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CMRC-NRC

May 29, 1997

Dr. M. Kalin
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Dear Dr. Kalin (Margarete):

Please find enclosed a copy of our final report on the Bacterial Consortia in Acid Mine Groundwater Seepage.

I will be happy to answer any specific question which you may have. I hope this preliminary work sets the stage for further collaboration.

Sincerely,

Peter C.K. Lau. Ph.D

cc. A. Pilon
E. Raymond



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Bacterial Consortia in Acid Mine Groundwater Seepage

Final Report (26 pages)

NRCC # 40499

Submitted to:

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May 28, 1997

BATERIAL CONSORTIA IN ACID MINE
GROUNDWATER SEEPAGE

MAY 28, 1997

Executive Summary

What is expected to be there (bacteria) is there and much more. This study reiterates the versatility and powerfulness of the 16S rDNA sequencing technology in the identification of microbial community in a natural environmental setting without prior cultivation. The challenge at hand is to assess activity and abundance of the culprit and beneficial bacteria in the groundwater seepage path and develop a knowledge-based strategy for the reduction of acidity to combat acid mine drainage problem. The importance of a multidisciplinary approach in this effort cannot be overemphasized.

Background (with notes from M. Kalin):

Ground water seepage originating from pyritic mining wastes (tailing ponds, waste rock piles and mine workings) will likely at one point of time emerge as surface water. It is proposed to treat the seepage while it is contaminated groundwater, resulting in discharge of greatly reduced contaminants to surface waters. The task at hand is to identify the microbial consortia which are present in the groundwater seepage path. This prerequisite information will serve as a base for treatment approaches that can be formulated and a proposal involving a multidisciplinary team developed for 1997 and beyond.

It is envisaged that technology development will take about 3 years. The South Bay site outside Toronto is to serve as a test site. In this site, a seepage path from a tailings pond to an adjacent lake is well defined hydrologically and stratigraphically. Monitoring methods for changes in seepage quality are also in place. Piezometers have been monitored for sometime. The anticipated flow of the groundwater is "clean" water at M28 (**Fig. 1**), it then flows to the section where it gets contaminated, in the vicinity of M5, M85. M39(A) is the deepest part of the "Kalin canyon" from which the water flows towards M80 which is in the gravel pit and Kalin canyon. Then the water flows to M60 which is located in the muskeg surrounding Mud Lake. From there it flows towards the outflow M63 passing M62.

The present report deals with a molecular analysis of the bacterial consortia in five water samples collected from sites, M28, M39A, M60A, M63 and M80 as described above. The molecular analysis makes use of 16S rDNA sequencing which is a well established method for identifying bacteria in the characterization of microbial ecology and community structure. This method which uses polymerase chain reaction (PCR) to generate ribosomal DNA (rDNA) of community nucleic acids, has substantial advantages over traditional culture-based methods since it is not dependent on growth and culturing conditions and hence it is generally accepted that environmental diversity is better represented than what cultural diversity is able to portray.

Materials and Methods

Water samples were collected by the Boojum personnel on September 9, 1996. They arrived in Montreal the same day in a cooler containing 40 X 250-ml plastic bottles which were completely filled. The cooler was kept in freezer overnight until processed the following morning. One litre of each water sample was filtered through a Millipore membrane of 0.22 μm and 5 cm diameter. The filters gave different shades of rusty orange color, a reflection perhaps on the purity of the water sample. The filters were then kept in sterile petri dishes at -20°C . The pH of the filtrates was 7.5 for M28 and 6.5 for the remaining samples.

Fig. 2 shows a flow chart of the main events leading to the characterization of

microbial communities without cultivation. For extraction of nucleic acids the membranes were thawed. One-half of each membrane was processed as follows; the other halves were kept for further use. The surface of the filter was washed with 2.5 ml of 0.75 M sucrose, 50 mM Tris-HCl pH 8.3, 40 mM EDTA and 1 mg/ml of lysozyme onto a sterile petri dish. With a razor blade materials from the surface of each membrane were scrapped and the suspension from each was transferred to individual 15 ml tubes. Incubate for 30 min at 37°C to mix. Add 400 µg of Proteinase K and SDS at a final concentration of 0.5%. Incubate for 2 hr at 37°C while mixing every 30 min. Freeze each mixture in dry ice for 15 min and then thaw at 60°C for 10 min. Adjust the extraction mixture to 0.7M NaCl with a stock solution of 5M. Add CTAB at a final concentration of 1% (w/v) to precipitate polysaccharides and proteins. Incubate at 65°C for 20 min. Add an equal volume of phenol:chloroform:isoamyl alcohol (50:49:1), mix well and spin in a refrigerated centrifuge (4°C) for 10 min at 7000 rpm. Discard lower phase. Extract aqueous phase with a volume of chloroform:isoamyl alcohol (49:1), mix well and centrifuge as before. Precipitate nucleic acids with 0.6 volume of isopropanol at -20°C overnight. Centrifuge at 8400 rpm at 4°C for 10 min. Wash pellet with 70% ethanol and resuspend nucleic acids in 100 µl sterile distilled water.

Amplifications of 16S rDNAs from the various samples were carried out by polymerase chain reactions (PCR) as follows: the eubacteria primers 27F and 1492R (15 pmole/reaction) which would amplify near full length 16S rDNA were used for each genomic preparation (15 µl DNA/reaction). In each reaction mixture of 100 µl volume add 100 µM dNTPs, 10X Taq polymerase buffer (Pharmacia) and 5U of Taq polymerase (Pharmacia). Conditions of amplification are: 1 cycle of 2 min at 94°C and 35 cycles of 1 min at 94°C, 1 min at 50°C and 2 min at 72°C. Keep reactions at 4°C.

Universal 16S small subunit (SSU) rDNA library construction: The PCR amplified products were separated on 0.8% agarose gel in 1X TBE buffer. The desired -1.4 kb bands were excised from the gels and purified with QIAEXII resin which was purchased from QIAGEN. pBlueScriptKSII vector (3.199 kb; Promega) which provides blue-white selection was used for cloning after digestion with *EcoRV* to linearize the plasmid and addition of a thymine to the 3' cohesive ends. Ligation with the PCR amplified fragments was carried out by routine procedures and the mixture was transformed in *Escherichia coli* DH5 cells. Recombinants were selected as white colonies when plated on XGal-containing media. The recombinants were then screened for the presence of 4.6 kb plasmids by direct lysis on gels. Positive candidates containing the expected plasmid size were purified on QIAprep8 columns (QIAGEN).

Using 27F oligomer as primer these DNAs were sequenced with an Applied Biosystems model 373A automated fluorescent sequencer and the AmpliTaq DNA polymerase FS system from Applied Biosystems (Perkin Elmer Canada Ltd.). The 300-500 bp generated sequences were analyzed by the BLASTN program available from the National Center for Biotechnology Information (NCBI). Phylogenetic trees were not constructed since we are only interested in the identity of the bacterial samples.

Results and Discussion

The number of recombinants from each transformation varied from 4 to 135. In descending order these numbers are in the following parentheses according to sampling sites: M28 (135), M63 (85), M39 (47), M60 (27) and M80 (4). The “clean” M28 sample gave the highest number of colonies. Whether this is a reflection of ease of preparation of nucleic acids from this relatively clean sample is not clear.

A total of 105 sequencing reactions were carried out. Forty of these actual 16S rDNA sequences are provided in Appendix I. In each case the five sequences (with their corresponding database and accession numbers) which gave the highest scores and probability according to the BLASTN search program are given. **Table 1** lists the most probable bacterial species in each of the given sample according to their location. Complete files of these searches are available upon request. A list of bacteria with the number of occurrences is shown in **Table 2**.

Some general observations:

1. No *apparent Eucarya*. As this represents the eukaryotic arm (fungi, plants, animals) of the life’s three domain tree absence of these members may not come as a surprise.

2. No *apparent Archaea*. Members of the Archaea include *Sulfolobus*, *Methanococcus*, *Thermococcus* etc. This domain has been referred to as “life’s last domain” or “the third form of life” as a result of sequence analysis of the first archaeal complete genome viz. that of *Methanococcus jannaschii*. This group of supposed bacteria (initially termed archaeobacteria) as Carl Woese predicted is neither typically bacteria nor typically eukaryotic, but in between.

In this study, no apparent archaea was detected. This would be expected since one of the two PCR primers used for amplification was not specifically designed to pick up members of this domain. Several archaeal sequences have been found recently in soil.

3. Bacteria (of the interesting kind) galore.

i) *Zoogloea/Cytophaga/Flexibacter/Flavobacterium*.

[Descriptions of the bacteria listed below are according to *Bergey’s Manual of Determinative Bacteriology*].

The *Zoogloea* genus occurs free-living in organically polluted fresh water and in waste water at all stages of treatment. The type species is *Z. ramigera*. These organisms are actively motile. Although aerobic, growth can occur anaerobically in the presence of nitrate (nitrate respiration). Denitrification occurs with the formation of nitrogen.

The genus *Cytophaga* is strict aerobe or facultative anaerobe. Some may use nitrite

(NO₃⁻) as terminal acceptor. These chemoorganotrophs are commonly found in soil, decomposing organic matter, freshwater and marine habitats.

Flexibacter genus is also chemoorganotrophic. Like cytophaga these species are strictly aerobic or facultatively anaerobic. They are also found widely distributed in soil and freshwater.

Flavobacteria are aerobic but nonmotile. They are chemoorganotrophic and are also widely distributed in soil and water, although also found in raw meats, milk and other food.

ii) ***Gallionella ferruginea***. This stands out in the crowd as well. *G. ferruginea* is a type species of the genus *Gallionella*. These are strictly aerobic and microaerophilic. Chemolithoautotrophic. Only Fe²⁺ serves as electron donor. It is typically found in oligotrophic ferrous iron-bearing waters; optimally Eh +200 to +300 mV. This is one of the most important iron bacteria, forming large masses of ferrihydrite in bodies of water and water supply systems. This is probably one of the major culprits for the dirty water samples.

iii). ***Thiobacillus ferrooxidans*** and ***Acidiphilium***. These are culprits as well. Bad to have but good to see them as an indication that the 16S rDNA technique which negates cultivation of the organisms works. *Acidiphilium* is common in acid mineral environments such as pyritic mine drainage and copper and mine tailings. It may be isolated with *T. ferrooxidans* in Fe²⁺ enrichment cultures, and a common contaminant in these cultures. *Acidiphilium* is chemoorganotrophic unlike *Thiobacillus* which may be obligately chemolithotrophic.

iv) ***Desulfitobacterium***. These species are reported to be most commonly found in anoxic marine or brackish sediments. A number of types have been found in anoxic freshwater sediments. These are strictly anaerobic. Sulfate and in some cases also sulfite and/or thiosulfate are reduced to hydrogen sulfide. Sulfate reducing bacteria (SRBs) are good to have since a common strategy of reducing acidity is to promote the growth of SRBs.

v) ***Nitrosolobus/Azorcus***. *Nitrosolobus* (type species *N. multiformis*) was reported to be isolated exclusively from soil. This cannot be completely true. These strains utilize urea as ammonia source and can assimilate limited amounts of organic compounds. *Azorcus* is a recently described genus for a special group of denitrifiers capable of metabolizing toluene.

vi). ***Paracoccus denitrificans***. This is a type species of *Paracoccus*. *Paracocci* are nonmotile and aerobic. Nitrate is reduced to nitrous oxide and molecular nitrogen under anaerobic condition. Although not halophilic, this genus is found to occur in soil and presumably in natural and artificial brines.

Table 1. Bacterial consortia in groundwater seepage samples

M28:

28.1-Zooglea ramigera/P. lemoignei
 28.2-P. lemoignei/Z. ramigera
 28.3-Flavobacterium
 28.4-Flavobacterium
 28.5-Helicobacter hepaticus
 28.6-Helicobacter hepaticus
 28.7-R. fermentans?
 28.8-Flavobacterium
 2M28.4-Zooglea sp.
 2M28.5-Zooglea sp.
 2M28.6-Zooglea sp.
 2M28.9-Zooglea sp.
 2M28.12-Zooglea sp.
 2M28.16-Zooglea sp.
 2M28.20-Zooglea sp.
 2M28.11-Cytophaga sp.
 2M28.18-Flavobacterium

M39:

39.1-Cytophaga
 39.2-Cytophaga
 39.4-Cytophaga/Flexibacter
 39.5-Zoogloea ramigera
 39.6-Streptococcus gordonii
 39.7-Cytophaga
 39.10-Flavobacterium
 39.11-Flavobacterium/flexibacter
 39.12-Cytophaga
 39.13-Zoogloea ramigera
 39.14-Cytophaga
 39.15-Cytophaga
 2M39.4-Cytophaga
 2M39.5-Zooglea ramigera
 3M39.6-Alcaligenes
 3M39.9-Gallionella ferruginea
 3M39.8-Gallionella ferruginea
 3M39.10-Gallionella ferruginea
 3M39.15-Flavobacterium
 3M39.73-Flavobacterium
 3M39.74-Flavobacterium
 3M39.75-Flavobacterium
 3M39.76-Flavobacterium
 3M39.77-Flavobacterium
 3M39.82-Flavobacterium
 3M39.83-Flavobacterium
 3M39.11-poor sequence (not analyzed)
 3M39.13-poor sequence (not analyzed)

M80:

80.1-Azorcus sp./Nitrosolobus multiformis
 80.2-Zooglea ramigera
 80.3-M. chitae/Propionibacterium acnes
 80.4-Desulfitobacterium dehalogenans

M60:

60.1-Desulfitobacterium dehalogenans
 60.2-Gallionella ferruginea
 60.3-Proteobacterium (possibly Azorcus denitrificans)
 60.4-Gallionella ferruginea
 60.5-Thiobacillus ferrooxidans
 60.6-Thermus flavus/fiji/thermophilus
 60.7-Paracoccus denitrificans
 60.8-Bacteria sp. R. fermentans?
 60.9-Gallionella ferruginea
 60.10-Bacteria sp. R. fermentans?
 60.11-Gallionella ferruginea
 60.12-Flavobacterium
 60.13-Gallionella ferruginea
 60.14-unknown/Chlorobium tepidum?
 60.18-R. fermentans
 60.20-Acidocella sp. or Acidophilum facilis

60.24-*R. fermentans*
 2M60.3-*Proteobacterium*
 2M60.73-*Flavobacterium*
 2M60.80-*Flavobacterium*
 2M60.81--*Flavobacterium*
 3M60.9-poor sequence (not analyzed)
 3M60.2--poor sequence (not analyzed)

M63

63.1-*Gallionella ferruginea*
 63.3-*Cytophaga*
 63.4-*Cytophaga/flexibacter*
 63.6-*Cytophaga*
 63.7-*Flavobacterium*
 63.8-*Flavobacterium*
 63.10-*Flavobacterium*
 63.11-*Cytophaga*
 63.12-*Flavobacterium*
 63.13-*Flavobacterium*
 63.15-*Cytophaga*
 63.16-*Cytophaga/flexibacter*
 63.17-*Cytophaga*
 2M63.71-*Flavobacterium*
 2M63.80-*Flavobacterium*
 2M63.77-*Flavobacterium*
 2M63.76-*Flavobacterium*
 2M63.75-*Flavobacterium*
 2M63.74-*Flavobacterium*
 3M63.6-*Flavobacterium*
 3M63.3-*Flavobacterium*
 2M63.79-*Flavobacterium*
 2M63.82-*Flavobacterium*
 2M63.78-poor sequence (not analyzed)

(9 other poor sequences- not listed)

Total: 105

Table 2. Candidate bacteria and their abundance

<i>Flavobacterium</i>	32
<i>Cytophaga</i> sp.	16
<i>Zooglea/Z. ramigera</i>	12
<i>Gallionella ferruginea</i>	10
<i>R. fermentans</i>	5
<i>Desulfitobacterium dehalogenans</i>	2
<i>Thiobacillus ferrooxidans</i>	1
<i>Proteobacterium</i>	2
<i>Acidocella</i> sp./ <i>Acidophilum</i>	1
<i>Paracoccus denitrificans</i>	1
<i>Thermus flavus</i>	1
<i>Pseudomonas lemoignei</i>	1
<i>Heliobacter hepaticus</i>	2
unknown/ <i>Chorobium tepidium</i>	1
<i>Mycobacterium chitae</i>	1
<i>Azorcus</i> sp.	1
<i>Alcaligenes</i>	1
<i>Streptococcus gordonii</i>	1

Conclusions.

Results of this study reiterate the versatility and power of 16S rDNA sequencing in the characterization of microbial community in their natural settings without the need for prior cultivation of the cells which may be dependent on growth and selective media and in some cases simply unculturable. This study provides a sampling of bacterial diversity present in the groundwater seepage path. Correct identification of the individual strains and assemblage into phylogenetic trees, however, will require near complete sequencing of the 16SrDNAs and additional criteria or polyphasic approaches.

Knowledge and identification of the microbial consortia which are present in the groundwater seepage path will likely provide a sound footage for development of possible treatment approaches for the universally occurring acid mine drainage problems. Future research and technical objectives to be sought include: i) quantification of selective microorganisms present in the groundwater seepage path using probes directed against specific rRNA; ii) further assessment of microbial community present in the groundwater seepage path using denaturing gradient gel electrophoresis (DGGE). DGGE separates different rRNA genes on the basis of their G+C contents. Metabolically active cells contain more rRNA than resting or dormant cells. Hence, the DGGE patterns of PCR-amplified rRNA conceptually represent the metabolically active rRNA-rich bacterial populations.

It is anticipated that promotion of alkalinity and reduction of acidity in groundwater will be solved by microbial solutions through a better understanding of the physiology and biology of the beneficial or culprit organisms, and also through multidisciplinary approaches.

Key References

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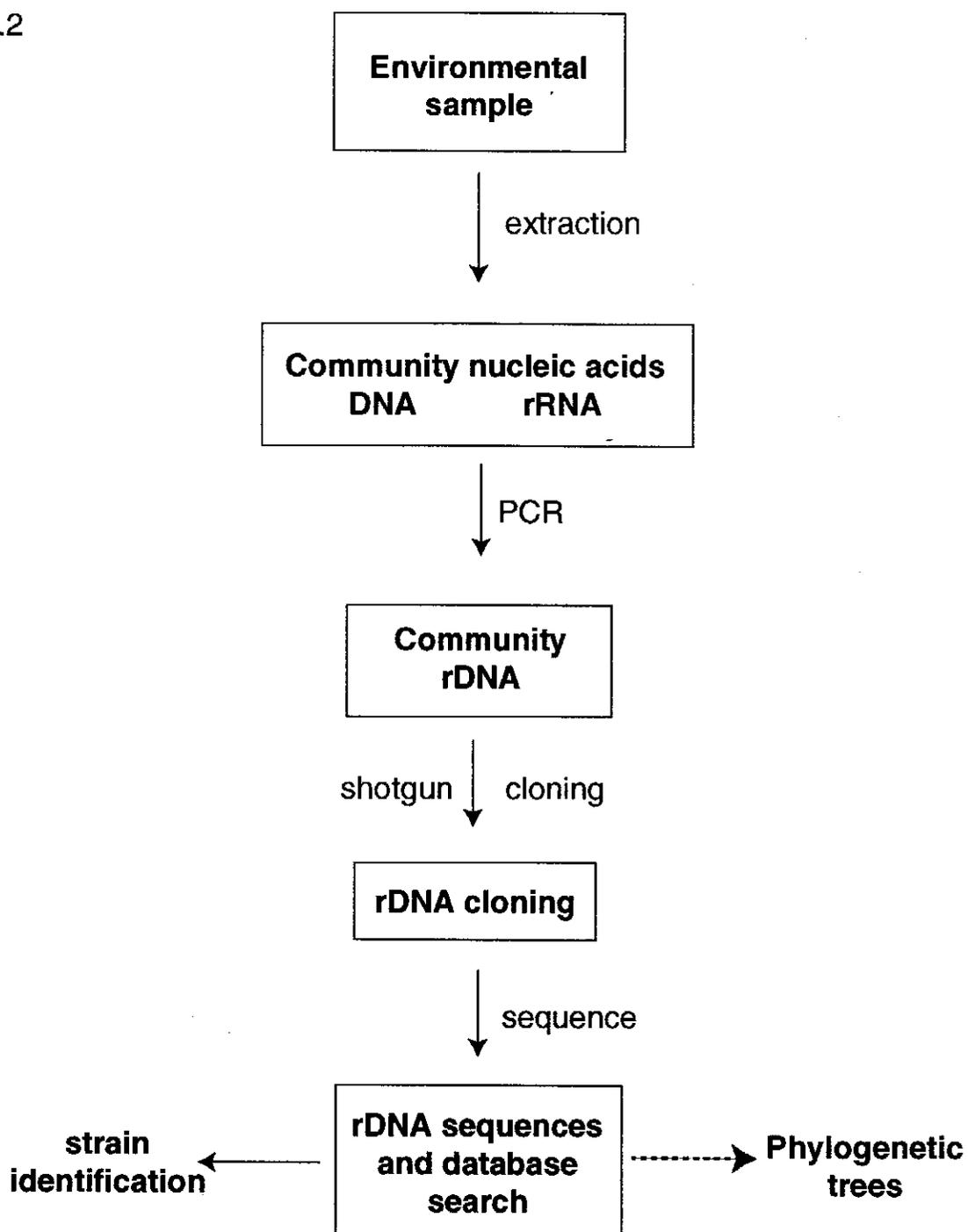
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Fig.2



Appendix I

>SAM281

TTACGGCTACCTTGTACGACTTCACCCCAGTCACGAATCCCACCGTGGTAAGCGCCCTCCTTACGGTTAAGCTACCT
 ACTTCTGGTGAAACCCGCTCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTACCCGCGACATGCTG
 ATCCGCGATTACTAGCGATTCCAACCTTCATGCAGTCGAGTTGCAGACTACTATCCGGACTACGATACTTTCTGGGA
 TTAGCTCCCCCTCGCGGGTTCGCGGCCCTCTGTATGTACCATTGTATGACGTGTGAAGCCCTAACCCATAAG

Probability		High	Smallest
Sequences producing High-scoring Segment Pairs:		Score	P(N)
N			Sum
emb X74914 ZR16SRRNB 1	Z.ramigera gene for 16S rRNA (ATCC ...	1466	1.4e-114
emb X92555 PL16SR220 1	P.lemoinei 16S ribosomal RNA (stra...	1457	7.9e-114
emb X92554 PL16SRA62 1	P.lemoinei 16S ribosomal RNA (stra...	1444	9.6e-113
gb U34035 UBU34035 1	Unidentified beta proteobacterium c...	1340	4.6e-104
dbj D14256 PSER16S3 1	Z.ramigera gene for 16S ribosomal RNA.	1333	1.7e-103

>SAM282

TTACGGTTACCTTGTACGACTTCACCCCAGTCACGAATCCCACCGTGGTAAGCGCCCTCCTTGCGGTTAAGCTACCT
 ACTTCTGGTGAAACCCGCGCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTACCCGCGACATGCTG
 ATCCGCGATTACTAGCGATTCCAACCTTCATGTAGTCGAGTTGCAGACTACAATCCGGACTACGATACTTTCTGGGA
 TTAGCTCCCCCTCGCGGGTTCGCGGCCCTCTGTATGTACCATTGTATGACGTGTGAAGCCCTAACCCATAAG

Probability		High	Smallest
Sequences producing High-scoring Segment Pairs:		Score	P(N)
N			Sum
emb X92555 PL16SR220 1	P.lemoinei 16S ribosomal RNA (stra...	1475	2.5e-115
emb X74914 ZR16SRRNB 1	Z.ramigera gene for 16S rRNA (ATCC ...	1466	1.5e-114
emb X92554 PL16SRA62 1	P.lemoinei 16S ribosomal RNA (stra...	1462	3.1e-114
gb U34035 UBU34035 1	Unidentified beta proteobacterium c...	1349	8.2e-105
dbj D14256 PSER16S3 1	Z.ramigera gene for 16S ribosomal RNA.	1342	3.1e-104

>SAM283

TTACGGCTACCTTGTACGACTTAGCCCTAGTTACCAGTTTACCCTAGGCAGCTCCTTGCGGTCACCGACTTCAGGC
 ACCCCCAGCTTCCATGGCTTGACGGGCGGTGTGTACAAGCCCGGGAACGTATTACCCGGATCATGGCTGATATCCGA
 TTACTAGCGATTCCAGCTTCACGGAGTCGAGTTGCAGACTCCGATCCGAACTGTGACCGGTTTATAGATTTCGCTCCT
 GGTACCCAGTGGCTGCTCTCTGTACCGGCCATTGTAGCACGTGTGTAGCCCAAGCCGTTAAGGGCCGTGATGATTTG
 ACCTCATCGCCACCTTCTCTCAGTT

Probability		High	
Sequences producing High-scoring Segment Pairs:		Score	P(N)
N			
gb L39067 FVBRRDA 2	Flavobacterium ameridies 16S ribosom...	1459	5.9e-127
gb M58781 FBCRR16SB 2	Flexibacter columnaris 16S ribosomal...	1344	2.4e-117
gb M59053 CYTRR16SI 2	Cytophaga johsonae 16S ribosomal RNA.	1344	2.6e-117
gb M62797 FVBRRD 2	F.aquatile 16S ribosomal RNA.	1338	8.3e-117
gb M62792 FBCRR16SZ 2	F.aurantiacus 16S ribosomal RNA.	1337	9.1e-117

>SAM286

TAGAGTTTGGATCCTGGCTCAGAGTGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGAACGATGATAGGAAGCTTGC
 TTCCTTGATTAGCGGCGCACGGGTGAGTAATGCATAGATAATGTGCCCTTAGTTTCGGGATAGCCACTGGAAACGGTG
 ATTAATACCGGATACTCCTTCTCGTTATAAGACGAGTCGGGAAAGTTTTTCGCTAAGGGATCAGTCTATGTTCCATCA
 GCTTGTGGTGAGGTAATGGCTCACCAAGGGCTATGACGGATATCTGGTTTGAGAGGATGATCAGACACACTGGAAC
 GAGACACGGTCCATACTCCTACGGGAAGC

Probability Sequences producing High-scoring Segment Pairs: N		High Score	Smallest Sum P(N)
gb L39122 HECRGD 4	Helicobacter hepaticus 16S ribosomal...	389	7.2e-93
gb M88144 HECRR16SBE 4	Helicobacter sp. (strain B52D Seymou...	385	3.8e-92
gb M88141 HECRR16SBC 4	Helicobacter sp. (strain B13A Seymou...	389	3.9e-92
gb L36143 HECFRC 4	Helicobacter pullorum (strain NCTC 1...	380	9.4e-92
gb L36146 HECFRF 4	Helicobacter pullorum (strain UB 316...	380	9.6e-92

>M287

CCTGGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGGAGCAATCCTGGTGGCGA
 GTGGCGAACGGGTGAGTAATATATCGGAACGTGCCAGTCGTGGGGGATAACGCAGCGAAAGCTGTGCTAATACCGCA
 TACGATCTCTGGATGAAAGCGGGGGACTCGCAAGGGCCTCGCGCGATTGGAGCGGCCGATATCAGATTAGCTAGTTGG
 TGGGGTAAAAGCCCACCAAGGCGACGATCTGTAGCTGGTCTGAGAAGACGACCAGCCACACTGGAACAGGACACGGT
 CCAGACTCCTACGGGAAGCACAGAAGGGAATTTTGGACAATGGGCGCAGCCTGATCCACAATGCCGCGTGCAGATGAA
 GCTC

Probability Sequences producing High-scoring Segment Pairs: N		High Score	Smallest Sum P(N)
dbj D84619 D84619 5	Unidentified beta proteobacterium D...	616	1.7e-120
dbj D16211 RHYFR2D 3	R.fermentans gene for 16S ribosomal...	833	1.9e-119
dbj D16212 RHYFR3E 3	R.fermentans gene for 16S ribosomal...	833	1.9e-119
emb X95837 BS16ST3 3	Bacteria species 16S rRNA gene, str...	847	2.9e-118
dbj D84645 D84645 4	Unidentified beta proteobacterium D...	620	2.0e-117

>2M28.4

GCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGAGCTTGCTCTGGTGGCGAGTGGCGAACGGGTGGGT
 AATATATCGGAACGTACCCTGGAGTGGGGGATAACGCAGCGAAAGTTGCGCTAATACCGCATAACGATCTACGGATGAA
 AGTGGGGGATCGCAAGACCTCATGCTCGTGGAGCGGCCGATATCTGATTAGCTAGTTGGTAGGGTAAAAGCCTACCAA
 GGCATCGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACGGCCCATACTCCTACGGGAGGC
 TTCAGTGGGGAATTTTGGACAATGGGGGCAACCCTGATCCATCAATGCCCGCGTGAGTGAAGAAGGCCTTCGGGT

Sequences producing High-scoring Segment Pairs:		High Score	Smalles t Sum P(N)	N
gb U63941 ZSU63941	Zoogloea sp. 16S ribosomal RNA gene, ...	1542	1.7e-145	3
dbj D84625 D84625	Unidentified beta proteobacterium DN...	1295	1.0e-144	4
dbj D84620 D84620	Unidentified beta proteobacterium DN...	1478	2.0e-142	3
dbj D84564 D84564	Zoogloea sp. DNA for 16S ribosomal R...	1287	3.0e-142	4
dbj D84572 D84572	Zoogloea sp. DNA for 16S ribosomal R...	1269	5.1e-140	4

>2M28.6

GCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGAGCTTGTCTCTGGTGGCGAGTGGCGAACGGGTGAGT
 AATATATCGGAACGTACCCTGGAGTGGGGGATAACCGCAGCGAAAGTTGCGCTAATACCGCATAACGATCTACGGATGAA
 AGTGGGGGATCGCAAGACCTCATGCTCGTGGAGCGGCCGATATCTGATTAGCTAGTTGGTAGGGTAAAAGCCTACCAA
 GGCATCGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGC
 AGCAGTGGGGAATTTTGGACAATGGGGGCAACCCTGATCCAGCAATGCCGCGTTGAGTGAAGAAGGCCTTCGGGTTGT
 TAAAGCTCTTTTGT CAGGGAAGAAACGGTGATTCCTTAATACCGATTGCTAATGACNGTACCTGAAGAATAAGCCCC
 T

Sequences producing High-scoring Segment Pairs:		High Probability Score	P(N)	Smallest Sum N
gb U63941 ZSU63941	Zoogloea sp. 16S ribosomal RNA gene,...	1735	7.3e-164	3
dbj D84564 D84564	Zoogloea sp. DNA for 16S ribosomal R...	1489	2.6e-161	4
dbj D84625 D84625	Unidentified beta proteobacterium DN...	1507	1.8e-160	4
dbj D84572 D84572	Zoogloea sp. DNA for 16S ribosomal R...	1462	2.5e-158	4
dbj D84574 D84574	Zoogloea sp. DNA for 16S ribosomal R...	1462	2.5e-158	4

>2M28.11

GACGCCTAACACATGCAAGTCAAACGGGATTGAGGGCGAGCTGTCATGACAGTGGCGCACGGGTGAGTAGACCGGTAT
 GCAACCTACCGTTTTGGCTGAGGGATAGCCCATATAAATGGGGATTAATACCTCATAGGTTCTTTTGTATCCGCATGGAT
 TGGAAAGATAAAGCTCCTGCGGTTAGAAGATGGGCATGCGTGACATTAGTTTGTGGTGGTAAACGGCTCACCAAGA
 CTACGATGTCTAGGGGTTCTGAAAGGATGATCCCCCACACTGGTACTGAGACACGGACCAGACTCCTACGGGAGGCAG
 CAGTGAGGAATATTGCTCAATGGGCGCAAGCCTGAACCAGCCATCCCCCGTGCAGGATGAAGGCCCTATGGGTCGTAA
 ACTGCTTTTATACACCAAGAA

Sequences producing High-scoring Segment Pairs:		High Probability Score	P(N)	Smallest Sum N
emb X84553 UNSR2008	Unknown organism, partial 16S rRNA ...	905	1.2e-101	5
gb U63940 CSU63940	Cytophaga sp. 16S ribosomal RNA gen...	911	1.2e-100	4
gb U64015 UEU64015	Unidentified eubacterium SCB38 16S ...	873	1.6e-100	5
gb U63938 FSU63938	Flavobacterium sp. 16S ribosomal RN...	939	2.0e-99	4
gb U63943 CSU63943	Cytophaga sp. 16S ribosomal RNA gen...	920	2.4e-98	4

>2M28.18

GCGGGGGCAGGCTTAACACGTGCAAGTCGAGGGGTANAGTTCGTGCGAAGTAGAGACCGGCGCACGGGTGCGTGACG
 CGTGTGCAATCTACCTTGCACAAAGGGATAGCCCATAGAAATTTGGATTAGTACCTTATAGTAGTACGACTTGGCATC
 AAGATGTGTTTAAAGATTTTTTCGGTGAAAAATGAGCATGCGTCCCGTTAGCGAGTGGGGGAGGTAACGGCTTACCAAG
 GCAACGATGGGTAGGGGTCCTGAGAGGGAGATCCCCACGCTGGTACTGAGACACGGACCAACTTCTACGGGAGGCA
 GCAGTGAGGAATATTGGACAATGGGCGCAAGCCTGATCCAACCATGCCGCGTGCAAGATGACGCTCCTATGGATTGTAA
 ACTGCTTTTATACAGGAAGAACACTCCGACT

Sequences producing High-scoring Segment Pairs:		High Probability Score	P(N)	Smallest Sum N
gb U63940 CSU63940	Cytophaga sp. 16S ribosomal RNA gen...	1313	1.1e-129	3
gb U85889 FSU85889	Flavobacterium sp. IC001 16S riboso...	1386	2.2e-128	3
dbj D84581 D84581	Flexibacter sp. DNA for 16S ribosom...	1463	2.6e-128	2
gb U85890 FSU85890	Flavobacterium sp. ACAM123 16S ribo...	1377	5.4e-127	3
gb U63943 CSU63943	Cytophaga sp. 16S ribosomal RNA gen...	1252	1.2e-124	3

>M3911

TACGGCTACCTTGTACGACTTAGCCCTAGTTACCAGTTTACCCTAGGCAGCTCCTTGCGGTCACCGACTTCAGGCA
 CCCCAGCTTCCATGGCTTGACGGGCGGTGTGTACAAGGCCCGGAACGTATTACCGGATCATGGCTGATATCCGAT
 TACTAGCGATTCCAGCTTACGGAGTTCGAGTTGCAGACTCCGATCCGAACTGTGACCGGTTTTATAGATTGCTCCTG
 GTCACCCAGTGGCTGCTCTCTGTACCGGCCATTGTAGCACGTGTGTTACCCAAGGCGTAAGGGCCGTGATGATTTGAC
 GTCATCCCCACCTTCCTCTCAGTTTGCAGTGGCATCTCGTTAAATTCCCACATGATCGCTGGCACTAACACAG

Sequences producing High-scoring Segment Pairs:	High Score	Smallest Sum High Probability	
		P(N)	N
gb L39067 FVBRDA Flavobacterium ameridies 16S ribosom...	1694	1.3e-133	1
gb M58781 FBCRR16SB Flexibacter columnaris 16S ribosomal...	1579	5.5e-124	1
gb M59053 CYTRR16SI Cytophaga johsonae 16S ribosomal RNA.	1579	5.8e-124	1
gb M62797 FVBRD F.aquatile 16S ribosomal RNA.	1573	1.8e-123	1
gb M62792 FBCRR16SZ F.aurantiacus 16S ribosomal RNA.	1572	2.1e-123	1

M396

AGAGTTTGTATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCTAATACATGCAAGTGGAAACGCATGATTGATACCGGA
 CTTGCTCTATCATTAAATCATAAGTCGCGAACGGGTGAGTAACGCGTAGGTAACCTACCTCATAGCGGGGGATAACTA
 TGAAACGATAGCTAATACCGCATAACAGTCTTTGACACATGTTAGAGACTTAAAGGAGCAATTGCTTCACTATGA
 ATGGACCTGCGTTTTGTATTAGCTAGTTGGTGAGGTAAAGGCTCACCAAGGCGACGATACATAGCCGACCTGAGAAG
 GATCGGCCACACTGGGACTGAGACACGGCCAGACTCCCTACGGGAAGCACATTAG

Sequences producing High-scoring Segment Pairs:	High Score	Smallest Sum Probability	
		P(N)	N
gb M58835 STRRR16SB Streptococcus bovis 16S ribosomal RNA.	632	6.3e-104	3
dbj D38483 STR16SRR2 Streptococcus gordonii 16S rRNA gene	884	2.2e-101	2
emb X89237 SPOPPDACA S.pyogenes DNA for oppA, oppB, oppC,...	614	5.9e-101	3
emb X68418 ST16SRRN S.thermophilus gene for 16S rRNA	586	4.0e-97	3
gb M58839 STRRR16SE Streptococcus salivarius 16S ribosom...	566	6.1e-97	3

M3913

AGAGTTTGTATCCTGGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGGGCAACC
 GNTGGCGAGTGGCGAACGGGTGAGTAATATATCGGAATGTACCCCTAGAGTGGGGGATAACGTAGCGAAAGTTACGCT
 ATACCGCATAACGATCTTCGGATGAAAGTGGGGGATCGCAAGACCTCATGCTCATGGAGCAGCCGATATCTGATTAGC
 AGTTGGTAGGGTAAAAGCCTACCAAGGCGACGATCAGTAGCTGGTTTTGAGAGAACGACCAGCCACACTGGAAGTGG
 CACGGTCCAGACTCCTACG

Sequences producing High-scoring Segment Pairs:	High Score	Smallest Sum High Probability	
		P(N)	N
gb U63941 ZSU63941 Zoogloea sp. 16S ribosomal RNA gene,...	1187	5.4e-120	2
emb X74914 ZR16SRRNB Z.ramigera gene for 16S rRNA (ATCC 2...	1526	1.6e-119	1
dbj D84625 D84625 Unidentified beta proteobacterium DN...	1200	5.3e-115	2
dbj D84564 D84564 Zoogloea sp. DNA for 16S ribosomal R...	1440	9.9e-115	1
dbj D84572 D84572 Zoogloea sp. DNA for 16S ribosomal R...	1422	3.1e-113	1

>2M394

AAACACGAACACGTCGAGGGGTCAGAGTTCGTCAGGAAGTATAGACCGGGCCACGGGTGCGTAACGCGTATGCAATCTA
CCTTTCACAAAGGGGATAGCCCAGAGAAATTTGGATTAATACCTTATAGTAATACGACTTGGCATCAAGATGTATTTA
AAGATTTATCGGTGAAAGATGAGCATGCGTCCCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATGGGT
AGGGGTCTTGAGAGGGAGGTCCCCCACACTGGTACCGAGACACGGACCAGACTCCTACGGGAGGCAGCAGTGAGGAAT
ATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGCAGGATGACGGTCTTATGGATTGTAAACTGCTTTTAT
ACAGGAAGAAACACTCGCGACGTGTCCGAGCTTGACGGTACTGTAGGAATAAGGATCGGCTAACTCCGTGCCAGCAGC
CGCGGTAATACGGCAGGATC

Sequences producing High-scoring Segment Pairs:		High Probability Score	P(N)	Smalles t Sum N
gb U63940 CSU63940	Cytophaga sp. 16S ribosomal RNA gen...	1432	1.5e-148	3
dbj D84581 D84581	Flexibacter sp. DNA for 16S ribosom...	1382	4.6e-145	3
gb M59053 CYTRR16SI	Cytophaga johsonae 16S ribosomal RNA -	1358	1.6e-144	3
gb M62797 FVBRRD	F.aquatile 16S ribosomal RNA.	1338	4.2e-144	3
gb U63936 FSU63936	Flavobacterium sp. 16S ribosomal RN...	1387	3.2e-142	3

>2M395

CACAAGCCAGTCGAACGGCCGCACGGGGCCAACCTGGTGGCGAGCGGCGAACGGGTGAGTAATATATCGGAATGTACC
CTAGAGTGGGGGATAACGTAGCGAAAGTTACGCTAATACCGCATAACGATCTACGGATGAAAGTGGGGGATCGCAAGAC
CTCATGCTCATGGAGCAGCCGATATCTGATTAGCTAGTTGGTAGGGTAAAAGCCTACCAAGGCGACGATCAGTAGCTG
GTTTGAGAGAACGACCAGCCACACTGGAAGTATACACGGTCCATACTCCTACGGGAGGCAGCAGTGGGGAATTTTGG
ACAATGGGGGCAACCCTGATCCAGCAATGCCGCGTGGTGAAGAAGGCCTTTCGGGTTGTAAAGCTCTTTTGTGAGGGA
AGAAAAGGTAGCCTCTAATACAGGCTGCTCATGACGGTACCTGAAGAATAAGCACCGGCTAACTACGTGCCAGCAGCC
CGGTAATACGTAGGGTGAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCCGAGGCGGTTATATAAGT

Sequences producing High-scoring Segment Pairs:		High Probability Score	P(N)	Smalles t Sum N
emb X74914 ZR16SRRNB	Z.ramigera gene for 16S rRNA (ATCC ...	2309	5.8e-190	2
dbj D14256 PSER16S3	Z.ramigera gene for 16S ribosomal RNA.	2281	8.7e-183	1
gb U34035 UBU34035	Unidentified beta proteobacterium c...	776	5.0e-178	5
emb X92555 PL16SR220	P.lemoinei 16S ribosomal RNA (stra...	2167	7.7e-178	2
emb X92554 PL16SRA62	P.lemoinei 16S ribosomal RNA (stra...	2152	2.1e-175	2

>3M965 396

CGAACGCGAAAGTAGGGGCAACCCTGCGAGTAGAGTGGCGAACGGGTGAGTAATACATCGGAACGTACCCAGGCAGTG
GGGGACAACCTCGAGAAATCGAGGCTAACACCCGCATACGTCTGAGGGAGAAAGCGGGGGATCCGTAAGGACCTCCGG
CTCATGGAGCGGCCGATGTCCGATTAGCTAGTTGGCGGGGTAAGAGCCCAACCAAGGCTACGATCCGTAGCTGGTTTGA
GAGAACCAGCCACACTGGGACTGATACACCGCCACACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG
GGGAAACCCTGATCCAGCC

Sequences producing High-scoring Segment Pairs:		High Probability Score	P(N)	Smalles t Sum N
emb X84466 UNSBR1022	Unknown organism, partial 16S rRNA ...	761	1.9e-92	2
emb X84518 UNSBR1090	Unknown organism, partial 16S rRNA ...	773	1.9e-91	3
dbj D84625 D84625	Unidentified beta proteobacterium D...	795	7.0e-91	3
emb X84493 UNSBR1058	Unknown organism, partial 16S rRNA ...	982	2.3e-90	2
emb X84610 UNSBR2080	Unknown organism, partial 16S rRNA ...	773	4.8e-90	3

>3M3910

AACCGGCTTTGCGTGCTTGCACCGGAGTTAGTGGCGAACGGGTGAGTAATATATCGGAACATATCCGGAAGTGGGGGA
 TAACGTGACGAAAGTTTCGCTAATACCGCATATGCCCTGAGGGGGAAAGGGGGGATCGCAAGACCGTCTCGCTTTTCG
 GAGTGGCCGATAACCGGATTAGCTACATGGTGAGGTAAAGGCTCACCATGGCGACGATCCGTAGCTGGTCTGAGAGGAC
 GACCAGCCACTCTGGAACCTGAGACACGGTCCAGACTCCTACGGGAGGC

Sequences producing High-scoring Segment Pairs:		High Score	Smallest Sum P(N)	N
gb L07897 GLLRGDA 2	Gallionella ferruginea 16S ribosoma...	641	3.4e-87	
emb X84620 UNSB2090 2	Unknown organism, partial 16S rRNA ...	544	5.5e-73	
emb X84544 UNSB1119 2	Unknown organism, partial 16S rRNA ...	524	2.0e-71	
emb X84465 UNSB1021 2	Unknown organism, partial 16S rRNA ...	587	3.0e-71	
emb X84518 UNSB1090 2	Unknown organism, partial 16S rRNA ...	542	1.7e-70	

>SAM601

TAGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGAACGGCCTTTGCGAGGTTTCG
 AAGCTCGAGGTTGCAAGTTGCAATTAAATTGACTTCTGAGGTATTTAAAGGCCACAGAGAAATTTCTTAATTCGCACAT
 CGTGCATCGCACTTTCGAACCTTCGCGGGTAGTGGCGGACGGGTGAGTAACCGGAGGTAACCTACCCATAAACCCGGGA
 CAACCCTTGAAACGAGGGCTAATACCGGATAATCTTTTAGCTTGGCATCAAGCAATAAGAAAAGGTGGCCTCTGAAA
 ATGCTACCGATTATGGATGGACCCGCGTCTGATTAGCTAGTTGCTG

Sequences producing High-scoring Segment Pairs:		High Score	Smallest Sum P(N)
gb M34417 DSORR1618 3	Desulfotomaculum orientis 16S ribos...	388	2.7e-71
gb L28946 DTORRD 2	Desulfitobacterium dehalogenans 16S...	681	1.1e-70
gb U68528 DCU68528 2	Desulfitobacterium chlororespirans ...	668	2.7e-61
emb X94975 DH16SRRNA 2	D.hafniense 16S ribosomal RNA	625	1.0e-58
emb X99706 SG16SRR1 3	S.glycolicus 16S rRNA gene	375	1.3e-52

>SAM602

TAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGTATGCTTTACACATGCAAGTCGAACGGATTGCGGGGCTTGCT
 CCCAAGTTAGTGGCGAACGGGTGAGTAATATATCGGAACATATCCGGAAGTGGGGGATAACGTAGCGAAAGTTACGCT
 AATACCGCATATGCCCTGAGGGGGAAAGGGGGGATCGCAAGACCTCTCGCTTTTCGGAGTGGCCGATATCGGATTAGC
 TAGTAGGTGAGGTAAAGGCTCACCTAGGCGACGATCCGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGAACCTGAG
 ACACCGTCCACACTCCTACCGGAAGCAGCAGTG

Sequences producing High-scoring Segment Pairs:		High Score	Smallest Sum P(N)
gb L07897 GLLRGDA 1	Gallionella ferruginea 16S ribosoma...	1436	4.6e-112
gb U63941 ZSU63941 2	Zoogloea sp. 16S ribosomal RNA gene...	958	9.5e-96
emb X65589 TM16SR 2	T.mixta 16S rRNA	996	1.4e-95
gb U63953 ASU63953 2	Alcaligenes sp. 16S ribosomal RNA g...	958	4.4e-94
gb L35509 NNTL16SR 2	Nitrosolobus multififormis (ATCC 2519...	958	5.3e-93

>SAM604

TAGAGTTTGGATCCTGGCTCAGATTGAACGCTGGCGGTATGCTTTACACATGCAAGTCGAACGGGCTTTGGTGCTTGCA
 CCGGAGTTAGTGGCGAACGGGTGAGTAATATATCGGAACATATCCGGAAGTGGGGGATAACGTAGCGAAAGTTACGCT
 AATACCGCATATGCCCTGAGGGGGAAAGGGGGGATCGCAAGACCTCTCGCTTTCGGAGTGGCCGATACCGGATTAGC
 TAGATGGTGAAGTAAAGGCTCACCATGGCGACGATCCGTAGCTGGTCTGAAAAGACGACCAGCCACACTGGAAGTGA
 ACACGGTCCAGACTCCTACGGAAGCACCAGTG

Probability Sequences producing High-scoring Segment Pairs: N		High Score	Smallest Sum P(N)
gb L07897 GLLRGDA 1	Gallionella ferruginea 16S ribosoma...	1382	1.5e-107
gb U63941 ZSU63941 2	Zoogloea sp. 16S ribosomal RNA gene...	913	5.0e-92
emb X65589 TM16SR 2	T.mixta 16S rRNA	951	7.7e-92
gb U63953 ASU63953 2	Alcaligenes sp. 16S ribosomal RNA g...	913	2.3e-90
gb L35509 NTL16SR 2	Nitrosolobus multiformis (ATCC 2519...	913	3.0e-89

>SAM605

TAGAGTTTGGATCCTGGCTCAGATTGAACGCTGGCGGCATGCCTAACACATGCAAGTCGAACGGTAGCAGGCCTTCGGG
 TGCTGACGAGTGGCGGACGGGTGAGTAATGCGTAGGAATCTGTCTTTTAGTGGGGGACAACCCACGGAAACTTGGGCT
 AATACCGCATGAGCCCTGAGGGGGAAAGCGGGGGATCTTCCGACCTCGCGCTAAGAGGAGAGCCTACGTCCTGATTAC
 CTAGTTGGTACGGTAAAGGCCTACCAAGGCGACAATCACTAGCTGGTCTGAGAGGAC

Probability Sequences producing High-scoring Segment Pairs: N		High Score	Smallest Sum P(N)
emb X75266 TF16SRRN 2	T.ferrooxidans (N-Fe2) gene for 16S ...	921	4.9e-89
emb X75267 TF16SRNA 2	T.ferrooxidans (N-Fe4) gene for 16S ...	912	2.8e-88
emb X98210 TS16SRDNA 2	Thiobacillus sp. 16S ribosomal DNA	921	3.6e-88
emb X93478 PBDSM2111 2	Phototrophic bacterium 16S rRNA gene...	952	2.4e-87
emb X75268 TFN16SRRN 2	T.ferrooxidans (N-Fe3) gene for 16S ...	926	1.1e-85

>SAM606

TTACGGTTACCTTGTACGACTTAGCGCCAGTCACCAGTTTTACCTTCAGCCCCGATTACTCGGAGATTTACGGTACC
 ACCAGCTCCCATCGCTTGACGGGCGGTGTGTACAAGCCCCGGGAACGTATTACGGCGGCGTAGCTGATCCGCCATTA
 CTAGTGATTCCGTCTTCATGGAGTCGAATTGCAGACTCCAATCTGAACTGAGCCCACTTTTTTTCGATTAGCTCCACC
 TCGCGGTTTTGGCAACGCTTTGGAGTGGGCATTGTAACACGTGTGTAGCCCAAGGCATAAAGGCCGTACTGACTTGACC
 TCATCTCCATCTTCCTCCCGCTTATCGCG

Probability Sequences producing High-scoring Segment Pairs: N		High Score	Smallest Sum P(N)
gb L09660 TTHAT62 2	Thermus flavus AT-62 16S ribosomal R...	975	2.0e-82
gb L10067 TTHDNAFRA 2	Thermus Fiji 3A DNA fragment.	975	2.0e-82
gb M26923 TTH16SRAA 2	T.thermophilus 16S rRNA gene, comple...	975	4.5e-82
gb L09670 TTHHS 2	Thermus sp. HS A.1 16S ribosomal RNA...	966	1.1e-81
gb L10069 TTHDNAFRC 2	Thermus Tok3 A.1 DNA fragment.	957	1.1e-81

>SAM607
 TTACGGCTACCTTGTTACGACTTCACCCCAGTCACTGAGCCTACCGTGGTTGGCTGCCTCCATTGCTGGTTGGCGCAC
 CACCTTCGGGTAGACCCAATCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGTCATGC
 TGTTACGCGATTACTAGCGATTCCGACTTCATGGGGTTCGAGTTGCAGACCCCAATCCGAAGTGAAGTGGCTTTTGGG
 ATTAACCCATTGTCACCACCATTGTAGCACGTGTGTAGCCCAACCCGTAAGGGCCATGAAGACTTGACGTCATCCACA
 CCTTCCTCCGGCTTATCACCGGCAGTTTTTCCTA

Probability		High	Smallest
Sequences producing High-scoring Segment Pairs:		Score	P(N)
N			
emb X69159 PD16SRRNA	P.denitrificans 16S rRNA	1538	1.3e-120
1			
emb X53855 RSRRNC	R. sphaeroides ribosomal RNA operon...	1302	5.6e-119
2			
emb X53853 RSRRNA	R. sphaeroides ribosomal RNA operon...	1302	5.9e-119
2			
emb X53854 RSRRNB	R. sphaeroides ribosomal RNA operon...	1302	6.0e-119
2			
dbj D16427 RCAC5J	R. capsulatus 16S rRNA gene.	1506	6.0e-118
1			

>SAM608
 TAGAGTTTGTATCCTGGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCGGCACGGGAGCAAT
 CCAGGTGGCGAGTGGCGAACGGGTGAGTAATATATCGGAACGTGCCAGTCGTGGGGGATAACGCAGCGAAAGCTGTG
 CTAATACCGCATAACGATCTCTGGATGAAAGCGGGGGACTCGCAAGGGCCTCGCGCGATTGGAGCGGCCGATATCAGAT
 TAGCTAGTTGGTGGGGTAAAAGCCCACCAAGCGCAGCATCTGTAGCTGGTCTGAGAAGACGACCAGCCACACTGGAAC
 TGAGACCCCTCCACACTCCTACGGGAAGCACAGTG

Probability		High	Smallest
Sequences producing High-scoring Segment Pairs:		Score	P(N)
N			
emb X95837 BS16ST3	Bacteria species 16S rRNA gene, str...	870	1.9e-109
3			
dbj D84619 D84619	Unidentified beta proteobacterium D...	598	1.9e-107
5			
dbj D16211 RHYFR2D	R.fermentans gene for 16S ribosomal...	815	1.0e-105
3			
dbj D16212 RHYFR3E	R.fermentans gene for 16S ribosomal...	815	1.0e-105
3			
gb L33981 LTTRRDC	Leptothrix sp. (strain NC-1) 16S ri...	953	8.0e-105
3			

>SAM609
 TTACGGCTACCTTGTTACGACTTCACCCCAGTCACTGAAACCCACCGTGGTAAGCGCCCTCCTTACGGTTAGGCTACCT
 ACTTCTGGCAGATTCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCGACATGCTG
 ATCCGCGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGATCGGCTTTCTGAGA
 TTAGCTCCCCCTCGCGGGTTTGGCAACCCTCTGTACCGACCATTGTATTACGTGTGAAGCCCTACCCATAAG

Probability		High	Smallest
Sequences producing High-scoring Segment Pairs:		Score	P(N)
N			
gb L07897 GLLRGDA	Gallionella ferruginea 16S ribosoma...	1242	6.6e-112
2			
gb U22536 ZSSSURNAS2	Zoogloea sp. small subunit ribosoma...	1129	1.8e-109
2			
emb X92415 ASP16SRRN	Alcaligenes sp. 16S ribosomal RNA	1179	1.2e-106
2			
emb X74913 ZR16SRRNA	Z.ramigera gene for 16S rRNA (ATCC ...	1116	7.1e-103
2			
gb S55008 S55000S2	16S rRNA [Burkholderia mallei, ATCC...	1062	3.6e-102
2			

>M6010

TAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGGAGCAAT
 CCTGGTGGCGAGTGGCGAACGGGTGAGTAATATATCGGAACGTGCCAGTCGTGGGGGATAACGCAGCGAAAGCTGTG
 CTAATACCGCATAACGATCTCTGGATGAAAGCGGGGGACTCGCAAGGGCCTCGCGCGATTGGAGCGGGCCGATATCAGAT
 TAGCTAGTTGGTGGGGTAAAAGCCCACCAAGGCGACGATCTGTAGCTGGTCTGAGAAGACGACCAGCCACACTGGAAC
 TGAGACACGGTCCAGACTCCTACGGGAAG

Sequences producing High-scoring Segment Pairs:	High Probability Score	Smallest Sum		
		P(N)	N	
emb X95837 BS16ST3	Bacteria species 16S rRNA gene, str...	888	3.6e-115	2
dbj D16211 RHYFR2D	R.fermentans gene for 16S ribosomal...	833	2.1e-111	2
dbj D16212 RHYFR3E	R.fermentans gene for 16S ribosomal...	833	2.1e-111	2
dbj D84619 D84619	Unidentified beta proteobacterium D...	616	5.5e-109	4
gb U37344 BSU37344	Burkholderia sp. isolate N3P2 16S r...	834	6.2e-107	2

>M6011

TACGGTTACCTTGTTACGACTTCACCCCAGTCATGAAACCCACCGTGGTAAGCGCCCCCTTACGGTTAGGCTACCTA
 CTTCTGGCAGATTCCACTCCCATGGTGTGACGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCGACATGCTGA
 TCCGCGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGATCGGCTTTCTGAGAT
 TAGCTCCCCCTCGCGGGTTGGCAACCCTCTGTACCGACCATTGTATTACCTGTGAAGCCCTACCCATAAGGGCCATGA
 AGAATTGACTCATCCCCACTTCCTCCGGTTGTACGGCAGTCTCATTAAAGTGCCAACT

Sequences producing High-scoring Segment Pairs:	High Probability Score	Smallest Sum		
		P(N)	N	
gb L07897 GLLRGDA	Gallionella ferruginea 16S ribosoma...	1515	6.9e-127	3
emb X92415 ASP16SRRN	Alcaligenes sp. 16S ribosomal RNA	1470	4.7e-123	3
gb U22536 ZSSSURNAS2	Zoogloea sp. small subunit ribosoma...	1420	8.7e-120	2
emb X74913 ZR16SRRNA	Z.ramigera gene for 16S rRNA (ATCC ...	1407	8.1e-118	3
emb X57026 BB16SRNA	B.bronchiseptica 16S ribosomal RNA	1407	9.8e-118	3

>M6014

TGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCTACGAGAAAAGAGTANCNATACTCTGAG
 TAAAGTGGCGCAAGGGTGGTAACCCGTAAGCAATCTACCTTTAGGCGGGGAATAATCCAGCGAAAGCCGGACTAATA
 CCCCATAATGCAGCGGCACCGCATGGTGTGTTGTTAAAGTCTATATGACGTCTANAGATGAGCTTGGCTCTGATTAG
 CTAGTTGGTGGGTAACGGCTACCAAGGCTACGATCAGTAGCTGGTCTGAGAAGATGATCAGCCACACTGGAAGTGA
 GACACGGTCCAGACTCCTACGGGAA

Sequences producing High-scoring Segment Pairs:	High Probability Score	Smallest Sum		
		P(N)	N	
emb X84451 UNSBR1003	Unknown organism, partial 16S rRNA g...	468	5.6e-71	3
gb M58468 CHBSSRIBRR	Chlorobium tepidum small subunit rib...	448	1.9e-70	3
emb X85131 SBRRNA16S	s.buswellii 16S rRNA gene	493	1.1e-69	3
gb M31769 CHBS6RNA	C.limicola ribosomal RNA small subunit.	444	2.1e-69	3
emb Y07607 BS16SRM13	Bacterial species 16S rRNA gene (par...	426	3.8e-69	3

>M6020

21

TAGAGTTTGGATCCTGGCTCAGAGCGAACGCTGGCGGCATGCTTAACACATGCAAGTCGCGCGGTGAGTAATGGCAGCG
GCGGACGGGTGAGTAACACCTAGGAATCTATCCCAGGGTGGGGGACAACAGCGGGAAACTGCTGCTAATACCGCATGA
TACCTGAGGGTCAAAGGCGCAAGTCGCCTGGGAGGAGCCTGCGTCTGATTAGCTTGTGGTGGGGTAAAGGCCTACC
AAGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGCCAAACTCCTACGGGAAG
CAGCAGTG

Sequences producing High-scoring Segment Pairs:		High Probability Score	P(N)	Smallest Sum N
dbj D86510 D86510	Acidocella sp. DNA for 16S rRNA	1372	1.3e-112	2
dbj D30774 ACD16SRNAG	Acidiphilium facilis gene for 16S r...	1354	4.2e-111	2
dbj D30771 ACD16SRNAD	Acidiphilium aminolytica gene for 1...	1293	5.1e-106	2
emb Y07647 BS16SR3C	Bacterial species 16S rRNA gene (pa...	525	3.1e-102	4
emb X68471 UPBMC106	Unknown Proteobacterium, alpha-1 su...	937	7.3e-99	3

>2M603

CGCTGGCGGCATGCCTTACACATGCAAGTCGAACGCGCAAAGTAGGGGCAACCCTGCGAGTAGAGTGGCGAACGGGTG
AGTAATACATCGGAACGTACCCAGGAGTGGGGGACAACCTCGAGAAATCGAGGCTAACACCCGCATACGTCCTGAGGGA
GAAAGCGGGGGATCCGTAAGGACCTCGCGCTCATGGAGCGGCCGATGTCGGATTAGCTAGTTGGCGGGTAAAAGCCC
ACCAAGGCTACGATCCGTAAGGACCTCGCGCTCATGGAGCGGCCGATGTCGGATTAGCTAGTTGGCGGGTAAAAGCCC
GAGGCAGCAGTGGGGAATTTTGGACAATGGGGGAAACCCTGATCCAGCCATGCCGCGTGAGTGAAGAAGGCCTTCGGG
TTGTAAAGCTCTTTCGGCCGGAACGAAATCGCGTACGTGAATAACGTGCGTGGATGACGGTACTGGAAGAAGAAGCAC
CGGCTAACTACGTGCCAGCAGCCGCGGGTAATACGTTAGGTGCGAACGTTAATCGGAATTACTGGGCCTTAAAGCGTG
CGTTAGCGGTTCT

Sequences producing High-scoring Segment Pairs:		High Probability Score	P(N)	Smallest Sum N
emb X83532 PBPBN116S	Proteobacteria 16S rDNA gene (strai...	1368	6.2e-159	4
emb X86583 AS054416S	Alcaligenes 05-44 16S rRNA gene >em...	929	3.9e-158	5
emb X86577 AS002516S	Alcaligenes 00-25 16S rRNA gene	929	4.0e-158	5
emb X86575 AS001916S	Alcaligenes 00-19 16S rRNA gene >em...	929	4.1e-158	5
emb X86592 ASS20416S	Alcaligenes S2-04 16S rRNA gene	929	4.3e-158	5

>2M6080

CGCTTAACACATGCAAGTCGAGGGGTATAGTTCTTCGGAACTAGAGACCGGGCGCACGGGTGCGTAACGCGTATGCAAT
CTACCTTTCACAAAGGGATAGCCCAGAGAAATTTGGATTAATACCTTATAGTAATACGACTTGGCATCAAGATGTATT
TAAAGATTTACCGGTGAAAGATGAGCATGCGTCCCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATGG
GTAGGGGTCTGAGAGGGAGATCCCCACACTGGTACTGAGACACGGACCAGACTCCTACGGGAGGCAGCAGTGAGGA
ATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGACAGGATGACGGTACTATGGATTGTAAACTGCTTTT
ATACAGGAAGAAACACTAGGACGTGTCCGAGCTTGACGGTACTGTTAGAATAAGGATCGGCTAACTCCGTGCCAACCA
G

Sequences producing High-scoring Segment Pairs:		High Probability Score	P(N)	Smallest Sum N
gb U85889 FSU85889	Flavobacterium sp. IC001 16S riboso...	1934	1.1e-160	2
gb U85890 FSU85890	Flavobacterium sp. ACAM123 16S ribo...	1936	2.3e-160	2
dbj D84581 D84581	Flexibacter sp. DNA for 16S ribosom...	1981	1.0e-159	1
gb M59053 CYTRR16SI	Cytophaga johsonae 16S ribosomal RNA.	1982	1.2e-157	1
gb U63940 CSU63940	Cytophaga sp. 16S ribosomal RNA gen...	1841	2.3e-157	2

>M6310

TACGGCTACCTTGTACGACTTAGCCCTAGTTACCAGCTTTACCCTAGGCAGCTCCTTGCGGTCACTGACTTCAGGCA
CCCCAGCTTCCATGGCTTGACGGGCGGTGTGTACAAGGCCCGGAACGTATTCACCGGATCATGGCTGATATCCGAT
TACTAGCGATTCCAGCTTACGAGTTCGAGTTGCGGACTCCGATCCGAACTGTGACCGGTTTATAGATTGCTCCTG
GTCACCCAGTGGCTGCTCTCTGTACCGGCCATTGTAACACGTGTGTAGCCCAAGGCGTAAGGGCCGTGATGATTTGAC
GTCATCCCCACCTTCCTCTCAGTTTGCAGTGGCAGTCTCGTTAGATCCCGAGATGACTCGCTG

Sequences producing High-scoring Segment Pairs:	High Score	Smallest Sum	Probability P(N)	N
gb L39067 FVBRRDA Flavobacterium ameridies 16S ribosom...	1722	6.1e-136	1	
gb M62797 FVBRRD F.aquatile 16S ribosomal RNA.	1610	1.9e-129	2	
gb M58781 FBCRR16SB Flexibacter columnaris 16S ribosomal...	1607	3.0e-129	2	
gb M59053 CYTRR16SI Cytophaga johsonae 16S ribosomal RNA.	1607	3.3e-129	2	
gb M58764 CYTRR16SA Cytophaga aquatile 16S ribosomal RNA.	1581	4.4e-127	2	

M631

AGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGTATGCTTTACACATGCAAGTCGAACGGGCTTGGGGGCTTGCT
CCGAGTTAGTGGCGAACGGGTGAGTAATATATCGGAACATATCCGGAAGTGGGGGATAACGTANCGAAAGTTACGCT
ATACCGCATATGCCCTGAGGGGGAAAGGGGGGGATCGCAAGACCTCTCGCTCTCGGAGTGGCCGATATCGGATTAGC
AGTAAGTGAGGTAAAGGCTCACCTAAGCGACGATCCGTAGCGGTCTGAGAAGACAACCGCCACACTGGAAGTGA
ACGGTCCAACCTCCCTAC

Sequences producing High-scoring Segment Pairs:	High Score	Smallest Sum	Probability P(N)	N
gb L07897 GLLRGDA Gallionella ferruginea 16S ribosoma...	1138	4.5e-95		2
gb U63941 ZSU63941 Zoogloea sp. 16S ribosomal RNA gene...	696	9.4e-84		3
gb U22534 ZSSSURNAS1 Zoogloea sp. small subunit ribosoma...	743	1.4e-83		3
gb L33976 SHLRRD Sphaerotilus natans 16S ribosomal R...	682	2.5e-83		3
gb L33978 SHLRRDB Sphaerotilus natans 16S ribosomal R...	676	3.0e-83		3

>M634

AGAGTTTGATCCTGGCTCAGGATGAACGCTAGCGGCAGGCTTAACACATGCAAGTCGAGGGGTATAGTTCTTCGGAAC
TAGAGACCGACGCACGGGTGCGTAACCGGTATGCAATCTACCTTTCACAAAGGGATAGCCCAGAGAAATTTGGATTAA
TACCTTATAGTAATACGACTTGGCATCAAGATGTATTTAAAGATTTATCGGTGAAAGATGAGCATGCGTCCCATTAGC
TAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATGGGTTAGGGTCTGAGAAGGAGATCCCCCACACTGGTACTGAG
ACACGGACCAGACTCCCTACGGGAAGCAGCAGTGAAGAATATTGGACAATG

Sequences producing High-scoring Segment Pairs:	High Score	Smallest Sum	Probability P(N)	N
gb U63940 CSU63940 Cytophaga sp. 16S ribosomal RNA gen...	1078	5.1e-118		3
gb M59053 CYTRR16SI Cytophaga johsonae 16S ribosomal RNA.	1378	2.2e-116		2
ibj D84581 D84581 Flexibacter sp. DNA for 16S ribosom...	1306	1.1e-115		2
gb M93151 SORRR16S Sporocytophaga cauliformis 16S ribo...	1360	6.2e-115		2
gb U63938 FSU63938 Flavobacterium sp. 16S ribosomal RN...	1297	2.3e-114		2

>M637

TTACGGCTACCTTGTTACGACTTAGCCCTAGTTACCAGTTTTACCCTAGGCAGCTCCTTGCGGTCACCGACTTCAGGC
 ACCCCCAGCTTCCATGGCTTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTACCGGATCATGGCTGATATCCGA
 TTACTAGCGATTCCAGCTTCACGGAGTCGAGTTGCAGACTCCGATCCGAACTGTGACCGGTTTTATAGATTCGCTCCT
 GGTACCCAGTGGCTGCTCTCTGTACCGGCCATTGTAACACGTGTGTAACCCAAGGCGTAAGGGCCGTGATGATTGA
 CGTCATCC

Probability		High	Smallest
Sequences producing High-scoring Segment Pairs:		Score	P(N)
N			
gb L39067 FVBRRDA 1	Flavobacterium ameridies 16S ribosom...	1568	4.2e-123
gb M58781 FBCRR16SB 1	Flexibacter columnaris 16S ribosomal...	1453	1.7e-113
gb M59053 CYTRR16SI 1	Cytophaga johsonae 16S ribosomal RNA.	1453	1.8e-113
gb M62797 FVBRRD 1	F.aquatile 16S ribosomal RNA.	1447	5.6e-113
gb M62792 FBCRR16SZ 1	F.aurantiacus 16S ribosomal RNA.	1446	6.6e-113

>M638

TTACGGCTACCTTGTTACGACTTAGCCCTAGTTACCAGTTTTACCCTAGGCAGCTCCTTGCGGTCACTGACTTCAGGC
 ACCCCCAGCTTCCATGGCTTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTACCGGATCATGGCTGATATCCGA
 TTACTAGCGATTCCAGCTTCACGGAGTCGAGTTGCAGACTCCGATCCGAACTGTGACCGGTTTTATAGATTCGCTCCT
 GGTACCCAGTGGCTGCTCTATGTACCGGCCATTGTAGCACGTGTGTAGCCCAAGGCGTAAGGGCCGTGATGATTTGA
 CGTCATCCCCACCTTCTCTCAGTTTGCAGTCTCGTTAGATTCCCGACATGANTCGCTGGCAACTAACAACA
 G

Probability		High	Smallest
Sequences producing High-scoring Segment Pairs:		Score	P(N)
N			
gb L39067 FVBRRDA 2	Flavobacterium ameridies 16S riboso...	1747	3.5e-146
gb M62797 FVBRRD 2	F.aquatile 16S ribosomal RNA.	1635	1.7e-137
gb M58781 FBCRR16SB 2	Flexibacter columnaris 16S ribosoma...	1632	2.6e-137
gb M59053 CYTRR16SI 2	Cytophaga johsonae 16S ribosomal RNA.	1632	3.0e-137
gb M58764 CYTRR16SA 2	Cytophaga aquatile 16S ribosomal RNA.	1606	3.9e-135

>M6316

TAGAGTTTGATCCTGGCTCAGGATGAACGCTAGCGGCAGGCTTAACACATGCAAGTCGAGGGGTATAGTTCTTCGGAA
 CTAGAGACCGGCGCACGGGTGCGTAACCGGTATGCAATCTACCTTTCACAAAGGGATAGCCCAGAGAAATTTGGATTA
 ATACCTTATAGTAATACGACTTGGCATCAAGATGTATTTAAAGATTTATCGGTGAAAGATGAGCATGCGTCCCATTAG
 CTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATGGGTAAGGGTCTGAGAAGGAAATCCCCACACTGGTACTGA
 GACACGGACCAGACTCCTACCGGAAGCACAGTGAAGAATATTGGACAATGGGCGCCAGCCTGATCCAGCC

Sequences producing High-scoring Segment Pairs:		High	Smallest
		Score	Sum
		P(N)	N
gb U63940 CSU63940	Cytophaga sp. 16S ribosomal RNA gen...	1124	2.9e-124
gb M59053 CYTRR16SI	Cytophaga johsonae 16S ribosomal RNA.	1424	4.2e-122
dbj D84581 D84581	Flexibacter sp. DNA for 16S ribosom...	1352	5.8e-122
gb U63938 FSU63938	Flavobacterium sp. 16S ribosomal RN...	1341	4.7e-121
gb U63943 CSU63943	Cytophaga sp. 16S ribosomal RNA gen...	1068	6.0e-121

>SAM801

TAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGAGTGCTTTACACATGCAAGTCGAACGGCAGCACGGGGGCTTG
CTCCTGGTGGCGAGTGGCGAACGGGTGAGTAATGCGTCGGAACGTACCGAGTAATGGGGGATAACGCACCGAAAGGTG
TGCTAATACCGCCTACGCCCTGAGGGGGAAAGCANGGGATCATTAGACCTTGC GTTATTCGAGCGGCCGACCTTCTGA
TTAGCTAGTTGGTGGGGTAAAG

Table with 5 columns: Probability, Sequences producing High-scoring Segment Pairs: N, High Score, Smallest Sum, P(N). Rows include Nitrosolobus multiformis, Azoarcus sp., Beta-proteobacterium 16S rRNA gene, and Neisseria canis 16S ribosomal RNA.

>SAM802

TAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGGGCAACC
TGGTGGCGAGTGGCGAACGGGTGAGTAATATATCGGAATGTACCCTAGAGTGGGGGATAACGTAGCGAAAGTTACGCT
AATACCGCATAACGATCTACGGATGAAAGTGGGGGATCGCAAGACCTCATGCTCATGGAGCAGCCGATATCTGATTAGC
TAGTTGGTAGGGTAAAAGCCTACCAAGGCGACGATCAGTAGCTGGTTTTGAGAGAACGACCAGCCACACTGGAAGTGG
ACACGGTCCAGACTCCTACGGGAAGCAGCAGTGGGAATTCCTGGACAATG

Table with 5 columns: Probability, Sequences producing High-scoring Segment Pairs: N, High Score, Smallest Sum, P(N). Rows include Zoogloea sp. 16S ribosomal RNA gene, Z. ramigera gene for 16S rRNA, and Unidentified beta proteobacterium DNA.

>803

GACGAACGCTGGCGCCGTGCTTAACACATGCAAGTCGAACGGAAAGGCCCTGCTTTTGTGGGGTGCTCGAGTGGCGAA
CGGGTGGTAAACACGTGAGTAACCTGCCCTTGACTTTGGGATAACTTCAGGAAACTGGGGCTAATACCGGATAGGAGC
TCCTGCTGCATGGTGGGGTTGGAAAGTTTCGGCGGTTGGGGATGGACTCGCGGCTTATCAGCTTGTGGTGGGGTAG
TGGCTTACCAAGGCTTTGACGGGTAGCCGGCCTGAGAGGTGACCGGCCACATTTGGGACTGAGATACGGCCAAACTCCT
ACGGGAAGCAGCAGTGGGAATATTGCACAATGGGCGGAACCTGATGCACAACGCGCGTGGGGATGACGGCTCGGTGT

Table with 5 columns: Probability, Sequences producing High-scoring Segment Pairs: N, High Score, Smallest Sum, P(N). Rows include M. chitae 16S ribosomal RNA, Propionibacterium acnes small subunit, and Fusobacterium prausnitzii small subunit.

>SAM804
 TAGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGAACGGAGAATTTCGAAGAGT
 TTACTCGGAGAAATTTTGTAGTGGCGGACGGGTGAGTAACGCGTGGGTAACCTACCCATAAACCCGGGACAACCCTTGG
 AAACGAGGGCTAATACCGGATAATCTCTTAGCTTGGCACCAAGTTTTAAGAAAAGGTGGCCTCTGAGTATGCTACCGA
 TTATGGATGGACCCGCGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTACCAAGGCGACGATCAGTAGCCGGCCTGAG
 AAGGTGAACGGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAAGCACAGTGGGAATCTCCGCAATGGACA
 A

Probability Sequences producing High-scoring Segment Pairs: N		High Score	Smallest Sum P(N)
gb M34417 DSORR1618 4	-Desulfotomaculum orientis 16S ribos...	788	7.1e-116
gb L28946 DTORRD 3	Desulfitobacterium dehalogenans 16S...	1119	8.4e-112
gb U68528 DCU68528 3	Desulfitobacterium chlororespirans ...	1115	3.7e-103
emb X94975 DH16SRRNA 3	D.hafniense 16S ribosomal RNA	1081	8.5e-101
emb X99706 SG16SRR1 4	S.glycolicus 16S rRNA gene	580	2.3e-95

ADDENDUM

Color of Millipore membranes after filtration of the respective water sample
(M28 is control "clean" water)

