Emergency Room	68 (19.4%)	2 (0.9%)
Hospitalized	262 (74.6%)	18 (7.8%)
Long-Term Care	2 (0.6%)	0 (0.0%)
Outpatient	1 (0.3%)	0 (0.0%)
Status Unknown	18 (5.1%)	211 (91.3%)
Total	351 (100.0%)	231 (100.0%)
Blood Culture Bottle Type		
BD BACTEC Lytic Anaerobic	65(18.5%)	8 (3.5%)
BD BACTEC Plus Aerobic	61(17.4%)	20 (8.7%)
BD BACTEC Standard Aerobic	19(5.4%)	89 (38.5%)
BacT/ALERT FA Plus	72(20.5%)	29 (12.6%)
BacT/ALERT FN Plus	77(21.9%) -	26 (11.3%)
BacT/ALERT PF Plus	3 (0.9%)	0 (0.0%)
BacT/ALERT SA Standard Aerobic	22(6.3%)	0 (0.0%)
BacT/ALERT SN Standard Anaerobic	16(4.6%)	0 (0.0%)
BD BACTEC Plus Anaerobic	1 (0.3%)	0 (0.0%)
BD BACTEC Peds Plus	10 (2.8%)	1 (0.4%)
BD BACTEC (Unknown Aerobic)	0 (0.0%)	5 (2.2%)
BD BACTEC (Unknown Anaerobic)	0 (0.0%)	3 (1.3%)
BD BACTEC (Unknown)	0 (0.0%)	15 (6.5%)
Unknown Aerobic	0 (0.0%)	4 (1.7%)
Unknown Anaerobic	0 (0.0%)	1 (0.4%)
Bottle Type Unknown	0 (0.0%)	30 (13.0%)
Total	351 (100.0%)	231 (100.0%)

The LIASON PLEX® BCN Assay results were compared to culture followed by automated microbiological/biochemical identification using VITEK 2, PCR followed by BDS, or a combination according to the algorithm described in **Table 19** below.

Table 19 – Reference Method Algorithm

LIAISON PLEX® BCN Assay Target	Comparator Method
Acinetobacter spp.	Culture followed by Automated microbiological/biochemical identification using VITEK 2
Citrobacter spp.	
Enterobacter spp.	
Enterobacteriaceae/Morganellaceae	
Escherichia coli(1)	
Haemophilus influenzae	
Morganella morganii	

LIAISON PLEX® BCN Assay Target	Comparator Method
Neisseria meningitidis	
Proteus spp.	
Pseudomonas aeruginosa	
Pseudomonas spp.	
Salmonella spp.	
Serratia marcescens	
Stenotrophomonas maltophilia	
Acinetobacter baumannii	Culture followed by Automated microbiological/biochemical identification using VITEK 2 with positive confirmation of the clinical isolate by PCR/BDS
Klebsiella oxytoca	
Klebsiella pneumoniae	
Klebsiella variicola	PCR followed by bi-directional sequencing
CTX-M (*bla*$_{CTX-M}$)	
IMP (*bla*$_{IMP}$)	
KPC (*bla*$_{KPC}$)	
NDM (*bla*$_{NDM}$)	
OXA (*bla*$_{OXA}$)	
VIM (*bla*$_{VIM}$)	
MCR	
SME	

(1)The LIAISION PLEX® BCN Assay is not designed to distinguish between *Escherichia coli* and *Shigella* spp. (*S. dysenteriae, S. boydii, S. flexneri,* and *S. sonnei*).

Of the 582 clinical specimens collectively included in the prospective and pre-selected study analysis (Arms 1 and 2 combined), 556 samples (95.5%) generated valid LIAISON PLEX® BCN Assay results (i.e., Detected or Not Detected) on the first attempt. There were 26 specimens (4.5%) with an invalid result on the initial run. Of the 26 specimens retested, 24 (4.1%) specimens generated valid BCN results after a single retest for a final testing success rate of 99.7% (580/582).

For each target in the LIAISON PLEX® BCN Assay Panel, the diagnostic performance of the LIAISON PLEX® BCN Assay was determined using Sensitivity/PPA and Specificity/NPA, along with the associated 95% confidence intervals, (95% CI as compared to the reference method). The results of the combined prospective and pre-selected specimen analysis are summarized in **Table 20**.

Table 20 – Sensitivity/PPA and Specificity/NPA of Combined Prospective and Pre-Selected Data Set

Pathogen Target		Sensitivity/PPA			Specificity/NPA		
		TP / (TP+FN)	Sensitivity/ PPA (%)	95% CI	TN / (TN+FP)	Specificity/N PA (%)	95% CI
Bacteria							
Acinetobacter baumannii	Prospective	0/0	N/A	N/A	350/350	100%	98.9% - 100%
	Pre-selected	30/31	96.8%	83.8% - 99.4%	199/199	100%	98.1% - 100%
	Combined	**30/31**	**96.8%**	**83.8% - 99.4%**	**549/549**	**100%**	**99.3% - 100%**
Acinetobacter spp.	Prospective	3/5	60%	23.1% - 88.2%	345/345	100%	98.9% - 100%
	Pre-selected	33/35	94.3%	81.4% - 98.4%	195/195	100%	98.1% - 100%
	Combined	**36/40[1]**	**90%**	**76.9% - 96%**	**540/540**	**100%**	**99.3% - 100%**
Citrobacter spp.	Prospective	6/6	100%	61% - 100%	344/344	100%	98.9% - 100%
	Pre-selected	23/24	95.8%	79.8% - 99.3%	206/206	100%	98.2% - 100%
	Combined	**29/30**	**96.7%**	**83.3% - 99.4%**	**550/550**	**100%**	**99.3% - 100%**

Pathogen Target		Sensitivity/PPA			Specificity/NPA		
		TP / (TP+FN)	Sensitivity/ PPA (%)	95% CI	TN / (TN+FP)	Specificity/N PA (%)	95% CI
Enterobacter spp.	Prospective	20/20	100%	83.9% - 100%	330/330	100%	98.8% - 100%
	Pre-selected	9/10	90%	59.6% - 98.2%	220/220	100%	98.3% - 100%
	Combined	**29/30**	**96.7%**	**83.3% - 99.4%**	**550/550**	**100%**	**99.3% - 100%**
Enterobacteriaceae/ Morganellaceae	Prospective	305/306	99.7%	98.2% - 99.9%	44/44	100%	92% - 100%
	Pre-selected	123/123	100%	97% - 100%	106/107	99.1%	94.9% - 99.8%
	Combined	**428/429**	**99.8%**	**98.7% - 100%**	**150/151**	**99.3%**	**96.3% - 99.9%**
Escherichia coli	Prospective	178/179	99.4%	96.9% - 99.9%	169/171	98.8%	95.8% - 99.7%
	Pre-selected	1/1	100%	20.7% - 100%	229/229	100%	98.4% - 100%
	Combined	**179/180**	**99.4%**	**96.9% - 99.9%**	**398/400[2]**	**99.5%**	**98.2% - 99.9%**
Haemophilus influenzae	Prospective	8/8	100%	67.6% - 100%	342/342	100%	98.9% - 100%
	Pre-selected	24/24	100%	86.2% - 100%	206/206	100%	98.2% - 100%
	Combined	**32/32**	**100%**	**89.3% - 100%**	**548/548**	**100%**	**99.3% - 100%**
Klebsiella oxytoca	Prospective	9/9	100%	70.1% - 100%	340/341	99.7%	98.4% - 99.9%
	Pre-selected	26/27	96.3%	81.7% - 99.3%	203/203	100%	98.1% - 100%
	Combined	**35/36**	**97.2%**	**85.8% - 99.5%**	**543/544[3]**	**99.8%**	**99% - 100%**
Klebsiella pneumoniae	Prospective	44/45	97.8%	88.4% - 99.6%	304/305	99.7%	98.2% - 99.9%
	Pre-selected	1/1	100%	20.7% - 100%	227/229	99.1%	96.9% - 99.8%
	Combined	**45/46**	**97.8%**	**88.7% - 99.6%**	**531/534[4]**	**99.4%**	**98.4% - 99.8%**
Klebsiella variicola	Prospective	8/8	100%	67.6% - 100%	341/341	100%	98.9% - 100%
	Pre-selected	4/4	100%	51% - 100%	197/197	100%	98.1% - 100%
	Combined	**12/12**	**100%**	**75.8% - 100%**	**538/538**	**100%**	**99.3% - 100%**
Morganella morganii	Prospective	3/3	100%	43.9% - 100%	347/347	100%	98.9% - 100%
	Pre-selected	5/5	100%	56.6% - 100%	225/225	100%	98.3% - 100%
	Combined	**8/8**	**100%**	**67.6% - 100%**	**572/572**	**100%**	**99.3% - 100%**
Neisseria meningitidis	Prospective	0/0	N/A	N/A	350/350	100%	98.9% - 100%
	Pre-selected	1/3	33.3%	6.1% - 79.2%	227/227	100%	98.3% - 100%
	Combined	**1/3[5]**	**33.3%**	**6.1% - 79.2%**	**577/577**	**100%**	**99.3% - 100%**
Proteus spp.	Prospective	23/23	100%	85.7% - 100%	327/327	100%	98.8% - 100%
	Pre-selected	14/14	100%	78.5% - 100%	216/216	100%	98.3% - 100%
	Combined	**37/37**	**100%**	**90.6% - 100%**	**543/543**	**100%**	**99.3% - 100%**
Pseudomonas aeruginosa	Prospective	28/29	96.6%	82.8% - 99.4%	321/321	100%	98.8% - 100%
	Pre-selected	6/6	100%	61% - 100%	224/224	100%	98.3% - 100%
	Combined	**34/35**	**97.1%**	**85.5% - 99.5%**	**545/545**	**100%**	**99.3% - 100%**
Pseudomonas spp.	Prospective	29/30	96.7%	83.3% - 99.4%	320/320	100%	98.8% - 100%
	Pre-selected	7/7	100%	64.6% - 100%	223/223	100%	98.3% - 100%
	Combined	**36/37**	**97.3%**	**86.2% - 99.5%**	**543/543**	**100%**	**99.3% - 100%**
Salmonella spp.	Prospective	1/1	100%	20.7% - 100%	349/349	100%	98.9% - 100%
	Pre-selected	16/16	100%	80.6% - 100%	214/214	100%	98.2% - 100%
	Combined	**17/17**	**100%**	**81.6% - 100%**	**563/563**	**100%**	**99.3% - 100%**
Serratia marcescens	Prospective	9/9	100%	70.1% - 100%	340/341	99.7%	98.4% - 99.9%
	Pre-selected	20/20	100%	83.9% - 100%	209/210	99.5%	97.4% - 99.9%

Pathogen Target		Sensitivity/PPA			Specificity/NPA		
		TP / (TP+FN)	Sensitivity/ PPA (%)	95% CI	TN / (TN+FP)	Specificity/N PA (%)	95% CI
	Combined	**29/29**	**100%**	**88.3% - 100%**	**549/551**	**99.6%**	**98.7% - 99.9%**
Stenotrophomonas maltophilia	Prospective	1/1	100%	20.7% - 100%	349/349	100%	98.9% - 100%
	Pre-selected	10/10	100%	72.2% - 100%	219/220	99.5%	97.5% - 99.9%
	Combined	**11/11**	**100%**	**74.1% - 100%**	**568/569**	**99.8%**	**99% - 100%**
Resistance Marker Genes[6]							
CTX-M (bla_{CTX-M})	Prospective	40/41	97.6%	87.4% - 99.6%	295/297	99.3%	97.6% - 99.8%
	Pre-selected	5/5	100%	56.6% - 100%	169/169	100%	97.8% - 100%
	Combined	**45/46**	**97.8%**	**88.7% - 99.6%**	**464/466**	**99.6%**	**98.4% - 99.9%**
IMP (bla_{IMP})	Prospective	0/0	N/A	N/A	338/338	100%	98.9% - 100%
	Pre-selected	0/0	N/A	N/A	174/174	100%	97.8% - 100%
	Combined	**0/0**	**N/A**	**N/A**	**512/512**	**100%**	**99.3% - 100%**
KPC (bla_{KPC})	Prospective	1/1	100%	20.7% - 100%	336/336	100%	98.9% - 100%
	Pre-selected	0/0	N/A	N/A	164/164	100%	97.7% - 100%
	Combined	**1/1**	**100%**	**20.7% - 100%**	**500/500**	**100%**	**99.2% - 100%**
NDM (bla_{NDM})	Prospective	0/0	N/A	N/A	338/338	100%	98.9% - 100%
	Pre-selected	1/1	100%	20.7% - 100%	173/173	100%	97.8% - 100%
	Combined	**1/1**	**100%**	**20.7% - 100%**	**511/511**	**100%**	**99.3% - 100%**
OXA (bla_{OXA})	Prospective	0/0	N/A	N/A	332/337	98.5%	96.6% - 99.4%
	Pre-selected	26/26	100%	87.1% - 100%	137/138	99.3%	96% - 99.9%
	Combined	**26/26**	**100%**	**87.1% - 100%**	**469/475**	**98.7%**	**97.3% - 99.4%**
VIM (bla_{VIM})	Prospective	0/0	N/A	N/A	338/338	100%	98.9% - 100%
	Pre-selected	0/0	N/A	N/A	174/174	100%	97.8% - 100%
	Combined	**0/0**	**N/A**	**N/A**	**512/512**	**100%**	**99.3% - 100%**
MCR	Prospective	0/0	N/A	N/A	334/334	100%	98.9% - 100%
	Pre-selected	0/0	N/A	N/A	131/131	100%	97.2% - 100%
	Combined	**0/0**	**N/A**	**N/A**	**465/465**	**100%**	**99.2% - 100%**
SME	Prospective	0/0	N/A	N/A	10/10	100%	72.2% - 100%
	Pre-selected	0/0	N/A	N/A	21/21	100%	84.5% - 100%
	Combined	**0/0**	**N/A**	**N/A**	**31/31**	**100%**	**89% - 100%**

[1]Clinical isolates from 2/4 *Acinetobacter* spp. false negative specimens were negative for *Acinetobacter* spp. by BDS.
[2]The clinical isolate from 1/2 *Escherichia coli* false positive specimens was positive for *Escherichia coli* by BDS.
[3]The *Klebsiella oxytoca* false positive specimen was positive for *Klebsiella oxytoca* by Standard of Care.
[4]Two of the three (2/3) *Klebsiella pneumoniae* false positive specimens were positive for *Klebsiella pnuemoniae* by Standard of Care.
[5]Both *Neisseria meningitidis* false negative specimens were positive by another FDA-cleared molecular assay.
[6]The LIAISON PLEX® BCN assay will report the presence or absence of resistance markers only if an applicable organism is also detected, therefore the total number of evaluable samples for each resistance marker is dependent on the number of applicable organisms enrolled.

Out of the 746 specimens included in the contrived study analysis, 717 specimens (96.1%) generated valid LIAISON PLEX® BCN Assay results (i.e., Detected or Not Detected) on the first attempt. There were 29 specimens (3.9%) with an invalid result on the initial run. Of the 29 specimens retested, 28 (3.8%) specimens generated a valid result after a single retest for a final

testing success rate of 99.9% (745/746).

The performance (Sensitivity/PPA and Specificity/NPA) of the LIAISION PLEX® BCN Assay for contrived specimens is presented separately in **Table 21**.

Table 21 – Sensitivity/PPA and Specificity/NPA for the Contrived Data Set

Pathogen Target	Sensitivity/PPA			Specificity/NPA		
Analyte	**TP / (TP+FN)**	**Sensitivity/ PPA (%)**	**95% CI**	**TN / (TN+FP)**	**Specificity/ NPA (%)**	**95% CI**
Bacterial Identification						
Acinetobacter baumannii	25/25	100%	86.7% - 100%	720/720	100%	99.5% - 100%
Acinetobacter spp.	45/45	100%	92.1% - 100%	700/700	100%	99.5% - 100%
Citrobacter spp.	32/32	100%	89.3% - 100%	713/713	100%	99.5% - 100%
Enterobacter spp.	54/54	100%	93.4% - 100%	691/691	100%	99.4% - 100%
Enterobacteriaceae/ Morganellaceae	460/460	100%	99.2% - 100%	284/285	99.6%	98% - 99.9%
Escherichia coli	41/41	100%	91.4% - 100%	704/704	100%	99.5% - 100%
Haemophilus influenzae	0/0	0%	0% - 0%	745/745	100%	99.5% - 100%
Klebsiella oxytoca	20/20	100%	83.9% - 100%	725/725	100%	99.5% - 100%
Klebsiella pneumoniae	46/46	100%	92.3% - 100%	698/699	99.9%	99.2% - 100%
Klebsiella variicola	50/50	100%	92.9% - 100%	695/695	100%	99.5% - 100%
Morganella morganii	62/62	100%	94.2% - 100%	683/683	100%	99.4% - 100%
Neisseria meningitidis	50/50	100%	92.9% - 100%	695/695	100%	99.5% - 100%
Proteus spp.	30/30	100%	88.6% - 100%	715/715	100%	99.5% - 100%
Pseudomonas aeruginosa	35/36	97.2%	85.8% - 99.5%	709/709	100%	99.5% - 100%
Pseudomonas spp.	57/58	98.3%	90.9% - 99.7%	687/687	100%	99.4% - 100%
Salmonella spp.	70/70	100%	94.8% - 100%	675/675	100%	99.4% - 100%
Serratia marcescens	55/55	100%	93.5% - 100%	690/690	100%	99.4% - 100%
Stenotrophomonas maltophilia	49/49	100%	92.7% - 100%	696/696	100%	99.5% - 100%
Resistance Marker Genes[1]						
CTX-M (bla_{CTX-M})	105/105	100%	96.5% - 100%	305/306	99.7%	98.2% - 99.9%
IMP (bla_{IMP})	54/54	100%	93.4% - 100%	357/357	100%	98.9% - 100%
KPC (bla_{KPC})	61/61	100%	94.1% - 100%	350/350	100%	98.9% - 100%
NDM (bla_{NDM})	67/67	100%	94.6% - 100%	344/344	100%	98.9% - 100%
OXA (bla_{OXA})	35/35	100%	90.1% - 100%	375/376	99.7%	98.5% - 100%
VIM (bla_{VIM})	50/50	100%	92.9% - 100%	361/361	100%	98.9% - 100%
MCR	50/50	100%	92.9% - 100%	326/326	100%	98.8% - 100%
SME	50/50	100%	92.9% - 100%	5/5	100%	56.6% - 100%

[1]The LIAISON PLEX® BCN assay will report the presence or absence of resistance markers only if an applicable organism is also detected, therefore the total number of evaluable samples for each resistance marker is dependent on the number of applicable organisms enrolled.

The pre-defined acceptance criteria for the clinical study were:

- The assay shall achieve a target Sensitivity/Positive Percent Agreement of ≥90% for all targets except *Klebsiella oxytoca* and *Stenotrophomonas maltophilia* which shall achieve ≥85%.
- The Specificity/Negative Percent Agreement for each target should be established at a level of ≥95%.
- Failure rate shall be ≤10%.

Acceptance Criteria are based on Prospective, Pre-selected, and Contrived sets combined.

As all predefined acceptance criteria were met, the study results demonstrate that the diagnostic accuracy of the LIAISON PLEX® BCN Assay is acceptable for the safe and effective detection and identification of gram-negative pathogens from blood culture media identified as positive by a continuous monitoring blood culture system and which contain gram-negative organism as determined by Gram stain from patients exhibiting clinical signs and symptoms of bloodstream infection.

N. Proposed Labeling:

The labeling provided in the submission satisfies the requirements of 21 CFR 809.10.

O. Conclusion:

The submitted information in this premarket notification is complete and supports a substantial equivalence decision.