

**510(k) SUBSTANTIAL EQUIVALENCE DETERMINATION  
DECISION MEMORANDUM  
ASSAY AND INSTRUMENT COMBINATION TEMPLATE**

**A. 510(k) Number:** K181412

**B. Purpose for Submission:** To add additional organism identification claims (Gram-positive aerobic and anaerobic bacteria, Gram-negative aerobic and anaerobic bacteria, *Brucella* species, and yeasts) to previously cleared devices; DEN130013/K124067 (VITEK MS) and K162950 (VITEK MS v3 KB v3.0).

**C. Measurand:** See Intended Use

**D. Type of Test:** A mass spectrometer system for clinical use for the identification of microorganisms is a qualitative in vitro diagnostic device intended for the identification of microorganisms cultured from human specimens. The device is comprised of an ionization source, a mass analyzer and a spectral database. The device is indicated for use in conjunction with other clinical and laboratory findings to aid in the diagnosis of bacterial and fungal infections.

**E. Applicant:** bioMérieux, Inc.

**F. Proprietary and Established Names:** VITEK MS

**G. Regulatory Information:**

1. Regulation section: 21 CFR 866.3378
2. Classification: Class II (special controls)
3. Product code: QBN
4. Panel: Microbiology (83)

**H. Intended Use:**

1. Intended use(s):  
VITEK MS is a mass spectrometry system using matrix-assisted laser desorption/ionization time to flight mass spectrometry (MALDI-TOF MS) for the identification of microorganisms cultured from human specimens.

The VITEK MS 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, yeast and mould infections.

The following organisms are claimed:

|  |                                     |
|--|-------------------------------------|
| <i>Abiotrophia defectiva</i>                 | <i>Burkholderia gladioli</i>        |
| <i>Achromobacter denitrificans</i>           | <i>Burkholderia multivorans</i>     |
| <i>Achromobacter xylosoxidans</i>            | <i>Burkholderia vietnamiensis</i>   |
| <i>Acinetobacter baumannii</i>               | <i>Campylobacter coli</i>           |
| <i>Acinetobacter calcoaceticus</i>           | <i>Campylobacter jejuni</i>         |
| <i>Acinetobacter haemolyticus</i>            | <i>Campylobacter rectus</i>         |
| <i>Acinetobacter johnsonii</i>               | <i>Candida albicans</i>             |
| <i>Acinetobacter junii</i>                   | <i>Candida auris</i>                |
| <i>Acinetobacter lwoffii</i>                 | <i>Candida dubliniensis</i>         |
| <i>Acinetobacter nosocomialis</i>            | <i>Candida duobushaemulonii</i>     |
| <i>Acinetobacter pittii</i>                  | <i>Candida famata</i>               |
| <i>Actinomyces bovis</i>                     | <i>Candida glabrata</i>             |
| <i>Actinomyces israelii</i>                  | <i>Candida guilliermondii</i>       |
| <i>Actinomyces meyeri</i>                    | <i>Candida haemulonii</i>           |
| <i>Actinomyces naeslundii</i>                | <i>Candida inconspicua</i>          |
| <i>Actinomyces neuui</i>                     | <i>Candida intermedia</i>           |
| <i>Actinomyces odontolyticus</i>             | <i>Candida kefyr</i>                |
| <i>Actinotignum schaalii</i>                 | <i>Candida krusei</i>               |
| <i>Aerococcus viridans</i>                   | <i>Candida lambica</i>              |
| <i>Aeromonas hydrophila</i>                  | <i>Candida lipolytica</i>           |
| <i>Aeromonas jandaei</i>                     | <i>Candida lusitaniae</i>           |
| <i>Aeromonas punctata (caviae)</i>           | <i>Candida metapsilosis</i>         |
| <i>Aeromonas sobria</i>                      | <i>Candida norvegensis</i>          |
| <i>Aggregatibacter actinomycetemcomitans</i> | <i>Candida orthopsilosis</i>        |
| <i>Aggregatibacter aphrophilus</i>           | <i>Candida parapsilosis</i>         |
| <i>Aggregatibacter segnis</i>                | <i>Candida pelliculosa</i>          |
| <i>Alcaligenes faecalis ssp faecalis</i>     | <i>Candida rugosa</i>               |
| <i>Bacteroides caccae</i>                    | <i>Candida tropicalis</i>           |
| <i>Bacteroides eggerthii</i>                 | <i>Candida utilis</i>               |
| <i>Bacteroides fragilis</i>                  | <i>Candida zeylanoides</i>          |
| <i>Bacteroides ovatus / xylanisolvens</i>    | <i>Cedecea davisae</i>              |
| <i>Bacteroides pyogenes</i>                  | <i>Cedecea lapagei</i>              |
| <i>Bacteroides stercoris</i>                 | <i>Cedecea neteri</i>               |
| <i>Bacteroides thetaiotaomicron</i>          | <i>Chryseobacterium gleum</i>       |
| <i>Bacteroides uniformis</i>                 | <i>Chryseobacterium indologenes</i> |
| <i>Bacteroides vulgatus</i>                  | <i>Citrobacter amalonaticus</i>     |
| <i>Bifidobacterium spp</i>                   | <i>Citrobacter braakii</i>          |
| <i>Bilophila wadsworthia</i>                 | <i>Citrobacter farmeri</i>          |
| <i>Bordetella avium</i>                      | <i>Citrobacter freundii</i>         |
| <i>Bordetella bronchiseptica</i>             | <i>Citrobacter koseri</i>           |
| <i>Bordetella parapertussis</i>              | <i>Citrobacter youngae</i>          |
| <i>Bordetella pertussis</i>                  | <i>Clostridium baratii</i>          |
| <i>Brevundimonas diminuta</i>                | <i>Clostridium beijerinckii</i>     |
| <i>Brevundimonas vesicularis</i>             | <i>Clostridium butyricum</i>        |
| <i>Brucella spp</i>                          | <i>Clostridium cadaveris</i>        |
| <i>Burkholderia cenocepacia</i>              | <i>Clostridium clostridioforme</i>  |
| <i>Burkholderia cepacia</i>                  | <i>Clostridium difficile</i>        |
| <i>Burkholderia contaminans</i>              | <i>Clostridium innocuum</i>         |

|                                       |  |
|---------------------------------------|--|
| <i>Clostridium novyi</i>              | <i>Granulicatella adiacens</i>         |
| <i>Clostridium perfringens</i>        | <i>Haemophilus influenzae</i>          |
| <i>Clostridium ramosum</i>            | <i>Haemophilus parahaemolyticus</i>    |
| <i>Clostridium septicum</i>           | <i>Haemophilus parainfluenzae</i>      |
| <i>Clostridium sporogenes</i>         | <i>Hafnia alvei</i>                    |
| <i>Clostridium tertium</i>            | <i>Hathewayia histolytica</i>          |
| <i>Clostridium tetani</i>             | <i>Kingella denitrificans</i>          |
| <i>Comamonas testosteroni</i>         | <i>Kingella kingae</i>                 |
| <i>Corynebacterium jeikeium</i>       | <i>Klebsiella oxytoca</i>              |
| <i>Cronobacter muytjensii</i>         | <i>Klebsiella pneumoniae</i>           |
| <i>Cronobacter sakazakii</i>          | <i>Klebsiella variicola</i>            |
| <i>Cronobacter turicensis</i>         | <i>Khuyvera ascorbata</i>              |
| <i>Cryptococcus gattii</i>            | <i>Khuyvera cryocrescens</i>           |
| <i>Cryptococcus neoformans</i>        | <i>Khuyvera intermedia</i>             |
| <i>Curtobacterium flaccumfaciens</i>  | <i>Kocuria rhizophila</i>              |
| <i>Delftia acidovorans</i>            | <i>Kodamaea ohmeri</i>                 |
| <i>Edwardsiella hoshinae</i>          | <i>Lactococcus garvieae</i>            |
| <i>Edwardsiella tarda</i>             | <i>Lactococcus lactis</i>              |
| <i>Eikenella corrodens</i>            | <i>Leclercia adecarboxylata</i>        |
| <i>Elizabethkingia anophelis</i>      | <i>Legionella pneumophila</i>          |
| <i>Elizabethkingia meningoseptica</i> | <i>Lelliottia amnigena</i>             |
| <i>Elizabethkingia miricola</i>       | <i>Leuconostoc mesenteroides</i>       |
| <i>Enterobacter aerogenes</i>         | <i>Leuconostoc pseudomesenteroides</i> |
| <i>Enterobacter asburiae</i>          | <i>Listeria monocytogenes</i>          |
| <i>Enterobacter cancerogenus</i>      | <i>Malassezia furfur</i>               |
| <i>Enterobacter cloacae</i>           | <i>Malassezia pachydermatis</i>        |
| <i>Enterobacter hormaechei</i>        | <i>Mannheimia haemolytica</i>          |
| <i>Enterobacter kobei</i>             | <i>Micrococcus luteus</i>              |
| <i>Enterobacter ludwigii</i>          | <i>Mobiluncus curtisii</i>             |
| <i>Enterococcus avium</i>             | <i>Moraxella catarrhalis</i>           |
| <i>Enterococcus casseliflavus</i>     | <i>Moraxella lacunata</i>              |
| <i>Enterococcus durans</i>            | <i>Moraxella nonliquefaciens</i>       |
| <i>Enterococcus faecalis</i>          | <i>Moraxella osloensis</i>             |
| <i>Enterococcus faecium</i>           | <i>Morganella morganii</i>             |
| <i>Enterococcus gallinarum</i>        | <i>Myroides spp</i>                    |
| <i>Enterococcus hirae</i>             | <i>Neisseria cinerea</i>               |
| <i>Escherichia coli</i>               | <i>Neisseria gonorrhoeae</i>           |
| <i>Escherichia fergusonii</i>         | <i>Neisseria meningitidis</i>          |
| <i>Escherichia hermannii</i>          | <i>Neisseria mucosa / sicca</i>        |
| <i>Escherichia vulneris</i>           | <i>Ochrobactrum anthropi</i>           |
| <i>Ewingella americana</i>            | <i>Oligella ureolytica</i>             |
| <i>Fingoldia magna</i>                | <i>Oligella urethralis</i>             |
| <i>Fusobacterium mortiferum</i>       | <i>Paeniclostridium sordellii</i>      |
| <i>Fusobacterium necrophorum</i>      | <i>Pantoea agglomerans</i>             |
| <i>Fusobacterium nucleatum</i>        | <i>Pantoea dispersa</i>                |
| <i>Fusobacterium periodonticum</i>    | <i>Paraclostridium bifermentans</i>    |
| <i>Gardnerella vaginalis</i>          | <i>Parvimonas micra</i>                |
| <i>Gemella haemolysans</i>            | <i>Pasteurella aerogenes</i>           |
| <i>Gemella morbillorum</i>            | <i>Pasteurella multocida</i>           |

|  |  |
|--|--|
| <i>Pediococcus acidilactici</i>                | <i>Serratia marcescens</i>                                   |
| <i>Peptoniphilus asaccharolyticus</i>          | <i>Serratia odorifera</i>                                    |
| <i>Peptostreptococcus anaerobius</i>           | <i>Serratia plymuthica</i>                                   |
| <i>Plesiomonas shigelloides</i>                | <i>Serratia proteamaculans</i>                               |
| <i>Pluralibacter gergoviae</i>                 | <i>Serrtia quinivorans</i>                                   |
| <i>Porphyromonas asaccharolytica / uenonis</i> | <i>Serratia rubidaea</i>                                     |
| <i>Porphyromonas gingivalis</i>                | <i>Shewanella putrefaciens</i>                               |
| <i>Prevotella bivia</i>                        | <i>Sphingobacterium multivorum</i>                           |
| <i>Prevotella buccae</i>                       | <i>Sphingobacterium spiritivorum</i>                         |
| <i>Prevotella denticola</i>                    | <i>Sphingomonas paucimobilis</i>                             |
| <i>Prevotella intermedia</i>                   | <i>Staphylococcus aureus</i>                                 |
| <i>Prevotella loescheii</i>                    | <i>Staphylococcus auricularis</i>                            |
| <i>Prevotella melaninogenica</i>               | <i>Staphylococcus capitis</i>                                |
| <i>Prevotella oralis</i>                       | <i>Staphylococcus chromogenes</i>                            |
| <i>Prevotella oris</i>                         | <i>Staphylococcus cohnii ssp cohnii</i>                      |
| <i>Propionibacterium acidipropionici</i>       | <i>Staphylococcus cohnii ssp urealyticus</i>                 |
| <i>Propionibacterium acnes</i>                 | <i>Staphylococcus epidermidis</i>                            |
| <i>Propionibacterium avidum</i>                | <i>Staphylococcus haemolyticus</i>                           |
| <i>Propionibacterium granulosum</i>            | <i>Staphylococcus hominis</i>                                |
| <i>Propionibacterium propionicum</i>           | <i>Staphylococcus hyicus</i>                                 |
| <i>Proteus mirabilis</i>                       | <i>Staphylococcus intermedius</i>                            |
| <i>Proteus penneri</i>                         | <i>Staphylococcus pseudintermedius</i>                       |
| <i>Proteus vulgaris</i>                        | <i>Staphylococcus kloosii</i>                                |
| <i>Providencia alcalifaciens</i>               | <i>Staphylococcus lentus</i>                                 |
| <i>Providencia rettgeri</i>                    | <i>Staphylococcus lugdunensis</i>                            |
| <i>Providencia rustigianii</i>                 | <i>Staphylococcus saprophyticus</i>                          |
| <i>Providencia stuartii</i>                    | <i>Staphylococcus schleiferi</i>                             |
| <i>Pseudomonas aeruginosa</i>                  | <i>Staphylococcus sciuri</i>                                 |
| <i>Pseudomonas alcaligenes</i>                 | <i>Staphylococcus simulans</i>                               |
| <i>Pseudomonas fluorescens</i>                 | <i>Staphylococcus warneri</i>                                |
| <i>Pseudomonas luteola</i>                     | <i>Staphylococcus xylosum</i>                                |
| <i>Pseudomonas mendocina</i>                   | <i>Stenotrophomonas maltophilia</i>                          |
| <i>Pseudomonas oryzihabitans</i>               | <i>Streptococcus agalactiae</i>                              |
| <i>Pseudomonas putida</i>                      | <i>Streptococcus alactolyticus</i>                           |
| <i>Pseudomonas stutzeri</i>                    | <i>Streptococcus anginosus</i>                               |
| <i>Ralstonia pickettii</i>                     | <i>Streptococcus canis</i>                                   |
| <i>Raoultella ornithinolytica</i>              | <i>Streptococcus constellatus</i>                            |
| <i>Raoultella planticola</i>                   | <i>Streptococcus cristatus</i>                               |
| <i>Raoultella terrigena</i>                    | <i>Streptococcus dysgalactiae ssp dysgalactiae</i>           |
| <i>Rhizobium radiobacter</i>                   | <i>Streptococcus dysgalactiae ssp equisimilis</i>            |
| <i>Rhodotorula mucilaginosa</i>                | <i>Streptococcus equi ssp equi</i>                           |
| <i>Rothia mucilaginosa</i>                     | <i>Streptococcus equi ssp zooepidemicus</i>                  |
| <i>Saccharomyces cerevisiae</i>                | <i>Streptococcus equinus</i>                                 |
| <i>Salmonella enterica ssp enterica</i>        | <i>Streptococcus gallolyticus ssp gallolyticus</i>           |
| <i>Saprochaete capitata</i>                    | <i>Streptococcus gallolyticus ssp pasteurianus</i>           |
| <i>Serratia ficaria</i>                        | <i>Streptococcus gordonii</i>                                |
| <i>Serratia fonticola</i>                      | <i>Streptococcus infantarius ssp coli (Str. lutetiensis)</i> |
| <i>Serratia grimesii</i>                       | <i>Streptococcus infantarius ssp infantarius</i>             |
| <i>Serratia liquefaciens</i>                   | <i>Streptococcus intermedius</i>                             |

|   |   |
|---|---|
| <i>Streptococcus mitis / Streptococcus oralis</i> | <b>NOCARDIA</b>                         |
| <i>Streptococcus mutans</i>                       | <i>Nocardia abscessus</i>               |
| <i>Streptococcus parasanguinis</i>                | <i>Nocardia africana / nova</i>         |
| <i>Streptococcus pneumoniae</i>                   | <i>Nocardia asteroides</i>              |
| <i>Streptococcus pseudoporcinus</i>               | <i>Nocardia brasiliensis</i>            |
| <i>Streptococcus pyogenes</i>                     | <i>Nocardia cyriacigeorgica</i>         |
| <i>Streptococcus salivarius ssp salivarius</i>    | <i>Nocardia farcinica</i>               |
| <i>Streptococcus sanguinis</i>                    | <i>Nocardia otitidiscaviarum</i>        |
| <i>Streptococcus sobrinus</i>                     | <i>Nocardia paucivorans</i>             |
| <i>Streptococcus suis</i>                         | <i>Nocardia pseudobrasiliensis</i>      |
| <i>Streptococcus uberis</i>                       | <i>Nocardia transvalensis</i>           |
| <i>Streptococcus vestibularis</i>                 | <i>Nocardia veterana</i>                |
| <i>Tannerella forsythia</i>                       | <i>Nocardia wallacei</i>                |
| <i>Veillonella dispar</i>                         |   |
| <i>Vibrio alginolyticus</i>                       | <b>MOULD</b>                            |
| <i>Vibrio cholerae</i>                            | <i>Acremonium sclerotigenum</i>         |
| <i>Vibrio fluvialis</i>                           | <i>Alternaria alternata</i>             |
| <i>Vibrio metschnikovii</i>                       | <i>Aspergillus brasiliensis</i>         |
| <i>Vibrio mimicus</i>                             | <i>Aspergillus calidoustus / ustus</i>  |
| <i>Vibrio parahaemolyticus</i>                    | <i>Aspergillus flavus / oryzae</i>      |
| <i>Vibrio vulnificus</i>                          | <i>Aspergillus fumigatus</i>            |
| <i>Yersinia aldovae</i>                           | <i>Aspergillus lentulus</i>             |
| <i>Yersinia enterocolitica</i>                    | <i>Aspergillus nidulans</i>             |
| <i>Yerinia frederiksenii</i>                      | <i>Aspergillus niger complex</i>        |
| <i>Yersinia intermedia</i>                        | <i>Aspergillus sydowii</i>              |
| <i>Yersinia kristensenii</i>                      | <i>Aspergillus terreus complex</i>      |
| <i>Yersinia pseudotuberculosis</i>                | <i>Aspergillus versicolor</i>           |
| <i>Yersinia ruckeri</i>                           | <i>Blastomyces dermatitidis</i>         |
|   | <i>Cladophialophora bantiana</i>        |
| <b>MYCOBACTERIUM</b>                              | <i>Coccidioides immitis / posadasii</i> |
| <i>Mycobacterium abscessus</i>                    | <i>Curvularia hawaiiensis</i>           |
| <i>Mycobacterium avium</i>                        | <i>Curvularia spicifera</i>             |
| <i>Mycobacterium chelonae</i>                     | <i>Epidermophyton floccosum</i>         |
| <i>Mycobacterium fortuitum group</i>              | <i>Exophiala dermatitidis</i>           |
| <i>Mycobacterium gordonae</i>                     | <i>Exophiala xenobiotica</i>            |
| <i>Mycobacterium haemophilum</i>                  | <i>Exserohilum rostratum</i>            |
| <i>Mycobacterium immunogenum</i>                  | <i>Fusarium oxysporum complex</i>       |
| <i>Mycobacterium intracellulare</i>               | <i>Fusarium proliferatum</i>            |
| <i>Mycobacterium kansasii</i>                     | <i>Fusarium solani complex</i>          |
| <i>Mycobacterium lentiflavum</i>                  | <i>Histoplasma capsulatum</i>           |
| <i>Mycobacterium malmoense</i>                    | <i>Lecythophora hoffmannii</i>          |
| <i>Mycobacterium marinum</i>                      | <i>Lichtheimia corymbifera</i>          |
| <i>Mycobacterium mucogenicum</i>                  | <i>Microsporum audouinii</i>            |
| <i>Mycobacterium scrofulaceum</i>                 | <i>Microsporum canis</i>                |
| <i>Mycobacterium simiae</i>                       | <i>Microsporum gypseum</i>              |
| <i>Mycobacterium smegmatis</i>                    | <i>Mucor racemosus complex</i>          |
| <i>Mycobacterium szulgai</i>                      | <i>Paecilomyces variotii complex</i>    |
| <i>Mycobacterium tuberculosis complex</i>         | <i>Penicillium chrysogenum</i>          |
| <i>Mycobacterium xenopi</i>                       | <i>Pseudallescheria boydii</i>          |

|                                      |   |
|--------------------------------------|---|
| <i>Purpureocillium lilacinum</i>     | <i>Trichophyton interdigitale</i>       |
| <i>Rasamsonia argillacea</i> complex | <i>Trichophyton rubrum</i>              |
| <i>Rhizopus arrhizus</i> complex     | <i>Trichophyton tonsurans</i>           |
| <i>Rhizopus microsporus</i> complex  | <i>Trichophyton verrucosum</i>          |
| <i>Sarocladium kiliense</i>          | <i>Trichophyton violaceum</i>           |
| <i>Scedosporium apiospermum</i>      | <i>Trichosporon asahii</i>              |
| <i>Scedosporium prolificans</i>      | <i>Trichosporon dermatis / mucoides</i> |
| <i>Sporothrix schenckii</i> complex  | <i>Trichosporon inkin</i>               |

2. Indication(s) for use: Same as Intended Use.

3. Special conditions for use statement(s):

The VITEK MS is for prescription use only in accordance with 21 CFR 866.3378.

4. Special instrument requirements:

- VITEK MS: Shimadzu AXIMA Assurance mass spectrometer
- VITEK MS Prep Station
- VITEK MS-DS Target Slides

Reagents:

- VITEK MS-CHCA (Alpha-cyano-4-hydroxy-cinnamic acid) solution
- VITEK MS-FA (Formic acid) reagent
- VITEK MS MYCOBACTERIUM/NOCARDIA KIT
- VITEK MS LIQUID MYCO SUPPLEMENTAL KIT (to process liquid samples)
- VITEK MS MOULD KIT
- *Brucella* inactivation solvent mixture reagents

Software:

- VITEK MS Sample Prep Station software (V2.3.2)
- VITEKMS V3 Acquisition Station 1.5.0
- VITEK MS Analysis Server / Software
- VITEK MS Computation Engine
- Myla Middleware

Database:

- VITEKMS V3.2.0 Knowledge Base (KB)

Due to updates in the database (KB v3.2.0), the following organism identification notes have been added. For a complete list of identification interpretations, please see DEN130013/K124067 and K162950.

**Table 1. VITEK MS Identification Interpretations Based on KB Update (v3.2)**

| Organism  | Interpretation  |
|---|---|
| <b>Gram-positive and Gram-negative Bacteria</b> |   |
| <i>Aeromonas hydrophila</i>                     | <i>Aeromonas hydrophila</i> ssp <i>dhakensis</i> and <i>Aeromonas hydrophila</i> ssp <i>ranae</i> are also correctly identified as <i>A. hydrophila</i> .   |
| <i>Aeromonas sobria</i>                         | In KB V3.0.0, <i>Aeromonas sobria</i> is displayed as a low discrimination result with <i>Aeromonas veronii</i> but only <i>Aeromonas sobria</i> has been clinically validated. There is a possibility of cross-identification between <i>Aeromonas sobria</i> and <i>Aeromonas salmonicida/bestiarum</i> .   |
| <i>Brucella</i> spp                             | <p>For some samples the VITEK MS result for <i>Brucella</i> spp will report as a low discrimination result of <i>Brucella</i> spp/<i>Brucella</i> spp, even though it is a single choice correct identification of <i>Brucella</i> spp. This will be corrected in a future software release.</p> <p>bioMérieux tested the following species reported in the literature to be misidentified to <i>Brucella</i> species: <i>Aggregatibacter aphrophilus</i>, <i>Bordetella bronchiseptica</i>, <i>Corynebacterium urealyticum</i>, <i>Haemophilus influenzae</i>, <i>Micrococcus luteus</i>, <i>Ochrobactrum intermedium</i>, <i>Ochrobactrum anthropi</i>, <i>Oligella urealytica</i>, <i>Pasteurella multocida</i>, <i>Pasteurella pneumotropica</i>, <i>Psychrobacter phenylpyruvicus</i>, <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i>. In the study, no cross reactivity was observed using the <i>Brucella</i> sample preparation. All tested strains were identified to the expected species by direct deposit, and none of the strains were identified to <i>Brucella</i> species.</p> <p><i>Bacillus anthracis</i>, <i>Yersinia pestis</i>, <i>Francisella tularensis</i> ssp. <i>holarctica</i>, <i>Burkholderia mallei</i> and <i>Burkholderia pseudomallei</i> species were tested using the VITEK MS V3.2 KB. No cross-identification with closely-related species were observed. These species are expected to provide an unidentified (No ID) result using the VITEK MS V3.2 KB.</p> |
| <i>Clostridium butyricum</i>                    | The reference method cannot differentiate between <i>Clostridium saccharoperbutylacetonicum</i> and <i>Clostridium butyricum</i> .  |
| <i>Clostridium tertium</i>                      | The reference method cannot differentiate between <i>Clostridium chauvoei</i> , <i>Clostridium sartagoforme</i> , <i>Clostridium septicum</i> , and <i>Clostridium tertium</i> .  |
| <i>Hafnia alvei</i>                             | In KB V3.2.0, <i>Hafnia alvei</i> is displayed as a low discrimination result with <i>Obesumbacterium proteus</i> but only <i>H. alvei</i> has been clinically validated.   |
| <i>Moraxella lacunata</i>                       | In KB V3.2.0, <i>Moraxella lacunata</i> is displayed as a low discrimination result with <i>Moraxella (Neisseria) ovis</i> but only <i>M. lacunata</i> has been clinically validated.   |
| <i>Moraxella osloensis</i>                      | In KB V3.2.0, <i>Moraxella osloensis</i> is displayed as a low discrimination result with <i>Enhydrobacter aerosaccus</i> but only <i>M. osloensis</i> has been clinically validated.   |
| <i>Pseudomonas oryzihabitans</i>                | The reference method cannot differentiate between <i>Pseudomonas oryzihabitans</i> , <i>Pseudomonas psychrotolerans</i> , and <i>Pseudomonas oleovorans</i> .   |
| <i>Staphylococcus hyicus</i>                    | The reference method cannot differentiate between <i>Staphylococcus chromogenes</i> , <i>Staphylococcus agnetis</i> , <i>Staphylococcus lutrae</i> , <i>Staphylococcus delphini</i> , and <i>Staphylococcus hyicus</i> .  |
| <i>Staphylococcus xylosus</i>                   | The reference method cannot differentiate between <i>Staphylococcus saprophyticus</i> and <i>Staphylococcus xylosus</i> .   |
| <i>Streptococcus equi</i> ssp                   | In KB V3.2.0, <i>Streptococcus equi</i> ssp <i>zooepidemicus</i> is displayed as a low  |

| Organism  | Interpretation   |
|---|--|
| <i>zooepidemicus</i>                            | discrimination result with <i>Streptococcus equi</i> ssp <i>ruminatorum</i> but only <i>Streptococcus equi</i> ssp <i>zooepidemicus</i> has been clinically validated. |
| <b>Nocardia</b>                                 |  |
| <i>Nocardia africana</i> / <i>nova</i>          | In KB V3.2.0, <i>Nocardia africana</i> is grouped in a slashline with <i>Nocardia nova</i> . It is not possible to distinguish between the 2 species.                  |
| <b>Moulds</b>                                   |  |
| <i>Aspergillus calidoustus</i> / <i>ustus</i>   | In KB V3.2.0, <i>Aspergillus calidoustus</i> is grouped in a slashline with <i>Aspergillus ustus</i> . It is not possible to distinguish between the 2 species.        |
| <i>Trichosporon dermatis</i> / <i>mucooides</i> | In KB V3.2.0, <i>Trichosporon dermatis</i> is grouped in a slashline with <i>Trichosporon mucooides</i> . It is not possible to distinguish between the 2 species.     |

## I. Device Description:

The VITEK MS v3.0 system is a system consisting of kit reagents (VITEK MS-CHCA, VITEK MS-FA, VITEK MS Mycobacterium/Nocardia Kit, VITEK MS Mould Kit), VITEK MS-DS target slides, VITEK MS Prep Station, Knowledge Base v3.2, software, and the VITEK MS (original equipment manufacturer (OEM)-labeled Shimadzu AXIMA Assurance mass spectrometer).

### Reagent Description:

- The VITEK MS-CHCA (Alpha-cyano-4-hydroxy-cinnamic acid) is a solution that serves as a matrix which will crystalize with the microbial sample on the target slide spot. One microliter of the matrix is added to the spot with the sample and allowed to dry forming crystals.
- The VITEK MS-FA (Formic acid) reagent is used to pre-treat yeast in order to extract protein before the VITEK MS-CHCA matrix is added to the spot containing the sample.
- The VITEK MS MYCOBACTERIUM/NOCARDIA KIT includes ethanol and vials with glass beads to inactivate *Mycobacterium* and *Nocardia* species by disrupting the cells. The kit also includes formic acid and acetonitrile to complete the extraction of proteins.
- The VITEK MS LIQUID MYCO SUPPLEMENTAL KIT includes the addition consumables (i.e., 5mL conical bottom tubes and safety backed absorbent pads) needed to process samples for *Mycobacterium* with liquid media.
- The VITEK MS MOULD KIT method uses ethanol, formic acid, and acetonitrile to inactivate moulds and extract their proteins.
- The *Brucella* inactivation solvent mixture contains API Suspension Medium or sterile deionized water, absolute ethanol (HPLC grade), acetonitrile (HPLC grade), and trifluoroacetic acid (TFA) (HPLC grade).

### VITEK MS-DS Target Slides:

VITEK MS-DS target slides are single-use disposable slides which contain three acquisition groups of 16 sample spots. Each group includes one calibration spot.

### Knowledge Base:

The reference database for the VITEK MS system includes data representing 1316 species and 1158 taxa displayed. VITEK MS Knowledge Base v3.2.0 includes 1095 species of

bacteria (863 single species and 77 groups including 232 species) and 221 species of fungi (195 single species and 12 groups including 26 species).

Additional laboratory tests as determined by microbiology laboratory protocols for low discrimination results or non-clinically validated organisms are necessary for the completion of the organism identification. Non-clinically validated organisms are displayed as (N) in the report.

Testing of non-clinically validated species or species not found in the database may result in an unidentified result or a misidentification.

Interpretation of results and use of the VITEK MS system require a competent laboratorian who should judiciously make use of experience, specimen information, and other pertinent procedures before reporting the identification of test organisms. Additional information known to the user, such as Gram stain reaction, colonial and cellular morphology, and growth aerobically or in CO<sub>2</sub> should be considered when accepting VITEK MS results.

*Brucella* species are included in the VITEK MS Knowledge Base (KB) v3.2.0 database. However, the VITEK MS will only report *Brucella* spp.

#### Software:

The VITEK MS system consists of a suite of applications that perform the overall system function. The system functions as a kiosk, not allowing the end-user to access any operating system functions. The end-user cannot access the native operating system or any system configuration panels. The software application contains several processes that include handling all user interactions, all network activity, communication, and synchronization with all the components. The VITEK MS system software is comprised of four software components and MYLA middleware.

1. VITEK MS Sample Prep Station software: The VITEK MS Prep Station is used to prepare VITEK MS-DS target slides. It consists of a computer workstation equipped with a barcode reader, touch screen, and virtual keyboard.
2. VITEK MS Acquisition Station: The Acquisition Station Software controls the VITEK MS to acquire spectral data from each sample and displays the spectra for the operator to review. The Acquisition Station displays the spectra and peak lists and transfers the peak lists to the VITEK MS Analysis Server.
3. VITEK MS Analysis Server / Software: The VITEK MS Analysis Server is the software that manages the VITEK MS workflow and computes VITEK MS identification results. It is a software component that resides on the Myla Server (PC).
4. VITEK MS Computation Engine: The VITEK MS analysis server sends the acquired data to the computation engine that calculates the identification results. The algorithms and mapping files required for identification are contained within the computation engine.
5. Myla Middleware: Myla is a computer application ("Middleware"), based on web technology, which allows data related to the laboratory workflow, laboratory instruments, Laboratory Information System (LIS), analysis results, etc. to be grouped together. Myla interfaces between the bioMérieux instruments connected to the application (e.g., VITEK

MS) and the Laboratory Information System (LIS). Myla manages the VITEK MS workflow and computes the identification results with the use of a computation engine and organism knowledge bases.

**VITEK MS:**

bioMérieux’s VITEK MS, is the same instrument as the Shimadzu Axima Assurance MALDI-TOF spectrometer. The VITEK MS is manufactured for bioMérieux by Kratos Analytical (a Shimadzu subsidiary) in Manchester, UK. The VITEK MS contains a Class 1 laser product containing a Class 3b invisible-light laser. The laser is a 337 nm nitrogen laser, fixed focus. This speed depends on the mass of the ions with heavier molecules having a higher moment of inertia resulting in a lower velocity. The time of transit is measured precisely by the ions’ arrival at a particle detector. Based on the time of flight, the m/z ratio of each particle can be determined, and a mass spectrum of the sample mixture is generated. The recorded signal is processed by the Acquisition Station software and presented as a spectrum of intensity versus mass in Daltons (Da).

**J. Substantial Equivalence Information:**

1. Predicate device name(s):

MALDI Biotyper CA System

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

DEN170081

3. Comparison with predicate:

| <b>Similarities</b>   |  |   |
|-----------------------|--|---|
| <b>Characteristic</b> | <b>New Device<br/>VITEK MS v3 / KB v3.2.0</b>  | <b>Predicate Device<br/>MALDI Biotyper CA System<br/>(DEN170081)</b>  |
| <b>Classification</b> | 21 CFR 866.3378<br>Class II<br>Clinical Mass Spectrometry Microorganism Identification and Differentiation System  | 21 CFR 866.3378<br>Class II<br>Clinical Mass Spectrometry Microorganism Identification and Differentiation System   |
| <b>Product Code</b>   | QBN  | QBN   |
| <b>Intended Use</b>   | <p>The VITEK MS is a mass spectrometry system using matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF MS) for the identification of microorganisms cultured from human specimens.</p> <p>The VITEK MS 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, yeast and mould infections.</p> <p style="text-align: center;"><b>NOTE:</b></p> | <p>The MALDI Biotyper CA System is a mass spectrometer system using matrix-assisted laser desorption/ionization – time of flight (MALDI-TOF) for the identification and differentiation of microorganisms cultured from human specimens.</p> <p>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 fungal infections.</p> |

| <b>Similarities</b>        |   |  |
|----------------------------|---|--|
| <b>Characteristic</b>      | <b>New Device<br/>VITEK MS v3 / KB v3.2.0</b>   | <b>Predicate Device<br/>MALDI Biotyper CA System<br/>(DEN170081)</b>   |
|                            | Additional organism identification claims (Gram-positive aerobic and anaerobic bacteria, Gram-negative aerobic and anaerobic bacteria, <i>Brucella</i> species, and yeasts) to the already cleared device DEN130013 (K124067) and K162950 using the VITEK MS v3.0 / KB v3.2.  | <b>NOTE:</b><br>Please see DEN170081 for a complete list of organisms.   |
| <b>Type of Test</b>        | Automated Mass Spectrometry System  | Automated Mass Spectrometry System   |
| <b>Matrix</b>              | Alpha-cyano-4-hydroxy-cinnamic acid   | Alpha-cyano-4-hydroxy-cinnamic acid  |
| <b>Method of Testing</b>   | (For bacteria and yeast)<br>Direct testing from isolated colonies<br><br>(For mycobacteria, <i>Nocardia</i> , moulds)<br>Inactivation and extraction prior to sample spotting on the target slide<br><br>(For <i>Brucella</i> spp)<br>Inactivation required prior to sample spotting on the target slide  | (For bacteria and yeast)<br>Direct testing from isolated colonies;<br>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.  |
| <b>Age of Culture</b>      | (For bacteria and yeast)<br>Incubation of culture should be 18 – 72hrs  | (For bacteria and yeast)<br>Incubation of culture should be between 18 – 36hrs   |
| <b>Sample / Media Type</b> | Isolate colony from a patient sample source, from media including: <ul style="list-style-type: none"> <li>• BacT/ALERT MP</li> <li>• Brucella agar base</li> <li>• Buffered charcoal yeast extract</li> <li>• Campylosel agar</li> <li>• Chocolate polyvitex agar</li> <li>• chromID CPS</li> <li>• Colestos</li> <li>• Columbia blood agar with 5% sheep blood</li> <li>• Lowenstein-Jensen*</li> <li>• MacConkey agar**</li> <li>• MGIT</li> <li>• Middlebrook 7H10 agar*</li> <li>• Middlebrook 7H11 agar*</li> <li>• Modified Sabouraud dextrose agar (glucose: 20 g/l – pH: 6.1)</li> <li>• Potato dextrose agar</li> <li>• Sabouraud dextrose agar (glucose: 40 g/l – pH: 5.6)</li> <li>• Sabouraud dextrose agar with Gentamicin &amp; Chloramphenicol</li> <li>• Trypticase soy agar</li> <li>• Trypticase soy agar with 5% sheep blood</li> <li>• Trypticase soya agr with neutralizers</li> </ul> | Isolate colony from any patient sample source.<br><br>Acceptable media: <ul style="list-style-type: none"> <li>• Columbia blood agar with 5% sheep blood (Gram-negative bacteria)</li> <li>• Columbia CNA agar with 5% sheep blood (Gram-positive bacteria)</li> <li>• Trypticase soy agar with 5% sheep blood (Gram-negative bacteria, Gram-positive bacteria, yeasts)</li> <li>• Chocolate agar (Gram-negative bacteria, Gram-positive bacteria)</li> <li>• MacConkey agar (Gram-negative bacteria)</li> <li>• Brucella agar with 5% horse blood (Gram-negative anaerobic bacteria, Gram-positive anaerobic bacteria)</li> <li>• Sabouraud dextrose agar (yeasts)</li> <li>• CDC anaerobe agar with 5% sheep blood (Gram-negative anaerobic bacteria, Gram-positive anaerobic bacteria)</li> <li>• CDC anaerobe 5% sheep blood agar with phenylethyl alcohol (Gram-negative anaerobic bacteria, Gram-positive anaerobic bacteria)</li> <li>• CDC anaerobe laked sheep blood</li> </ul> |

| Similarities        |  |   |
|---------------------|--|---|
| Characteristic      | New Device<br>VITEK MS v3 / KB v3.2.0  | Predicate Device<br>MALDI Biotyper CA System<br>(DEN170081)   |
|                     | *Non-bioMérieux media<br>**Use of this medium from some suppliers may show less than optimal performance   | agar with kanamycin and vancomycin (Gram-negative anaerobic bacilli) <ul style="list-style-type: none"> <li>• Bacteroides bile esculin agar with amikacin (<i>Bacteroides</i> species)</li> <li>• Clostridium difficile agar with 7% sheep blood (<i>Clostridium difficile</i>)</li> <li>• Brain heart infusion agar (yeasts)</li> <li>• Campylobacter agar with 5 antimicrobics and 10% sheep blood (<i>Campylobacter</i> species)</li> <li>• Bordet-Gengou agar with 15% sheep blood (<i>Bordetella</i> species)</li> </ul> |
| Algorithm           | An algorithm process known as "mass binning" is used for the differentiation of the species included in the knowledge base   | Calculates matches by comparing a new spectrum against each single reference entry of a reference database  |
| Result Reporting    | To detect microbial growth, the VITEK MS uses a knowledge base developed from spectra of a number of microbial species. The resulting spectra from the VITEK MS / Acquisition Station are evaluated against this knowledge.<br><br>Identifications are displayed, with a confidence value when an organism or organism group is identified. Low-discrimination identifications are displayed when more than one, but not more than four identifications, are made. When more than four identifications are made, or when no match is found, the organism is considered unidentified.<br><br>Data analysis is performed using software embedded on the MYLA Server. | Organism identification is reported with high confidence if the log(score) is >2.0. An organism identification is reported with low confidence if the log(score) is between 1.70 and <2.00.   |
| Recorded Mass Range | 2,000 – 20,000 m/z   | 2,000 – 20,000 m/z  |
| Laser               | Class 1 Laser Product – 337 nm fixed focus, nitrogen laser   | Class 1 Laser Product (class 4 with safety cover opened) – 337 nm fixed focus, nitrogen laser; microflex LT/SH<br><br>Solid state laser; microflex LT/SH Smart  |

| Differences             |  |  |
|-------------------------|--|--|
| Characteristic          | New Device<br>VITEK MS v3 / KB v 3.2.0 | Predicate Device<br>MALDI Biotyper CA System<br>(DEN170081)                  |
| Knowledge Base          | VITEK MS v3.2 Knowledge Base           | MALDI Biotyper Reference Library for Clinical Applications (MBT-CA)          |
| MALDI-TOF MS Instrument | Shimadzu AXIMA Assurance MS            | Bruker microflex LT/SH (benchtop)<br>Bruker microflex LT/SH smart (benchtop) |
| Target Slide            | VITEK MSDS Target Slides 48 positions  | US IVD 48 Spot Target (48 positions,   |

| Differences                           |   |   |
|---------------------------------------|---|---|
| Characteristic                        | New Device<br>VITEK MS v3 / KB v 3.2.0  | Predicate Device<br>MALDI Biotyper CA System<br>(DEN170081)   |
|                                       | disposable plastic targets  | reusable steel targets)<br>MBT Biotarget 96 US IVD plate (96 positions, disposable targets)   |
| System Components, Software, Reagents | The VITEK MS system consists of a number of components (e.g., a Prep Station, the MS Instrument, and an Acquisition Station), software/middleware solutions (e.g., Acquisition Station Software, an Analysis Server, a Computation Engine, and MYLA), and disposables/consumables (e.g., the VITEK MS-DS Target Slides, CHCA Matrix, Formic Acid as applicable, VITEK MS <i>Mycobacterium/Nocardia</i> Kit, VITEK MS Mould Kit, and the <i>Brucella</i> inactivation solvent mixture reagents). | The MBT-CA System consists of the microflex LT/SH mass spectrometer, reference library, kit reagents (e.g., US IVD Bacterial Test Standard [BTS]), US IVD HCCA portioned ( $\alpha$ -cyano-4-hydroxycinnamic acid), US IVD 48 Spot Target or MBT Biotarget 96 US IVD plate, and software (e.g., MBT-CA System Software Package [including the MBT-CA System client software displaying the user interface, MBT-CA System Server, and MBT-CA System DB Server] and the flexControl Software Package including GTPS firmware and flexControl acquisition software). |
| Calibration                           | <i>E. coli</i> ATCC 8739  | Bruker US IVD Bacterial Test Standard   |
| Age of Culture                        | Includes new <i>Brucella</i> spp indication for use: Incubation of <i>Brucella</i> spp should be 48-96 hrs (2-4 days)   | As there are no indications for use for <i>Brucella</i> spp., there are no applicable culture age requirements  |
| Sample Preparation                    | (For <i>Brucella</i> spp)<br>Inactivation required prior to sample spotting on the target slide; Bacteria are mixed in the <i>Brucella</i> solvent mixture, vortexed, and incubated at room temperature – supernatant is discarded and CHCA matrix is added to the pelleted organism; no vortexing or resuspension; preparation is spotted on the target slide and allowed to dry before processing   | NA  |

**K. Standard/Guidance Document Referenced (if applicable):**

**Table 2. FDA Guidance Documents**

| Title  | Date       |
|--|------------|
| De Novo Classification Process (Evaluation of Automatic Class III Designation), Guidance for Industry and Food and Drug Administration Staff   | 02/19/1998 |
| Guidance on Informed Consent for <i>In Vitro</i> Diagnostic Device Studies Using Leftover Human Specimens that are Not Individually Identifiable, Guidance for Sponsors, Institutional Review Boards, and Food and Drug Administration Staff | 04/25/2006 |
| Statistical Guidance on Reporting Results from Studies Evaluation Diagnostic Tests   | 03/13/2007 |

**Table 3. Clinical & Laboratory Standards Institute (CLSI) Standards**

| Standards No. | Standards Title  | Date       |
|---------------|--|------------|
| MM09-A        | Nucleic Acid Sequencing Methods in Diagnostic Laboratory Medicine; Approved Guideline, 2 <sup>nd</sup> Edition                       | 08/14/2015 |
| MM18-A        | Interpretive Criteria for Identification of Bacteria and Fungi by DNA Target Sequencing; Approved Guideline, 1 <sup>st</sup> Edition | 04/28/2008 |
| M35-A2        | Abbreviated Identification of Bacteria and Yeast; Approved Guideline, 2 <sup>nd</sup> Edition  | 11/24/2008 |
| EP12-A2       | User Protocol for Evaluation of Qualitative Test Performance; Approved Guideline, 2 <sup>nd</sup> Edition                            | 01/25/2008 |

**L. Test Principle:**

The VITEK MS system is based on a matrix-assisted laser desorption ionization-time of flight mass spectrometer (MALDI-TOF MS). The colony is mixed with a saturated matrix solution and forms crystals. The ionization of this mixture by the laser induces the desorption and transfer of protons from photo-excited matrix to analyte to form a protonated molecule. During the analysis process, proteins are ionized without fragmentation by the coordinated action of the laser and the small organic acids of the matrix are separated on the basis of their mass-to-charge ratios, a process which results in a characteristic mass spectral profile. Microbial identification is based on the comparison of the protein spectrum generated from intact whole bacterial cells to the knowledge database of species-specific reference protein profiles using a particular algorithm.

**M. Performance Characteristics (if/when applicable):**1. Analytical performance:

a. *Addition of Brucella spp. to Knowledge Base v3.2*

**Table 4. All *Brucella* spp. Strains Used Throughout Various Studies**

| Strain ID                                   | Resource Center | Comment                             |
|---|-----------------|-------------------------------------|
| <i>Brucella abortus</i> , NR-69, ATCC 23448 | ATCC/USDA       | Reproducibility, Proficiency, Clone |
| <i>Brucella abortus</i> , B99-0165          | USDA            | Challenge                           |
| <i>Brucella abortus</i> , B90-1449          | USDA            | Challenge                           |
| <i>Brucella abortus</i> , NR-229            | ATCC/USDA       | Clone                               |
| <i>Brucella abortus</i> , NR-231            | ATCC/USDA       | Clone                               |
| <i>Brucella abortus</i> , NR-233            | ATCC/USDA       | Clone                               |
| <i>Brucella canis</i> , B17-0225            | USDA            | Challenge                           |
| <i>Brucella canis</i> , NR-683, ATCC 23365  | ATCC/USDA       | Clone                               |
| <i>Brucella canis</i> , B17-0194            | ATCC/USDA       | Clone                               |
| <i>Brucella canis</i> , B17-0193            | ATCC/USDA       | Clone                               |
| <i>Brucella canis</i> , B17-0225            | ATCC/USDA       | Clone                               |
| <i>Brucella canis</i> , B17-0244            | ATCC/USDA       | Clone                               |
| <i>Brucella ceti</i> , B13-0078             | ATCC/USDA       | Challenge, Clone                    |
| <i>Brucella ceti</i> , B06-0757             | ATCC/USDA       | Challenge, Clone                    |
| <i>Brucella ceti</i> , B04-0019             | ATCC/USDA       | Clone                               |

| Strain ID                                       | Resource Center | Comment                             |
|---|-----------------|-------------------------------------|
| <i>Brucella ceti</i> , B92-1350                 | ATCC/USDA       | Clone                               |
| <i>Brucella ceti</i> , B13-014                  | ATCC/USDA       | Clone                               |
| <i>Brucella melitensis</i> , NR-256, ATCC 23456 | ATCC            | Reproducibility, Proficiency, QC    |
| <i>Brucella melitensis</i> , B94-0130           | ATCC/USDA       | Challenge, Clone                    |
| <i>Brucella melitensis</i> , B90-1447           | ATCC/USDA       | Clone                               |
| <i>Brucella melitensis</i> , B90-1444           | ATCC/USDA       | Challenge, Clone                    |
| <i>Brucella melitensis</i> , B00-0076           | ATCC/USDA       | Clone                               |
| <i>Brucella ovis</i> , B14-0018                 | USDA            | Challenge                           |
| <i>Brucella ovis</i> , NR-682, ATCC 25840       | ATCC/USDA       | Clone                               |
| <i>Brucella ovis</i> , B90-0828                 | ATCC/USDA       | Clone                               |
| <i>Brucella ovis</i> , B08-1348                 | ATCC/USDA       | Challenge, Clone                    |
| <i>Brucella ovis</i> , B99-0596                 | ATCC/USDA       | Clone                               |
| <i>Brucella ovis</i> , B91-0507                 | ATCC/USDA       | Clone                               |
| <i>Brucella papionis</i> , B07-0224             | ATCC/USDA       | Challenge, Clone                    |
| <i>Brucella papionis</i> , B07-0026             | ATCC/USDA       | Challenge, Clone                    |
| <i>Brucella pinnipedialis</i> , B05-0747        | ATCC/USDA       | Challenge, Clone                    |
| <i>Brucella pinnipedialis</i> , B00-0777        | ATCC/USDA       | Challenge, Clone                    |
| <i>Brucella pinnipedialis</i> , B03-0094        | ATCC/USDA       | Clone                               |
| <i>Brucella pinnipedialis</i> , B03-0058        | ATCC/USDA       | Clone                               |
| <i>Brucella pinnipedialis</i> , B07-0215        | ATCC/USDA       | Clone                               |
| <i>Brucella suis</i> , NR-302, ATCC 23444       | ATCC/USDA       | Reproducibility, Proficiency, Clone |
| <i>Brucella suis</i> , NR-303                   | ATCC/USDA       | Clone                               |
| <i>Brucella suis</i> , NR-304                   | ATCC/USDA       | Clone                               |
| <i>Brucella suis</i> , B15-0008                 | ATCC/USDA       | Clone                               |
| <i>Brucella suis</i> , B17-0007                 | ATCC/USDA       | Challenge, Clone                    |
| <i>Brucella suis</i> , B11-0281                 | USDA            | Challenge                           |

b. Precision/Reproducibility:

A panel of three well-characterized *Brucella* strains were tested at one clinical trial site by two technologists in duplicate for five days with two runs per day for a total of 60 replicates per organism. Three different lots of solvent mixture were used during reproducibility testing. On each day of testing, sequential positions on the target slide were assigned to the first run of the selected reproducibility samples, and randomized for the second run. Spot positions were alternated with each run when testing samples in a randomized order. One organism was used for positive quality control, and reagents alone were used for the negative control. The quality control strain was *Brucella melitensis*, NR-256. Results are shown in Table 5 below.

**Table 5. Reproducibility Testing for *Brucella* spp – All Sites Combined**

| Sample | Organism                   | Day   |       |       |       |       | Total (%)        | 95% CI         |
|--------|----------------------------|-------|-------|-------|-------|-------|------------------|----------------|
|        |                            | 1     | 2     | 3     | 4     | 5     |                  |                |
| R1     | <i>Brucella abortus</i>    | 12/12 | 12/12 | 12/12 | 12/12 | 12/12 | 60/60 (100.0%)   | [94.0, 100.0]% |
| R2     | <i>Brucella melitensis</i> | 12/12 | 12/12 | 12/12 | 12/12 | 12/12 | 60/60 (100.0%)   | [94.0, 100.0]% |
| R3     | <i>Brucella suis</i>       | 12/12 | 12/12 | 12/12 | 12/12 | 12/12 | 60/60 (100.0%)   | [94.0, 100.0]% |
| All    |                            | 36/36 | 36/36 | 36/36 | 36/36 | 36/36 | 180/180 (100.0%) | [98.0, 100.0]% |

NOTE: Reproducibility display the *Brucella* species tested (*Brucella abortus*, *Brucella melitensis*, and *Brucella suis*). However, the VITEK MS will only provide a genus level identification of *Brucella* spp. in Myla.

c. *Linearity/assay reportable range:*

Not applicable, qualitative assay.

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

Calibrator: *E. coli* ATCC 8739 is used as a calibrator. This organism is deposited with VITEK MS-CHCA matrix on positions: xA1, xB1, xC1, of the VITEK MS-DS target slides depending on the number of samples tested (one calibrator per acquisition group of 16 spots). The VITEK MS goes to the calibration spot in an acquisition group and performs a calibration. If the calibration passes, the instrument goes to the first spot in the acquisition group. If the calibration fails, an error is reported and VITEK MS proceeds to the next acquisition group without collecting sample spectra. After spectra have been acquired from each sample spot in an acquisition group, the calibration spot is checked again. The calibration sample should provide *E. coli* identification at 99.9% in Myla software.

Stability:

See Section M. 1. i. below on *Brucella* stability

Controls:

During the reproducibility, proficiency, and clinical isolate testing, three organisms were used for positive quality control, with reagents alone (VITEK MS-FA and/or VITEK MS-CHCA) used for the negative control. Quality control organism were tested by VITEK MS each day a bacterium, yeast, or *Brucella* isolate was tested as well as with each new batch of VITEK MS-CHCA or VITEK MS-DS target slides. The quality control strains were as follows:

- *Brucella melitensis*, NR-256 (VITEK MS reports as *Brucella* spp)
- *Candida glabrata*, ATCC MYA-2950
- *Enterobacter aerogenes*, ATCC 13048
- Negative control (reagents alone)

A minimum of 20 replicates of each appropriate quality control strain was tested at each clinical study site. Result for quality control testing are presented in Table 6.

**Table 6. Quality Control Strains and Repeat Testing**

| QC Species                        | N   | 1 Repeat (Percent) | 2 Repeats (Percent) |
|-----------------------------------|-----|--------------------|---------------------|
| * <i>Brucella melitensis</i>      | 48  | 11 (22.9%)         | 5 (10.4%)           |
| <i>Candida glabrata</i>           | 51  | 0 (0.0%)           | 0 (0.0%)            |
| <i>Enterobacter aerogenes</i>     | 94  | 0 (0.0%)           | 0 (0.0%)            |
| Negative control (reagents alone) | 148 | 0 (0.0%)           | 0 (0.0%)            |
| Total                             | 341 | 11 (3.2%)          | 5 (1.5%)            |

\*Quality control result displays as *Brucella melitensis*. However, VITEK MS will only provide a genus level identification of *Brucella* spp in Myla.

e. *Detection limit:* See DEN130013 (K124067)

f. *Regression Study Comparing VITEK MS v3.0 KB v3.0.0 and v3.0 KB v3.2.0 (Biological Performance Equivalency Study)*

Identification performance of the new knowledge base (KB v3.2) was verified by comparing to spectra generated during the VITEK MS v3/KB v3.0.0 system development. A total of 209 well characterized strains (species or subspecies level) were tested from the 193 FDA claimed species: 179 samples representative of bacteria species (gram positive, gram negative) and 30 samples representative of fungi species (only yeast samples).

In addition, spectra that were acquired during the clinical validation of KB v3.0 were reprocessed with KB v3.2 in order to obtain new identification results. To assess if there was a between knowledge base regression, KB v3.2 results were compared to KB v3.0 results. A total of 2692 out of 2695 spectra that were acquired for KB v3.0 clinical studies were used to perform the regression testing (1508 moulds spectra, 802 *Mycobacterium* spectra, 382 *Nocardia* spectra). No Identification, Incorrect Identification, and Correct Identification were considered equivalent for both identification databases.

The overall correct identification rate is 94.6% (2549/2695) from VITEK MS KB v3.0 and 94.8% (2552/2692) from VITEK MS KB v3.2. Results are presented in Tables 7 and 8 below. The percentage of correct identification is similar between both KBs (0.22% difference) and therefore, no regression is observed with the new knowledge base release.

**Table 7. KB v3.2 Performance Using KB v3.0 Spectra**

| Organism            | Correct ID            |             |                     |            |             |             | Incorrect Identification |            |                       |            |           |            | No Identification |            |                              |            |                   |            | Total      |            |             |
|---------------------|-----------------------|-------------|---------------------|------------|-------------|-------------|--------------------------|------------|-----------------------|------------|-----------|------------|-------------------|------------|------------------------------|------------|-------------------|------------|------------|------------|-------------|
|                     | Correct Single Choice |             | Correct Low Discrim |            | Total       |             | Incorrect Single Choice  |            | Incorrect Low Discrim |            | Total     |            | Bad Spectrum      |            | Low Discrim Different Genera |            | No Matching Class |            |            | Total      |             |
|                     | N                     | %           | N                   | %          | N           | %           | N                        | %          | N                     | %          | N         | %          | N                 | %          | N                            | %          | N                 | %          |            | N          | %           |
| <b>Moulds</b>       | 1388                  | 92.0        | 26                  | 1.7        | 1414        | 93.8        | 15                       | 1.0        | 0                     | 0.0        | 15        | 1.0        | 10                | 0.7        | 9                            | 0.6        | 60                | 4.0        | 79         | 5.2        | 1508        |
| <b>Mycobacteria</b> | 766                   | 95.5        | 0                   | 0.0        | 766         | 95.5        | 3                        | 0.4        | 0                     | 0.0        | 3         | 0.4        | 4                 | 0.5        | 0                            | 0.0        | 29                | 3.6        | 33         | 4.1        | 802         |
| <b>Nocardia</b>     | 372                   | 97.4        | 0                   | 0.0        | 372         | 97.4        | 4                        | 1.0        | 0                     | 0.0        | 4         | 1.0        | 0                 | 0.0        | 0                            | 0.0        | 6                 | 1.6        | 6          | 1.6        | 382         |
| <b>Total</b>        | <b>2526</b>           | <b>93.8</b> | <b>26</b>           | <b>1.0</b> | <b>2552</b> | <b>94.8</b> | <b>22</b>                | <b>0.8</b> | <b>0</b>              | <b>0.0</b> | <b>22</b> | <b>0.8</b> | <b>14</b>         | <b>0.5</b> | <b>9</b>                     | <b>0.3</b> | <b>95</b>         | <b>3.5</b> | <b>118</b> | <b>4.4</b> | <b>2692</b> |

**Table 8. Global Performance for Both KB v3.0 and v3.2**

|                                 |  |   | Performance Including No ID Results |             | Performance Excluding No ID Results |             |
|---------------------------------|--|---|-------------------------------------|-------------|-------------------------------------|-------------|
|                                 |  |   | KB 3.0                              | KB 3.2      | KB 3.0                              | KB 3.2      |
| <b>Correct Identification</b>   | Correct Single Choice  | N | 2494                                | 2526        | 2494                                | 2526        |
|                                 |  | % | 92.5                                | 93.8        | 97.1                                | 98.1        |
|                                 | Correct Low Discrim  | N | 55                                  | 26          | 55                                  | 26          |
|                                 |  | % | 2.0                                 | 1.0         | 2.1                                 | 1.0         |
|                                 | <b>Total (Correct Single Choice + Correct Low Discrim)</b>   | N | <b>2549</b>                         | <b>2552</b> | <b>2549</b>                         | <b>2552</b> |
|                                 |  | % | <b>94.6</b>                         | <b>94.8</b> | <b>99.3</b>                         | <b>99.1</b> |
| <b>Incorrect Identification</b> | Incorrect Single Choice                                      | N | 19                                  | 22          | 19                                  | 22          |
|                                 |  | % | 0.7                                 | 0.8         | 0.7                                 | 0.9         |
|                                 | Incorrect Low Discrim  | N | 0                                   | 0           | 0                                   | 0           |
|                                 |  | % | 0.0                                 | 0.0         | 0.0                                 | 0.0         |
|                                 | <b>Total (Incorrect Single Choice + Correct Low Discrim)</b> | N | <b>19</b>                           | <b>22</b>   | <b>19</b>                           | <b>22</b>   |
|                                 |  | % | <b>0.7</b>                          | <b>0.8</b>  | <b>0.7</b>                          | <b>0.9</b>  |
| <b>No Identification</b>        | Bad Spectrum/ No Matching Class                              | N | 121                                 | 109         | -                                   | -           |
|                                 |  | % | 4.5                                 | 4.0         | -                                   | -           |
|                                 | Low Discrim: Different Genera                                | N | 6                                   | 9           | -                                   | -           |
|                                 |  | % | 0.2                                 | 0.3         | -                                   | -           |
|                                 | <b>Total</b>   | N | <b>127</b>                          | <b>118</b>  | -                                   | -           |
|                                 |  | % | <b>4.7</b>                          | <b>4.4</b>  | -                                   | -           |
| <b>Total Number of Spectra</b>  |  | N | 2695                                | 2692        | 2568                                | 2574        |

*g. Age of Culture Study for VITEK MS Testing*

An evaluation of different media and incubation times on *Brucella* identification results and score values was evaluated. A panel of *Brucella* species were grown on Columbia blood agar (CBA/COS), *Brucella* blood agar, and chocolate agar at different incubation times (2, 3, and 4 days) at two external development sites.

Results demonstrated that the culture media and the age of culture recommended for *Brucella* spp isolates for VITEK MS acquisition is either Columbia blood agar or *Brucella* blood agar with an incubation time of 2 to 4 days. Acceptability of chocolate agar cannot be concluded due to an insufficient number of spectra and limited incubation time data (n=23 spectra and only 2 days of incubation data available).

*h. Validation of Inactivation of Brucella Sample Preparation Study (Biological Slide Viability)*

The same preparation of *Brucella* spp. requires additional steps as compared to the standard VITEK MS procedure due to the infectious potential of this genera. Manipulation of *Brucella* isolates requires a BSL3/P3 laboratory and a safety cabinet. A set of three *Brucella* isolates were inoculated onto Columbia blood agar according to their growth requirements and incubated in appropriate conditions. The general inactivation procedure remained unchanged. To ensure that *Brucella* was inactivated completely, CHCA is added to the pelleted organism followed by vortexing. Ten microliters of the suspension was added to Trypticase Soy Broth (TSB) tubes and incubation followed for 3 days at 35-37°C in 5% CO<sub>2</sub> and then a re-incubation period

of 11 days at 35-37°C in 5% CO<sub>2</sub> (14 day total incubation). From both the 3-day and 14-day TSB cultures, 200µl was inoculated onto 10-15 CBA plates (60-75 plates total). Plates were incubated for 3, 7, and 14 days at 35-37°C in 5% CO<sub>2</sub>. *Brucella* samples were successfully inactivated using the designed *Brucella* protocol.

i. *Stability of Brucella Sample Preparation and Sample Deposits Study*

The stability of the *Brucella* sample preparation method prior to and following spotting on the target slide was evaluated (sample preparation stability, slide stability). *B. neotomae* was initially part of the testing protocol; however, this organism is not part of KB v3.2 and results were not included for analysis. In this stability study, *B. neotomae* cross-identified with other *Brucella* species; however, the VITEK MS will report *Brucella* spp. at the genus level.

For this study, eight inactivated samples were prepared for five *Brucella* spp. strains (including *B. neotomae*). Following addition of the CHCA matrix, the added matrix was removed without disturbing the pellet and pooled into a new tube. The pooled CHCA matrix was vortexed and dispensed into five separate tubes (15µl). Between each dispensation, the pooled matrix was vortexed to ensure uniform preparation in each tube. For preparation stability, one tube served as the control (T=0). The remaining sample preparation tubes were divided according to the following: one tube at worst case room temperature (30°C) for T=1 day, and three tubes refrigerated (2-8°C) for T=1, 4, and 7 days.

Sample extract storage at refrigerated temperatures for four and seven days generated several NoID results, indicating sample instability. Similarly, when sample extracts remained at room temperature for one day, testing showed poor agreement with the reference result. Overall, *Brucella* extract preparation is stable for one day at refrigerated temperature.

Further, testing demonstrated that *Brucella* sample deposits are stable for up to three days at room temperature on the target slide when using fresh sample preparation. In addition, when sample extracts were refrigerated for one day and then deposited on the target slide and read one and three days following deposit, results were acceptable.

j. *Demonstration of Non-Viability of Clostridium tetani Spores*

Due to reports of laboratory personnel exposure to *Clostridium tetani* cultures, a study was conducted to demonstrate non-viability of *C. tetani* spores after spotting and addition of the CHCA matrix on the VITEK MS target slide. Deposits on two target slides were performed in duplicate for a panel of five organisms. One slide was used for identification and the second slide was used for inactivation testing of the *C. tetani* spores. For the inactivation slide, a swab of the dried spot (after matrix addition) was inoculated on appropriate media and incubated for 18-24h, 3 days, and 7 days. Two of the five *C. tetani* strains grew after CHCA matrix addition following 3

days of incubation even when no spores were observed on Gram stain. These results indicated that CHCA did not inactivate the spores.

Inactivation protocols have been validated for each specific species they are intended for (e.g., *Brucella*, Mycobacteria, Moulds) and are dedicated to those species only. They must not be used to test any other species (including BSL-3 or spore forming bacteria). Direct preparation with CHCA matrix is insufficient for the inactivation of spore forming bacteria, such as *Clostridium tetani*.

k. *Internal and External Contamination of the VITEK MS Instrument*

A study was performed to determine if the VITEK MS instrument becomes contaminated following strain manipulation. Both external contamination including the door, slide, and plateholder and internal contamination of spare parts (accessed during annual maintenance) was evaluated. The strains used to assess contamination included *Salmonella* ser. Typhimurium and *Bacillus licheniformis* in its sporulative form. The door and plateholder were cleaned with 70% ethanol before testing. The baseline level of contamination before testing was evaluated by swabbing the door, plateholder, and slides (between spots). The two species were spotted on a target slide both with and without matrix, followed by laser firing on the spots. Possible external contamination during sample manipulation was evaluated by swabbing the slide, instrument door, and plateholder. Determining internal contamination involved swabbing of 21 instrument parts that the user cannot contact. Only during maintenance can these parts (i.e., slide adapter, sample stage, SAC, ion optics, flight tube turbo pump, SAC turbo pump, foreline trap sorbent, rotary pump) be accessed. For each sampling event, the swabs were plated on four different media plates.

No external contamination was found on the different tested parts except for the slide without CHCA which corresponded to the inoculated samples; however, this was expected and confirmed the inactivation power of the CHCA matrix. The Clinical Workflow User Manual has instructions on how to perform maintenance tasks to clean the outside of the instrument. Results of internal contamination testing showed only sporadic environmental contaminants on different internal parts and therefore, no risk of biological contamination.

l. *Analytical Specificity - Cross-Reactivity with Other Genera:*

Also see DEN130013 / K124067 and K162950

*Aggregatibacter/Haemophilus, Bordetella, Corynebacterium, Micrococcus, Ochrobactrum, Oligella, Pasteurella, Psychrobacter/Moraxella, Staphylococcus*  
study: In this study, a panel of 13 species represented by 21 strains (includes representative strains of each genus) were tested with VITEK MS V3, KB v3.2. Specific species were chosen from the abovementioned genera because they have been reported in the literature to be misidentified as *Brucella* species.

The specific sample preparation and inactivation procedure for *Brucella* (as described in section M.1.h.) was followed for each of the non-*Brucella* species mentioned previously. Each sample preparation was spotted in duplicate on a VITEK MS DS slide. These strains were tested in parallel using direct deposit. None of the tested strains were identified as *Brucella* spp., which is in agreement with the acceptance criterion. Additionally, the negative control gave the expected result of NoID.

Additional exclusivity testing was performed for BSL-3 organisms including *Bacillus anthracis*, *Yersinia pestis*, *Francisella tularensis*, *Burkholderia mallei*, and *Burkholderia pseudomallei*. These species are not currently included in the v3.2 KB; however, to demonstrate that there was no risk of cross-contamination between these BSL-3 pathogens and closely related species, exclusivity testing was conducted. Available RUO spectra for each of the abovementioned BSL-3 organisms were reprocessed using KB v3.2 and produced NoID results as expected. Overall, using this set of acquired RUO spectra, there was no cross-identification between *Bacillus anthracis*, *Yersinia pestis*, *Francisella tularensis* ssp. *holarctica*, *Burkholderia mallei*, and *Burkholderia pseudomallei* and other species present in KB v3.2.

The following claimed and unclaimed species were identified as cross-reacting with claimed organisms in KB v3.2 (See Tables 9 and 10 below). Please refer to previous clearances (DEN130013/K124067, K162950) for a complete list of cross identifications.

**Table 9. Cross-Identification of the VITEK MS of Claimed Displayed Taxa and Unclaimed Taxa**

| Clinial Claimed Displayed Taxon                | Reference ID of Unclaimed Taxa <sup>a</sup>    | # Cross-ID | # Tests | # Unique Isolates |
|--|--|------------|---------|-------------------|
| <i>Salmonella enterica</i> ssp <i>enterica</i> | <i>Salmonella enterica</i> ssp <i>arizonae</i> | 3          | 24      | 10                |
| <i>Shewanella putrefaciens</i>                 | <i>Shewanella baltica</i>                      | 1          | 1       | 1                 |
|  | <i>Shewanella xiamenensis</i>                  | 4          | 4       | 4                 |

<sup>a</sup> Unclaimed taxa include both species not included in the knowledge base or non-clinically validated species.

**Table 10. Cross-Identification of the VITEK MS Between Claimed Displayed Taxa**

| Clinial Claimed Displayed Taxon | Reference ID  | # Cross-ID | # Tests | # Unique Isolates |
|---------------------------------|---|------------|---------|-------------------|
| <i>Klebsiella pneumoniae</i>    | <i>Klebsiella variicola</i>   | 3          | 35      | 10                |
| <i>Serratia ficaria</i>         | <i>Serratia proteamaculans/grimesii/liquefaciens</i>                                | 1          | 1       | 1                 |
|                                 | <i>Serratia quinivorans/liquefaciens/proteamaculans/grimesii/myotis*/plymuthica</i> | 1          | 1       | 1                 |
|                                 | <i>Serratia grimesii</i>  | 1          | 28      | 3                 |
| <i>Serratia liquefaciens</i>    | <i>Serratia grimesii</i>  | 1          | 28      | 3                 |
|                                 | <i>Serratia quinivorans</i>   | 3          | 35      | 5                 |

\**Serratia myotis* is not in the database.

*m. Assay cut-off:*

After the calibration is accepted for an acquisition group, the VITEK MS acquires the spectra for the samples in that group. A perfect match between the spectrum and the

unique spectrum of a single organism or organism group would provide a percent probability of 99.9. Results are displayed as follows:

- A single identification is displayed with confidence value of 60 to 99.9 when one significant organism or organism group is retained.
- Low Discrimination identifications are displayed when more than one significant organism or organism group are retained, but not for more than four organisms. In this case, the sum of confidence values is equal to 100.
- When more than four organisms or organism groups are found, the organism is considered as non-identified. In this case, a list of possible organisms is displayed and the sum of confidence values is less than 100.
- When no match is found, the organism is considered as non-identified.

2. Comparison studies:

a. *Method comparison with predicate device:*

N/A

b. *Matrix comparison:*

N/A

3. Clinical studies:

a. *Clinical Sensitivity:*

*Challenge Study:* Fifteen well-characterized *Brucella* strains were evaluated for the challenge study. Each challenge organism was tested on the VITEK MS in triplicate. One trial site tested the *Brucella* challenge strains. Organism identifications were masked to the technologist performing the testing. Results from this study are summarized in Table 11 below.

**Table 11. Challenge Study Results with VITEK MS v3.2 Knowledge Base**

| Site | Organism             | # of Isolates Tested | Correct One Choice (OC) | Low Discrim (LD) Correct Genus | Correct OC + LD Correct Genus | Mis ID   | LD Incorrect Genus | MisID + LD Incorrect Genus | No ID         | No ID Multiple Genera | No ID + Multiple Genera |
|------|----------------------|----------------------|-------------------------|--------------------------------|-------------------------------|----------|--------------------|----------------------------|---------------|-----------------------|-------------------------|
| ATCC | <i>Brucella</i> spp. | 45                   | 64.4% (29)              | 0.0% (0)                       | 64.4% (29)                    | 0.0% (0) | 0.0% (0)           | 0.0% (0)                   | 35.6% (16/45) | 0.0% (0)              | 0.0% (0)                |

The objective of the clinical study was to evaluate the percent agreement of the VITEK MS in identifying microorganisms in a clinical setting as compared to the reference method. Each VITEK MS identification was compared to a reference identification determined by molecular sequencing supplemented as needed by additional testing or previously well-characterized strains were used. The following performance characteristics (see Table 12 below) were obtained for aerobic and

anaerobic Gram-positive and Gram-negative bacteria, including *Brucella*, and yeasts, at one external and one internal clinical trial site. For *Brucella*, clinical trial testing occurred at one external clinical trial site.

**Table 12. Overall Study Performance Results for Gram-positive bacteria, Gram-negative bacteria (including *Brucella* spp.), and Yeasts with VITEK MS v3.2 Knowledge Base**

| Organism Group         | N           | Number of Unique Isolates | Correct Identification (ID)            |  |   | Single Choice Incorrect ID <sup>1</sup> (no. of results) | No ID <sup>2</sup> (no. of results) |                |
|------------------------|-------------|---------------------------|--|--|---|--|-------------------------------------|----------------|
|                        |             |                           | Correct Single Choice (no. of results) | Low Discrim Correct Genus (no. of results) | Combined Correct Single Choice and Low Discrim Correct Genus (no. of results) |  |                                     |                |
| Gram-positive bacteria | Aerobic     | 801                       | 281                                    | 86.6% (694/801)                            | 12.7% (102/801)   | 99.4% (796/801)  | 0.0% (0/801)                        | 0.6% (5/801)   |
|                        | Anaerobic   | 693                       | 205                                    | 99.1% (687/693)                            | 0.1% (1/693)  | 99.3% (688/693)  | 0.0% (0/693)                        | 0.7% (5/693)   |
|                        | Total       | 1494                      | 486                                    | 92.4% (1381/1494)                          | 6.9% (103/1494)   | 99.3% (1484/1494)  | 0.0% (0/1494)                       | 0.7% (10/1494) |
| Gram-negative bacteria | Aerobic     | 2119                      | 570                                    | 92.6% (1962/2119)                          | 5.6% (118/2119)   | 98.2% (2080/2119)  | 0.6% (12/2119)                      | 1.3% (27/2119) |
|                        | Anaerobic   | 424                       | 72                                     | 99.3% (421/424)                            | 0.2% (1/424)  | 99.5% (422/424)  | 0.0% (0/424)                        | 0.5% (2/424)   |
|                        | Total       | 2543                      | 642                                    | 93.7% (2383/2543)                          | 4.7% (119/2543)   | 98.4% (2502/2543)  | 0.5% (12/2543)                      | 1.1% (29/2543) |
| Yeasts                 | Total       | 204                       | 44                                     | 99.5% (203/204)                            | 0.0% (0/204)  | 99.5% (203/204)  | 0.0% (0/204)                        | 0.5% (1/204)   |
| All                    | Grand Total | 4241                      | 1172                                   | 93.5% (3967/4241)                          | 5.2% (222/4241)   | 98.8% (4189/4241)  | 0.3% (12/4241)                      | 0.9% (40/4241) |

<sup>1</sup> The discordant column includes single choice incorrect identifications and low discrimination results with >1 choice in same genus but genus does not match the reference genus. See Single Choice Discordant (Incorrect) Results (Table 15) below.

<sup>2</sup> The No Identification column includes Low Discrimination with multiple genera or No ID (Bad Spectra, Not Enough Peaks, Too Many Peaks (Bad spectrum), or No ID (Good spectrum)).

**Table 13. Gram-positive Bacteria Performance with VITEK MS v3.2 Knowledge Base**

| Species                                  | Number of Unique Isolates | Correct Identification (ID)            |  |   | Discordant | No Identification |
|--|---------------------------|--|--|---|------------|-------------------|
|  |                           | Correct for Genus & Species (1 choice) | Low Discrimination (>1 Choice in Same Genus) | Combined (1 Choice + >1 Choice in Same Genus) |            |                   |
| <i>Actinomyces bovis</i>                 | 4                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                  | 0% (0/30)  | 0% (0/30)         |
| <i>Actinomyces israelii</i>              | 5                         | 93.3% (28/30)                          | 0% (0/30)                                    | 93.3% (28/30)                                 | 0% (0/30)  | 6.7% (2/30)       |
| <i>Actinomyces naeslundii</i>            | 4                         | 96.7% (29/30)                          | 0% (0/30)                                    | 96.7% (29/30)                                 | 0% (0/30)  | 3.3% (1/30)       |
| <i>Actinotignum schaalii</i>             | 14                        | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                  | 0% (0/30)  | 0% (0/30)         |
| <i>Bifidobacterium</i> spp               | 17                        | 100% (32/32)                           | 0% (0/32)                                    | 100% (32/32)                                  | 0% (0/32)  | 0% (0/32)         |
| <i>Clostridium baratii</i>               | 7                         | 100% (32/32)                           | 0% (0/32)                                    | 100% (32/32)                                  | 0% (0/32)  | 0% (0/32)         |
| <i>Clostridium beijerinckii</i>          | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                  | 0% (0/30)  | 0% (0/30)         |
| <i>Clostridium butyricum</i>             | 11                        | 100% (36/36) <sup>a</sup>              | 0% (0/36)                                    | 100% (0/36)                                   | 0% (0/36)  | 0% (0/36)         |
| <i>Clostridium cadaveris</i>             | 6                         | 100% (31/31)                           | 0% (0/31)                                    | 100% (0/31)                                   | 0% (0/31)  | 0% (0/31)         |
| <i>Clostridium innocuum</i>              | 17                        | 100% (32/32)                           | 0% (0/32)                                    | 100% (32/32)                                  | 0% (0/32)  | 0% (0/32)         |
| <i>Clostridium novyi</i>                 | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                  | 0% (0/30)  | 0% (0/30)         |
| <i>Clostridium septicum</i>              | 19                        | 97.1% (33/34)                          | 2.9% (1/34)                                  | 100% (34/34)                                  | 0% (0/34)  | 0% (0/34)         |
| <i>Clostridium sporogenes</i>            | 12                        | 100% (32/32)                           | 0% (0/32)                                    | 100% (32/32)                                  | 0% (0/32)  | 0% (0/32)         |
| <i>Clostridium tertium</i>               | 19                        | 100% (34/34) <sup>b</sup>              | 0% (0/34)                                    | 100% (34/34)                                  | 0% (0/34)  | 0% (0/34)         |
| <i>Clostridium tetani</i>                | 4                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                  | 0% (0/30)  | 0% (0/30)         |
| <i>Curtobacterium flaccumfaciens</i>     | 5                         | 100% (33/33)                           | 0% (0/33)                                    | 100% (33/33)                                  | 0% (0/33)  | 0% (0/33)         |
| <i>Enterococcus hirae</i>                | 16                        | 100% (31/31)                           | 0% (0/31)                                    | 100% (0/31)                                   | 0% (0/31)  | 0% (0/31)         |
| <i>Hathewayia histolytica</i>            | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                  | 0% (0/30)  | 0% (0/30)         |
| <i>Kocuria rhizophila</i>                | 8                         | 100% (33/33)                           | 0% (0/33)                                    | 100% (33/33)                                  | 0% (0/33)  | 0% (0/33)         |
| <i>Paenicostridium sordellii</i>         | 17                        | 100% (32/32)                           | 0% (0/32)                                    | 100% (32/32)                                  | 0% (0/32)  | 0% (0/32)         |
| <i>Paracostridium bifementans</i>        | 9                         | 100% (34/34)                           | 0% (0/34)                                    | 100% (34/34)                                  | 0% (0/34)  | 0% (0/34)         |
| <i>Propionibacterium acidipropionici</i> | 1                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                  | 0% (0/30)  | 0% (0/30)         |
| <i>Propionibacterium avidum</i>          | 14                        | 100% (34/34)                           | 0% (0/34)                                    | 100% (34/34)                                  | 0% (0/34)  | 0% (0/34)         |
| <i>Propionibacterium granulosum</i>      | 5                         | 96.7% (29/30)                          | 0% (0/30)                                    | 96.7% (29/20)                                 | 0% (0/30)  | 3.3% (1/30)       |
| <i>Propionibacterium propionicum</i>     | 5                         | 96.7% (29/30)                          | 0% (0/30)                                    | 96.7% (29/20)                                 | 0% (0/30)  | 3.3% (1/30)       |
| <i>Staphylococcus auricularis</i>        | 14                        | 100% (34/34)                           | 0% (0/34)                                    | 100% (34/34)                                  | 0% (0/34)  | 0% (0/34)         |
| <i>Staphylococcus chromogenes</i>        | 5                         | 100% (33/33)                           | 0% (0/33)                                    | 100% (33/33)                                  | 0% (0/33)  | 0% (0/33)         |
| <i>Staphylococcus hyicus</i>             | 7                         | 100% (32/32) <sup>c</sup>              | 0% (0/32)                                    | 100% (32/32)                                  | 0% (0/32)  | 0% (0/32)         |
| <i>Staphylococcus intermedius</i>        | 9                         | 0% (0/34)                              | 100% (34/34)                                 | 100% (34/34)                                  | 0% (0/34)  | 0% (0/34)         |
| <i>Staphylococcus pseudintermedius</i>   |                           |  |  |   |            |                   |
| <i>Staphylococcus kloosii</i>            | 7                         | 96.9% (31/32)                          | 0% (0/32)                                    | 96.9% (31/32)                                 | 0% (0/32)  | 3.1% (1/32)       |

| Species   | Number of Unique Isolates | Correct Identification (ID)            |  |  | Discordant | No Identification |
|---|---------------------------|--|--|--|------------|-------------------|
|   |                           | Correct for Genus & Species (1 choice) | Low Discrimination (>1 Choice in Same Genus) | Combined (1 Choice + > 1 Choice in Same Genus) |            |                   |
| <i>Staphylococcus lentus</i>                              | 8                         | 100% (33/33)                           | 0% (0/33)                                    | 100% (33/33)                                   | 0% (0/33)  | 0% (0/33)         |
| <i>Staphylococcus xylosus</i>                             | 12                        | 91.9% (34/37) <sup>d</sup>             | 0% (0/37)                                    | 91.9% (34/37)                                  | 0% (0/37)  | 8.1% (3/37)       |
| <i>Streptococcus alactolyticus</i>                        | 5                         | 100% (35/35)                           | 0% (0/35)                                    | 100% (35/35)                                   | 0% (0/35)  | 0% (0/35)         |
| <i>Streptococcus canis</i>                                | 28                        | 100% (33/33)                           | 0% (0/33)                                    | 100% (33/33)                                   | 0% (0/33)  | 0% (0/33)         |
| <i>Streptococcus cristatus</i>                            | 16                        | 100% (31/31)                           | 0% (0/31)                                    | 100% (31/31)                                   | 0% (0/31)  | 0% (0/31)         |
| <i>Streptococcus equi</i> ssp <i>equi</i>                 | 5                         | 100% (35/35)                           | 0% (0/35)                                    | 100% (35/35)                                   | 0% (0/35)  | 0% (0/35)         |
| <i>Streptococcus equi</i> ssp <i>zooepidemicus</i>        | 9                         | 0% (0/34)                              | 100% (34/34)                                 | 100% (34/34)                                   | 0% (0/34)  | 0% (0/34)         |
| <i>Streptococcus equinus</i>                              | 5                         | 96.9% (31/32)                          | 3.1% (1/32)                                  | 100% (32/32)                                   | 0% (0/32)  | 0% (0/32)         |
| <i>Streptococcus gallolyticus</i> ssp <i>pasteurianus</i> | 26                        | 100% (31/31)                           | 0% (0/31)                                    | 100% (31/31)                                   | 0% (0/31)  | 0% (0/31)         |
| <i>Streptococcus gordonii</i>                             | 19                        | 100% (34/34)                           | 0% (0/34)                                    | 100% (34/34)                                   | 0% (0/34)  | 0% (0/34)         |
| <i>Streptococcus parasanguinis</i>                        | 20                        | 100% (46/46)                           | 0% (0/46)                                    | 100% (46/46)                                   | 0% (0/46)  | 0% (0/46)         |
| <i>Streptococcus pseudoporcinus</i>                       | 20                        | 96.7% (29/30)                          | 3.3% (1/30)                                  | 100% (30/30)                                   | 0% (0/30)  | 0% (0/30)         |
| <i>Streptococcus sobrinus</i>                             | 7                         | 96.7% (29/30)                          | 0% (0/30)                                    | 96.7% (29/30)                                  | 0% (0/30)  | 3.3% (1/30)       |
| <i>Streptococcus suis</i>                                 | 5                         | 100% (33/33)                           | 0% (0/33)                                    | 100% (0/33)                                    | 0% (0/33)  | 0% (0/33)         |
| <i>Streptococcus uberis</i>                               | 8                         | 100% (33/33)                           | 0% (0/33)                                    | 100% (0/33)                                    | 0% (0/33)  | 0% (0/33)         |
| <i>Streptococcus vestibularis</i>                         | 17                        | 0% (32/32)                             | 100% (32/32)                                 | 100% (32/32)                                   | 0% (0/32)  | 0% (0/32)         |

<sup>a</sup> The reference method cannot differentiate between *Clostridium saccharoperbutylacetonicum* and *Clostridium butyricum*. 23/36 replicates (63.9%) had a multiple choice reference result and 13/36 replicates (36.1%) had a one choice reference result.

<sup>b</sup> The reference method cannot differentiate between *Clostridium chauvoei*, *Clostridium sartagoforme*, *Clostridium septicum* and *Clostridium tertium*. 2/34 replicates (5.9%) had a multiple choice reference result and 32/34 replicates (94.1%) had a one choice reference result.

<sup>c</sup> The reference method cannot differentiate between *Staphylococcus chromogenes*, *Staphylococcus agnetis*, *Staphylococcus lutrae*, *Staphylococcus delphini* and *Staphylococcus hyicus*. 2/32 replicates (6.3%) had a multiple choice reference result and 30/32 replicates (93.8%) had a one choice reference result.

<sup>d</sup> The reference method cannot differentiate between *Staphylococcus saprophyticus* and *Staphylococcus xylosus*. 2/37 replicates (5.4%) had a multiple choice reference result and 32/37 replicates (86.5%) had a one choice reference result.

**Table 14. Gram-negative Bacteria Performance with VITEK MS v3.2 Knowledge Base**

| Species                                  | Number of Unique Isolates | Correct Identification (ID)            |  |  | Discordant | No Identification |
|--|---------------------------|--|--|--|------------|-------------------|
|  |                           | Correct for Genus & Species (1 choice) | Low Discrimination (>1 Choice in Same Genus) | Combined (1 Choice + > 1 Choice in Same Genus) |            |                   |
| <i>Acinetobacter baumannii</i>           | 5                         | 100% (15/15)                           | 0% (0/15)                                    | 100% (15/15)                                   | 0% (0/15)  | 0% (0/15)         |
| <i>Acinetobacter calcoaceticus</i>       | 5                         | 100% (15/15)                           | 0% (0/15)                                    | 100% (15/15)                                   | 0% (0/15)  | 0% (0/15)         |
| <i>Acinetobacter johnsonii</i>           | 16                        | 100% (31/31)                           | 0% (0/31)                                    | 100% (31/31)                                   | 0% (0/31)  | 0% (0/31)         |
| <i>Acinetobacter nosocomialis</i>        | 5                         | 93.3% (14/15)                          | 6.7% (1/15)                                  | 100% (15/15)                                   | 0% (0/15)  | 0% (0/15)         |
| <i>Acinetobacter pittii</i>              | 5                         | 100% (15/15)                           | 0% (0/15)                                    | 100% (15/15)                                   | 0% (0/15)  | 0% (0/15)         |
| <i>Aeromonas hydrophila</i> <sup>a</sup> | 5                         | 100% (20/20)                           | 0% (0/20)                                    | 100% (20/20)                                   | 0% (0/20)  | 0% (0/20)         |
| <i>Aeromonas jandaei</i>                 | 5                         | 93.3% (28/30)                          | 6.7% (2/30)                                  | 100% (30/30)                                   | 0% (0/30)  | 0% (0/30)         |
| <i>Aeromonas punctata</i> (caviae)       | 5                         | 100% (20/20)                           | 0% (0/20)                                    | 100% (20/20)                                   | 0% (0/20)  | 0% (0/20)         |
| <i>Bacteroides eggertii</i>              | 4                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)  | 0% (0/30)         |
| <i>Bacteroides pyogenes</i>              | 5                         | 96.6% (28/29)                          | 0% (0/29)                                    | 96.6% (28/29)                                  | 0% (0/29)  | 3.4% (1/29)       |
| <i>Bacteroides stercoris</i>             | 10                        | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)  | 0% (0/30)         |
| <i>Bilophila wadsworthia</i>             | 6                         | 100% (31/31)                           | 0% (0/31)                                    | 100% (31/31)                                   | 0% (0/31)  | 0% (0/31)         |
| <i>Bordetella avium</i>                  | 6                         | 100% (31/31)                           | 0% (0/31)                                    | 100% (31/31)                                   | 0% (0/31)  | 0% (0/31)         |
| <i>Bordetella bronchiseptica</i>         | 9                         | 100% (34/34)                           | 0% (0/34)                                    | 100% (34/34)                                   | 0% (0/34)  | 0% (0/34)         |
| <i>Brevundimonas vesicularis</i>         | 8                         | 93.8% (30/32)                          | 0% (0/32)                                    | 93.8% (30/32)                                  | 0% (0/32)  | 6.3% (2/32)       |
| <i>Brucella</i> spp <sup>b, c, d</sup>   | 50                        | 91.7% (220/240)                        | 0% (0/240)                                   | 91.7% (220/240)                                | 0% (0/240) | 8.3% (20/240)     |
| <i>Burkholderia cenocepacia</i>          | 19                        | 100% (34/34)                           | 0% (0/34)                                    | 100% (34/34)                                   | 0% (0/34)  | 0% (0/34)         |
| <i>Burkholderia cepacia</i>              | 9                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)  | 0% (0/30)         |
| <i>Burkholderia contaminans</i>          | 6                         | 96.9% (31/32)                          | 3.1% (1/32)                                  | 100% (32/32)                                   | 0% (0/32)  | 0% (0/32)         |
| <i>Burkholderia gladioli</i>             | 18                        | 100% (33/33)                           | 0% (0/33)                                    | 100% (33/33)                                   | 0% (0/33)  | 0% (0/33)         |
| <i>Burkholderia vietnamiensis</i>        | 8                         | 100% (39/39)                           | 0% (0/39)                                    | 100% (39/39)                                   | 0% (0/39)  | 0% (0/39)         |

| Species                                       | Number of Unique Isolates | Correct Identification (ID)            |  |  | Discordant  | No Identification |
|---|---------------------------|--|--|--|-------------|-------------------|
|   |                           | Correct for Genus & Species (1 choice) | Low Discrimination (>1 Choice in Same Genus) | Combined (1 Choice + > 1 Choice in Same Genus) |             |                   |
| <i>Campylobacter rectus</i>                   | 6                         | 100% (32/32)                           | 0% (32/32)                                   | 100% (32/32)                                   | 0% (0/32)   | 0% (0/32)         |
| <i>Cedecea davisae</i>                        | 11                        | 100% (31/31)                           | 0% (0/31)                                    | 100% (31/31)                                   | 0% (0/31)   | 0% (0/31)         |
| <i>Cedecea lapagei</i>                        | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Cedecea neteri</i>                         | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Chryseobacterium gleum</i>                 | 12                        | 100% (32/32)                           | 0% (32/32)                                   | 100% (32/32)                                   | 0% (0/32)   | 0% (0/32)         |
| <i>Citrobacter farmeri</i>                    | 16                        | 93.5% (29/31)                          | 3.2% (1/31)                                  | 96.8% (30/31)                                  | 3.2% (1/31) | 0% (0/31)         |
| <i>Comamonas testosteroni</i>                 | 5                         | 100% (32/32)                           | 0% (32/32)                                   | 100% (32/32)                                   | 0% (0/32)   | 0% (0/32)         |
| <i>Cronobacter mytjensii</i>                  | 6                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Cronobacter turicensis</i>                 | 5                         | 96.7% (29/30)                          | 3.3% (1/30)                                  | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Delftia acidovorans</i>                    | 17                        | 100% (32/32)                           | 0% (32/32)                                   | 100% (32/32)                                   | 0% (0/32)   | 0% (0/32)         |
| <i>Elizabethkingia anophelis</i>              | 9                         | 94.1% (32/34)                          | 5.9% (2/34)                                  | 100% (34/34)                                   | 0% (0/34)   | 0% (0/34)         |
| <i>Elizabethkingia miricola</i>               | 9                         | 100% (34/34)                           | 0% (0/34)                                    | 100% (34/34)                                   | 0% (0/34)   | 0% (0/34)         |
| <i>Enterobacter hormaechei</i>                | 8                         | 78.8% (26/33)                          | 18.2% (6/33)                                 | 97.0% (32/33)                                  | 0% (0/33)   | 3.0% (1/33)       |
| <i>Enterobacter kobei</i>                     | 5                         | 33.3% (10/30)                          | 66.7% (20/30)                                | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Enterobacter ludwigii</i>                  | 6                         | 45.2% (14/31)                          | 54.8% (17/31)                                | 100% (31/31)                                   | 0% (0/31)   | 0% (0/31)         |
| <i>Escherichia vulneris</i>                   | 11                        | 100% (36/36)                           | 0% (0/36)                                    | 100% (36/36)                                   | 0% (0/36)   | 0% (0/36)         |
| <i>Fusobacterium mortiferum</i>               | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Fusobacterium periodonticum</i>            | 3                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (0/30)                                    | 0% (0/30)   | 0% (0/30)         |
| <i>Klebsiella variicola</i>                   | 10                        | 71.4% (25/35)                          | 20.0% (7/35)                                 | 91.4% (32/35)                                  | 8.6% (3/35) | 0% (0/35)         |
| <i>Kluyvera ascorbata</i>                     | 13                        | 100% (31/31)                           | 0% (0/31)                                    | 100% (31/31)                                   | 0% (0/31)   | 0% (0/31)         |
| <i>Kluyvera cryocrescens</i>                  | 6                         | 96.7% (29/30)                          | 0% (0/30)                                    | 96.7% (29/30)                                  | 3.3% (1/30) | 0% (0/30)         |
| <i>Kluyvera intermedia</i>                    | 9                         | 100% (34/34)                           | 0% (0/34)                                    | 100% (34/34)                                   | 0% (0/34)   | 0% (0/34)         |
| <i>Lelliottia amnigena</i>                    | 8                         | 100% (28/28)                           | 0% (0/28)                                    | 100% (0/28)                                    | 0% (0/28)   | 0% (0.28)         |
| <i>Mannheimia haemolytica</i>                 | 6                         | 100% (31/31)                           | 0% (0.31)                                    | 100% (0/31)                                    | 0% (0/31)   | 0% (0/31)         |
| <i>Moraxella lacunata</i>                     | 4                         | 0% (0/29)                              | 100% (29/29)                                 | 100% (0/29)                                    | 0% (0/29)   | 0% (0/29)         |
| <i>Moraxella nonliquefaciens</i>              | 13                        | 100% (31/31)                           | 0% (0/31)                                    | 100% (31/31)                                   | 0% (0/31)   | 0% (0/31)         |
| <i>Moraxella sloensis</i>                     | 15                        | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Myroides spp</i>                           | 10                        | 97.1% (34/35)                          | 0% (0/35)                                    | 97.1% (34/35)                                  | 0% (0/35)   | 2.9% (1/35)       |
| <i>Pantoea dispersa</i>                       | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Pasteurella aerogenes</i>                  | 7                         | 100% (32/32)                           | 0% (0/32)                                    | 100% (32/32)                                   | 0% (0/32)   | 0% (0/32)         |
| <i>Plesiomonas shigelloides</i>               | 13                        | 100% (33/33)                           | 0% (0/33)                                    | 100% (33/33)                                   | 0% (0/33)   | 0% (0/33)         |
| <i>Porphyromonas asaccharolytica/ uenonis</i> | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Porphyromonas gingivalis</i>               | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Prevotella loescheii</i>                   | 4                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Prevotella oralis</i>                      | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Prevotella oris</i>                        | 6                         | 100% (31/31)                           | 0% (0/31)                                    | 100% (31/31)                                   | 0% (0/31)   | 0% (0/31)         |
| <i>Proteus penneri</i>                        | 5                         | 100% (20/20)                           | 0% (0/20)                                    | 100% (20/20)                                   | 0% (0/20)   | 0% (0/20)         |
| <i>Proteus vulgaris</i>                       | 5                         | 100% (20/20)                           | 0% (0/20)                                    | 100% (20/20)                                   | 0% (0/20)   | 0% (0/20)         |
| <i>Providencia alcalifaciens</i>              | 13                        | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Providencia rustigianii</i>                | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Pseudomonas alcaligenes</i>                | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Pseudomonas luteola</i>                    | 15                        | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Pseudomonas mendocina</i>                  | 15                        | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Pseudomonas oryzihabitans<sup>c</sup></i>  | 20                        | 100% (30/30) <sup>c</sup>              | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Raoultella terrigena</i>                   | 5                         | 66.7% (20/30)                          | 33.3% (10/30)                                | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Serratia ficaria</i>                       | 7                         | 93.3% (28/30)                          | 0% (0/30)                                    | 93.3% (28/30)                                  | 6.7% (2/30) | 0% (0/30)         |
| <i>Serratia grimesii</i>                      | 3                         | 32.1% (9/28)                           | 50.0% (14/28)                                | 82.1% (23/28)                                  | 7.1% (2/28) | 10.7% (3/28)      |
| <i>Serratia plymuthica</i>                    | 4                         | 100% (28/28)                           | 0% (0/28)                                    | 100% (28/28)                                   | 0% (0/28)   | 0% (0/28)         |
| <i>Serratia proteamaculans</i>                | 4                         | 96.6% (28/29)                          | 3.4% (1/29)                                  | 100% (0/29)                                    | 0% (0/29)   | 0% (0/29)         |
| <i>Serratia quinivorans</i>                   | 5                         | 82.9% (29/35)                          | 8.6% (3/35)                                  | 91.4% (32/35)                                  | 8.6% (3/35) | 0% (0/35)         |
| <i>Serratia rubidaea</i>                      | 11                        | 100% (31/31)                           | 0% (0/31)                                    | 100% (0/31)                                    | 0% (0/31)   | 0% (0/31)         |
| <i>Shewanella putrefaciens</i>                | 1                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Tannerella forsythia</i>                   | 4                         | 96.8% (30/31)                          | 0% (0/31)                                    | 96.8% (30/31)                                  | 0% (0/31)   | 3.2% (1/31)       |
| <i>Veillonella dispar</i>                     | 4                         | 96.7% (29/30)                          | 3.3% (1/30)                                  | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Vibrio alginolyticus</i>                   | 6                         | 100% (34/34)                           | 0% (0/34)                                    | 100% (34/34)                                   | 0% (0/34)   | 0% (0/34)         |
| <i>Vibrio fluvialis</i>                       | 7                         | 90.6% (29/32)                          | 9.4% (2/32)                                  | 100% (32/32)                                   | 0% (0/32)   | 0% (0/32)         |
| <i>Vibrio metschnikovii</i>                   | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Vibrio mimicus</i>                         | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Yersinia aldovae</i>                       | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                   | 0% (0/30)   | 0% (0/30)         |
| <i>Yersinia ruckeri</i>                       | 5                         | 100% (31/31)                           | 0% (0/31)                                    | 100% (0/31)                                    | 0% (0/31)   | 0% (0/31)         |

<sup>a</sup> *Aeromonas hydrophila* ssp *dhakensis* and *Aeromonas hydrophila* ssp *ranae* are also correctly identified as *A. hydrophila*.

<sup>b</sup> On occasions the VITEK MS result for *Brucella* spp will report as a low discrimination result of *Brucella* spp/*Brucella* spp, even though it is a single choice correct identification of *Brucella* spp. This will be corrected in a future software release. See Table 18 for a break down of *Brucella* species No IDs.

<sup>c</sup> bioMérieux tested the following species reported in the literature to be misidentified to *Brucella* species: *Aggregatibacter aphrophilus*, *Bordetella bronchiseptica*, *Corynebacterium urealyticum*, *Haemophilus influenzae*, *Micrococcus luteus*, *Ochrobactrum intermedium*, *Ochrobactrum anthropi*, *Oligella urealytica*, *Pasteurella multocida*, *Pasteurella pneumotropica*, *Psychrobacter phenylpyruvicus*, *Staphylococcus aureus* and *Staphylococcus epidermidis*. In the study, no cross reactivity was observed using the *Brucella* sample preparation. All tested strains were identified to the expected species by direct deposit, and none of the strains were identified to *Brucella* species.

<sup>d</sup> *Bacillus anthracis*, *Yersinia pestis*, *Francisella tularensis* ssp. *holarctica*, *Burkholderia mallei* and *Burkholderia pseudomallei* species were tested using the VITEK MS V3.2 KB. No cross-identification with closely-related species were observed. These species are expected to provide an unidentified (No ID) result using the VITEK MS V3.2 KB.

<sup>e</sup> The reference method cannot differentiate between *Pseudomonas oryzae*, *Pseudomonas psychrotolerans* and *Pseudomonas oleovorans*. 2/30 replicates (6.7%) had a multiple choice reference result and 28/30 replicates (93.3%) had a one choice reference result.

**Table 15. Yeast Performance with VITEK MS v3.2 Knowledge Base**

| Species                                | Number of Unique Isolates | Correct Identification (ID)            |  |   | Discordant | No Identification |
|--|---------------------------|--|--|---|------------|-------------------|
|  |                           | Correct for Genus & Species (1 choice) | Low Discrimination (>1 Choice in Same Genus) | Combined (1 Choice + >1 Choice in Same Genus) |            |                   |
| <i>Candida auris</i>                   | 11                        | 97.2% (35/36)                          | 0% (0/36)                                    | 97.2% (36/36)                                 | 0% (0/36)  | 2.8% (1/36)       |
| <i>Candida duobushaemulonii</i>        | 6                         | 100% (36/36)                           | 0% (0/36)                                    | 100% (36/36)                                  | 0% (0/36)  | 0% (0/36)         |
| <i>Candida metapsilosis</i>            | 6                         | 100% (36/36)                           | 0% (0/36)                                    | 100% (0/36)                                   | 0% (0/36)  | 0% (0/36)         |
| <i>Candida orthopsilosis</i>           | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                  | 0% (0/30)  | 0% (0/30)         |
| <i>Cryptococcus gattii</i>             | 5                         | 100% (30/30)                           | 0% (0/30)                                    | 100% (30/30)                                  | 0% (0/30)  | 0% (0/30)         |
| <i>Trichosporon dermatis/mucooides</i> | 11                        | 100% (36/36) <sup>a</sup>              | 0% (0/36)                                    | 100% (36/36)                                  | 0% (0/36)  | 0% (0/36)         |

<sup>a</sup> 1/36 replicates (2.8%) had a multiple choice reference result and 35/36 replicates (97.2%) had a one choice reference result.

Table 16 below reflects the single choice discordant results associated with the addition of new organisms into the Knowledge Base (KB v3.2.0). Please refer to DEN130013/K124067 and K162950 for single choice discordants for previously cleared organisms.

**Table 16. Single Choice Discordants**

| Number of Isolates | Reference Result                                     | VITEK MS Result              |
|--------------------|--|------------------------------|
| 3                  | <i>Klebsiella variicola</i>                          | <i>Klebsiella pneumoniae</i> |
| 1                  | <i>Serratia grimesii</i>                             | <i>Serratia ficaria</i>      |
| 1                  | <i>Serratia proteamaculans/grimesii/liquefaciens</i> | <i>Serratia ficaria</i>      |

| Number of Isolates | Reference Result   | VITEK MS Result                 |
|--------------------|--|---------------------------------|
| 1                  | <i>Serratia quinivorans/liquefaciens/ proteamaculans/grimesii/myotis/ plymuthica</i> | <i>Serratia ficaria</i>         |
| 1                  | <i>Serratia grimesii</i>   | <i>Serratia liquefaciens</i>    |
| 3                  | <i>Serratia quinivorans</i>  | <i>Serratia liquefaciens</i>    |
| 1                  | <i>Kluyvera cryocrescens</i>   | <i>Citrobacter werkmanii</i>    |
| 1                  | <i>Citrobacter farmeri</i>   | <i>Citrobacter amalonaticus</i> |

**Table 17. Repeat Testing Rate by Organism in Clinical Study**

| Group           |           | Number of Samples Tested | Number of Samples- Same Extraction Tested (Repeat 1) | Number of Samples- New Extraction Tested (Repeat 2) |
|-----------------|-----------|--------------------------|--|---|
| Gram + Bacteria | Aerobic   | 801                      | 30 (3.7%)  | 16 (2.0%)   |
|                 | Anaerobic | 693                      | 23 (3.3%)  | 10 (1.4%)   |
|                 | Total     | 1494                     | 53 (3.5%)  | 26 (1.7%)   |
| Gram – Bacteria | Aerobic   | 2119                     | 142 (6.7%)   | 84 (4.0%)   |
|                 | Anaerobic | 424                      | 12 (2.8%)  | 10 (2.4%)   |
|                 | Total     | 2543                     | 154 (6.1%)   | 94 (3.7%)   |
| Yeasts          | Total     | 204                      | 4 (2.0%)   | 2 (1.0%)  |
| Unclaimed       | Total     | 65                       | 9 (13.8%)  | 8 (12.3%)   |
| All Organisms   | Total     | 4306                     | 220 (5.1%)   | 130 (3.0%)  |

**Table 18. Clinical, Challenge, and Reproducibility *Brucella* spp No ID Report**

| Study           | <i>Brucella</i> spp     | Total # of Samples Tested | # of Unique Strains | Number and Percent of No ID |                         |   | # of Unique Strains w/No ID Result |
|-----------------|-------------------------|---------------------------|---------------------|-----------------------------|-------------------------|---|------------------------------------|
|                 |                         |                           |                     | Initial Spot Read           | Re-Read of Initial Spot | Repeat Newly Inactivated Sample on New Spot |                                    |
| Challenge       | <i>B. abortus</i>       | 6                         | 2                   | 83.3% (5/6)                 | 83.3% (5/6)             | 83.3% (5/6)                                 | 2                                  |
|                 | <i>B. canis</i>         | 3                         | 1                   | 100.0% (3/3)                | 100.0% (3/3)            | 100.0% (3/3)                                | 1                                  |
|                 | <i>B. ceti</i>          | 6                         | 2                   | 16.7% (1/6)                 | 16.7% (1/6)             | 16.7% (1/6)                                 | 1                                  |
|                 | <i>B. melitensis</i>    | 6                         | 2                   | 16.7% (1/6)                 | 16.7% (1/6)             | 16.7% (1/6)                                 | 1                                  |
|                 | <i>B. ovis</i>          | 6                         | 2                   | 83.3% (5/6)                 | 83.3% (5/6)             | 83.3% (5/6)                                 | 2                                  |
|                 | <i>B. papionis</i>      | 6                         | 2                   | 0.0% (0/6)                  | NA                      | NA  | 0                                  |
|                 | <i>B. pinnipedialis</i> | 6                         | 2                   | 0.0% (0/6)                  | NA                      | NA  | 0                                  |
|                 | <i>B. suis</i>          | 6                         | 2                   | 16.7% (1/6)                 | 16.7% (1/6)             | 16.7% (1/6)                                 | 1                                  |
| Clinical        | <i>B. abortus</i>       | 30                        | 13                  | 0.0% (0/30)                 | NA                      | NA  | 0                                  |
|                 | <i>B. canis</i>         | 30                        | 6                   | 70.0% (21/30)               | 50.0% (15/30)           | 26.7% (8/30)                                | 2                                  |
|                 | <i>B. ceti</i>          | 30                        | 5                   | 16.7% (5/30)                | 3.3% (1/30)             | 3.3% (1/30)                                 | 1                                  |
|                 | <i>B. melitensis</i>    | 30                        | 6                   | 23.3% (7/30)                | 6.7% (2/30)             | 3.3% (1/30)                                 | 1                                  |
|                 | <i>B. ovis</i>          | 30                        | 5                   | 36.7% (11/30)               | 33.3% (10/30)           | 26.7% (8/30)                                | 4                                  |
|                 | <i>B. papionis</i>      | 30                        | 2                   | 36.7% (11/30)               | 36.7% (11/30)           | 3.3% (1/30)                                 | 1                                  |
|                 | <i>B. pinnipedialis</i> | 30                        | 5                   | 13.3% (4/30)                | 3.3% (1/30)             | 0.0% (0/30)                                 | 0                                  |
|                 | <i>B. suis</i>          | 30                        | 8                   | 36.7% (11/30)               | 3.3% (1/30)             | 3.3% (1/30)                                 | 1                                  |
| Reproducibility | <i>B. abortus</i>       | 60                        | 1                   | 16.7% (10/60)               | 13.3% (8/60)            | 0.0% (0/60)                                 | 0                                  |
|                 | <i>B. melitensis</i>    | 60                        | 1                   | 18.3% (11/60)               | 6.7% (4/60)             | 0.0% (0/60)                                 | 0                                  |
|                 | <i>B. suis</i>          | 60                        | 1                   | 13.3% (8/60)                | 6.7% (4/60)             | 0.0% (0/60)                                 | 0                                  |
| All             | <i>Brucella</i> spp     | 465                       | 50*                 | 24.7% (115/465)             | 15.7% (73/465)          | 7.7% (36/465)                               | 17                                 |

\*The number is less than the sum of all the unique strains in each type of study since the same strains were used across all studies.

b. Clinical specificity:

See clinical sensitivity section above.

*c. Other clinical supportive data (when a. and b. are not applicable):*

4. Clinical cut-off:

N/A

5. Expected values/Reference range:

See M.1.c.

**N. Instrument Name :**

VITEK MS

**O. System Descriptions :**

1. Modes of Operation:

Does the applicant's device contain the ability to transmit data to a computer, webserver, or mobile device?

Yes \_\_\_X\_\_\_ or No \_\_\_\_\_

Does the applicant's device transmit data to a computer, webserver, or mobile device using wireless transmission?

Yes \_\_\_X\_\_\_ or No \_\_\_\_\_

2. Software:

FDA has reviewed applicant's Hazard Analysis and software development processes for this line of product types:

Yes \_\_\_X\_\_\_ or No \_\_\_\_\_

a. FDA has reviewed the applicant's cybersecurity processes and were found to be acceptable.

b. The following software has remained unchanged from VITEK MS v2 (DEN130013 / K124067):

- VITEK MS Sample Prep Station software
- Myla Middleware

#### VITEK MS Acquisition Station:

There was an update to the VITEK MS Acquisition Station in K162950 from v1.4.2 to v1.5.0. The most significant change to the Acquisition Station algorithms in v1.5.0 was the rastering strategy. As the spectrum is acquired for each target spot, it is visible in the Spectrum Display on the Acquisition Screen with the number of profiles incrementing as they are collected. In the Acquisition Station v1.5.0, the acquisition process stops when the target of 100 good profiles is achieved, or when all raster points have been visited. If the final total of good profiles is less than 30 then the acquisition has failed, and if more than 30 good profiles are obtained then the spectrum is acceptable.

No updates to the VITEK MS Acquisition Station or software occurred with the VITEK MS v3.0 KB v3.2.

#### VITEK MS Analysis Server and VITEK MS Computation Engine:

The computation server consists of three components – Brice v1.1., MSCE v1.2., and the KB v3.2.0. Brice and MSCE are the modules used to compute identification results based on the algorithms and knowledge bases within the knowledge set (i.e. KSets).

For the VITEK MS KB v3.2 update, Brice remains unchanged. However, the VITEK MS v3 / KB v3.2.0 update includes an update to the VITEK MS computation engine (MSCE), a subcomponent of the VITEK MS Analysis Server. To communicate with the Knowledge Base, the MSCE uses the MatLab library which was updated to assure the MSCE is compatible with the new hardware platforms used by bioMérieux for its systems. The MSCE was updated from v1.1 to v1.2 and as a result, the VITEK MS Analysis Server was updated from v1.4.1 to v1.4.3.

#### 3. Specimen Identification:

Same as DEN130013 (K124067).

#### 4. Specimen Sampling and Handling:

Cultures of *Brucella* species must be processed and inactivated before spotting to the target slide in a BSL-3 facility and safety cabinet.

#### 5. Calibration:

See Section M.1.c. above

#### 6. Quality Control:

See Section M.1.c. above

**P. Other Supportive Instrument Performance Characteristics Data Not Covered In The “Performance Characteristics” Section above:**

N/A

**Q. Proposed Labeling:**

The labeling supports the finding of substantial equivalence for this device.

**R. Conclusion:**

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