

es

- SP100 Stenotrophomonas maltophilia
- SP101 Parasutterella excrementihominis
- SP104 Mucispirillum schaedleri
- SP107 Robinsoniella sp._strain_[D2-1X-13]
- SP11 Enterococcus gallinarum;
- SP113 Lachnospiraceae_[G-14] bacterium_MOT-185
- SP114 Staphylococcus hominis;_
- SP117 Paracoccus laevigulosivorans
- SP119 Enterobacter sp._MOT-050
- SP12 Faecalibaculum rodentium
- SP12 Adlercreutzia muris
- SP122 Corynebacterium pilbarensis
- SP123 Erysipelatoclostridium_[Clostridium]_cocleatum
- SP127 Acidipropionibacterium thoenii
- SP13 Cutibacterium acnes
- SP130 Coprococcus sp._strain_[1XD21-23]
- SP139 Eubacteriales_[G-1] bacterium_MOT-159
- SP140 Absiella sp._strain_[1XD42-72]
- SP141 Anaerotignum sp._strain_[1XD42-85]
- SP142 Clostridium chromiireducens
- SP146 Roseburia sp._strain_[MGB-1]
- SP15 Lactobacillus johnsonii;_
- SP156 Oscillospiraceae_[G-3] bacterium_MOT-150
- SP157 Shigella flexneri;_
- SP16 Limosilactobacillus fermentum
- SP167 Eubacteriales_[G-4] bacterium_MOT-164
- SP17 Enterococcus faecalis
- SP174 Salmonella enterica
- SP178 Eubacteriales_[G-2] bacterium_MOT-162
- SP18 Mordavella sp._strain_[D2-1X-71]
- SP185 Enterococcus olivae
- SP188 Lachnoclostridium sp._strain_[1XD42-54]
- SP2 Streptococcus sp._MOT-012
- SP22 Oscillospiraceae_[G-7] bacterium_MOT-154
- SP23 Corynebacterium tuberculostearicum
- SP235 Trichococcus pasteurii;_
- SP26 Staphylococcus ureilyticus;_
- SP3 Ligilactobacillus murinus
- SP30 Peptoniphilus lacydonensis
- SP31 Shigella boydii;_
- SP32 Cutibacterium granulosum
- SP33 Phyllobacterium myrsinacearum
- SP36 Finegoldia magna
- SP37 Escherichia coli;_
- SP371 Tessaracoccus aquimaris
- SP4 Enterococcus camelliae
- SP40 Actinomyces polyneisensis
- SP41 Escherichia fergusonii;_
- SP46 Kineothrix sp._strain_[1XD8-87]
- SP48 Oscillibacter sp._strain_[128x]
- SP49 Alkalibacterium pelagium
- SP5 Shigella sonnei;_
- SP50 Akkermansia muciniphila
- SP51 Duncaniella freteri
- SP52 Clostridium disporicum;_
- SP58 Limosilactobacillus reuteri
- SP59 Lactobacillus intestinalis
- SP60 Romboutsia ilealis;_
- SP63 Anaerobium sp._strain_[C-37]
- SP64 Alistipes sp._MOT-127
- SP66 Streptococcus mitis;_
- SP7 Mammaliococcus sciuri
- SP70 Anaerotignum sp._strain_[D2-1X-72]
- SP72 Streptococcus chosunense
- SP73 Corynebacterium mucifaciens
- SP75 Paracoccus mangrovi
- SP76 Marvinbryantia sp._strain_[D2-1X-79]
- SP84 Achromobacter pulmonis;_
- SP85 Listeria monocytogenes
- SP89 Acutalibacter muris
- SP90 Lachnospiraceae_[G-1] bacterium_MOT-166
- SP91 Eisenbergiella sp._strain_[1XD8-92]
- SP92 Ruminococcus sp._strain_[C-28]
- SP94 Pseudomonas aestus
- SP98 Mammaliococcus lentus
- SPN1009 Lachnospiraceae_[G-7] bacterium_MOT-172_nov_94.617%
- SPN1020 Duncaniella freteri_nov_89.463%
- SPN1037 Streptococcus danieliae_nov_97.379%
- SPN1063 Actinomyces polyneisensis_nov_97.183%
- SPN108 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_97.015%
- SPN1101 Actinomyces polyneisensis_nov_94.153%
- SPN1146 Streptococcus danieliae_nov_93.952%
- SPN1181 Duncaniella freteri_nov_88.577%
- SPN120 Alistipes senegalensis_nov_93.483%
- SPN1220 Cutibacterium granulosum_nov_96.788%
- SPN1253 Lachnospiraceae_[G-7] bacterium_MOT-172_nov_91.770%
- SPN1292 Duncaniella freteri_nov_89.780%
- SPN132 Muribaculaceae_[G-2] bacterium_MOT-104_nov_88.911%
- SPN1332 Wolinella succinogenes_nov_80.044%
- SPN1406 Salinibacillus xinjiangensis_nov_86.160%
- SPN144 Lachnospiraceae_[G-6] bacterium_MOT-171_nov_94.179%
- SPN1450 Lachnospiraceae_[G-12] bacterium_MOT-180_nov_89.676%
- SPN150 Streptococcus danieliae_nov_95.582%
- SPN1521 Duncaniella freteri_nov_86.373%
- SPN156 Duncaniella freteri_nov_95.510%
- SPN1565 Alkalibacterium olivapovliticus_nov_97.595%
- SPN161 Eisenbergiella massiliensis_nov_85.744%
- SPN1638 Muribaculaceae_[G-1] bacterium_MOT-129_nov_88.200%
- SPN168 Glucerbacter canis_nov_93.542%
- SPN1682 Lacrimispora xylanolytica_nov_94.398%
- SPN1754 Duncaniella freteri_nov_91.515%
- SPN1799 Lachnoclostridium_[Clostridium]_aminophilum_nov_86.983%
- SPN180 Duncaniella freteri_nov_92.121%
- SPN1869 Duncaniella freteri_nov_86.922%
- SPN192 Acetivibrio sp._strain_[D16-59]_nov_90.812%
- SPN204 Muribaculaceae_[G-1] bacterium_MOT-129_nov_85.972%
- SPN206 Oscillospiraceae_[G-6] bacterium_MOT-153_nov_91.684%
- SPN218 Duncaniella freteri_nov_90.982%
- SPN229 Phocaecicola massiliensis_nov_93.509%
- SPN240 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_95.745%
- SPN252 Muribaculaceae_[G-1] bacterium_MOT-129_nov_86.720%
- SPN264 Bariatricus massiliensis_nov_89.506%
- SPN278 Eubacteriales_[G-1] bacterium_MOT-159_nov_81.420%
- SPN285 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_97.228%
- SPN29 Anaerotignum sp._strain_[1XD42-85]_nov_97.098%
- SPN295 Pseudoflavonifractor sp._strain_[136x]_nov_93.407%
- SPN306 Muribaculaceae_[G-2] bacterium_MOT-104_nov_87.873%
- SPN318 Muribaculaceae_[G-1] bacterium_MOT-129_nov_91.870%
- SPN321 Blautia hominis_nov_89.583%
- SPN332 Kineothrix alysoides_nov_89.855%
- SPN344 Coprococcus sp._strain_[1XD21-23]_nov_95.595%
- SPN356 Murimonas sp._strain_[WYJ26-X68]_nov_93.873%
- SPN368 Duncaniella freteri_nov_87.298%
- SPN380 Lachnospiraceae_[G-6] bacterium_MOT-171_nov_92.931%
- SPN392 Lachnospiraceae_[G-7] bacterium_MOT-172_nov_93.320%
- SPN396 Cellulomonas bogoriensis_nov_97.872%
- SPN404 Anaerocolumna cellulositytica_nov_86.071%
- SPN416 Eisenbergiella sp._strain_[1XD8-92]_nov_97.309%
- SPN428 Eubacterium coprostanoligenes_nov_91.667%
- SPN442 Turicibacter sanguinis_nov_95.949%
- SPN443 Alistipes senegalensis_nov_93.522%
- SPN454 Magnetovibrio blakemorei_nov_83.259%
- SPN466 Muribaculaceae_[G-1] bacterium_MOT-129_nov_85.111%
- SPN478 Duncaniella freteri_nov_87.273%
- SPN526 Muribaculaceae_[G-2] bacterium_MOT-104_nov_88.340%
- SPN538 Anaerotaenia torta_nov_88.773%
- SPN540 Muricomes intestini_nov_89.648%
- SPN549 Lachnoclostridium_[Clostridium]_polysaccharolyticum_nov_92.946%
- SPN561 Streptococcus danieliae_nov_96.787%
- SPN562 Duncaniella freteri_nov_87.976%
- SPN573 Duncaniella freteri_nov_87.976%
- SPN585 Duncaniella freteri_nov_94.898%
- SPN597 Lachnoclostridium_[Clostridium]_herbivorans_nov_92.562%
- SPN609 Lachnoclostridium_[Clostridium]_scindens_nov_89.300%
- SPN621 Eubacterium coprostanoligenes_nov_91.489%
- SPN625 Lachnospiraceae_[G-3] bacterium_MOT-168_nov_93.776%
- SPN633 Lachnospiraceae_[G-3] bacterium_MOT-168_nov_94.606%
- SPN644 Phoceia massiliensis_nov_89.787%
- SPN655 Anaeromassilibacillus senegalensis_nov_93.008%
- SPN666 Anaerotignum sp._strain_[D2-1X-45]_nov_96.205%
- SPN677 Duncaniella freteri_nov_91.952%
- SPN679 Eubacteriales_[G-1] bacterium_MOT-161_nov_97.881%
- SPN690 Lachnoclostridium_[Clostridium]_polysaccharolyticum_nov_90.496%
- SPN702 Adlercreutzia equolifaciens_nov_89.530%
- SPN714 Faecalicatena fissicatena_nov_94.824%
- SPN726 Clostridium disporicum_nov_97.849%
- SPN738 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_92.537%
- SPN743 Muribaculaceae_[G-2] bacterium_MOT-104_nov_89.264%
- SPN749 Lachnospiraceae_[G-6] bacterium_MOT-171_nov_95.218%
- SPN762 Cutibacterium acnes_nov_96.815%
- SPN773 Lachnospiraceae_[G-11] bacterium_MOT-178_nov_95.344%
- SPN785 Fusicatenaibacter saccharivorans_nov_88.912%
- SPN798 Muribaculaceae_[G-2] bacterium_MOT-104_nov_89.703%
- SPN799 Adlercreutzia equolifaciens_nov_96.983%
- SPN81 Prevotella shahii_nov_87.903%
- SPN810 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_92.766%
- SPN82 Streptococcus danieliae_nov_93.387%
- SPN822 Lachnospiraceae_[G-14] bacterium_MOT-183_nov_97.868%
- SPN832 Adlercreutzia caecimuris_nov_89.270%
- SPN844 Streptococcus danieliae_nov_96.774%
- SPN855 Lachnospiraceae_[G-14] bacterium_MOT-183_nov_94.670%
- SPN859 Lachnospiraceae_[G-11] bacterium_MOT-177_nov_95.679%
- SPN866 Eubacterium coprostanoligenes_nov_90.213%
- SPN878 Anaerocolumna cellulositytica_nov_91.909%
- SPN902 Marinisporobacter balticus_nov_82.839%
- SPN913 Duncaniella freteri_nov_88.668%
- SPN914 Murimonas sp._strain_[WYJ26-X68]_nov_94.105%
- SPN926 Eisenbergiella sp._strain_[1XD8-92]_nov_92.841%
- SPN935 Anaerocolumna cellulositytica_nov_90.683%
- SPN947 Beduini massiliensis_nov_86.708%
- SPN95 Lachnospiraceae_[G-14] bacterium_MOT-185_nov_95.949%
- SPN959 Phoceia massiliensis_nov_89.787%
- SPN972 Pilibacter termitis_nov_90.581%
- SPN975 Lachnospiraceae_[G-11] bacterium_MOT-177_nov_92.608%
- SPN984 Duncaniella freteri_nov_93.750%
- SPN996 Anaerocolumna xylanovorans_nov_88.212%
- SPP100 Streptococcus mitis_pneumoniae_pseudopneumoniae
- SPP110 Bacillus halotolerans_spizizenii
- SPP18 Staphylococcus argenteus_aureus_rotterdamii
- SPP19 Staphylococcus capitis_epidermidis
- SPP3 Enterococcus casseliflavus_gallinarum
- SPP33 Lactobacillus johnsonii_taiwanensis
- SPP42 Agrobacterium_Rhizobium_lusitanum_rhizogenes
- SPP54 Staphylococcus saprophyticus_xylosum
- SPP65 Achromobacter aegrifaciens_insuavis
- SPP74 Burkholderia contaminans_lata_multivorans
- SPP78 Burkholderia_Caenibaculum_aenigmatica_baiyandianus_cepacia_contaminans_diffu...(8 s
- SPP79 Burkholderia_aenigmatica_cepacia_contaminans_lata_multivorans
- SPP97 Escherichia_Shigella_albertii_sonnei
- SPPN31 Faecalicatena multispecies_sppn31_2_nov_93.802%
- SPPN9 Faecalicatena multispecies_sppn9_2_nov_93.568%