

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

TCCTACGGGAGGCAGCAGTCGGAATTTTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGGATGAT
GAAGGCCTTAGGGTTGTAAATCCTTTTCGTCAGGGACGATAATGACGGTACCTGAAGAAGAAGCCCCGGCTAA
CTTCGTGCCAGCAGCCGCGGTAAT

+	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
GACGGTCCTATGGATTGTAACTGCTTTTGTACGGGAAGAAACACTCCTACGAGTAGGAGCCTGACGGTACCGT
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-

TCCTACGGGAGGCAGCAGTAGGGAATTTTGC GCAATGGAGGAACTCTGACGCAGCAACGCCATGTGTGGGAT
GAAGCATTTTCGGTGTGTAAACCACTGTCAGCAGGGAATAAAAGGTCGCCTCGGCGGCACTTGAATGTACCTGC
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-

TATTACCGCGGCTGCTGGCACGTAGTTAGCCGTGGCTTATTACCGGGTACCTTCAAGTTCCCACGCATGGGATT
TTTATCCCCCGGCAAAAGCAGTTTACAACCCAGAAGGCCTTCTTCCTGCACGCGGCATGGCTGGTTCAGACTTG
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-

TCCTACGGGAGGCAGCAGTGGGGAATTTTGC GCAATGGGCTAACGCCTGACGCAGCAACGCCGCGTGGAGGAT
GAAGGTCTTTGGATTGTAACTCCTGTGTCAGCAGGGAAGGGAGTGGGCCTAATACGTCCGCAACTTGATTGT
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-

TATTACCGCGGCTGCTGGCACGAAGTTAGCCGGGGCTTCCTTTGCAGGTACATTCAACTGCCTCCGAAGAGACC
ATTTATTCCTGTGACAGTGGTTTACACACCGAAATGCTTCATCCACACATGGCGTTGCTGCGTCAGAGTTTC
CTCCATTGCGCAAAATTCCTACTGCTGCCTCCCGTAGG

+ 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
ATGGCCTCTTTCTCCCCACTGAAAGTGCTTTACAACCTCAGGCCTTCTTCACACACGCGGCATTGCTGGATCA
GGCTTGCGCCCACTGTCCAATATTCCCCACTGCTGCCTCCCGTAGG

+ 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-

TATTACCGCGGCTGCTGGCACGGAGTTAGCCGGTGCTTATTCCTAGGGTACCGTCAGTCTCTTTAGAAAAAGAG
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
GAAGGCCTGCGGGTTGTAAAGCACTTTCAGAGGGGAAGAAAAAATTGGAGCTAACACCTCCGATCTTGACGTT
ACCCTTAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAAT

+ 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
GAAGGCCCTATGGGTTGTAACTGCTTTTGCCAGGGGATAAACGAGCATGCGTGCTTAATTGAAGGTACCTGG
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
GAAGATCTTCGGGTCGTAACTCCTGTGCGAGTGGGAAGAACATCTTTCCGATGAATATTCGGAGAGACTGACGG
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
CCGACTGCTGCCTCCCGTAGG

+ 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
GAAGGCCTTCGGGTCGTAAACTCTGTGATAGGGGAAGATGATGACGGTACCCTATCAGAAAGGACCGGCTAA
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