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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:

Dr. M. Kalin, President
Boojum Research Ltd., Toronto

Submitted by:

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May 28, 1997

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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 ^{0}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 filterwas 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^{0}C while mixing every 30 min. Freeze each mixture in dry ice for 15 min and then thaw at 60^{0}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^{0}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^{0}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^{0}C overnight. Centrifuge at 8400 rpm at 4^{0}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^{0}C and 35 cycles of 1 min at 94^{0}C, 1 min at 50^{0}C and 2 min at 72^{0}C. Keep reactions at 4^{0}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 *Eco*RV 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 occurences 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 memebrs 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 *Methanococcous jannaschii*. This group of supposed bacteria (initially termed archaebacteria) 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 archael sequences have been found recently in soil.

3. Bacteria (of the interesting kind) galore.

i) ***Zooglea/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 in *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

(NO;) 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 Fe^{2+} 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*** ferrooxidansand ***Acidophilum.*** 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 Fe^{2+} 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 frshwater sediments. These are strictly anaerobic. Sulfate and in some cases also sulfite and/or thiosulfate are reduced to hydrogen sulfide. Sulfate reducing beateria (SRBs) are good to have since a common strategy of reducing acidity is to promote the growth of SRBs.

v) ***Nitrosolubus/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 ramigeraa*
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 dehalogenas*
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 tepidium?*
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

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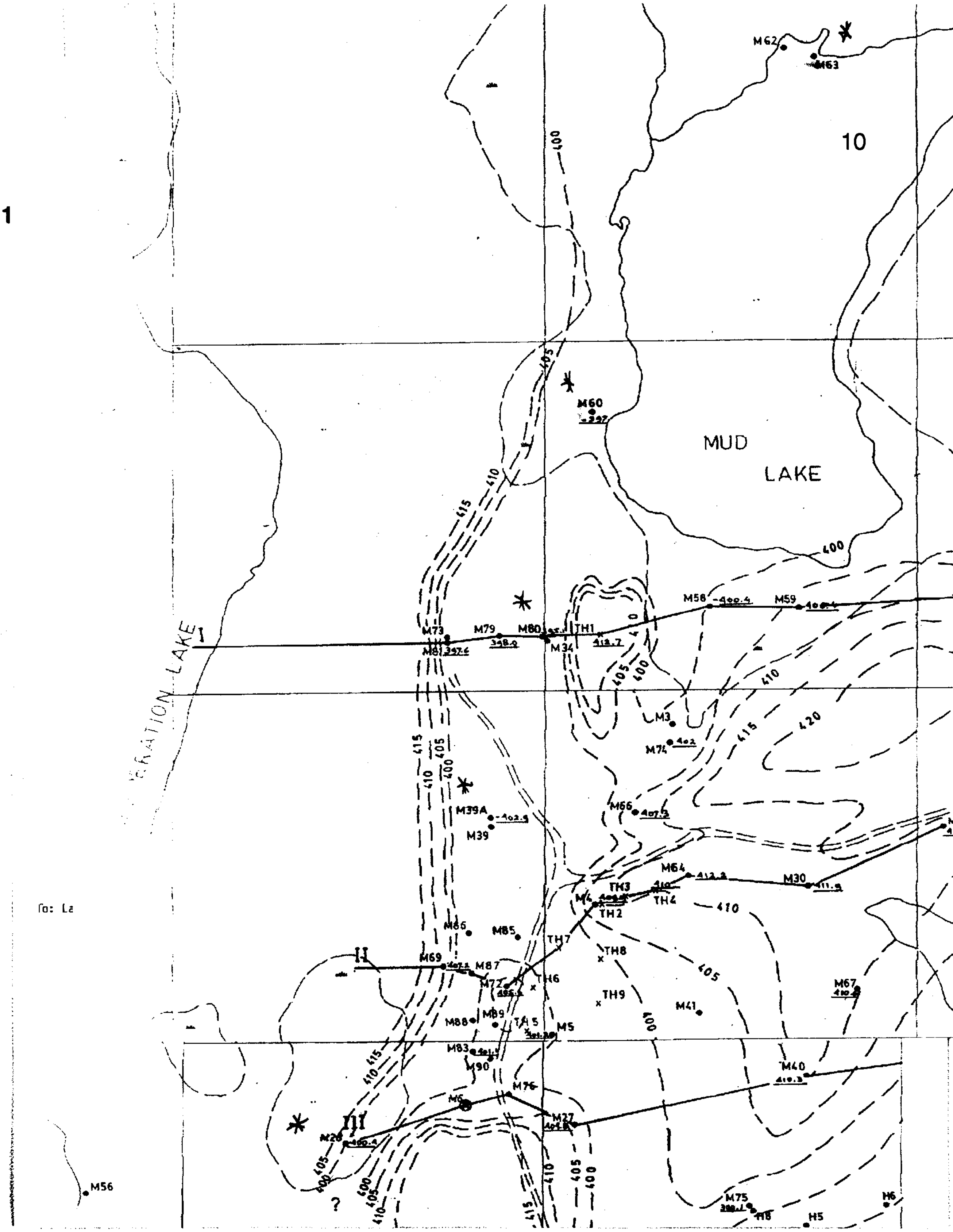
Fig. 1



10
MUD
LAKE
...RATION LAKE
fo: La
I
II
III
M62
M63
M60
M58
M59
M73
M81
M79
M80
M34
TH1
M3
M74
M66
M39A
M39
M64
M30
TH3
TH4
TH2
M4
TH7
TH8
TH6
TH9
M86
M85
M69
M87
M72
M88
M89
TH5
M5
M41
M67
M83
M90
M76
M6
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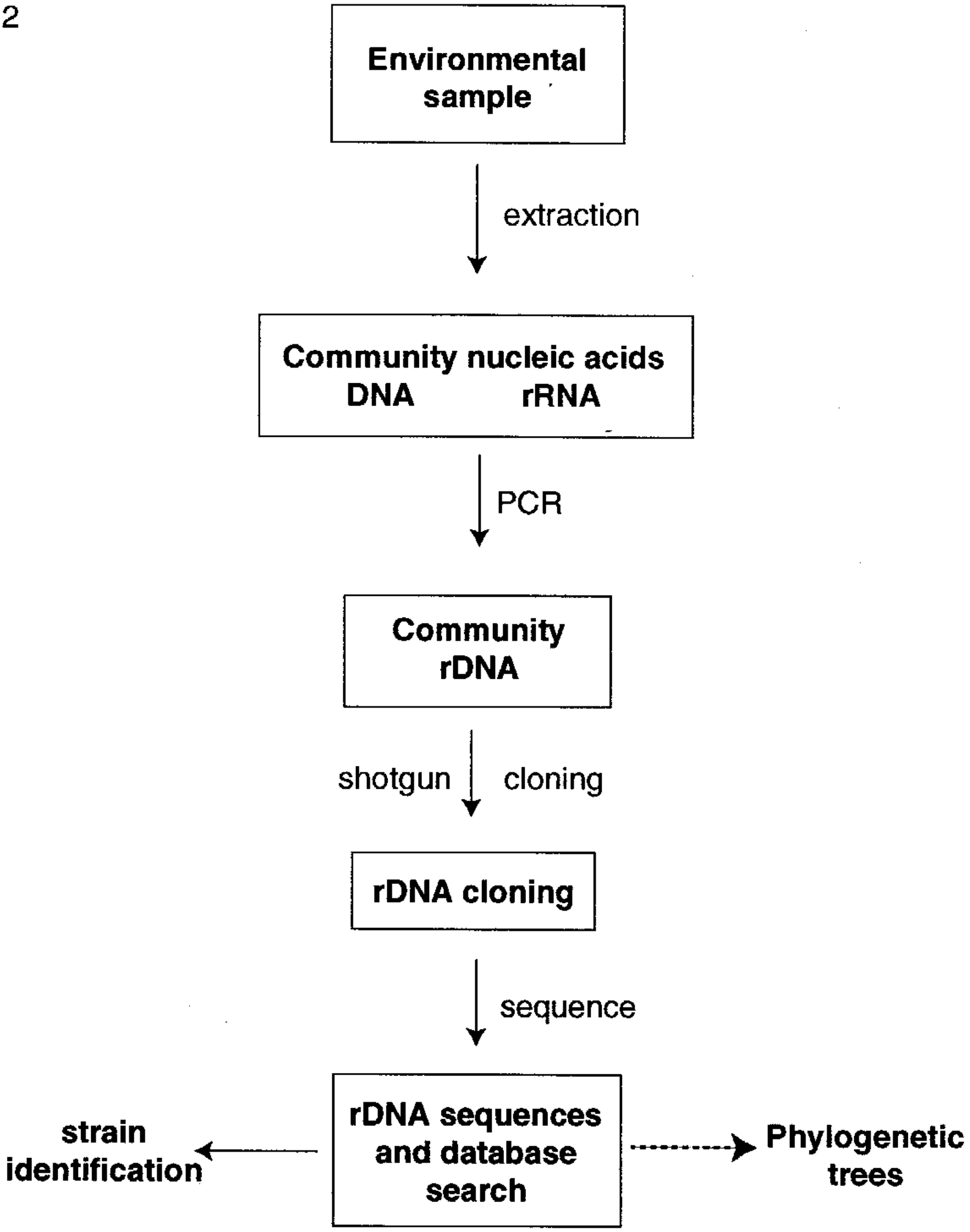
M40
M75
H8
H5
H6
M56
400
405
410
415
420
?

Fig.2


Environmental sample
extraction
Community nucleic acids
DNA
rRNA
PCR
Community rDNA
shotgun
cloning
rDNA cloning
sequence
strain identification
rDNA sequences and database search
Phylogenetic trees

Appendix I

```
>SAM281
TTACGGCTACCTTGTTACGACTTCACCCCAGTCACGAATCCCACCGTGGTAAGCGCCCTCCTTACGGTTAAGCTACCT
ACTTCTGGTGAAACCCGCTCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCGACATGCTG
ATCCGCGATTACTAGCGATTCCAACTTCATGCAGTCGAGTTGCAGACTACTATCCGGACTACGATACACTTTCTGGGA
TTAGCTCCCCCTCGCGGGTTGGCGGCCCTCTGTATGTACCATTGTATGACGTGTGAAGCCCTAACCATAAG
```

```
                                                                     Smallest
                                                                        Sum
                                                              High
 Probability
Sequences producing High-scoring Segment Pairs:               Score  P(N)
     N

emb|X74914|ZR16SRRNB   Z.ramigera gene for 16S rRNA (ATCC ...  1466  1.4e-114
 1
emb|X92555|PL16SR220   P.lemoignei 16S ribosomal RNA (stra...  1457  7.9e-114
 1
emb|X92554|PL16SRA62   P.lemoignei 16S ribosomal RNA (stra...  1444  9.6e-113
 1
gb|U34035|UBU34035     Unidentified beta proteobacterium c...  1340  4.6e-104
 1
dbj|D14256|PSER16S3    Z.ramigera gene for 16S ribosomal RNA.  1333  1.7e-103
 1
```

```
>SAM282
TTACGGTTACCTTGTTACGACTTCACCCCAGTCACGAATCCCACCGTGGTAAGCGCCCTCCTTGCGGTTAAGCTACCT
ACTTCTGGTGAAACCCGCGCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCGACATGCTG
ATCCGCGATTACTAGCGATTCCAACTTCATGTAGTCGAGTTGCAGACTACAATCCGGACTACGATACACTTTCTGGGA
TTAGCTCCCCCTCGCGGGTTGGCGGCCCTCTGTATGTACCATTGTATGACGTGTGAAGCCCTACCCATAAG
```

```
                                                                     Smallest
                                                                        Sum
                                                              High
 Probability
Sequences producing High-scoring Segment Pairs:               Score  P(N)
     N

emb|X92555|PL16SR220   P.lemoignei 16S ribosomal RNA (stra...  1475  2.5e-115
 1
emb|X74914|ZR16SRRNB   Z.ramigera gene for 16S rRNA (ATCC ...  1466  1.5e-114
 1
emb|X92554|PL16SRA62   P.lemoignei 16S ribosomal RNA (stra...  1462  3.1e-114
 1
gb|U34035|UBU34035     Unidentified beta proteobacterium c...  1349  8.2e-105
 1
dbj|D14256|PSER16S3    Z.ramigera gene for 16S ribosomal RNA.  1342  3.1e-104
 1
```

```
>SAM283
TTACGGCTACCTTGTTACGACTTAGCCCTAGTTACCAGTTTTACCCTAGGCAGCTCCTTGCGGTCACCGACTTCAGGC
ACCCCCAGCTTCCATGGCTTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGGATCATGGCTGATATCCGA
TTACTAGCGATTCCAGCTTCACGGAGTCGAGTTGCAGACTCCGATCCGAACTGTGACCGGTTTTATAGATTCGCTCCT
GGTCACCCAGTGGCTGCTCTCTGTACCGGCCATTGTAGCACGTGTGTAGCCCAAGGCGTTAAGGGCCGTGATGATTTG
ACGTCATCGCCACCTTCCTCTCAGTT
```

```
                                                              High
 Probability
Sequences producing High-scoring Segment Pairs:               Score  P(N)
     N

gb|L39067|FVBRRDA      Flavobacterium ameridies 16S ribosom...  1459  5.9e-127
 2
gb|M58781|FBCRR16SB    Flexibacter columnaris 16S ribosomal...  1344  2.4e-117
 2
gb|M59053|CYTRR16SI    Cytophaga johsonae 16S ribosomal RNA.    1344  2.6e-117
 2
gb|M62797|FVBRRD       F.aquatile 16S ribosomal RNA.            1338  8.3e-117
 2
gb|M62792|FBCRR16SZ    F.aurantiacus 16S ribosomal RNA.         1337  9.1e-117
 2
```

```
>SAM286
TAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGAACGATGATAGGAAGCTTGC
TTCCTTGATTAGCGGCGCACGGGTGAGTAATGCATAGATAATGTGCCCCTTAGTTCGGGATAGCCACTGGAAACGGTG
ATTAATACCGGATACTCCTTCTCGTTATAAGACGAGTCGGGAAAGTTTTTCGCTAAGGGATCAGTCTATGTTCCATCA
GCTTGTTGGTGAGGTAATGGCTCACCAAGGGCTATGACGGATATCTGGTTTGAGAGGATGATCAGACACACTGGAACT
GAGACACGGTCCATACTCCTACGGGAAGC
```

```
                                                                       Smallest
                                                                         Sum
                                                                High
 Probability
Sequences producing High-scoring Segment Pairs:                 Score  P(N)
      N

gb|L39122|HECRGD       Helicobacter hepaticus 16S ribosomal...   389   7.2e-93
    4
gb|M88144|HECRR16SBE Helicobacter sp. (strain B52D Seymou...     385   3.8e-92
    4
gb|M88141|HECRR16SBC Helicobacter sp. (strain B13A Seymou...     389   3.9e-92
    4
gb|L36143|HECFRC       Helicobacter pullorum (strain NCTC 1...   380   9.4e-92
    4
gb|L36146|HECFRF       Helicobacter pullorum (strain UB 316...   380   9.6e-92
    4
```

```
>M287
CCTGGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGGAGCAATCCTGGTGGCGA
GTGGCGAACGGGTGAGTAATATATCGGAACGTGCCCAGTCGTGGGGGATAACGCAGCGAAAGCTGTGCTAATACCGCA
TACGATCTCTGGATGAAAGCGGGGGACTCGCAAGGGCCTCGCGCGATTGGAGCGGCCGATATCAGATTAGCTAGTTGG
TGGGGTAAAAGCCCACCAAGGCGACGATCTGTAGCTGGTCTGAGAAGACGACCAGCCACACTGGAACTGAGACACGGT
CCAGACTCCTACGGGAAGCACAGAAGGGAATTTTGGACAATGGGCGCAGCCTGATCCACAATGCCGCGTGCAGATGAA
GCTC
```

```
                                                                       Smallest
                                                                         Sum
                                                                High
 Probability
Sequences producing High-scoring Segment Pairs:                 Score  P(N)
      N

dbj|D84619|D84619      Unidentified beta proteobacterium D...    616   1.7e-120
    5
dbj|D16211|RHYFR2D     R.fermentans gene for 16S ribosomal...    833   1.9e-119
    3
dbj|D16212|RHYFR3E     R.fermentans gene for 16S ribosomal...    833   1.9e-119
    3
emb|X95837|BS16ST3     Bacteria species 16S rRNA gene, str...    847   2.9e-118
    3
dbj|D84645|D84645      Unidentified beta proteobacterium D...    620   2.0e-117
    4
```

```
>2M28.4
GCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGAGCTTGCTCTGGTGGCGAGTGGCGAACGGGTGGGT
AATATATCGGAACGTACCCTGGAGTGGGGGATAACGCAGCGAAAGTTGCGCTAATACCGCATACGATCTACGGATGAA
AGTGGGGGATCGCAAGACCTCATGCTCGTGGAGCGGCCGATATCTGATTAGCTAGTTGGTAGGGTAAAAGCCTACCAA
GGCATCGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACGGCCCATACTCCTACGGGAGGC
TTCAGTGGGGAATTTTTGGACAATGGGGGCAACCCTGATCCATCAATGCCCGCGTGAGTGAAGAAGGCCTTCGGGT
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                                                                    Smalles t
                                                                       Sum
                                                               High Probability
Sequences producing High-scoring Segment Pairs:               Score   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
```

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>2M28.6
GCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGAGCTTGCTCTGGTGGCGAGTGGCGAACGGGTGAGT
AATATATCGGAACGTACCCTGGAGTGGGGATAACGCAGCGAAAGTTGCGCTAATACCGCATACGATCTACGGATGAA
AGTGGGGGATCGCAAGACCTCATGCTCGTGGAGCGGCCGATATCTGATTAGCTAGTTGGTAGGGTAAAAGCCTACCAA
GGCATCGATCAGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGC
AGCAGTGGGGAATTTTGGACAATGGGGGCAACCCTGATCCAGCAATGCCGCGTTGAGTGAAGAAGGCCTTCGGGTTGT
TAAAGCTCTTTTGTCAGGGAAGAAACGGTGATTCCTTAATACCGATTGCTAATGACNGTACCTGAAGAATAAGCCCCG
T
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                                                                    Smalles t
                                                                       Sum
                                                               High  Probability
Sequences producing High-scoring Segment Pairs:                Score   P(N)      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
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>2M28.11
GACGCCTAACACATGCAAGTCAAACGGGATTGAGGGCGAGCTGTCATGACAGTGGCGCACGGGTGAGTAGACGCGTAT
GCAACCTACCGTTTGGCTGAGGGATAGCCCATATAAATGGGGATTAATACCTCATAGGTTCTTTTGATCCGCATGGAT
TGGAAAGATAAAGCTCCTGCGGTTAGAAGATGGGCATGCGTGACATTAGTTTGTTGGTGAGGTAACGGCTCACCAAGA
CTACGATGTCTAGGGGTTCTGAAAGGATGATCCCCCACACTGGTACTGAGACACGGACCAGACTCCTACGGGAGGCAG
CAGTGAGGAATATTGGTCAATGGGCGCAAGCCTGAACCAGCCATCCCCCGTGCAGGATGAAGGCCCTATGGGTCGTAA
ACTGCTTTTATACACCAAGAA
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                                                                     Smalles t
                                                                        Sum
                                                                 High  Probability
Sequences producing High-scoring Segment Pairs:                  Score   P(N)      N

emb|X84553|UNSBR2008     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
```

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>2M28.18
GCGGGGGGCAGGCTTAACACGTGCAAGTCGAGGGGTANAGTTCGTCGGAAGTAGAGACCGGCGCACGGGTGCGTGACG
CGTGTGCAATCTACCTTGCACAAAGGGATAGCCCATAGAAATTTGGATTAGTACCTTATAGTAGTACGACTTGGCATC
AAGATGTGTTTAAAGATTTTTCGGTGAAAAATGAGCATGCGTCCCGTTAGCGAGTGGGGGAGGTAACGGCTTACCAAG
GCAACGATGGGTAGGGGTCCTGAGAGGGAGATCCCCCACGCTGGTACTGAGACACGGACCAACTTCCTACGGGAGGCA
GCAGTGAGGAATATTGGACAATGGGCGCAAGCCTGATCCAACCATGCCGCGTGCAAGATGACGTCCTATGGATTGTAA
ACTGCTTTTATACAGGAAGAACACTCCGACT
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                                                                     Smalles t
                                                                        Sum
                                                                 High  Probability
Sequences producing High-scoring Segment Pairs:                  Score   P(N)      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
```

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>M3911
TACGGCTACCTTGTTACGACTTAGCCCTAGTTACCAGTTTTACCCTAGGCAGCTCCTTGCGGTCACCGACTTCAGGCA
CCCCCAGCTTCCATGGCTTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGGATCATGGCTGATATCCGAT
TACTAGCGATTCCAGCTTCACGGAGTCGAGTTGCAGACTCCGATCCGAACTGTGACCGGTTTTATAGATTCGCTCCTG
GTCACCCAGTGGCTGCTCTCTGTACCGGCCATTGTAGCACGTGTGTTACCCAAGGCGTAAGGGCCGTGATGATTTGAC
GTCATCCCCACCTTCCTCTCAGTTTGCACTGGCATCTCGTTAAATTCCCGACATGATCGCTGGCACTAACACAG
```

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                                                                    Smalles t
                                                                       Sum
                                                              High Probability
Sequences producing High-scoring Segment Pairs:              Score  P(N)     N

gb|L39067|FVBRRDA    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|FVBRRD     F.aquatile 16S ribosomal RNA.            1573 1.8e-123  1
gb|M62792|FBCRR16SZ  F.aurantiacus 16S ribosomal RNA.         1572 2.1e-123  1 -
```

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M396
AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCTAATACATGCAAGTGGAACGCATGATTGATACCGGA
CTTGCTCTATCATTAATCATAAGTCGCGAACGGGTGAGTAACGCGTAGGTAACCTACCTCATAGCGGGGGATAACTA
TGGAAACGATAGCTAATACCGCATAACAGTCTTTGACACATGTTAGAGACTTAAAAGGAGCAATTGCTTCACTATGA
ATGGACCTGCGTTTGTATTAGCTAGTTGGTGAGGTAAAGGCTCACCAAGGCGACGATACATAGCCGACCTGAGAAGG
GATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCCTACGGGAAGCACATTAG
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                                                                    Smallest
                                                                      Sum
 Probability                                                  High
Sequences producing High-scoring Segment Pairs:
      N                                                       Score  P(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
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M3913
AGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGGGCAACC
GNTGGCGAGTGGCGAACGGGTGAGTAATATATCGGAATGTACCCTAGAGTGGGGGATAACGTAGCGAAAGTTACGCT
ATACCGCATACGATCTTCGGATGAAAGTGGGGGATCGCAAGACCTCATGCTCATGGAGCAGCCGATATCTGATTAGC
AGTTGGTAGGGTAAAAGCCTACCAAGGCGACGATCAGTAGCTGGTTTGAGAGAACGACCAGCCACACTGGAACTGAG
CACGGTCCAGACTCCTACG
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                                                                    Smalles t
                                                                       Sum
                                                              High Probability
Sequences producing High-scoring Segment Pairs:              Score  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
AACACGAACACGTCGAGGGGTCAGAGTTCGTCAGGAAGTATAGACCGGCGCACGGGTGCGTAACGCGTATGCAATCTA
CCTTTCACAAAGGGGATAGCCCAGAGAAATTTGGATTAATACCTTATAGTAATACGACTTGGCATCAAGATGTATTTA
AAGATTTATCGGTGAAAGATGAGCATGCGTCCCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATGGGT
AGGGGTCCTGAGAGGGAGGTCCCCCACACTGGTACCGAGACACGGACCAGACTCCTACGGGAGGCAGCAGTGAGGAAT
ATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGCAGGATGACGGTCCTATGGATTGTAAACTGCTTTTAT
ACAGGAAGAAACACTCGCGACGTGTCCGAGCTTGACGGTACTGTAGGAATAAGGATCGGCTAACTCCGTGCCAGCAGC
CGCGGTAATACGGCAGGATC

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                                                                        Smalles t
                                                                           Sum
                                                                   High  Probability
Sequences producing High-scoring Segment Pairs:                    Score   P(N)      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
CTAGAGTGGGGGATAACGTAGCGAAAGTTACGCTAATACCGCATACGATCTACGGATGAAAGTGGGGGATCGCAAGAC
CTCATGCTCATGGAGCAGCCGATATCTGATTAGCTAGTTGGTAGGGTAAAAGCCTACCAAGGCGACGATCAGTAGCTG
GTTTGAGAGAACGACCAGCCACACTGGAACTGATACACGGTCCATACTCCTACGGGAGGCAGCAGTGGGGAATTTTGG
ACAATGGGGGCAACCCTGATCCAGCAATGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTTGTCAGGGA
AGAAAAGGTAGCCTCTAATACAGGCTGCTCATGACGGTACCTGAAGAATAAGCACCGGCTAACTACGTGCCAGCAGCC
GCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTTATATAAGT

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                                                                        Smalles t
                                                                           Sum
                                                                   High  Probability
Sequences producing High-scoring Segment Pairs:                    Score   P(N)      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.lemoignei 16S ribosomal RNA (stra...   2167  7.7e-178   2
emb|X92554|PL16SRA62    P.lemoignei 16S ribosomal RNA (stra...   2152  2.1e-175   2
```

>3M9~~65~~ 396
CGAACGCGAAAGTAGGGGCAACCCTGCGAGTAGAGTGGCGAACGGGTGAGTAATACATCGGAACGTACCCAGGCAGTG
GGGGACAACCTCGAGAAATCGAGGCTAACACCGCATACGTCCTGAGGGAGAAAGCGGGGGATCCGTAAGGACCTCGCG
CTCATGGAGCGGCCGATGTCGGATTAGCTAGTTGGCGGGGTAAAAGCCCACCAAGGCTACGATCCGTAGCTGGTTTGA
GAGAACGACCAGCCACACTGGGACTGATACACCGCCCACACTCCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATG
GGGGAAACCCTGATCCAGCC

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                                                                        Smalles t
                                                                           Sum
                                                                   High  Probability
Sequences producing High-scoring Segment Pairs:                    Score   P(N)      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
AACCGGCTTTGCGTGCTTGCACCGGAGTTAGTGGCGAACGGGTGAGTAATATATCGGAACATATCCGGAAGTGGGGA
TAACGTGACGAAAGTTTCGCTAATACCGCATATGCCCTGAGGGGGAAAGGGGGGGATCGCAAGACCGTCTCGCTTTCG
GAGTGGCCGATACCGGATTAGCTACATGGTGAGGTAAAGGCTCACCATGGCGACGATCCGTAGCTGGTCTGAGAGGAC
GACCAGCCACTCTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGC

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                                                                    Smalles t
                                                                       Sum
                                                               High  Probability
Sequences producing High-scoring Segment Pairs:                Score  P(N)     N

gb|L07897|GLLRGDA        Gallionella ferruginea 16S ribosoma...  641  3.4e-87
  2
emb|X84620|UNSBR2090     Unknown organism, partial 16S rRNA ...  544  5.5e-73
  2
emb|X84544|UNSBR1119     Unknown organism, partial 16S rRNA ...  524  2.0e-71
  2
emb|X84465|UNSBR1021     Unknown organism, partial 16S rRNA ...  587  3.0e-71
  2
emb|X84518|UNSBR1090     Unknown organism, partial 16S rRNA ...  542  1.7e-70
  2
```

>SAM601
TAGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGAACGGCCTTTGCGAGGTTCG
AAGCTCGAGGTTCGAAGTTCGAATTAAATTGACTTCTGAGGTATTAAAAGGCCACAGAGAAATTCTTAATTCGCACAT
CGTGCATCGCACTTCGAACTTCGCGGGTAGTGGCGGACGGGTGAGTAACGCGAGGGTAACCTACCCATAAACCCGGGA
CAACCCTTGGAAACGAGGGCTAATACCGGATAATCTTTTAGCTTGGCATCAAGCAATAAGAAAAGGTGGCCTCTGAAA
ATGCTACCGATTATGGATGGACCCGCGTCTGATTAGCTAGTTGGTG

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                                                                 Smallest
                                                                   Sum
                                                           High
 Probability
Sequences producing High-scoring Segment Pairs:            Score  P(N)
     N

gb|M34417|DSORR1618     Desulfotomaculum orientis 16S ribos...   388  2.7e-71
  3
gb|L28946|DTORRD        Desulfitobacterium dehalogenans 16S...  ·681  1.1e-70
  2
gb|U68528|DCU68528      Desulfitobacterium chlororespirans ...   668  2.7e-61
  2
emb|X94975|DH16SRRNA    D.hafniense 16S ribosomal RNA            625  1.0e-58
  2
emb|X99706|SG16SRR1     S.glycolicus 16S rRNA gene               375  1.3e-52
  3
```

>SAM602
TAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGTATGCTTTACACATGCAAGTCGAACGGATTTGGGGGCTTGCT
CCCAAGTTAGTGGCGAACGGGTGAGTAATATATCGGAACATATCCGGAAGTGGGGGATAACGTAGCGAAAGTTACGCT
AATACCGCATATGCCCTGAGGGGGAAAGGGGGGGATCGCAAGACCTCTCGCTTTCGGAGTGGCCGATATCGGATTAGC
TAGTAGGTGAGGTAAAGGCTCACCTAGGCGACGATCCGTAGCTGGTCTGAGAGGACGACCAGCCACACTGGAACTGAG
ACACCGTCCACACTCCTACCGGAAGCAGCAGTG

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                                                                 Smallest
                                                                   Sum
                                                           High
 Probability
Sequences producing High-scoring Segment Pairs:            Score  P(N)
     N

gb|L07897|GLLRGDA       Gallionella ferruginea 16S ribosoma...  1436  4.6e-112
  1
gb|U63941|ZSU63941      Zoogloea sp. 16S ribosomal RNA gene...   958  9.5e-96
  2
emb|X65589|TM16SR       T.mixta 16S rRNA                         996  1.4e-95
  2
gb|U63953|ASU63953      Alcaligenes sp. 16S ribosomal RNA g...   958  4.4e-94
  2
gb|L35509|NTL16SR       Nitrosolobus multiformis (ATCC 2519...   958  5.3e-93
  2
```

>SAM604
TAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGTATGCTTTACACATGCAAGTCGAACGGCTTTGGTGCTTGCA
CCGGAGTTAGTGGCGAACGGGTGAGTAATATATCGGAACATATCCGGAAGTGGGGGATAACGTAGCGAAAGTTACGCT
AATACCGCATATGCCCTGAGGGGGAAAGGGGGGATCGCAAGACCTCTCGCTTTCGGAGTGGCCGATACCGGATTAGC
TAGATGGTGAGGTAAAGGCTCACCATGGCGACGATCCGTAGCTGGTCTGAAAAGACGACCAGCCACACTGGAACTGAG
ACACGGTCCAGACTCCTACGGAAGCACCAGTG

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                                                                   Smallest
                                                                    Sum
                                                             High
 Probability
Sequences producing High-scoring Segment Pairs:              Score  P(N)
     N

gb|L07897|GLLRGDA       Gallionella ferruginea 16S ribosoma...  1382  1.5e-107
  1
gb|U63941|ZSU63941      Zoogloea sp. 16S ribosomal RNA gene...   913  5.0e-92
  2
emb|X65589|TM16SR       T.mixta 16S rRNA                         951  7.7e-92
  2
gb|U63953|ASU63953      Alcaligenes sp. 16S ribosomal RNA g...   913  2.3e-90
  2
gb|L35509|NTL16SR       Nitrosolobus multiformis (ATCC 2519...   913  3.0e-89
  2
```

>SAM605
TAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCCTAACACATGCAAGTCGAACGGTAGCAGGCCTTCGGG
TGCTGACGAGTGGCGGACGGGTGAGTAATGCGTAGGAATCTGTCTTTTAGTGGGGGACAACCCACGGAAACTTGGGCT
AATACCGCATGAGCCCTGAGGGGGAAAGCGGGGGATCTTCGGACCTCGCGCTAAGAGGAGAGCCTACGTCCTGATTAC
CTAGTTGGTACGGTAAAGGCCTACCAAGGCGACAATCACTAGCTGGTCTGAGAGGAC

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                                                                   Smallest
                                                                    Sum
                                                             High
 Probability
Sequences producing High-scoring Segment Pairs:              Score  P(N)
     N

emb|X75266|TF16SRRN  T.ferrooxidans (N-Fe2) gene for 16S ...   921  4.9e-89
  2
emb|X75267|TF16SRNA  T.ferrooxidans (N-Fe4) gene for 16S ...   912  2.8e-88
  2
emb|X98210|TS16SRDNA Thiobacillus sp. 16S ribosomal DNA        921  3.6e-88
  2
emb|X93478|PBDSM2111 Phototrophic bacterium 16S rRNA gene...   952  2.4e-87
  2
emb|X75268|TFN16SRRN T.ferrooxidans (N-Fe3) gene for 16S ...   926  1.1e-85
  2
```

>SAM606
TTACGGTTACCTTGTTACGACTTAGCGCCAGTCACCAGTTTTACCTTCAGCCCCGATTACTCGGAGATTTCAGGTACC
ACCAGCTCCCATCGCTTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACGGCGGCGTAGCTGATCCGCCATTA
CTAGTGATTCCGTCTTCATGGAGTCGAATTGCAGACTCCAATCTGAACTGAGCCCACTTTTTTGCGATTAGCTCCACC
TCGCGGTTTGGCAACGCTTTGGAGTGGGCATTGTAACACGTGTGTAGCCCAAGGCATAAAGGCCGTACTGACTTGACG
TCATCTCCATCTTCCTCCCGCTTATCGCG

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                                                                   Smallest
                                                                    Sum
                                                             High
 Probability
Sequences producing High-scoring Segment Pairs:              Score  P(N)
     N

gb|L09660|TTHAT62     Thermus flavus AT-62 16S ribosomal R...   975  2.0e-82
  2
gb|L10067|TTHDNAFRA   Thermus Fiji 3A DNA fragment.             975  2.0e-82
  2
gb|M26923|TTH16SRAA   T.thermophilus 16S rRNA gene, comple...   975  4.5e-82
  2
gb|L09670|TTHHS       Thermus sp. HS A.1 16S ribosomal RNA...   966  1.1e-81
  2
gb|L10069|TTHDNAFRC   Thermus Tok3 A.1 DNA fragment.            957  1.1e-81
  2
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>SAM607
TTACGGCTACCTTGTTACGACTTCACCCCAGTCACTGAGCCTACCGTGGTTGGCTGCCTCCATTGCTGGTTGGCGCAC
CACCTTCGGGTAGACCCAATTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGTCATGC
TGTTACGCGATTACTAGCGATTCCGACTTCATGGGGTCGAGTTGCAGACCCCAATCCGAACTGAGATGGCTTTTTGGG
ATTAACCCATTGTCACCACCATTGTAGCACGTGTGTAGCCCAACCCGTAAGGGCCATGAAGACTTGACGTCATCCACA
CCTTCCTCCGGCTTATCACCGGCAGTTTTTCCTA
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                                                                Smallest
                                                                  Sum
                                                            High
  Probability
 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
TAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCGGCACGGGAGCAAT
CCAGGTGGCGAGTGGCGAACGGGTGAGTAATATATCGGAACGTGCCCAGTCGTGGGGGATAACGCAGCGAAAGCTGTG
CTAATACCGCATACGATCTCTGGATGAAAGCGGGGGACTCGCAAGGGCCTCGCGCGATTGGAGCGGCCGATATCAGAT
TAGCTAGTTGGTGGGGTAAAAGCCCACCAAGGCGACGATCTGTAGCTGGTCTGAGAAGACGACCAGCCACACTGGAAC
TGAGACCCGTCCACACTCCTACGGGAAGCACAGTG
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                                                                Smallest
                                                                  Sum
                                                            High
 Probability
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
TTACGGCTACCTTGTTACGACTTCACCCCAGTCATGAAACCCACCGTGGTAAGCGCCCTCCTTACGGTTAGGCTACCT
ACTTCTGGCAGATTCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCGACATGCTG
ATCCGCGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGATCGGCTTTCTGAGA
TTAGCTCCCCCTCGCGGGTTTGGCAACCCTCTGTACCGACCATTGTATTACGTGTGAAGCCCTACCCATAAG
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                                                                Smallest
                                                                  Sum
                                                            High
  Probability
 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
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>M6010
TAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGGAGCAAT
CCTGGTGGCGAGTGGCGAACGGGTGAGTAATATATCGGAACGTGCCCAGTCGTGGGGGATAACGCAGCGAAAGCTGTG
CTAATACCGCATACGATCTCTGGATGAAAGCGGGGGACTCGCAAGGGCCTCGCGCGATTGGAGCGGCCGATATCAGAT
TAGCTAGTTGGTGGGGTAAAAGCCCACCAAGGCGACGATCTGTAGCTGGTCTGAGAAGACGACCAGCCACACTGGAAC
TGAGACACGGTCCAGACTCCTACGGGAAG
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                                                                   Smalles t
                                                                     Sum
                                                              High  Probability
Sequences producing High-scoring Segment Pairs:              Score   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
```

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>M6011
TACGGTTACCTTGTTACGACTTCACCCCAGTCATGAAACCCACCGTGGTAAGCGCCCCCCTTACGGTTAGGCTACCTA
CTTCTGGCAGATTCCACTCCCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGCGACATGCTGA
TCCGCGATTACTAGCGATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGATCGGCTTTCTGAGAT
TAGCTCCCCCTCGCGGGTTGGCAACCCTCTGTACCGACCATTGTATTACGTGTGAAGCCCTACCCATAAGGGCCATGA
AGAATTGACTCATCCCCACTTCCTCCGGTTTGTCACGGCAGTCTCATTAAAGTGCCAACT
```

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                                                                   Smalles t
                                                                     Sum
                                                              High  Probability
Sequences producing High-scoring Segment Pairs:              Score   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
```

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>M6014
TGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCTACGAGAAAAGAGTANCNATACTCTGAG
TAAAGTGGCGCAAGGGTGCGTAACCCGTAAGCAATCTACCTTTAGGCGGGGAATAATCCAGCGAAAGCCGGACTAATA
CCCCATAATGCAGCGGCACCGCATGGTGATGTTGTTAAAGTCTATATGACGTCTANAGATGAGCTTGCGTCTGATTAG
CTAGTTGGTGAGGTAACGGCTCACCAAGGCTACGATCAGTAGCTGGTCTGAGAAGATGATCAGCCACACTGGAACTGA
GACACGGTCCAGACTCCTACGGGAA
```

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                                                                   Smalles t
                                                                     Sum
                                                              High  Probability
Sequences producing High-scoring Segment Pairs:              Score   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
```

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>M6020
TAGAGTTTGATCCTGGCTCAGAGCGAACGCTGGCGGCATGCTTAACACATGCAAGTCGCGCGGTCAGTAATGGCAGCG
GCGGACGGGTGAGTAACACGTAGGAATCTATCCCAGGGTGGGGGACAACAGCGGGAAACTGCTGCTAATACCGCATGA
TACCTGAGGGTCAAAGGCGCAAGTCGCCTTGGGAGGAGCCTGCGTCTGATTAGCTTGTTGGTGGGGTAAAGGCCTACC
AAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACATTGGGACTGAGACACGGCCAAACTCCTACGGGAAG
CAGCAGTG
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                                                                Smalles t
                                                                    Sum
                                                              High  Probability
Sequences producing High-scoring Segment Pairs:               Score   P(N)      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
```

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>2M603
CGCTGGCGGCATGCCTTACACATGCAAGTCGAACGCGCAAAGTAGGGGCAACCCTGCGAGTAGAGTGGCGAACGGGTG
AGTAATACATCGGAACGTACCCAGGAGTGGGGGACAACCTCGAGAAATCGAGGCTAACACCGCATACGTCCTGAGGGA
GAAAGCGGGGGATCCGTAAGGACCTCGCGCTCATGGAGCGGCCGATGTCGGATTAGCTAGTTGGCGGGGTAAAAGCCC
ACCAAGGCTACGATCCGTAGCTGGTTTGAGAGAACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGG
GAGGCAGCAGTGGGGAATTTTGGACAATGGGGGAAACCCTGATCCAGCCATGCCGCGTGAGTGAAGAAGGCCTTCGGG
TTGTAAAGCTCTTTCGGCCGGAACGAAATCGCGTACGTGAATAACGTGCGTGGATGACGGTACTGGAAGAAGAAGCAC
CGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTTAGGTGCGAACGTTAATCGGAATTACTGGGCCTTAAAGCGTG
CGTTAGCGGTTCT
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                                                             Smalles t
                                                                 Sum
                                                           High  Probability
Sequences producing High-scoring Segment Pairs:            Score   P(N)      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
```

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>2M6080
CGCTTAACACATGCAAGTCGAGGGGTATAGTTCTTCGGAACTAGAGACCGGCGCACGGGTGCGTAACGCGTATGCAAT
CTACCTTTCACAAAGGGATAGCCCAGAGAAATTTGGATTAATACCTTATAGTAATACGACTTGGCATCAAGATGTATT
TAAAGATTTACCGGTGAAAGATGAGCATGCGTCCCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATGG
GTAGGGGTCCTGAGAGGGAGATCCCCCACACTGGTACTGAGACACGGACCAGACTCCTACGGGAGGCAGCAGTGAGGA
ATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGCAGGATGACGGTACTATGGATTGTAAACTGCTTTT
ATACAGGAAGAAACACTAGGACGTGTCCGAGCTTGACGGTACTGTTAGAATAAGGATCGGCTAACTCCGTGCCAACCA
G
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                                                            Smalles t
                                                                Sum
                                                          High  Probability
Sequences producing High-scoring Segment Pairs:           Score   P(N)      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
TACGGCTACCTTGTTACGACTTAGCCCTAGTTACCAGCTTTACCCTAGGCAGCTCCTTGCGGTCACTGACTTCAGGCA
CCCCCAGCTTCCATGGCTTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGGATCATGGCTGATATCCGAT
TACTAGCGATTCCAGCTTCACGGAGTCGAGTTGCGGACTCCGATCCGAACTGTGACCGGTTTTATAGATTCGCTCCTG
GTCACCCAGTGGCTGCTCTCTGTACCGGCCATTGTAACACGTGTGTAGCCCAAGGCGTAAGGGCCGTGATGATTTGAC
GTCATCCCCACCTTCCTCTCAGTTTGCACTGGCAGTCTCGTTAGATCCCGAGATGACTCGCTG

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                                                             Smalles  t
                                                               Sum
                                                        High  Probability
  Sequences producing High-scoring Segment Pairs:       Score  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
AGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGTATGCTTTACACATGCAAGTCGAACGGCTTGGGGCTTGCT
CCCGAGTTAGTGGCGAACGGGTGAGTAATATATCGGAACATATCCGGAAGTGGGGATAACGTANCGAAAGTTACGCT
ATACCGCATATGCCCTGAGGGGGAAAGGGGGGATCGCAAGACCTCTCGCTCTCGGAGTGGCCGATATCGGATTAGC
AGTAAGTGAGGTAAAGGCTCACCTAAGCGACGATCCGTAGCGGGTCTGAGAAGACAACCGCCACACTGGAACTGAGA
ACGGTCCAACTCCCTAC

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                                                                  Smallest
                                                                    Sum
                                                              High
  Probability
 Sequences producing High-scoring Segment Pairs:              Score  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
TAGAGACCGACGCACGGGTGCGTAACGCGTATGCAATCTACCTTTCACAAAGGGATAGCCCAGAGAAATTTGGATTAA
TACCTTATAGTAATACGACTTGGCATCAAGATGTATTTAAAGATTTATCGGTGAAAGATGAGCATGCGTCCCATTAGC
TAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATGGGTTAGGGTCCTGAGAAGGAGATCCCCCACACTGGTACTGAG
ACACGGACCAGACTCCCTACGGGAAGCAGCAGTGAAGAATATTGGACAATG

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                                                                  Smallest
                                                                    Sum
                                                              High
 Probability
Sequences producing High-scoring Segment Pairs:               Score  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
dbj|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
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>M637
TTACGGCTACCTTGTTACGACTTAGCCCTAGTTACCAGTTTTACCCTAGGCAGCTCCTTGCGGTCACCGACTTCAGGC
ACCCCCAGCTTCCATGGCTTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGGATCATGGCTGATATCCGA
TTACTAGCGATTCCAGCTTCACGGAGTCGAGTTGCAGACTCCGATCCGAACTGTGACCGGTTTTATAGATTCGCTCCT
GGTCACCCAGTGGCTGCTCTCTGTACCGGCCATTGTAACACGTGTGTAACCCAAGGCGTAAGGGCCGTGATGATTTGA
CGTCATCC
```

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                                                                     Smallest
                                                                      Sum
                                                              High
  Probability
 Sequences producing High-scoring Segment Pairs:              Score  P(N)
      N

gb|L39067|FVBRRDA    .Flavobacterium ameridies 16S ribosom...  1568  4.2e-123
 1
gb|M58781|FBCRR16SB  Flexibacter columnaris 16S ribosomal...  1453  1.7e-113
 1
gb|M59053|CYTRR16SI  Cytophaga johsonae 16S ribosomal RNA.    1453  1.8e-113
 1
gb|M62797|FVBRRD     F.aquatile 16S ribosomal RNA.            1447  5.6e-113
 1
gb|M62792|FBCRR16SZ  F.aurantiacus 16S ribosomal RNA.         1446  6.6e-113
 1
```

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>M638
TTACGGCTACCTTGTTACGACTTAGCCCTAGTTACCAGTTTTACCCTAGGCAGCTCCTTGCGGTCACTGACTTCAGGC
ACCCCCAGCTTCCATGGCTTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGGATCATGGCTGATATCCGA
TTACTAGCGATTCCAGCTTCACGGAGTCGAGTTGCAGACTCCGATCCGAACTGTGACCGGTTTTATAGATTCGCTCCT
GGTCACCCAGTGGCTGCTCTATGTACCGGCCATTGTAGCACGTGTGTAGCCCAAGGCGTAAGGGCCGTGATGATTTGA
CGTCATCCCCACCTTCCTCTCAGTTTGCACTGGCAGTCTCGTTAGATTCCCGACATGANTCGCTGGCAACTAACAACA
G
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                                                                     Smallest
                                                                      Sum
                                                              High
  Probability
 Sequences producing High-scoring Segment Pairs:              Score  P(N)
      N

gb|L39067|FVBRRDA     Flavobacterium ameridies 16S riboso...  1747  3.5e-146
 2
gb|M62797|FVBRRD     .F.aquatile 16S ribosomal RNA.           1635  1.7e-137.
 2
gb|M58781|FBCRR16SB   Flexibacter columnaris 16S ribosoma...  1632  2.6e-137
 2
gb|M59053|CYTRR16SI   Cytophaga johsonae 16S ribosomal RNA.   1632  3.0e-137
 2
gb|M58764|CYTRR16SA   Cytophaga aquatile 16S ribosomal RNA.   1606  3.9e-135
 2
```

```
>M6316
TAGAGTTTGATCCTGGCTCAGGATGAACGCTAGCGGCAGGCTTAACACATGCAAGTCGAGGGGTATAGTTCTTCGGAA
CTAGAGACCGGCGCACGGGTGCGTAACGCGTATGCAATCTACCTTTCACAAAGGGATAGCCCAGAGAAATTTGGATTA
ATACCTTATAGTAATACGACTTGGCATCAAGATGTATTTAAAGATTTATCGGTGAAAGATGAGCATGCGTCCCATTAG
CTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATGGGTAAGGGTCCTGAGAAGGAAATCCCCCACACTGGTACTGA
GACACGGACCAGACTCCTACCGGAAGCACAGTGAAGAATATTGGACAATGGGCGCCAGCCTGATCCAGCC
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                                                                   Smalles t
                                                                     Sum
                                                              High Probability
Sequences producing High-scoring Segment Pairs:               Score  P(N)     N

gb|U63940|CSU63940    Cytophaga sp. 16S ribosomal RNA gen...  1124 2.9e-124  3
gb|M59053|CYTRR16SI   Cytophaga johsonae 16S ribosomal RNA.   1424 4.2e-122  2
dbj|D84581|D84581     Flexibacter sp. DNA for 16S ribosom...  1352 5.8e-122  2
gb|U63938|FSU63938    Flavobacterium sp. 16S ribosomal RN...  1341 4.7e-121  2
gb|U63943|CSU63943    Cytophaga sp. 16S ribosomal RNA gen...  1068 6.0e-121  3
```

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>SAM801
TAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGAGTGCTTTACACATGCAAGTCGAACGGCAGCACGGGGCTTG
CTCCTGGTGGCGAGTGGCGAACGGGTGAGTAATGCGTCGGAACGTACCGAGTAATGGGGGATAACGCACCGAAAGGTG
TGCTAATACCGCCTACGCCCTGAGGGGGAAAGCANGGGATCATTAGACCTTGCGTTATTCGAGCGGCCGACCTTCTGA
TTAGCTAGTTGGTGGGGTAAAG
```

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                                                                    Smallest
                                                                      Sum
                                                              High
  Probability
 Sequences producing High-scoring Segment Pairs:              Score  P(N)
     N

 gb|L35508|NTL16SRA    Nitrosolobus multiformis (ATCC 2519...   552  1.3e-78
   3
 gb|L15532|AZORR16SC   Azoarcus sp. (strain S5b2) 16S ribo...   893  2.8e-71
   2
 emb|X97599|BP16SRT65  Beta-proteobacterium 16S rRNA gene,...   480  2.4e-70
   3
 emb|X97592|BP16SRT67  Beta-proteobacterium 16S rRNA gene,...   478  5.0e-70
   3
 gb|L06170|NGORR16SD   Neisseria canis 16S ribosomal RNA.       562  1.5e-69
   3
```

```
>SAM802
TAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCCTTACACATGCAAGTCGAACGGCAGCACGGGCAACC
TGGTGGCGAGTGGCGAACGGGTGAGTAATATATCGGAATGTACCCTAGAGTGGGGGATAACGTAGCGAAAGTTACGCT
AATACCGCATACGATCTACGGATGAAAGTGGGGGATCGCAAGACCTCATGCTCATGGAGCAGCCGATATCTGATTAGC
TAGTTGGTAGGGTAAAAGCCTACCAAGGCGACGATCAGTAGCTGGTTTGAGAGAACGACCAGCCACACTGGAACTGAG
ACACGGTCCAGACTCCTACGGGAAGCAGCAGTGGGAATTCTTGGACAATG
```

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                                                                     Smallest
                                                                       Sum
                                                               High
   Probability
  Sequences producing High-scoring Segment Pairs:              Score  P(N)
      N

  gb|U63941|ZSU63941    Zoogloea sp. 16S ribosomal RNA gene...  1317  8.2e-131
   2
  emb|X74914|ZR16SRRNB  Z.ramigera gene for 16S rRNA (ATCC ...  1656  1.9e-130
   1
  dbj|D84625|D84625     Unidentified beta proteobacterium D...  1330  8.0e-126
   2
  dbj|D84564|D84564     Zoogloea sp. DNA for 16S ribosomal ...  1570  1.4e-125
   1
  dbj|D84572|D84572     Zoogloea sp. DNA for 16S ribosomal ...  1552  4.3e-124
   1
```

```
>803
GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGAAAGGCCCTGCTTTTGTGGGGTGCTCGAGTGGCGAA
CGGGTGAGTAACACGTGAGTAACCTGCCCTTGACTTTGGGATAACTTCAGGAAACTGGGGCTAATACCGGATAGGAGC
TCCTGCTGCATGGTGGGGGTTGGAAAGTTTCGGCGGTTGGGGATGGACTCGCGGCTTATCAGCTTGTTGGTGGGGTAG
TGGCTTACCAAGGCTTTGACGGGTAGCCGGCCTGAGAGGTGACCGGCCACATTGGGACTGAGATACGGCCAAACTCCT
ACGGGAAGCAGCAGTGGGAATATTGCACAATGGGCGGAACCTGATGCACAACGCGCGTGCGGATGACGGCTCGGTGT
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                                                                   Smallest
                                                                     Sum
                                                             High
  Probability
 Sequences producing High-scoring Segment Pairs:             Score  P(N)
     N

 gb|M29560|MSGRR16SF   M.chitae 16S ribosomal RNA.             1365  8.1e-129
  4
 gb|M61903|PRSRROA     Propionibacterium acnes small subuni... 1361  9.3e-128
  4
 gb|M58682|FUSSRRNAD   Fusobacterium prausnitzii small subu... 1022  1.9e-115
  4
 dbj|D84616|D84616     Unidentified Actinomycetes bacterium...  424  1.6e-112
  6
 dbj|D84587|D84587     Unidentified Actinomycetes bacterium...  424  3.4e-108
  6
```

```
>SAM804
TAGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGAACGGAGAATTTCGAAGAGT
TTACTCGGAGAAATTTTTAGTGGCGGACGGGTGAGTAACGCGTGGGTAACCTACCCATAAACCCGGGACAACCCTTGG
AAACGAGGGCTAATACCGGATAATCTCTTAGCTTGGCACCAAGTTTTAAGAAAAGGTGGCCTCTGAGTATGCTACCGA
TTATGGATGGACCCGCGTCTGATTAGCTAGTTGGTGGGGTAAAGGCCTACCAAGGCGACGATCAGTAGCCGGCCTGAG
AAGGTGAACGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAAGCACAGTGGGAATCTCCGCAATGGACA
A
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                                                                   Smallest
                                                                     Sum
                                                              High
   Probability
  Sequences producing High-scoring Segment Pairs:            Score  P(N)
       N

  gb|M34417|DSORR1618    Desulfotomaculum orientis 16S ribos...   788  7.1e-116
   4
  gb|L28946|DTORRD       Desulfitobacterium dehalogenans 16S...  1119  8.4e-112
   3
  gb|U68528|DCU68528     Desulfitobacterium chlororespirans ...  1115  3.7e-103
   3
  emb|X94975|DH16SRRNA   D.hafniense 16S ribosomal RNA           1081  8.5e-101
   3
  emb|X99706|SG16SRR1    S.glycolicus 16S rRNA gene               580  2.3e-95
   4
```

ADDENDUM

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