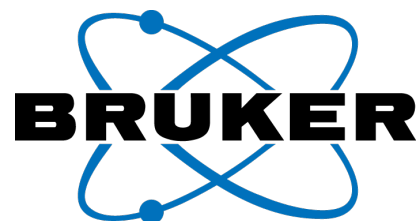


Bruker MALDI Biotyper Identification Results



Run Info:

Run Identifier: 210813-1138-10199
Comment:
Operator: MALDI@FLEX-PC
Run Creation Date/Time: 2021-08-13T11:43:12.136
Number of Tests: 7
Type: Standard
BTS-QC: not present
BTS-QC Position:
Instrument ID: 269944.01064
Server Version: 4.1.100 (PYTH) 174 2019-06-158_01-16-09

Result Overview

Sample Name	Sample ID	Organism (best match)	Score Value	Organism (second-best match)	Score Value
H2 (+++)(A)	DT KA 1 (Standard)	Streptococcus salivarius	2.03	Streptococcus salivarius	1.89
H3 (+++)(A)	DT KA 2 (Standard)	Streptococcus parasanguinis	2.15	Streptococcus parasanguinis	2.10
H4 (+)(B)	DT KA 3 (Standard)	Neisseria subflava	1.78	No Organism Identification Possible	1.69
H5 (+++)(A)	DT COKO 1 (Standard)	Haemophilus parainfluenzae	2.28	Haemophilus parainfluenzae	2.19
H6 (+++)(A)	DT COKO 2 (Standard)	Haemophilus sputorum	2.04	Haemophilus sputorum	1.97
H7 (+)(A)	DT COKO 2 (Standard)	Haemophilus sputorum	1.97	Haemophilus sputorum	1.81
H8 (-)(C)	XXX (Standard)	no peaks found	0.00	no peaks found	0.00

Matching Hints

Matched Pattern	Comment
Streptococcus mitis DSM 12643T BRB	Streptococcus mitis / oralis / peroris / pneumoniae / pseudopneumoniae are closely related! The result may be confirmed by a further test, e.g. bile test or optochin test, according to standard clinical microbiological practice.
Streptococcus oralis NRZ 26417 NRZ	Streptococcus mitis / oralis / peroris / pneumoniae / pseudopneumoniae are closely related! The result may be confirmed by a further test, e.g. bile test or optochin test, according to standard clinical microbiological practice.
Streptococcus peroris DSM 12493T DSM	Streptococcus mitis / oralis / peroris / pneumoniae / pseudopneumoniae are closely related! The result may be confirmed by a further test, e.g. bile test or optochin test, according to standard clinical microbiological practice.

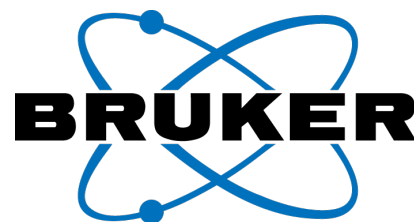
Meaning of Score Values

Range	Interpretation	Symbols	Color
2.00 - 3.00	High-confidence identification	(+++)	green
1.70 - 1.99	Low-confidence identification	(+)	yellow
0.00 - 1.69	No Organism Identification Possible	(-)	red

Meaning of Consistency Categories (A - C)

Category	Interpretation
(A)	High consistency: The best match is a high-confidence identification. The second-best match is (1) a high-confidence identification in which the species is identical to the best match, (2) a low-confidence identification in which the species or genus is identical to the best match, or (3) a non-identification.
(B)	Low consistency: The requirements for high consistency are not met. The best match is a high- or low-confidence identification. The second-best match is (1) a high- or low-confidence identification in which the genus is identical to the best match or (2) a non-identification.
(C)	No consistency: The requirements for high or low consistency are not met.

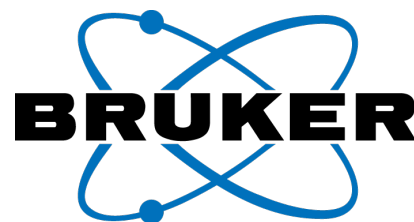
Sample 1



Sample Name: H2
Sample Description:
Sample ID: DT KA 1
Sample Creation Date/Time: 2021-08-13T11:41:06.113
Sample Type: Standard
Identification Method: MALDI Biotyper MSP Identification Standard Method 1.1
Preprocessing Method: MALDI Biotyper Preprocessing Standard Method 1.1
ACQ Method: D:\Methods\flexControlMethods\MBT_FC.par
AutoXecute Method: MBT_AutoX
Consistency Category (based on 2 best matches): A
Applied Taxonomy Tree: Bruker Taxonomy

Rank (Quality)	Matched Pattern	Score Value	NCBI Identifier
1 (+++)	Streptococcus salivarius 0807M25049501 IBS	<u>2.03</u>	<u>1304</u>
2 (+)	Streptococcus salivarius DSM 20560T DSM	<u>1.89</u>	<u>1304</u>
3 (+)	Streptococcus vestibularis CCUG 51352 CCUG	<u>1.88</u>	<u>1343</u>
4 (+)	Streptococcus salivarius ssp salivarius 140417_01 ETL	<u>1.79</u>	<u>1304</u>
5 (+)	Streptococcus salivarius DSM 20560T BRB	<u>1.73</u>	<u>1304</u>
6 (+)	Streptococcus vestibularis DSM 5636T DSM_2	<u>1.70</u>	<u>1343</u>
7 (-)	Streptococcus vestibularis 14147704_2 MVD	<u>1.67</u>	<u>1343</u>
8 (-)	Streptococcus salivarius IBS_MS_23 IBS	<u>1.65</u>	<u>1304</u>
9 (-)	Streptococcus vestibularis CCUG 61229 CCUG	<u>1.56</u>	<u>1343</u>
10 (-)	Streptococcus salivarius DSM 20067 DSM	<u>1.51</u>	<u>1304</u>

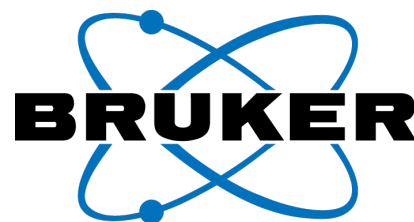
Sample 2



Sample Name: H3
Sample Description:
Sample ID: DT KA 2
Sample Creation Date/Time: 2021-08-13T11:41:06.114
Sample Type: Standard
Identification Method: MALDI Biotyper MSP Identification Standard Method 1.1
Preprocessing Method: MALDI Biotyper Preprocessing Standard Method 1.1
ACQ Method: D:\Methods\flexControlMethods\MBT_FC.par
AutoExecute Method: MBT_AutoX
Consistency Category (based on 2 best matches): A
Applied Taxonomy Tree: Bruker Taxonomy

Rank (Quality)	Matched Pattern	Score Value	NCBI Identifier
1 (+++)	Streptococcus parasanguinis 15001036_2 MVD	2.15	1318
2 (+++)	Streptococcus parasanguinis 14148475_4 MVD	2.10	1318
3 (+++)	Streptococcus parasanguinis 14137939_2 MVD	2.09	1318
4 (+++)	Streptococcus parasanguinis DSM 6778T DSM_2	2.06	1318
5 (+++)	Streptococcus parasanguinis CCUG 55521 CCUG	2.02	1318
6 (+)	Streptococcus parasanguinis CS 50_4 BRB	1.99	1318
7 (+)	Streptococcus parasanguinis 15025560_1 MVD	1.92	1318
8 (+)	Streptococcus mitis DSM 12643T BRB	1.88	28037
9 (+)	Streptococcus oralis NRZ 26417 NRZ	1.87	1303
10 (+)	Streptococcus peroris DSM 12493T DSM	1.85	68891

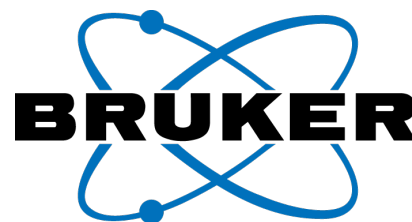
Sample 3



Sample Name: H4
Sample Description:
Sample ID: DT KA 3
Sample Creation Date/Time: 2021-08-13T11:41:06.114
Sample Type: Standard
Identification Method: MALDI Biotyper MSP Identification Standard Method 1.1
Preprocessing Method: MALDI Biotyper Preprocessing Standard Method 1.1
ACQ Method: D:\Methods\flexControlMethods\MBT_FC.par
AutoXecute Method: MBT_AutoX
Consistency Category (based on 2 best matches): B
Applied Taxonomy Tree: Bruker Taxonomy

Rank (Quality)	Matched Pattern	Score Value	NCBI Identifier
1 (+)	Neisseria subflava CCUG 29402 CCUG	1.78	28449
2 (-)	Neisseria flavescens C1 2 PGM	1.69	484
3 (-)	Neisseria flavescens DSM 17633T DSM	1.63	484
4 (-)	Neisseria subflava DSM 17610T DSM_2	1.58	28449
5 (-)	Neisseria subflava CCUG 30607 CCUG	1.57	28449
6 (-)	Neisseria subflava CCUG 32186 CCUG	1.56	28449
7 (-)	Neisseria sp[2] 0807M15057901 IBS	1.56	482
8 (-)	Neisseria subflava CCUG 24850 CCUG	1.51	28449
9 (-)	Neisseria perflava DSM 18009T DSM	1.46	33053
10 (-)	Neisseria subflava DSM 17610T DSM	1.42	28449

Sample 4



Sample Name: H5
Sample Description:
Sample ID: DT COKO 1
Sample Creation Date/Time: 2021-08-13T11:41:06.115
Sample Type: Standard
Identification Method: MALDI Biotyper MSP Identification Standard Method 1.1
Preprocessing Method: MALDI Biotyper Preprocessing Standard Method 1.1
ACQ Method: D:\Methods\flexControlMethods\MBT_FC.par
AutoXecute Method: MBT_AutoX
Consistency Category (based on 2 best matches): A
Applied Taxonomy Tree: Bruker Taxonomy

Rank (Quality)	Matched Pattern	Score Value	NCBI Identifier
1 (+++)	Haemophilus parainfluenzae 21086307 MLD	2.38	729
2 (+++)	Haemophilus parainfluenzae CIP 102513T CTL	2.19	729
3 (+++)	Haemophilus parainfluenzae CIP 102204 CIP	2.17	729
4 (+++)	Haemophilus parainfluenzae VP 58646 BOM	2.14	729
5 (+++)	Haemophilus parainfluenzae P2bue_re2AN USH	2.12	729
6 (+++)	Haemophilus parainfluenzae VA05021_10 ERL	2.05	729
7 (+)	Haemophilus parainfluenzae VP 58974 BOM	1.98	729
8 (+)	Haemophilus parainfluenzae CIP 102169 CIP	1.95	729
9 (+)	Haemophilus parainfluenzae DSM 8978T DSM	1.86	729
10 (-)	Haemophilus parainfluenzae CIP 102202 CIP	1.64	729

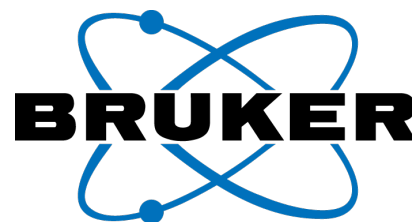
Sample 5



Sample Name: H6
Sample Description:
Sample ID: DT COKO 2
Sample Creation Date/Time: 2021-08-13T11:41:06.115
Sample Type: Standard
Identification Method: MALDI Biotyper MSP Identification Standard Method 1.1
Preprocessing Method: MALDI Biotyper Preprocessing Standard Method 1.1
ACQ Method: D:\Methods\flexControlMethods\MBT_FC.par
AutoXecute Method: MBT_AutoX
Consistency Category (based on 2 best matches): A
Applied Taxonomy Tree: Bruker Taxonomy

Rank (Quality)	Matched Pattern	Score Value	NCBI Identifier
1 (+++)	Haemophilus sputorum DSM 24472T DSM	2.04	724
2 (+)	Haemophilus sputorum 15104186 MMCA	1.97	724
3 (-)	Haemophilus parainfluenzae VP 58646 BOM	1.63	729
4 (-)	Haemophilus parahaemolyticus VP 58684 BOM	1.57	735
5 (-)	Haemophilus parahaemolyticus DSM 21417T DSM	1.48	735
6 (-)	Haemophilus parahaemolyticus VP 59343 BOM	1.46	735
7 (-)	Haemophilus parahaemolyticus VP 58628 BOM	1.40	735
8 (-)	Haemophilus parainfluenzae VA05021_10 ERL	1.39	729
9 (-)	Mannheimia haemolytica ISU 29322 ISUV	1.37	75985
10 (-)	Haemophilus pittmaniae VA15632_10 ERL	1.36	249188

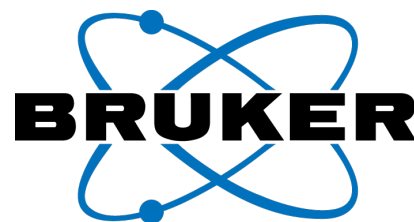
Sample 6



Sample Name: H7
Sample Description:
Sample ID: DT COKO 2
Sample Creation Date/Time: 2021-08-13T11:41:06.116
Sample Type: Standard
Identification Method: MALDI Biotyper MSP Identification Standard Method 1.1
Preprocessing Method: MALDI Biotyper Preprocessing Standard Method 1.1
ACQ Method: D:\Methods\flexControlMethods\MBT_FC.par
AutoXecute Method: MBT_AutoX
Consistency Category (based on 2 best matches): A
Applied Taxonomy Tree: Bruker Taxonomy

Rank (Quality)	Matched Pattern	Score Value	NCBI Identifier
1 (+)	Haemophilus sputorum DSM 24472T DSM	1.97	724
2 (+)	Haemophilus sputorum 15104186 MMCA	1.81	724
3 (+)	Haemophilus parainfluenzae 21086307 MLD	1.70	729
4 (-)	Haemophilus parainfluenzae CIP 102204 CIP	1.68	729
5 (-)	Haemophilus parainfluenzae CIP 102513T CTL	1.64	729
6 (-)	Haemophilus parainfluenzae VP 58646 BOM	1.59	729
7 (-)	Haemophilus parainfluenzae VA05021_10 ERL	1.55	729
8 (-)	Haemophilus parainfluenzae P2bue_re2AN USH	1.51	729
9 (-)	Haemophilus parahaemolyticus VP 58628 BOM	1.43	735
10 (-)	Haemophilus haemolyticus DN636 SLH	1.41	726

Sample 7



Sample Name: H8
Sample Description:
Sample ID: XXX
Sample Creation Date/Time: 2021-08-13T11:41:06.116
Sample Type: Standard
Identification Method: MALDI Biotyper MSP Identification Standard Method 1.1
Preprocessing Method: MALDI Biotyper Preprocessing Standard Method 1.1
ACQ Method: D:\Methods\flexControlMethods\MBT_FC.par
AutoExecute Method: MBT_AutoX
Consistency Category (based on 2 best matches): C
Applied Taxonomy Tree: Bruker Taxonomy

Rank (Quality)	Matched Pattern	Score Value	NCBI Identifier
1 (-)	no peaks found	<u>0.00</u>	-
2 (-)	no peaks found	<u>0.00</u>	-
3 (-)	no peaks found	<u>0.00</u>	-
4 (-)	no peaks found	<u>0.00</u>	-
5 (-)	no peaks found	<u>0.00</u>	-
6 (-)	no peaks found	<u>0.00</u>	-
7 (-)	no peaks found	<u>0.00</u>	-
8 (-)	no peaks found	<u>0.00</u>	-
9 (-)	no peaks found	<u>0.00</u>	-
10 (-)	no peaks found	<u>0.00</u>	-