DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service

Food and Drug Administration
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Silver Spring, MD 20993-0002

July 26, 2017

Bruker Daltonik GmbH
Mr. David Cromwick
Director of Quality
40 Manning Rd
Billerica, MA 01821 US

Re: K163536
Trade/Device Name: MALDI Biotyper CA (MBT-CA) System, MBT smart CA System
Regulation Number: 21 CFR 866.3361
Regulation Name: Mass spectrometer system for clinical use for the identification of microorganisms
Regulatory Class: II
Product Code: PEX
Dated: December 16, 2016
Received: December 16, 2016

Dear Mr. Cromwick:

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 (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. 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.

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 Parts 801 and 809); medical device reporting (reporting of

medical device-related adverse events) (21 CFR 803); good manufacturing practice requirements as set forth in the quality systems (QS) regulation (21 CFR Part 820); and if applicable, the electronic product radiation control provisions (Sections 531-542 of the Act); 21 CFR 1000-1050.

If you desire specific advice for your device on our labeling regulations (21 CFR Parts 801 and 809), please contact the Division of Industry and Consumer Education at its toll-free number (800) 638 2041 or (301) 796-7100 or at its Internet address http://www.fda.gov/MedicalDevices/ResourcesforYou/Industry/default.htm. Also, please note the regulation entitled, "Misbranding by reference to premarket notification" (21 CFR Part 807.97). For questions regarding the reporting of adverse events under the MDR regulation (21 CFR Part 803), please go to http://www.fda.gov/MedicalDevices/Safety/ReportaProblem/default.htm for the CDRH's Office of Surveillance and Biometrics/Division of Postmarket Surveillance.

You may obtain other general information on your responsibilities under the Act from the Division of Industry and Consumer Education at its toll-free number (800) 638-2041 or (301) 796-7100 or at its Internet address http://www.fda.gov/MedicalDevices/ResourcesforYou/Industry/default.htm.

Sincerely yours,

Kristian M. Roth -S

For: Uwe Scherf, M.Sc., Ph.D.
Director
Division of Microbiology Devices
Office of In Vitro Diagnostics and
Radiological Health
Center for Devices and
Radiological Health

Enclosure

Indications for Use

Form Approved: OMB No. 0910-0120
Expiration Date: January 31, 2017
See PRA Statement below.

510(k) Number *(if known)*
K163536

Device Name
MALDI Biotyper CA System

Indications for Use *(Describe)*
The MALDI Biotyper CA System is a mass spectrometer systems using matrix-assisted laser desorption/ionization - time of flight (MALDI-TOF) for the identification of microorganisms cultured from human specimens.

The MALDI Biotyper CA System is a qualitative in vitro diagnostic device indicated for use in conjunction with other clinical and laboratory findings to aid in the diagnosis of bacterial and yeast infections.

The following organisms are claimed:

Bacteria:
Abiotrophia defectiva
Achromobacter xylosoxidans
Acinetobacter baumannii / nosocomialis group
Acinetobacter calcoaceticus
Acinetobacter haemolyticus
Acinetobacter johnsonii
Acinetobacter junii
Acinetobacter lwoffii
Acinetobacter pittii
Acinetobacter radioresistens
Acinetobacter ursingii
Actinomyces europaeus
Actinomyces funkei
Actinomyces graevenitzii
Actinomyces hyovaginalis
Actinomyces meyeri
Actinomyces neuii
Actinomyces odontolyticus
Actinomyces oris
Actinomyces radingae
Actinomyces turicensis
Actinomyces urogenitalis
Actinotignum schaalii group
Aerococcus sanguinicola
Aerococcus urinae
Aerococcus viridans
Aeromonas salmonicida
Aeromonas sp[7]
Aggregatibacter actinomycetemcomitans
Aggregatibacter aphrophilus
Aggregatibacter segnis
Alcaligenes faecalis
Alloiococcus otitis
Alloscardovia omnicolens

Anaerococcus murdochii
Anaerococcus vaginalis
Arthrobacter cumminsii
Bacteroides caccae
Bacteroides fragilis
Bacteroides nordii
Bacteroides ovatus group
Bacteroides pyogenes
Bacteroides salyersiae
Bacteroides stercoris group
Bacteroides thetaiotaomicron group
Bacteroides uniformis
Bacteroides vulgatus group
Bifidobacterium breve
Bordetella group[3]
Bordetella hinzii
Brevibacterium casei
Brevundimonas diminuta group
Burkholderia cepacia complex [13]
Burkholderia gladioli
Burkholderia multivorans
Campylobacter coli
Campylobacter jejuni
Campylobacter ureolyticus
Capnocytophaga ochracea
Capnocytophaga sputigena
Chryseobacterium gleum
Chryseobacterium indologenes
Citrobacter amalonaticus complex
Citrobacter freundii complex
Citrobacter koseri
Clostridium beijerinckii
Clostridium bifermentans
Clostridium butyricum
Clostridium clostridioforme group
Clostridium difficile
Clostridium innocuum
Clostridium paraputrificum
Clostridium perfringens
Clostridium ramosum
Clostridium septicum
Clostridium sordellii
Clostridium sporogenes / Clostridium botulinum (group I)
Clostridium tertium
Corynebacterium accolens
Corynebacterium afermentans group
Corynebacterium amycolatum
Corynebacterium aurimucosum group
Corynebacterium bovis
Corynebacterium coyleae
Corynebacterium diphtheriae
Corynebacterium freneyi
Corynebacterium glucuronolyticum
Corynebacterium glutamicum

Corynebacterium jeikeium
Corynebacterium kroppenstedtii
Corynebacterium macginleyi
Corynebacterium minutissimum
Corynebacterium mucifaciens / ureicelerivorans group
Corynebacterium propinquum
Corynebacterium pseudodiphtheriticum
Corynebacterium pseudotuberculosis
Corynebacterium resistens
Corynebacterium riegelii
Corynebacterium striatum group
Corynebacterium tuberculostearicum
Corynebacterium ulcerans
Corynebacterium urealyticum
Corynebacterium xerosis
Cronobacter sakazakii group
Cupriavidus pauculus group
Delftia acidovorans group
Dermabacter hominis
Dermacoccus nishinomiyaensis
Edwardsiella tarda
Eikenella corrodens
Elizabethkingia meningoseptica group
Enterobacter aerogenes
Enterobacter amnigenus
Enterobacter cloacae complex
Enterococcus avium
Enterococcus casseliflavus
Enterococcus durans
Enterococcus faecalis
Enterococcus faecium
Enterococcus gallinarum
Enterococcus hirae
Enterococcus mundtii
Enterococcus raffinosus
Escherichia coli
Escherichia hermannii
Escherichia vulneris
Ewingella americana
Facklamia hominis
Finegoldia magna
Fluoribacter bozemanae
Fusobacterium canifelinum
Fusobacterium necrophorum
Fusobacterium nucleatum
Gardnerella vaginalis
Gemella haemolysans
Gemella morbillorum
Gemella sanguinis
Granulicatella adiacens
Haemophilus haemolyticus
Haemophilus influenzae
Haemophilus parahaemolyticus group
Haemophilus parainfluenzae

Hafnia alvei
Helcococcus kunzii
Kingella denitrificans
Kingella kingae
Klebsiella oxytoca / Raoultella ornithinolytica
Klebsiella pneumoniae
Klebsiella variicola
Kocuria kristinae
Kytococcus sedentarius
Lactobacillus gasseri
Lactobacillus jensenii
Lactobacillus rhamnosus
Lactococcus garvieae
Lactococcus lactis
Leclercia adecarboxylata
Legionella longbeachae
Legionella pneumophila
Leuconostoc citreum
Leuconostoc mesenteroides
Leuconostoc pseudomesenteroides
Listeria monocytogenes
Macrococcus caseolyticus
Mannheimia haemolytica group
Micrococcus luteus
Micrococcus lylae
Mobiluncus curtisii
Moraxella sg Branhamella catarrhalis*
Moraxella sg Moraxella nonliquefaciens*
Moraxella sg Moraxella osloensis*
Morganella morganii
Myroides odoratimimus
Myroides odoratus
Neisseria bacilliformis
Neisseria cinerea
Neisseria elongata
Neisseria flavescens / subflava group
Neisseria gonorrhoeae
Neisseria lactamica
Neisseria meningitidis
Neisseria sicca group
Neisseria weaveri
Nocardia brasiliensis
Nocardia cyriacigeorgica
Nocardia farcinica group
Nocardia nova
Nocardia otitidiscaviarum
Ochrobactrum anthropi
Oligella ureolytica
Oligella urethralis
Pantoea agglomerans
Parabacteroides distasonis
Parabacteroides goldsteinii
Parabacteroides johnsonii / merdae group
Parvimonas micra

Pasteurella multocida
Pediococcus acidilactici
Pediococcus pentosaceus
Peptoniphilus harei group
Peptostreptococcus anaerobius
Plesiomonas shigelloides
Pluralibacter gergoviae
Porphyromonas gingivalis
Porphyromonas somerae
Prevotella bivia
Prevotella buccae
Prevotella denticola
Prevotella intermedia
Prevotella melaninogenica
Propionibacterium acnes
Proteus mirabilis
Proteus vulgaris group
Providencia rettgeri
Providencia stuartii
Pseudomonas aeruginosa
Pseudomonas fluorescens group
Pseudomonas oryzihabitans
Pseudomonas putida group
Pseudomonas stutzeri
Ralstonia pickettii
Rhizobium radiobacter
Rothia aeria
Rothia dentocariosa
Rothia mucilaginosa
Salmonella sp**
Serratia fonticola
Serratia liquefaciens
Serratia marcescens
Serratia odorifera
Serratia plymuthica
Serratia rubidaea
Sphingobacterium multivorum
Sphingobacterium spiritivorum
Sphingomonas paucimobilis group
Staphylococcus aureus
Staphylococcus auricularis
Staphylococcus capitis
Staphylococcus caprae
Staphylococcus carnosus
Staphylococcus cohnii
Staphylococcus delphini
Staphylococcus epidermidis
Staphylococcus equorum
Staphylococcus felis
Staphylococcus haemolyticus
Staphylococcus hominis
Staphylococcus intermedius
Staphylococcus lentus
Staphylococcus lugdunensis

Staphylococcus pasteuri
Staphylococcus pettenkoferi
Staphylococcus pseudintermedius
Staphylococcus saccharolyticus
Staphylococcus saprophyticus
Staphylococcus schleiferi
Staphylococcus sciuri
Staphylococcus simulans
Staphylococcus vitulinus
Staphylococcus warneri
Staphylococcus xylosus
Stenotrophomonas maltophilia
Streptococcus agalactiae
Streptococcus anginosus
Streptococcus canis
Streptococcus constellatus
Streptococcus dysgalactiae
Streptococcus equi
Streptococcus gallolyticus
Streptococcus gordonii
Streptococcus intermedius
Streptococcus lutetiensis
Streptococcus mitis / oralis group
Streptococcus mutans
Streptococcus parasanguinis
Streptococcus pneumoniae
Streptococcus pyogenes
Streptococcus salivarius / vestibularis group
Streptococcus sanguinis
Streptococcus sobrinus
Streptococcus thermophilus
Sutterella wadsworthensis
Trueperella bernardiae
Turicella otitidis
Vagococcus fluvialis
Veillonella parvula group
Vibrio parahaemolyticus
Vibrio vulnificus
Weeksella virosa
Yersinia enterocolitica
Yersinia frederiksenii
Yersinia intermedia
Yersinia kristensenii
Yersinia pseudotuberculosis

*sg = subgenus
**sp = species

Yeasts:
Candida albicans
Candida boidinii
Candida dubliniensis
Candida duobushaemulonii

Candida famata
Candida glabrata
Candida guilliermondii
Candida haemulonis
Candida inconspicua
Candida intermedia
Candida kefyr
Candida krusei
Candida lambica
Candida lipolytica
Candida lusitaniae
Candida metapsilosis
Candida norvegensis
Candida orthopsilosis
Candida parapsilosis
Candida pararugosa
Candida pelliculosa
Candida tropicalis
Candida valida
Candida zeylanoides
Cryptococcus gattii
Cryptococcus neoformans var grubii*
Cryptococcus neoformans var neoformans*
Cyberlindnera jadinii
Geotrichum candidum
Geotrichum capitatum
Kloeckera apiculata
Malassezia furfur
Malassezia pachydermatis
Pichia ohmeri
Rhodotorula mucilaginosa
Saccharomyces cerevisiae
Trichosporon asahii
Trichosporon inkin
Trichosporon mucoides group

*var = variety

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)

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10. 510(k) SUMMARY

Date of Summary: June 21, 2017

Product Name MBT-CA System

Sponsor
Bruker Daltonik GmbH
Fahrenheitstrasse 4
28359 Bremen, Germany

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Device Identification

Trade or Proprietary Name: MALDI Biotyper CA System
Common or Usual Name: System, mass spectrometry, maldi tof, microorganism identification, cultured isolates
Product Code: PEX
Regulation Section: 21 CFR 866.3361 Instrumentation for clinical multiplex test systems
Device Class: Class II
Panel: Microbiology

Substantial Equivalency

The MBT-CA System (K163536) is substantially equivalent to the MBT-CA System (K142677). Table 1 compares the characteristics of the MBT-CA System (New Device) and the MBT-CA System (Predicate Device).

Table 1: Substantial Equivalency Table

Similarities		
Characteristic	**NEW DEVICE MBT-CA System (K163536)**	**PRIMARY PREDICATE DEVICE MBT-CA System (K142677)**
Product Codes	PEX	PEX
Intended use	The MALDI Biotyper CA System is a mass spectrometer systems using matrix-assisted laser desorption/ionization - time of flight (MALDI-TOF) for the identification of microorganisms cultured from human specimens. The MALDI Biotyper CA System is a qualitative *in vitro* diagnostic devices indicated for use in conjunction with other clinical and laboratory findings to aid in the diagnosis of bacterial and yeast infections.	The MALDI Biotyper CA System is a mass spectrometer system using matrix-assisted laser desorption/ionization - time of flight (MALDI-TOF) for the identification of microorganisms cultured from human specimens. The MALDI Biotyper CA System is a qualitative *in vitro* diagnostic device indicated for use in conjunction with other clinical and laboratory findings to aid in the diagnosis of bacterial and yeast infections.
Sample type	Isolated colony from any patient sample source. Acceptable media: • Columbia blood agar with 5% sheep blood (Gram-negative bacteria) • Trypticase soy agar with 5% sheep blood (Gram-negative bacteria, Gram-positive bacteria, yeasts) • Chocolate agar (Gram-negative bacteria, Gram-positive bacteria) • MacConkey Agar (Gram-negative bacteria) • Columbia CNA agar with 5% sheep blood (Gram-positive bacteria) • Brucella Agar with 5% horse blood (Gram-negative anaerobic bacteria, Gram-positive anaerobic bacteria) • CDC anaerobe Agar with 5% sheep blood (Gram-negative anaerobic bacteria, Gram-positive anaerobic bacteria) • CDC anaerobe 5% sheep blood Agar with phenylethyl alcohol (Gram-negative anaerobic bacteria, Gram-positive anaerobic bacteria) • CDC anaerobe laked sheep blood Agar with kanamycin and vancomycin (Gram-negative anaerobic bacteria) • Bacteroides bile esculin Agar with amikacin (*Bacteroides* species) • Clostridium difficile Agar with 7% sheep	Isolated colony from any patient sample source. Acceptable media: • Columbia blood agar with 5% sheep blood (Gram-negative bacteria) • Trypticase soy agar with 5% sheep blood (Gram-negative bacteria, Gram-positive bacteria, yeasts) • Chocolate agar (Gram-negative bacteria, Gram-positive bacteria) • MacConkey Agar (Gram-negative bacteria) • Columbia CNA agar with 5% sheep blood (Gram-positive bacteria) • Brucella Agar with 5% horse blood (Gram-negative anaerobic bacteria, Gram-positive anaerobic bacteria) • CDC anaerobe Agar with 5% sheep blood (Gram-negative anaerobic bacteria, Gram-positive anaerobic bacteria) • CDC anaerobe 5% sheep blood Agar with phenylethyl alcohol (Gram-negative anaerobic bacteria, Gram-positive anaerobic bacteria) • CDC anaerobe laked sheep blood Agar with kanamycin and vancomycin (Gram-negative anaerobic bacteria) • Bacteroides bile esculin Agar with amikacin (*Bacteroides* species) • Clostridium difficile Agar with 7% sheep

Similarities		
Characteristic	**NEW DEVICE MBT-CA System (K163536)**	**PRIMARY PREDICATE DEVICE MBT-CA System (K142677)**
	blood (*Clostridium difficile*) • Sabouraud-Dextrose Agar (Yeasts) • Brain Heart Infusion Agar (Yeasts) • Campylobacter Agar with 5 Antimicrobics and 10% Sheep Blood (*Campylobacter* species) • Bordet Gengou Agar with 15% sheep blood (*Bordetella* species) • plus three (3) additionally validated media (see differences).	blood (*Clostridium difficile*) • Sabouraud-Dextrose Agar (Yeasts) • Brain Heart Infusion Agar (Yeasts) • Campylobacter Agar with 5 Antimicrobics and 10% Sheep Blood (*Campylobacter* species) • Bordet Gengou Agar with 15% sheep blood (*Bordetella* species)
Type of Test	Automated Mass Spectrometry System	Automated Mass Spectrometry System
Matrix	α-Cyano-4-hydroxycinnamic acid	α-Cyano-4-hydroxycinnamic acid
Method of Testing	Bacteria & Yeast: Direct testing If after initial analysis the log(score) is reported at <2.00, organisms may be processed using the Extraction (Ext) procedure or extended Direct Transfer (eDT, 70% aqueous formic acid) procedure. If eDT procedure still yields log(score) <2.00, organisms may be processed via Ext procedure.	Bacteria & Yeast: Direct testing If after initial analysis the log(score) is reported at <2.00, organisms may be processed using the Extraction (Ext) procedure or extended Direct Transfer (eDT, 70% aqueous formic acid) procedure. If eDT method still yields log(score) <2.00, organisms may be processed via Ext procedure.
Result Reporting	Organism identification is reported with high confidence if the log(score) is ≥2.00. An organism identification is reported with low confidence if the log(score) is between 1.70 and <2.00.	Organism identification is reported with high confidence if the log(score) is ≥2.00. An organism identification is reported with low confidence if the log(score) is between 1.70 and <2.00.
Matching Algorithm	Calculates matches by comparing a new spectrum against each single reference entry of a reference database.	Calculates matches by comparing a new spectrum against each single reference entry of a reference database.
Recorded mass range	2,000 - 20,000 m/z	2,000 - 20,000 m/z
Calibration	Bruker US IVD Bacterial Test Standard (BTS)	Bruker US IVD Bacterial Test Standard (BTS)
Database	MALDI Biotyper Reference Library for Clinical Applications (MBT-CA) - update	MALDI Biotyper Reference Library for Clinical Applications (MBT-CA)

Differences		
Characteristic	**NEW DEVICE MBT-CA System (K163536)**	**PRIMARY PREDICATE DEVICE MBT-CA System (K142677)**
System Update	System claims additional organisms but no additional changes.	N/A
Media	Additional Media validated: • Buffered Charcoal Yeast Extract Agar (*Legionella* species) • Buffered Charcoal Yeast Extract Selective Agar with polymyxin, anisomycin and vancomycin (*Nocardia* species) • Modified Thayer-Martin Agar (*Neisseria* species)	See Similarities
MALDI-TOF MS instruments	Bruker microflex LT/SH (benchtop) Bruker microflex LT/SH smart (benchtop)	Bruker microflex LT/SH (benchtop)
MALDI Target Plates	US IVD 48 Spot Target (48 positions reusable steel targets) MBT Biotarget 96 US IVD (96 positions disposable targets)	US IVD 48 Spot Target (48 positions reusable steel targets)

The differences do not affect substantial equivalence of the MBT-CA System and MBT-CA System (K142677). Both systems are mass spectrometers using matrix-assisted laser desorption/ionization-time to flight (MALDI-TOF) for the identification of microorganisms cultured from human specimens. The differences noted above do not impact the intended use and do not raise questions as to the safety and effectiveness of the test (new) device.

Intended Use

The MALDI Biotyper CA System is a mass spectrometer system using matrix-assisted laser desorption/ionization - time of flight (MALDI-TOF) for the identification of microorganisms cultured from human specimens.

The MALDI Biotyper CA System is a qualitative *in vitro* diagnostic device indicated for use in conjunction with other clinical and laboratory findings to aid in the diagnosis of bacterial and yeast infections.

Methodology

Biochemical methods are currently the most commonly used methods for the identification of microorganisms. Organisms are tested against a range of reagents and organism identification is based on a microorganism's reaction to these reagents.

The MBT-CA System uses a different methodology for organism identification based on unique protein patterns of the microorganisms obtained from mass spectrometry. The test organism's spectrum (a pattern of mass peaks) is compared with a reference spectra library (database). Using biostatistical analysis, a probability ranking of the organism identification is generated. The probability ranking is represented as a log(score) between 0.00 and 3.00. Organism identification is reported with high confidence if the log(score) is ≥2.00. An organism identification is reported with low confidence if the log(score) is between 1.70 and <2.00.

Organisms to be identified with the MBT-CA System should be isolated for purity on appropriate isolation media.

Direct Transfer procedure (DT): An individual colony from a subculture plate is transferred to a selected position on a US IVD 48 Spot Target plate or a MBT Biotarget 96 US IVD Target plate (targets) and overlaid with US IVD HCCA portioned (matrix). The standard solvent (50% acetonitrile / 47.5% H_2O / 2.5% trifluoroacetic acid) in the matrix solution extracts proteins (mainly ribosomal proteins, which are present in high concentration) from the microorganisms. When dried matrix crystallizes, the inoculated target is ready to be analyzed on the MBT-CA System. If after initial analysis the log(score) is reported as <2.00, organisms can be processed using the extended Direct Transfer (eDT) procedure or the Extraction procedure and analysis repeated. If eDT is employed and log(score) is reported as <2.00, reanalysis via the Extraction procedure may be used.

extended Direct Transfer procedure (eDT):
If DT analysis yields a [log(score) <2.00] result, an individual colony from a subculture plate may be transferred to a selected position on a target and overlaid with 70% aqueous formic acid solution. The target is air-dried and then matrix is overlaid. When dried matrix crystallizes, the inoculated target is ready to be analyzed on the MBT-CA System. If a high confidence result is not achieved [log(score) is reported at <2.00], organisms can be processed using the Extraction procedure and analysis repeated.

Extraction procedure (Ext): If after initial analysis and eDT procedure the log(score) is reported at <2.00, organisms are processed using the Extraction procedure and analysis repeated. For this purpose, isolated colonies from the subculture plate are extracted in accordance with instructions of the user manual (Ext sample preparation procedure). An aliquot of extracted material is transferred to a selected position on a target, air-dried and then overlaid with matrix material. When dried matrix crystallizes, the inoculated target is ready to be analyzed on the MBT-CA System.

MALDI-TOF Analysis:
Samples are analyzed using MALDI (matrix-assisted laser desorption/ionization) TOF (time-of-flight) mass spectrometry. The matrix transfers protons onto the extracted proteins and absorbs UV light. A laser in the MALDI- TOF mass spectrometer irradiates the matrix sample composite, causing evaporation and release of positively charged intact proteins and peptides ("soft" ionization technique). These ions are electrostatically accelerated over a short distance and arrive in the flight tube at a mass-dependent speed. As different proteins/peptides have different masses, ions arrive at the detector at different times (time of flight). The system measures the time (in the nanosecond range) between pulsed acceleration and the corresponding detector signal, the speed is converted into an exact molecular mass. The mass-to-charge ratio of an ion is proportional to the square of its drift time.

Highly abundant microbial proteins (mainly ribosomal proteins) result in a mass spectrum with characteristic mass and intensity distribution. It is species-specific for many bacteria and is interpreted as a molecular fingerprint to identify the test organism.

Data acquisition is controlled with MBT-CA System software. The spectrum of the unknown organism is first transformed into a peak list. Using a biostatistical algorithm, this peak list is compared to the reference peak lists of organisms in the reference library (database) and a log(score) is generated. A higher log(score) indicates a higher degree of similarity to the organism in the reference library. Organism identification is reported with high confidence if the log(score) is ≥2.00. An organism identification is reported with low confidence if the log(score) is between 1.70 and <2.00.

The log(score) ranges, defined in the MBT-CA System, are indicative of the probability of organism identification. Results should be reviewed by a trained microbiologist and final organism identification should be based on all relevant information available. This information includes but is not limited to: Gram staining, colony morphology, growth characteristics, sample matrix, etc.

Performance Data

Media and Colony Stability

With the inclusion of further Gram-negative and Gram-positive microaerophilic, additional Gram-negative and Gram-positive anaerobic and further Gram-negative and Gram-positive aerobic bacteria and yeasts, a study on the following media was conducted to confirm acceptability of the recommended agar and the stability of the colony for up to 12 hours storage at room temperature prior to analysis:

- Trypticase Soy Agar with 5% sheep blood (TSA)
- Buffered Charcoal Yeast Extract Agar (BCYE)
- Buffered Charcoal Yeast Extract Selective Agar with polymyxin, anisomycin and vancomycin (BCYE/PAV)
- Modified Thayer-Martin Agar (MTM)

In the previousl submission (K142677) TSA medium was only validated for Gram-positive /-negative aerobic bacteria and yeast. Goal for TSA medium in this submission was to show the suitability of this medium for Gram-positive /-negative microaerophilic and anaerobic bacteria.

Testing was conducted using one (1) Gram-negative bacterium, one (1) microaerophilic Gram-negative bacterium, one (1) Gram-positive bacterium, one (1) microaerophilic Gram-positive bacterium, two (2) *Legionella* species, three (3) *Nocardia* species and three (3) *Neisseria* species, at varying incubation time points in replicates of eight (8). Additionally, thirteen (13) clinical isolates derived from *Neisseria* species were tested in duplicate at varying incubation time points.

Conclusion Media and Colony Stability: Three (3) additional media could be validated successfully. TSA medium could be validated for all kinds of organisms. Cultivation of *Neisseria* on Modified Thayer-Martin Agar (MTM) should not be longer than 24 hours plus 12 hours storage at room temperature.

Resolution of the *Acinetobacter baumannii* complex

This study served to evaluate an improved species resolution power of the MBT-CA System of the *Acinetobacter baumannii* complex (members: *A. baumannii*, *A. calcoaceticus*, *A. nosocomialis*, *A. pittii*) down to the species level after final extraction procedure. Sixty-six (66) clinical isolates of *Acinetobacter baumannii* complex collected during initial Clinical Method Comparison protocol (see K130831) and identified by 16S rRNA and/or protein gene sequencing were re-tested using Direct Transfer, extended Direct Transfer and Extraction procedure in parallel.

The study results showed that the *Acinetobacter baumannii* complex cannot be completely but partially resolved applying MBT-CA System workflow. The reference library/software will be updated to complex *Acinetobacter baumannii* and *Acinetobacter nosocomialis* under the *Acinetobater baumannii/nosocomialis* group. After formation of an *Acinetobacter baumannii/nosocomialis* group unambiguous MBT-CA identification with high confidence [log(score) ≥2.00] of *Acinetobacter baumannii/nosocomialis* group, *Acinetobacter calcoaceticus* and *Acinetobacter pittii* is possible if final Extraction procedure has been applied. A matching hint will be included in the system package insert which contains the following alert: The displayed species should be considered a member of the *Acinetobacter baumannii* complex. For organisms identified by the MBT-CA System as *Acinetobacter calcoaceticus*, *Acinetobacter pittii* or *Acinetobacter baumannii/nosocomialis* group the full Extraction procedure (Ext) is mandatory for secure species differentiation.

Cultivation of yeast organisms at 37 °C

This study served to show the general applicability of the MBT-CA System workflow for identification of yeasts cultivated at 37 (± 2)°C. Testing was conducted using three (3) yeast species at varying incubation time points in replicates of eight (8). After initial testing, isolates were further tested at room temperature after twelve (12) hours post-incubation.

The study results confirmed the acceptability of 37 (± 2)°C cultivation of yeasts and sample colony stability of up to 12 hours.

Reproducibility:

The reproducibility study for Gram-negative and Gram-positive aerobic bacteria, Gram-negative and Gram-positive microaerophilic bacteria, Gram-negative and Gram-positive anaerobic bacteria and yeasts was carried out to confirm day-to-day reproducibility and precision of the MALDI Biotyper CA System at different clinical study sites. The study was conducted for five (5) days with two (2) runs [two (2) operators] each day per clinical site. The sources of variability tested were:

- Two (2) operators/each clinical study site
- Three (3) clinical study sites
- At least two (2) target plates/each clinical study site
- Four (4) microflex LT/SH instruments

Ten (10) well-characterized organisms were chosen for this study and tested in duplicate via Direct Transfer procedure in accordance with product instructions. When the DT log(score) was <2.00, per product instructions, the test organism was tested following the extended Direct Transfer and Extraction procedure.

Note: As REPRO-2 was identified as Listeria monocytogenes after applying DT procedure test sites should have proceeded with testing of eDT and Ext procedure in parallel in accordance with the study protocol. Test sites did not conduct additional testing, therefore REPRO-02 was excluded from data analysis.

Table 2: Reproducibility Study Summary

Blinded Test Organism	**Reproducibility Panel**	*Site A:* **MBT-CA ID (DT+eDT+Ext)**	*Site B:* **MBT-CA ID (DT+eDT+Ext)**	*Site C:* **MBT-CA ID (DT+eDT+Ext)**
Dermabacter hominis	REPRO-01	20/20 (100%)	20/20 (100%)	20/20 (100%)
Listeria monocytogenes	REPRO-02*	N/A	N/A	N/A
Nocardia farcinica group	REPRO-03	19/20 (95%)	19/20 (95%)	19/20 (95%)
Legionella pneumophila	REPRO-04	20/20 (100%)	20/20 (100%)	20/20 (100%)
Clostridium tertium	REPRO-05	20/20 (100%)	20/20 (100%)	20/20 (100%)
Facklamia hominis	REPRO-06	20/20 (100%)	20/20 (100%)	20/20 (100%)
Bacteroides caccae	REPRO-07	20/20 (100%)	20/20 (100%)	20/20 (100%)
Trueperella bernardiae	REPRO-08	20/20 (100%)	20/20 (100%)	20/20 (100%)
Neisseria meningitidis	REPRO-09	20/20 (100%)	20/20 (100%)	20/20 (100%)
Rhodotorula mucilaginosa	REPRO-10	20/20 (100%)	20/20 (100%)	20/20 (100%)
TOTAL		**179/180 (99%)**	**179/180 (99%)**	**179/180 (99%)**

*REPRO-02: Organism skipped as MBT-CA ID applying DT procedure was not confirmed via eDT and Ext procedure.

Conclusion Reproducibility: 99% of test organisms were correctly identified with a log(score) ≥2.00 at each clinical test site. In addition, no isolates were falsely identified. Thus, data confirm reproducibility and precision of the whole MALDI Biotyper CA System independent from:

- Clinical Site
- System operators
- microflex LT/SH instruments
- Target plate

Challenge Panel:

A panel of 46 organisms (12 Gram-positive aerobic bacteria, 8 Gram-negative aerobic bacteria, 4 Gram-positive microaerophilic bacteria, 5 Gram-negative microaerophilic bacteria, 10 Gram-positive anaerobic bacteria, 4 Gram-negative anaerobic bacteria, 3 yeasts) was tested at three (3) study sites. All of the forty-six (46) organisms included in the panel were selected from stored organisms tested during the clinical study. The study interim reference laboratory prepared the panel. Organism identifications were blinded to test sites. Each site tested the challenge panel member via Direct Transfer, extended Direct Transfer and Extraction procedure in parallel.

Table 3: Challenge Panel Study Summary

Test procedure	Site A*	Site B**	Site C***
DT method	43/45 (96%)	38/44 (86%)	36/41 (88%)
eDT method	44/45 (98%)	36/44 (82%)	38/41 (93%)
Ext method	43/45 (96%)	36/44 (82%)	39/41 (95%)
MBT-CA workflow	**45/45 (100%)**	**40/44 (91%)**	**40/41 (98%)**

* One (1) sample was not identified due to isolate failure to grow.
** Two (2) samples were not identified due to isolate failure to grow.
*** Five (5) samples were not identified due to isolate failure to grow.

Conclusion Challenge Panel:

Testing of the challenge panel confirms reliability of the MBT-CA System workflow independently from

- Clinical Site
- Test-operator
- microflex LT/SH mass spectrometer system
- US IVD 48 Spot Target plate

Biological / Technical Equivalency Study - MBT-CA smart System

Objective of this validation was to demonstrate equivalence of the MBT-CA output when using MALDI-TOF mass spectrometers equipped with smartbeam laser technology and nitrogen laser technology.

A panel of thirty four (34) species which are part of the MBT-CA library were measured. The 34 species represent Gram negative, Gram positive, and yeast. All three sample preparation techniques (DT, eDT, Ext) were used in parallel (eDT and Ext were always additionally performed independent from the DT result). Each sample preparation technique (DT, eDT, Ext) was spotted 8 times onto the MALDI target. The measurement was performed on two nitrogen laser instruments and 3 smart laser instruments.

Overall 4080 spectra were represented in this study. The performance of all spectra for each single species, each single sample prep (DT, eDT and Ext), each MBT-CA result (no ID "*red*", low confidence ID "*yellow*", high confidence ID "*green*") for each instrument type is summarised in Table 4.

Table 4: Overall performance of 4080 measured samples. "High confidence ID" (green), "low confidence ID" (yellow) and "no ID" (ref) are shown. The table (left) shows the total numbers and table (right) the percentage.

	Nitrogen (544)			Smart (816)		
DT	187	72	285	300	117	399
eDT	37	61	446	63	120	633
Ext	2	3	539	0	13	803
∑	226	136	1270	363	250	1835

	Nitrogen (544)			Smart (816)		
DT	34.4%	13.2%	52.4%	36.8%	14.3%	48.9%
eDT	6.8%	11.2%	82.0%	7.7%	14.7%	77.6%
Ext	0.4%	0.6%	99.1%	0.0%	1.6%	98.4%
∑	13.8%	8.3%	77.8%	14.8%	10.2%	75.0%

As an example, the row "Ext" shows a similar percentage of "high confidence results" between both systems (99.1% for Nitrogen Laser versus 98.4% for Smartbeam Laser).

Conclusion: Based on these results the equivalence between the Nitrogen Laser System and the Smartbeam Laser System could be shown.

Equivalence Study MBT Biotarget 96 US IVD (Nitrogen Laser)

This study was designed to verify and validate the use of the MBT Biotarget 96 US IVD in conjunction with the MBT-CA System (Nitrogen Laser). Study goal was to show the equivalency between the already cleared US IVD MSP 48 Target Polished Steel and the new MBT Biotarget 96 US IVD. The functionality and performance of the MBT-CA System using the MBT Biotarget 96 US IVD under varying conditions was shown. Test runs were performed always in parallel using US IVD MSP 48 Target Polished Steel plates.

The following six studies were performed:

- Repeatability / Precision
- Tolerance range (dynamic range) - limit of detection (LOD)
- Sample stability prior to matrix application
- Sample stability post matrix application
- Mass Accuracy / Target Edge Effects
- Identification of 50 FDA cleared organisms according to MBT-CA System workflow.

Repeatability and Precision

In this study, approximately one thousand (1000) measurements were carried out. In total, seven hundred and twenty (720) MBT-CA System identifications (10 species, triplicates, two target plates, 1 operator per day, 2 runs per day, 6 days) were performed. 100% of test organisms were correctly MBT-CA identified at high confidence level [log(score) ≥2.0] applying the MBT-CA System workflow (combination of DT, eDT and Ext procedure). The rate of MBT-CA System false identification was 0% for all test samples after final sample preparation procedure.

Both target types performed similarly.

Tolerance Range (Dynamic Range) - Limit of Detection (LOD)

In this study, approximately one thousand five hundred (1500) measurements were performed. 10 different species were analysed representing Gram positive, Gram negative bacteria and yeast. All sample preparation techniques (DT, eDT and Ext) were conducted. Up to 5 dilutions steps were performed for each scenario. The rate of MBT-CA System false identifications at least at low confidence level [log(score) ≥1.70] was 0%. The estimated dynamic range (limit of detection) of bacteria and yeast onto the MBT Biotarget 96 US IVD / US IVD MSP 48 Target Polished Steel required for MBT-CA System identification did not show significant differences.

As a common limit of detection the amount of about $5*10^5$ cells (or cell equivalents using extraction) which must be placed on a target spot could be defined. Since a sharp boundary is hard to define, some exceptions occurred during this study. But these exceptions occurred for different species, different sample preparation techniques and different target types. Therefore there is no general trend for a better limit of detection for one kind of target.

Therefore the equivalence between the MBT Biotarget 96 US IVD / US IVD MSP 48 Target Polished Steel could be shown.

Sample Stability prior to Matrix application
In this study, approximately two thousand five hundred (2500) measurements were carried out. Five species were analyzed on two instruments. Measurement was applied directly after matrix application and after 15, 30, 60 and 120 minutes. All sample preparation techniques (DT, eDT and Ext) were conducted. Each sample was spotted and measured 8 times. The rate of MBT-CA System false identifications was 0% for all tests.

The performance was similar for both target types.

Sample Stability post Matrix application
In this study, approximately three thousand (3000) measurements were performed. Two temperature conditions were analysed in this study (21°C and 25°C). All measurements were conducted using 5 different species on two MALDI instruments. All sample preparation techniques (DT, eDT and Ext) were performed and each sample was spotted 8 times on both target types. The ready prepared sample stability was analyzed immediately after matrix application (standard condition) and after 4h, 8h and 24h of aging.

No MBT-CA false identifications occurred. The performance of the MBT Biotarget 96 US IVD as compared to that of the US IVD MSP 48 Target Polished Steel could be shown.

Validation Study - Validation of 50 Representative Claimed Species
Approximately three hundred (300) measurements were carried out. In this study 50 claimed species representing Gram negative aerobic / anaerobic, Gram positive aerobic / anaerobic bacteria and yeast were analysed. All sample preparation techniques (DT, eDT and Ext) were conducted. The rate of MBT-CA false identifications was 0% for this test. The overall identification rate of test samples at high confidence level (log(score) ≥2.0) was 100%.

General performance of the MBT Biotarget 96 US IVD and the US IVD MSP 48 Target Polished Steel was comparable.

Technical Study - Mass Accuracy / Target Edge Effects
In this study, approximately one thousand five hundred (1500) measurements were carried out. This study was designed for validation of the MBT Biotarget 96 US IVD in terms of "mass accuracy / target flatness" using BTS, MBT-CA System software and reference library and at least two (2) microflex LT/SH mass spectrometer systems. Validation was performed on five (5) MBT Biotarget 96 US IVD and five (5) US IVD MSP 48 Target Polished Steel. Targets were entirely prepared with dissolved BTS, dried and then overlaid with HCCA matrix.

Two parameters were evaluated during this study: Target Flatness (the mass accuracy was used as an indicator for target flatness) and edge effects (comparison of mass accuracy from edge positions vs inner target positions). For evaluation, one prominent reference protein (e.g. 6255.4 m/z) within the mass range of the BTS was analyzed concerning mass reproducibility. Additionally the log(scores) of each BTS spectrum were calculated as an indicator of identification performance.

Generally it can be stated that the technical performance between the MBT Biotarget 96 US IVD compared to the US IVD MSP 48 Target Polished Steel was comparable.

Equivalence Study MBT Biotarget 96 US IVD (Smartbeam Laser)

The study design of this study was identical to the previous chapter [*Equivalence Study MBT Biotarget 96 US IVD (Nitrogen Laser)*]. In contrast to the 10,000 measurements in the previous chapter using two nitrogen laser systems, in this study an additional 5000 measurements were performed on one MBT smart CA System (Smartbeam Laser) to further prove the equivalence of both target types.

The following six studies were performed:

- Repeatability / Precision
- Tolerance range (dynamic range) - limit of detection (LOD)
- Sample stability prior to matrix application
- Sample stability post matrix application
- Mass Accuracy / Target Edge Effects
- Identification of 50 FDA cleared organisms according to MBT-CA System workflow.

Generally it can be stated that the technical performance and equivalence between the MBT Biotarget 96 US IVD compared to the US IVD MSP 48 Target Polished Steel could be shown again in this study.

Nocardia Study

This study was designed to verify and validate the measurement and identification of different strains and different species of the genus *Nocardia* by using the MBT-CA System as well as the MBT smart CA System in parallel. In addition the study was performed using the US IVD MSP 48 Target Polished Steel and the MBT Biotarget 96 US IVD in parallel. The results of this study can be evaluated as analytical study for identification performance of the MBT-CA System for the genus *Nocardia* and additionally as demonstration of equivalence between the "MBT-CA and MBT smart CA Systems" as well as equivalence of the "MBT Biotarget 96 US IVD and US IVD MSP 48 Target Polished Steel".

Analytical Studies:

- Measurement of 30 strains covering 6 *Nocardia* species.
- DT, eDT and Ext was used for sample preparation.
- Each sample preparation technique was spotted 8 times on the targets.
- Each spot was measured twice.
- MALDI targets "US IVD MSP 48 Target Polished Steel" and "MBT Biotarget 96 US IVD" were used.
- Measurement on MBT smart CA System and MBT-CA System.
- *Nocardia* were measured after 24h, 48h and after 5 days of cultivation.

Altogether about 15,000 measurements were performed (30 strains * 3 sample preparations * 8 target spots * 2 measurements per spot * 2 target types * 2 instrument types * three cultivation times). The identification performance of *Nocardia* using the standard identification MBT-CA workflow was excellent. The general log(score) distribution was similar and the the equivalence for all examined components (MBT-CA System, MBT smart CA System, MBT Biotarget 96 US IVD, and US IVD MSP 48 Target Polished Steel) was shown successfully.

As an example all 5760 log(scores) after 48h cultivation are shown in the following diagram:

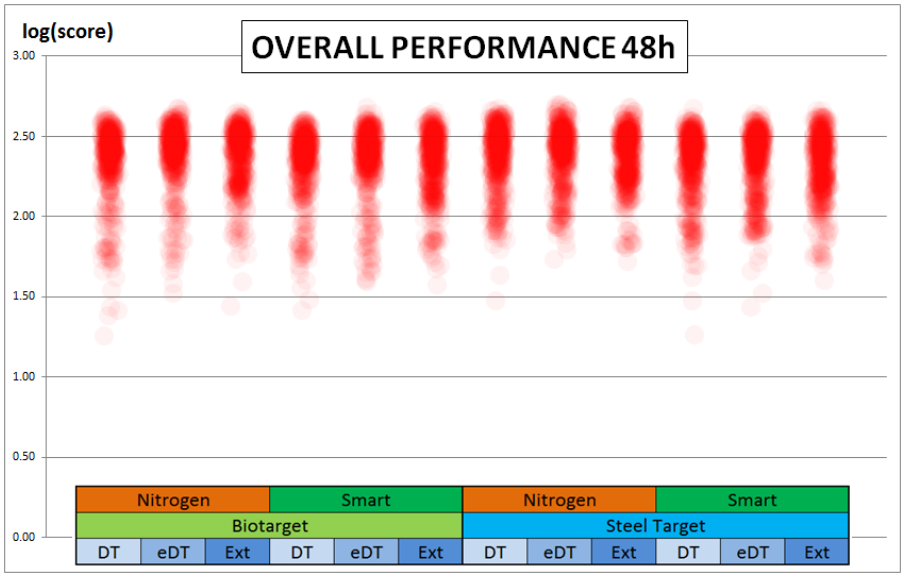

Figure 1: 5760 spectra derived log(scores) after 48h cultivation overlaid. Each "log(score) lane" represents 480 single log(scores). The "focal points" are very similar.

Conclusion:

Studies found that the MBT smart System and the MBT System, as well as the MBT Biotarget 96 US IVD and US IVD MSP 48 Target Polished Steel had comparable performance.

Method Comparison:

To demonstrate performance of the MALDI Biotyper CA (MBT-CA) System, a method comparison study was performed at four (4) US clinical test sites and in-house laboratory. 2,091 fresh and stored organisms were tested on the MALDI Biotyper CA System in accordance with manufacturer's instructions for use. All organisms included in the study were sub-cultured for purity. Testing on the MBT-CA System was done from a freshly isolated colony.

All organisms included in the study and tested by US study sites were also sub-cultured onto an agar slant or appropriate media for isolation and shipped to the study interim reference laboratory. The interim reference laboratory stored all organisms included in the study and when requested, sent organisms to the sequencing reference laboratory for 16S rRNA or ITS sequencing and protein gene sequencing when requested. In-house laboratory and some testing sites processed their own isolates to the sequencing reference laboratory.

The following Gram-negative, Gram-positive and yeast species are additionally included in the reference library (please refer to K130831 and K142677 for previously claimed organisms).

Table 5: Claimed Organisms

Organisms
Abiotrophia defectiva
Acinetobacter_baumannii_nosocomialis group
Acinetobacter calcoaceticus
Acinetobacter pittii
Actinomyces europaeus
Actinomyces funkei
Actinomyces graevenitzii
Actinomyces hyovaginalis
Actinomyces radingae
Actinomyces turicensis
Actinomyces urogenitalis
Actinotignum_schaalii group
Aerococcus sanguinicola
Aggregatibacter actinomycetemcomitans
Aggregatibacter aphrophilus
Aggregatibacter segnis
Alloiococcus otitis
Alloscardovia omnicolens
Anaerococcus murdochii
Arthrobacter cumminsii
Bacteroides caccae
Bacteroides nordii
Bacteroides pyogenes
Bacteroides salyersiae

Organisms
Bacteroides stercoris group
Bifidobacterium breve
Candida intermedia
Candida zeylanoides
Clostridium beijerinckii
Clostridium bifermentans
Clostridium butyricum
Clostridium_clostridioforme group
Clostridium innocuum
Clostridium paraputrificum
Clostridium ramosum
Clostridium septicum
Clostridium sordellii
Clostridium sporogenes/ Clostridium botulinum (group I)
Clostridium tertium
Corynebacterium accolens
Corynebacterium_afermentans group
Corynebacterium coyleae
Corynebacterium freneyi
Corynebacterium glutamicum
Corynebacterium_mucifaciens_ureicelerivorans group
Corynebacterium pseudotuberculosis
Corynebacterium resistens
Cyberlindnera jadinii
Dermabacter hominis
Enterococcus durans
Enterococcus mundtii
Enterococcus raffinosus
Escherichia hermannii
Escherichia vulneris
Ewingella americana
Facklamia hominis
Fluoribacter bozemanae
Gemella morbillorum
Helcococcus kunzii
Kingella denitrificans
Klebsiella variicola
Lactobacillus gasseri
Lactobacillus jensenii
Lactobacillus rhamnosus
Leclercia adecarboxylata
Legionella longbeachae
Legionella pneumophila
Leuconostoc citreum

Organisms
Leuconostoc pseudomesenteroides
Listeria monocytogenes
Malassezia furfur
Malassezia pachydermatis
Mannheimia_haemolytica group
Micrococcus lylae
Mobiluncus curtisii
Neisseria bacilliformis
Neisseria cinerea
Neisseria elongata
Neisseria_flavescens_subflava group
Neisseria gonorrhoeae
Neisseria lactamica
Neisseria meningitidis
Neisseria_sicca group
Neisseria weaveri
Nocardia brasiliensis
Nocardia cyriacigeorgica
Nocardia_farcinica group
Nocardia nova
Nocardia otitidiscaviarum
Ochrobactrum anthropi
Parabacteroides goldsteinii
Parabacteroides_johnsonii_merdae group
Parvimonas micra
Pediococcus acidilactici
Pluralibacter gergoviae
Porphyromonas somerae
Ralstonia pickettii
Rhodotorula mucilaginosa
Serratia fonticola
Serratia odorifera
Sphingobacterium multivorum
Sphingobacterium spiritivorum
Sphingomonas paucimobilis
Staphylococcus delphini
Staphylococcus intermedius
Staphylococcus lentus
Staphylococcus sciuri
Staphylococcus xylosus
Streptococcus canis
Streptococcus equi
Streptococcus parasanguinis
Streptococcus sanguinis

Organisms
Streptococcus sobrinus
Streptococcus_salivarius_vestibularis group
Streptococcus thermophilus
Trichosporon inkin
Trichosporon_mucoides group
Trueperella bernardiae
Turicella otitidis
Vagococcus fluvialis
Veillonella_parvula group
Weeksella virosa
Yersinia frederiksenii
Yersinia intermedia
Yersinia kristensenii

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Table 6 to **Table 8** below show the overall isolate performance.

Table 6: Overall Isolate Performance

Overall Performance - CLAIM 3				
MBT-CA RESULT	REFERENCE ALGORITHM			
	high resolution species	*low resolution species / genus*	*Negative*	*Total*
Organism ID ≥ 2.0 (High Confidence)	1904	130	21	2055
Organism ID (≥1.7; <2.0) (Low Confidence)	23	5	4	32
- INCORRECT MBT-CA ID (≥1.7) *- NO ID (<1.7)*	3	1	n/a	4
Total	1930	136	25	2091

Positive		***Negative***
high resolution	*high & low resolution*	
98.45%	99.81%	n/a

Table 7: Overall Bacteria Performance

Performance BACTERIA				
MBT-CA RESULT	REFERENCE ALGORITHM			
	high resolution species	*low resolution species / genus*	*Negative*	*Total*
Organism ID ≥ 2.0 (High Confidence)	1827	130	21	1978
Organism ID (≥1.7; <2.0) (Low Confidence)	21	5	4	30
- INCORRECT MBT-CA ID (≥1.7) *- NO ID (<1.7)*	2	1	n/a	3
Total	1850	136	25	2011

Positive		***Negative***
high resolution	*high & low resolution*	
98.54%	99.85%	n/a

Table 8: Overall Yeast Performance

Performance YEAST				
MBT-CA RESULT	REFERENCE ALGORITHM			
	high resolution species	*low resolution species / genus*	*Negative*	*Total*
Organism ID ≥ 2.0 (High Confidence)	77	0	0	77
Organism ID (≥1.7; <2.0) (Low Confidence)	2	0	0	2
- INCORRECT MBT-CA ID (≥1.7) *- NO ID (<1.7)*	1	0	n/a	1
Total	80	0	0	80

Positive		***Negative***
high resolution	*high & low resolution*	
96.25%	98.75%	n/a

Statement of Safety and Efficacy

The data presented clearly demonstrate the safety and efficacy of the MBT-CA System as compared to the reference algorithm, when the instructions for use are followed.