

>ZB05141030(XJ-1)-A1-M13-

TCCTACGGGAGGCAGCAGTCGGGAATTTTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGGATGAT
GAAGGCCTTAGGGTTGTAATAATCCTTTTCGTCAGGGACGATAATGACGGTACCTGAAGAAGAAGCCCCGGCTAA
CTTCGTGCCAGCAGCCGCGTAAT

- + domain Bacteria (0/20/1459456)
- + phylum "Proteobacteria" (0/20/418265)
- + class Alphaproteobacteria (0/20/88104)
- + order Caulobacterales (0/2/5084)
- + family Hyphomonadaceae (0/2/1610)
- + unclassified_Alphaproteobacteria (0/15/5054)
- [S002500928](#) not_calculated 0.883 1338 uncultured alpha proteobacterium; Ppss_Ma40; JF421149
- [S002903729](#) not_calculated 0.883 1298 uncultured alpha proteobacterium; HG-B02221; JN409270
- [S002904822](#) not_calculated 0.883 1312 uncultured bacterium; MPB1-64; AB630446
- [S002904826](#) not_calculated 0.877 1301 uncultured bacterium; MPB1-68; AB630450
- [S002972327](#) not_calculated 0.883 1346 uncultured alpha proteobacterium; E06L-1; HE614839

>ZB05141031(XJ-2)-A1-M13-

TCCTACGGGAGGCAGCAGTGAGGAATATTGGTCAATGGGCGCAAGCCTGAACCAGCCATGCCGCGTGCAGGAT
GACGGTCCTATGGATTGTAACCTGCTTTTGTACGGGAAGAAACACTCCTACGAGTAGGAGCCTGACGGTACCGT
AAGAATAAGGATCGGCTAACTCCGTGCCAGCAGCCGCGGTAAT

- + domain Bacteria (0/20/1459456)
- + phylum "Bacteroidetes" (0/20/177857)
- + class Flavobacteriia (0/20/48280)
- + order "Flavobacteriales" (0/20/48280)
- + family Flavobacteriaceae (0/20/29549)
- + genus Flavobacterium (0/20/4440)
- [S001098092](#) not_calculated 0.922 1314 Flavobacterium denitrificans; JS14-1; EU599190
- [S001327996](#) not_calculated 0.917 1398 Flavobacterium sp. TISTR 1610; AB465579
- [S001327997](#) not_calculated 0.917 1403 Flavobacterium sp. TISTR 1602; AB465580
- [S002035054](#) not_calculated 0.933 1395 Flavobacterium phragmitis; BLN_2; GU564236

>ZB05141032(XJ-3)-A1-M13-

TCCTACGGGAGGCAGCAGTAGGGAATTTTGCGCAATGGAGGAACTCTGACGCAGCAACGCCATGTGTGGGAT
GAAGCATTTCCGGTGTGTAACCCTGTCAGCAGGGAATAAAAGGTCGCCTCGCGGCCACTGAATGTACCTGC
AAAGGAAGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAAT

- + domain Bacteria (0/20/1459456)
- + unclassified_Bacteria (0/20/34557)
- [S000933198](#) not_calculated 0.773 1278 uncultured bacterium; FFCH12636; EU134604
- [S002195654](#) not_calculated 0.851 1322 uncultured bacterium; E2006TS6.35; GU983350
- [S002695007](#) not_calculated 0.768 1277 uncultured bacterium; ncd2021a05c1; JF175074
- [S002697389](#) not_calculated 0.768 1270 uncultured bacterium; ncd2060d08c1; JF177456

[S002893909](#) not_calculated 0.840 1349 uncultured bacterium; TX2_1021; JN177914

>ZB05141033(XJ-4)-A1-M13-

TATTACCGCGGCTGCTGGCACGTAGTTAGCCGTGGCTTATTACCGGGTACCTTCAAGTTCACGCATGGGATT
TTTATCCCCGGCAAAGCAGTTTACAACCCAGAAGGCCTTCTTCCTGCACGCGGCATGGCTGGTTCAGACTTG
CATCCATTGACCAATATTCCTACTGCTGCCTCCCGTAGG

- + domain Bacteria (0/20/1459456)
- + phylum "Bacteroidetes" (0/20/177857)
- + class "Bacteroidetes"_incertae_sedis (0/20/1617)
- + genus Ohtaekwangia (0/20/846)

[S001266288](#) - not_calculated 0.923 1299 uncultured Sphingobacteriales bacterium; AMJE10; AM934896
[S001266293](#) - not_calculated 0.929 1293 uncultured Sphingobacteriales bacterium; AMJF3; AM934901
[S001266297](#) - not_calculated 0.923 1299 uncultured Sphingobacteriales bacterium; AMJF8; AM934905
[S001266380](#) - not_calculated 0.923 1294 uncultured Sphingobacteriales bacterium; AMLG11; AM934988
[S001267856](#) - not_calculated 0.929 1275 uncultured Sphingobacteriales bacterium; CM38D11; AM936464

>ZB05141034(XJ-5)-A1-M13-

TCCTACGGGAGGCAGCAGTGGGGAATTTGCGCAATGGGCTAACGCCTGACGCAGCAACGCCGCGTGGAGGAT
GAAGGTCTTTGGATTGTAAACTCCTGTGTCAGCAGGGAAGGGAGTGGGCCTAATACGTCGCCAACTTGATTGT
ACCTGCAGAGGAAGCCCCGGCTAACTCTGTGCCAGCAGCCGCGTAAT

- + domain Bacteria (0/20/1459456)
- + phylum "Acidobacteria" (0/20/15997)
- + class Acidobacteria_Gp7 (0/20/446)
- + genus Gp7 (0/20/446)

[S001407496](#) not_calculated 0.904 1276 uncultured bacterium; nbw774f12c1; GQ016556
[S001598443](#) not_calculated 0.914 1408 uncultured bacterium; AK4AB1_10F; GQ396911
[S002508697](#) not_calculated 0.909 1352 uncultured Acidobacteria bacterium; QZ-B68; JF776898
[S002876698](#) not_calculated 0.898 1429 uncultured bacterium; 2f05; JF979346
[S002887682](#) not_calculated 0.904 1382 uncultured Acidobacteria bacterium; M-B249; JN038969

>ZB05141035(XJ-6)-A1-M13-

TATTACCGCGGCTGCTGGCACGAAGTTAGCCGGGGCTTCCTTGCAGGTACATTCAACTGCCTCCGAAGAGACC
ATTTATCCCTGTGACAGTGGTTTACACACCGAAATGCTTCATCCACACATGGCGTTGCTGCGTCAGATTTTC
CTCCATTGCGCAAATTCCTACTGCTGCCTCCCGTAGG

- + domain Bacteria (0/20/1459456)
- + unclassified_Bacteria (0/20/34557)

[S000933198](#) - not_calculated 0.821 1278 uncultured bacterium; FFCH12636; EU134604
[S002195654](#) - not_calculated 0.827 1322 uncultured bacterium; E2006TS6.35; GU983350
[S002695007](#) - not_calculated 0.765 1277 uncultured bacterium; ncd2021a05c1; JF175074

[S002893909](#) - not_calculated 0.899 1349 uncultured bacterium; TX2_1021; JN177914

[S002894364](#) - not_calculated 0.927 1424 uncultured bacterium; TX2_5J03; JN178369

>ZB05141036(XJ-7)-A1-M13-

TATTACCGCGGCTGCTGGCACAGAGTTAGCCGGTGCTTCTTCTGTGAGTAACATCATCCGCCATTGGTATTAACA
ATGGCCTCTTTCTCCCCACTGAAAGTGCTTTACAACCCTCAGGCCTTCTTACACACGCGGCATTGCTGGATCA
GGCTTGCGCCACTGTCCAATATTTCCCCACTGCTGCCTCCCGTAGG

+ domain Bacteria (0/20/1459456)

+ phylum "Proteobacteria" (0/20/418265)

+ class Gammaproteobacteria (0/20/198197)

+ order Legionellales (0/4/1471)

+ family Coxiellaceae (0/4/715)

+ genus Coxiella (0/4/368)

[S000830387](#) - not_calculated 0.755 1320 uncultured Methylococcaceae bacterium; Elev_16S_1037;
EF019533

[S002189518](#) - not_calculated 0.750 1321 uncultured bacterium; Llo_014; FR667312

[S003451402](#) - not_calculated 0.788 1303 uncultured bacterium; T30-An-20C-9; JX105588

[S004244955](#) - not_calculated 0.739 1380 uncultured bacterium; smkt_G-pro_012_002; AB806792

>ZB05141037(XJ-8)-A1-M13-

TATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTATTCTAGGGTACCAGTCAGTCTCTTTAGAAAAAGAG
GTTTCGTCCCCTATAAAAGAAGTTTACAATCCAGAGGACCTTCATCCTTCACGCGGCATGGCTGGTTCAGACTT
GCGTCCATTGACCAATATTCCTTACTGCTGCCTCCCGTAGG

+ domain Bacteria (0/20/1459456)

+ phylum "Bacteroidetes" (0/20/177857)

+ class Sphingobacteriia (0/20/17689)

+ order "Sphingobacteriales" (0/20/17689)

+ family Chitinophagaceae (0/20/4875)

+ genus Flavisolibacter (0/20/343)

[S000544377](#) - not_calculated 0.978 1380 uncultured bacterium; 21BSF3; AJ863256

[S001191728](#) - not_calculated 0.885 1388 uncultured bacterium; sl1307; EU244045

[S001192260](#) - not_calculated 0.885 1388 uncultured bacterium; sls1324; EU376237

[S002083376](#) - not_calculated 1.000 1288 uncultured bacterium; ncd553f01c1; HM278350

[S002134949](#) - not_calculated 0.874 1283 uncultured bacterium; ncd941e07c1; HM329923

>ZB05141038(XJ-9)-A1-M13-

TCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGGGCAACCCTGATCCAGCAATGCCGCGTGTGTGAA
GAAGGCCTGCGGGTTGTAAAGCACTTTCAGAGGGGAAGAAAAATTGGAGCTAACACCTCCGATCTTGACGTT
ACCCTTAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGTAAT

+ domain Bacteria (0/20/1459456)

+ phylum "Proteobacteria" (0/20/418265)

+ class Gammaproteobacteria (0/20/198197)

+ unclassified_Gammaproteobacteria (0/20/14896)

[S000493193](#) not_calculated 0.930 1310 uncultured gamma proteobacterium; AKYG1556;

AY921959

[S000493321](#) not_calculated 0.930 1312 uncultured gamma proteobacterium; AKYH1000;
AY922087

[S000493399](#) not_calculated 0.930 1313 uncultured gamma proteobacterium; AKYH885;
AY922165

[S000854373](#) not_calculated 1.000 1378 uncultured soil bacterium; MK6;

[S001800395](#) not_calculated 1.000 1409 uncultured bacterium; 2y-73; FJ444687

>ZB05141039(XJ-10)-A1-M13-

TCCTACGGGAGGCAGCAGTAGGGAATATTGGTCAATGGATGCAAGTCTGAACCAGCCATGCCGCGTGCAGGAA
GAAGGCCCTATGGGTTGTAAACTGCTTTTGCCAGGGGATAAAACGAGCATGCGTGCTTAATTGAAGGTACCTGG
TGAATAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAAT

+ domain Bacteria (0/20/1459456)

+ phylum "Bacteroidetes" (0/20/177857)

+ class "Bacteroidetes"_incertae_sedis (0/20/1617)

+ genus Ohtaekwangia (0/20/846)

[S000932249](#) not_calculated 0.907 1283 uncultured bacterium; FFCH599; EU133655

[S000932262](#) not_calculated 0.880 1230 uncultured bacterium; FFCH10617; EU133668

[S000932307](#) not_calculated 0.913 1334 uncultured bacterium; FFCH12631; EU133713

[S000944222](#) not_calculated 0.880 1362 uncultured bacterium; CK06-06_Mud_MAS4B-12;
AB369181

>ZB05141040(XJ-11)-A1-M13-

TCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGGGAAACCCTGATCCAGCGACGCCGCGTGGGTGAT
GAAGGCCTTCGGGTCGTAAAGCCCTGTCTGGGGGACGAATCCCCTGCCGGTGAACAATCGGCAGGAATGACG
GTACCTTCAAAGGAAGCACC GGCTAACTCTGTGCCAGCAGCCGCGGTAAT

+ domain Bacteria (0/20/1459456)

+ phylum "Proteobacteria" (0/20/418265)

+ class Deltaproteobacteria (0/18/30263)

+ order Myxococcales (0/1/3299)

+ unclassified_Deltaproteobacteria (0/17/6433)

[S000932930](#) not_calculated 0.842 1312 uncultured bacterium; FFCH2225; EU134336

[S000933293](#) not_calculated 0.784 1267 uncultured bacterium; FFCH6210; EU134699

[S001234328](#) not_calculated 0.889 1437 uncultured bacterium; p9j07ok; FJ478475

[S001234559](#) not_calculated 0.842 1430 uncultured bacterium; p7p03ok; FJ478706

>ZB05141041(XJ-12)-A1-M13-

TCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAA
GAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGCGGTGCGGTTAATAACCGCGCCGATTGACGT
TACCCGCAGAAGAAGCACC GGCTAACTCCGTGCCAGCAGCCGCGGTAAT

+ domain Bacteria (0/20/1459456)

+ phylum "Proteobacteria" (0/20/418265)

+ class Gammaproteobacteria (0/20/198197)

+ order "Enterobacteriales" (0/20/47931)

+ family Enterobacteriaceae (0/20/47931)

+ genus Pantoea (0/20/1644)

[S000333636](#) not_calculated 1.000 1397 Pantoea stewartii subsp. stewartii; 0028; AY642383

[S000514043](#) not_calculated 1.000 1406 Pantoea agglomerans; XW131; AY941841

[S000691536](#) not_calculated 1.000 1315 Pantoea sp. BD 639; DQ512489

[S000722635](#) not_calculated 1.000 1288 Pantoea sp. BD 500; DQ849042

[S000722636](#) not_calculated 1.000 1296 Pantoea sp. BD 502; DQ849043

>ZB05141042(XJ-13)-A1-M13-

CCTACGGGAGGCAGCAGTGGGGAATTGTTTCGCAATGGGCGCAAGCCTGACGACGCAACGCCGCGTGGAGGAC
GAAGATCTTCGGGTCGTAACCTCTGTCGAGTGGGAAGAACATCTTTCCGATGAATATTCGGAGAGACTGACGG
TACCACTAAAGGAAGCCCCGGCCAACTCCGTGCCAGCAGCCGCGTAAT

+ domain Bacteria (0/20/1459456)

+ phylum "Acidobacteria" (0/20/15997)

+ class Acidobacteria_Gp6 (0/20/4463)

+ genus Gp6 (0/20/4463)

[S000144968](#) not_calculated 0.831 1361 uncultured Acidobacterium sp.; KCM-C-55; AJ581627

[S000493217](#) not_calculated 0.831 1309 uncultured Acidobacteria bacterium; AKYG1751;
AY921983

[S000493346](#) not_calculated 0.915 1315 uncultured Acidobacteria bacterium; AKYH1441;
AY922112

[S000500777](#) not_calculated 0.847 1461 uncultured Acidobacteria bacterium; 23k22; AY281352

>ZB05141043(XJ-14)-A1-M13-

TATTACCGCGGCTGCTGGCACGTAGTTAGCCGTGGCTTCTTCCTCAGGTACCGTCATTATCGTCCCTGAGAAAAG
AGGTTTACAACCCGAAGGCCTTCATCCCTCACGCGGCGTTGCTGCGTCAGACTTTCGTCCATTGCGCAAAATTC
CCGACTGCTGCTCCCGTAGG

+ domain Bacteria (0/20/1459456)

+ phylum "Chloroflexi" (0/13/22092)

+ unclassified_"Chloroflexi" (0/13/9347)

[S000493143](#) - not_calculated 0.884 1284 uncultured Chloroflexi bacterium; AKYH943; AY921909

[S000829439](#) - not_calculated 0.902 1282 uncultured bacterium; Amb_16S_854; EF018585

[S001565917](#) - not_calculated 0.909 1352 uncultured bacterium; F2_63X2; GQ263112

[S002124329](#) - not_calculated 0.896 1244 uncultured bacterium; ncd352d01c1; HM319303

>ZB05141044(XJ-15)-A1-M13-

TCCTACGGGAGGCAGCAGTAGGGAATATTGCACAATGGACGAAAGTCTGATGCAGCGACGCCGCGTGAGTGAT
GAAGGCCTTCGGGTCGTAACCTCTGTGATAGGGGAAGATGATGACGGTACCCTATCAGAAAGGACCGGCTAA
CTACGTGCCAGCAGCCGCGTAAT

+ domain Bacteria (0/20/1459456)

+ phylum "Proteobacteria" (0/15/418265)

+ class Deltaproteobacteria (0/14/30263)

+ order Bdellovibrionales (0/10/1804)

+ family Bdellovibrionaceae (0/10/1139)

+	genus Bdellovibrio (0/10/274)			
S000344657	not_calculated	0.854	1394	Bdellovibrio sp. oral clone CA006; AF385539
S000840660	not_calculated	0.695	1381	uncultured bacterium; FCPT447; EF516218
S002495818	not_calculated	0.701	1382	uncultured bacterium; LJ-J64; JF319240
S002501426	not_calculated	0.701	1416	uncultured bacterium; B55; JF429081
S002648890	not_calculated	0.787	1271	uncultured bacterium; ncd1561c04c1; JF128957