U2BIO
Global Premier Medical Service Partner

U2BIO Molecular Biology Services

629/398 Sathupradit Road, Bangpongpang, Yannawa, Bangkok 10120 Thailand Tel : +66 2 294-3547 Fax: +66 2 053-1030

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DNA oligo synthesis

Since launching Oligo synthesis service in 1998, we have produced and supplied high quality DNA oligonucleotide based on the latest facilities and know-how. In addition, we are continuously improving our DNA Oligonucleotide quality with a Global Oligo manufacturing company together.
So, we are providing oligo synthesis service, which is one of the best in this industry.
With the introduction of the latest ESI MS in Korea, we carry out the oligo purity and molecular weight QC for the whole oligosaccharide (~ 130 mer).

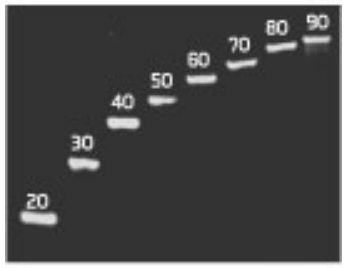
Benefit Summary of MALDI-TOF vs. ESI

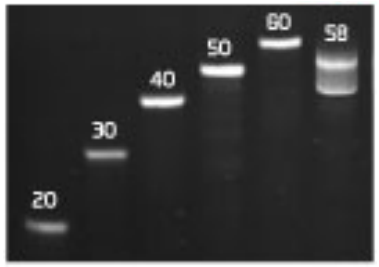
Criteria	MALDI-TOF	ESI
<50 bases	+	+
>50 bases	-	++
Photosensitive Modified Oligonucleotide	-	+
Degenerate (wobble) Oligonucleotide	-	+
Throughput	+++	+
N-1 Detection	+	+
Incomplete deprotection	+	+
Depurination	+	+
Mass accuracy	+	++

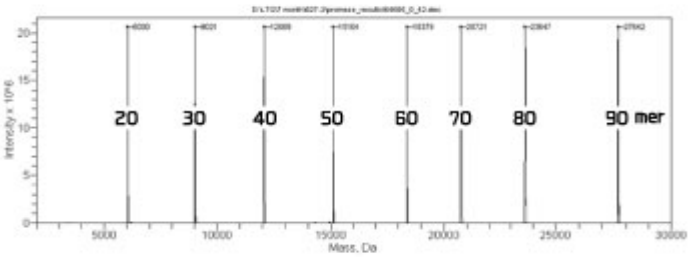
(refer. : Sigma - aldrich)

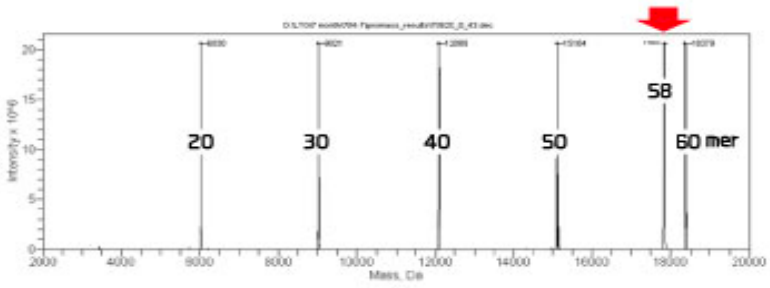
"Accurate Synthesis"
"High-purity Purification"
"Exact Quality Control"

Electrospray Ionization Mass Spectrometer (ESI-MS)









Gene Synthesis Service

Our products guarantee 100% accuracy of your ordered DNA or protein sequences with minimized time.

Service components

- Data of automated (bi-directional) fluorescent DNA sequencing
- Lyophilized DNA cloned into vector
- Plasmid map (vector species)
- Result of DNA sequencing

Features and Benefits

***Rapid and economical**
***Accurate quality**
- Guaranteed 100% sequence using Automatic DNA sequencer (ABI 3730xl)

***Codon optimization service**
- Accumulated experience and techniques for optimization of protein expression and codon

***Comprehensive vector choice**
- Wide range of choices for compatible vectors according to the desired applications at a reasonable price and time

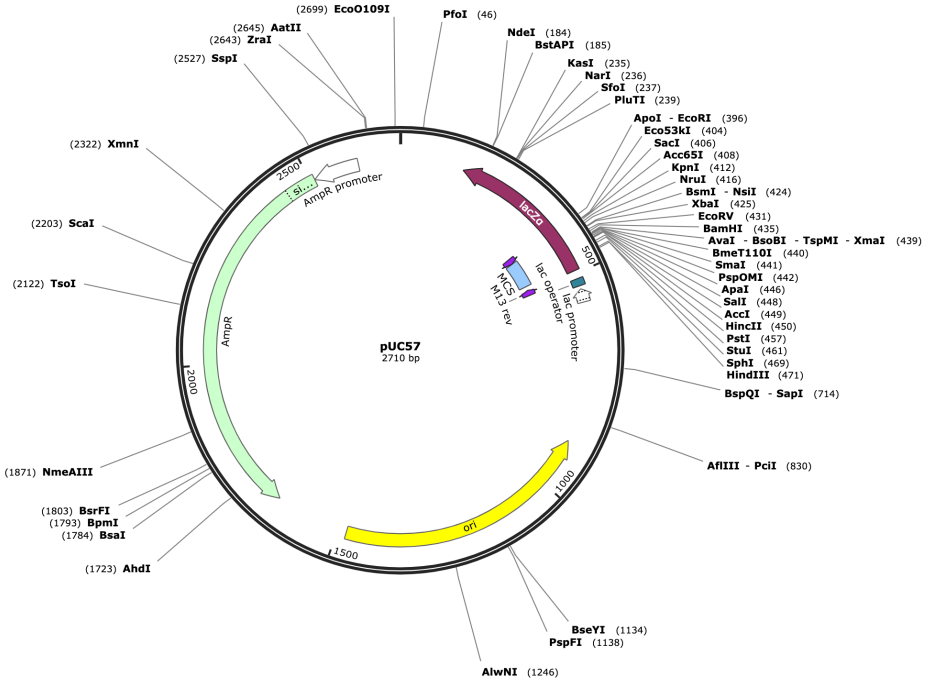
Vector Type

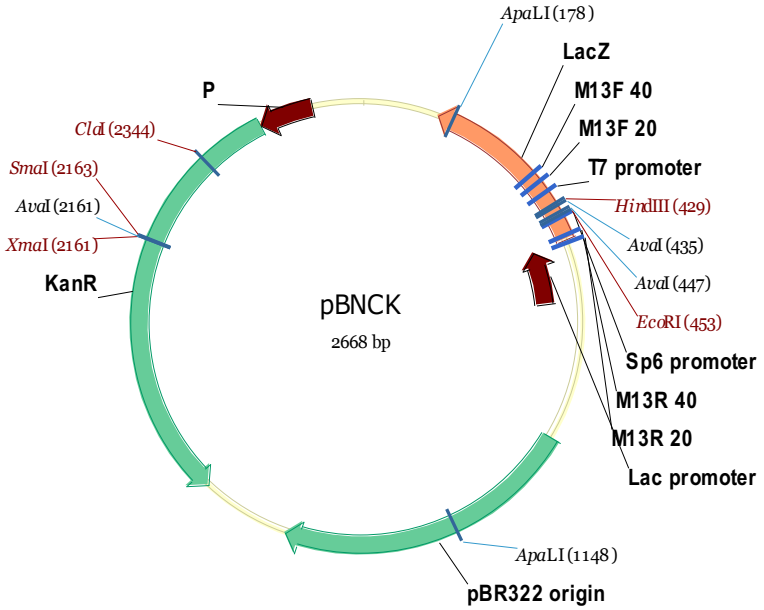
- pUC57-Amp (Free), pBNCK (Free, kanamycin), pBluescript II SK (+) (Free)
- pET21a, pET28b (It will be charged as custom vector, please contact sales person)

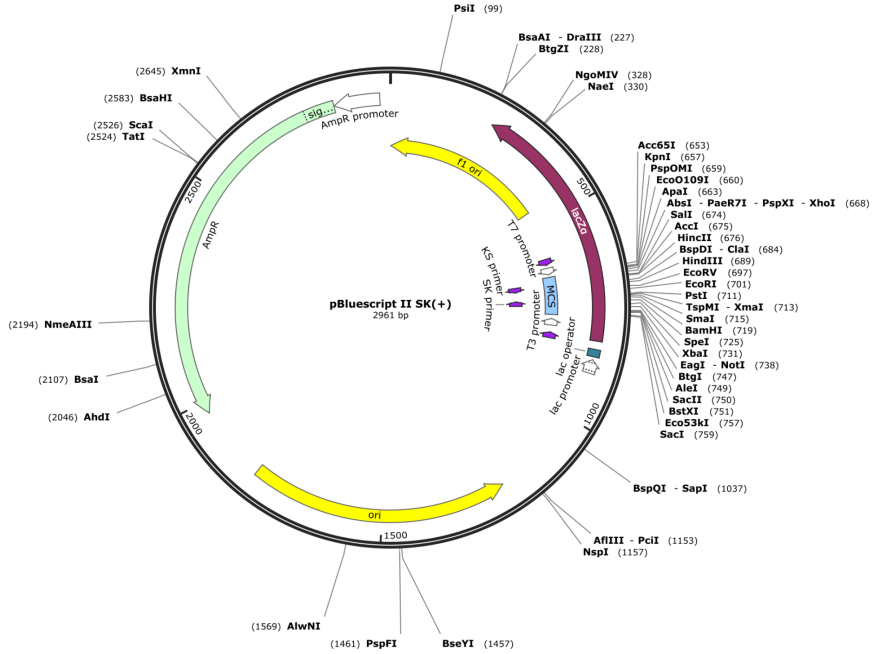
Turn Around Time (TAT)

Size of gene	Delivery
0 ~ 0.5kb	8 to 10 working days
0.5kb ~ 1kb	10 to 12 working days
1kb ~ 1.5kb	14 to 16 working days
1.5kb ~ 2kb	17 to 20 working days
2kb ~ 3kb	21 to 23 working days
< 5kb	inquire

Vector Map / pUC57-Amp (Free), pBNCK (Free, kanamycin), pBluescript II SK (+) (Free)







DNA sequencing service

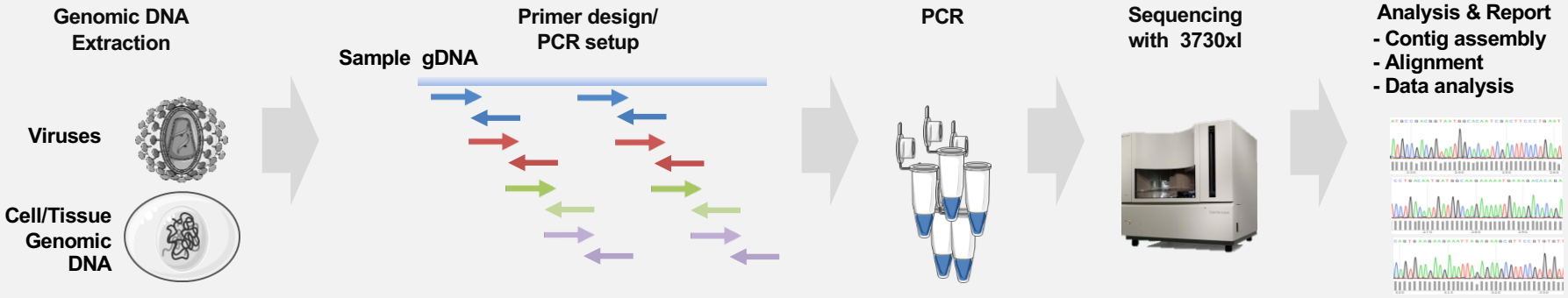
Based on the reference sequence of the genome to be analyzed, we provides ‘Primer design’ and ‘PCR setup’, and full/partial high-quality sequencing service by sanger sequencing method. This Sanger sequencing service is efficient for mutation detection and verification of NGS result.
We have extensive experience and expertise in the sequencing of various organisms such as viruses and bacteria, including the human genome.
You'll also get more complete results with the variety of service options you need for each project.

Services features

- High purity Genomic DNA preparation (Option)
- Re-Sequencing of genomic region
- Primer walking project
- PCR primer design and PCR setup
- PCR amplification
- Verification of NGS sequencing data
- NGS Gap-fill
- Verification of genomic mutation

Service workflow

STEP 1	STEP 2	STEP 3	STEP 4
1. Submit correct NCBI Acc. No. 2. Reference confirmation 3. Analysis availability notification	1. DNA sample delivery to BIONICS	1. Primer design 2. PCR Setup	Analysis & Report - Contig assembly - Alignment - Data analysis - Final report



Genomic DNA sequencing service (International)

Template DNA requirements

Please use ultrapure water or TE buffer

Sample Specification

All international samples are received in purified DNA or PCR fragment only.
Please use 1.5 ml tubes for sample submission.
Please provide the exact sample name on the tube
Please be sure to seal to prevent leakage.

Total range to analyze (kb)	Min. Concentration	Required total Quantity (ng)
Under 1 kb	10ng/ul	100 - 200 ng
Under 5 kb	10ng/ul	300 - 500 ng
Under 10 kb	10ng/ul	300 - 500 ng
Under 20 kb	10ng/ul	500 - 900 ng

Report

The final result report, including alignment and coting assemble, is sent.
Raw data file including Ab1 and chromatogram are also transmitted

Order

International services are not available online.
All service requests and result reporting are progressed by e-mail.

Mitochondrial Genomic Sequencing

Service Description

Mitochondrial DNA (mtDNA) analysis can be used for research on diseases and aging due to mutation of genetic sequence.
By utilizing highly conserved genetic characteristics, it can be used for identification of forensic medicine as well as biodiversity and classification also available. we provides mitochondrial genomic sequencing of analytical samples based on **Sanger sequencing method**, from reference selection for analysis to result analysis including primer design/arrange and alignment.

Sample requirement

- Only Total DNA sample (internal service only)
- Amount : minimum 200 ng DNA
- Specimens : contact for details
- DNA purify : OD260/280 >1.8

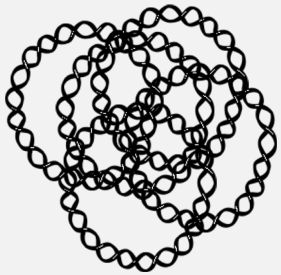
Service Turn-around

- Turnaround time : 3-5 weeks

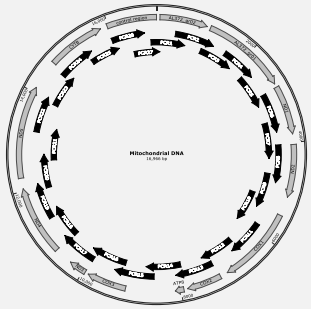
Service workflow

STEP 1	STEP 2	STEP 3	STEP 2	STEP 4
Submit samples	Q.C. of DNA samples	Primer design	PCR reaction	Sequencing/Reporting

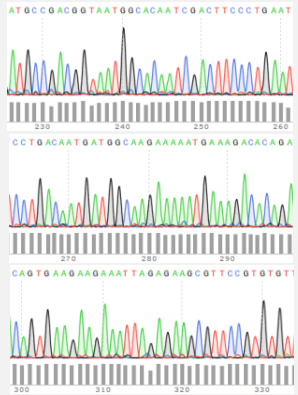
Mitochondria



Mitochondrial
Genomic DNA



PCR



Sequencing & Alignment

Viral Genome Sequencing

Service description

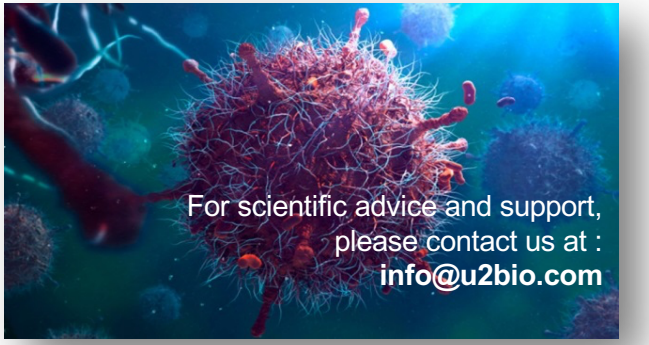
Based on a reference sequence of viruses, we provides full / partial sequencing service for virus genome using sanger sequencing method.
From primer set design to RACE PCR service for genome sequencing, various services can be provided according to the purpose of the customer.

Service features

- RNA and DNA virus available
- 5'-, 3'- end RACE service available
- Full length genome or Partial genome sequencing available

Sample requirement

- Only purified genome sample
- Amount
  1) in case of DNA viral genome : minimum 200 ng DNA
  2) in case of RNA viral genome : minimum 500 ng RNA
- DNA purity : OD260/280 >1.8
- RNA purity : OD260/280 >2.0



Service Turn-around

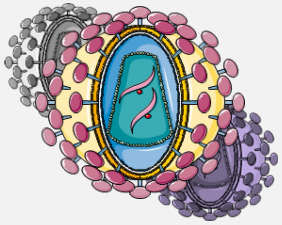
- contact for details

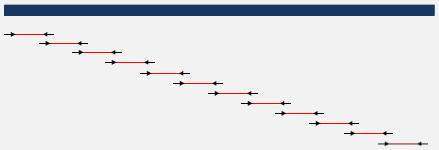
Service features

- RNA and DNA virus available

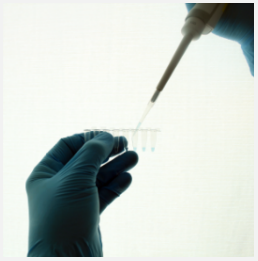
Service work flow

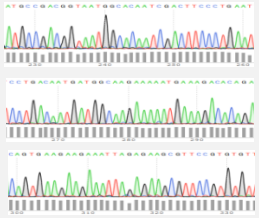
STEP 1	STEP 2	STEP 3	STEP 4
Sample - Viral gnome sample submit - Reference check	Preparation - Primer set design - PCR setup	PCR & Sequencing - PCR amplification - Sanger Sequencing	Analysis & Report - Contig assembly - Alignment - Data analysis





Oligo name 1	ACG TGA TCT AAG TCA AAG TCA
Oligo name 2	ACG AAG TCA TGA TCT AAG TCA
Oligo name 3	ACG TGA AAG TCA TCT TGA AAG
Oligo name 4	ACG TGA TCT AAG TCA AAG TCA
Oligo name 5	ACG TGA TCT AAG TGA AAG TCA
Oligo name 6	ACG TGA TGA AAG TCT AAG TCA AAG TCA
Oligo name 7	ACG TGA TCT AAG TCA TTT TGA AAG
Oligo name 8	ACG TGA TCT AAG TCA GAG TTT
Oligo name 9	ACG AAG TGA TCT AAG TCA





Mycoplasma Detection Service

Service Description

Mycoplasma infection changes the physical / chemical properties of the cultured cells. This can alter cell growth, protein synthesis, antigenic properties of the cell surface, efficiency of the virus production or transfection efficiency. Therefore, periodic testing of mycoplasma is essential for all studies using cell culture. Our Mycoplasma testing service was performed by a **Rapid PCR-based detection** method and provide information about infection, identification of infectious species, and so on, using very small samples.

Sample requirement

- Cultured media
- Amount : minimum 100 ul

Service turn-around

- Turnaround time : 1-2 days

Major Infection Source (Cytotechnology. 2002 Jul; 39(2): 75–90)

Species	Frequency	Host
M. orale	20-40%	Human
M. hyorhinis	10-40%	Swine
M. arginini	20-30%	Bovine
M. fermentans	10-20%	Human
M. hominis	10-20%	Human
A. laidlawii	5-20%	Bovine

Service workflow

STEP 1	STEP 2	STEP 3	STEP 2	STEP 4
Submit samples	Q.C. of samples	PCR reaction	Sequencing Identification	Reporting

Single nucleotide polymorphism (SNP) Genotyping

Service description

Single nucleotide polymorphism (SNP) refers to a single nucleotide sequence variation in the genomic sequence of a subject to be investigated, and SNP genotyping is a technique for analyzing the nucleotide polymorphism. Our SNP genotyping service is provided by two methods, Sanger sequencing method and Real-time PCR method, which can be used effectively for SNP screening and SNP locus validation. These analytical techniques can be used to identify genetic characteristics, disease prediction, and genetic lineage of the study subjects or groups, and also can be used for development of diagnostic kits.

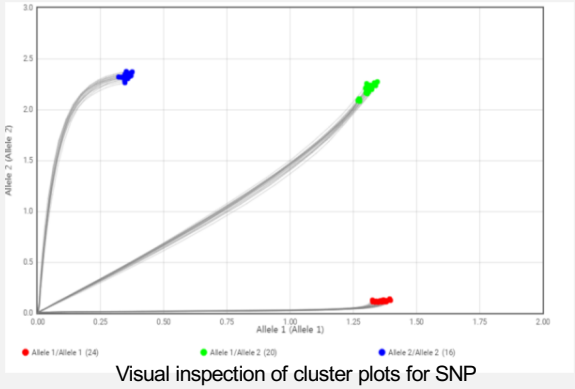
Sample requirement

- Purified DNA or PCR product
- Amount : minimum 10 ng/sample

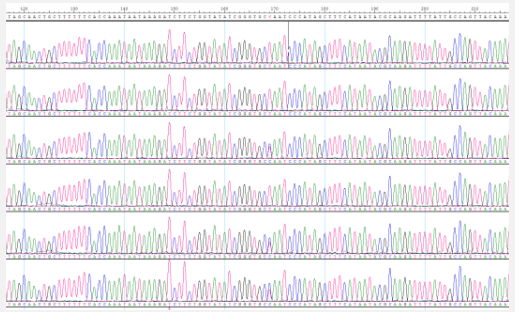
Service turn-around

- Depends on total sample number. Please contact for details

	Real-PCR	Sanger Sequencing
Analysis base	TaqMan Assay	Direct sequencing
Assay coverage	Annotated or non-annotated	Annotated or non-annotated
Provided data	Raw PCR data file Cluster plot data	Raw seq. data file, Align & SNP analysis data



Visual inspection of cluster plots for SNP
by TaqMan-based real-time PCR



Direct sequencing-based SNP analysis

Short Tandem Repeat (STR) Genotyping

Service description

Short Tandem Repeat (STR) refers to the repetition of a short (2-13bp) nucleotide sequence present in the non-coding region of each genome. This repeating sequence, also referred to as microsatellite, can exist in thousands of genomes within a single individual, where the repeating number has a unique value depending on the species. Using this techniques, genetic mapping with entity or interspecies deviation is possible, and finally analysis of repeated numbers is called 'fragment analysis'.

Application

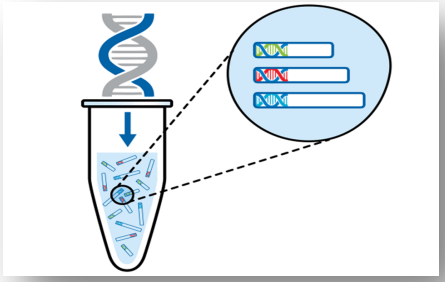
- Management of various genetic resources
- Biodiversity research
- Molecular classification studies

Sample requirement

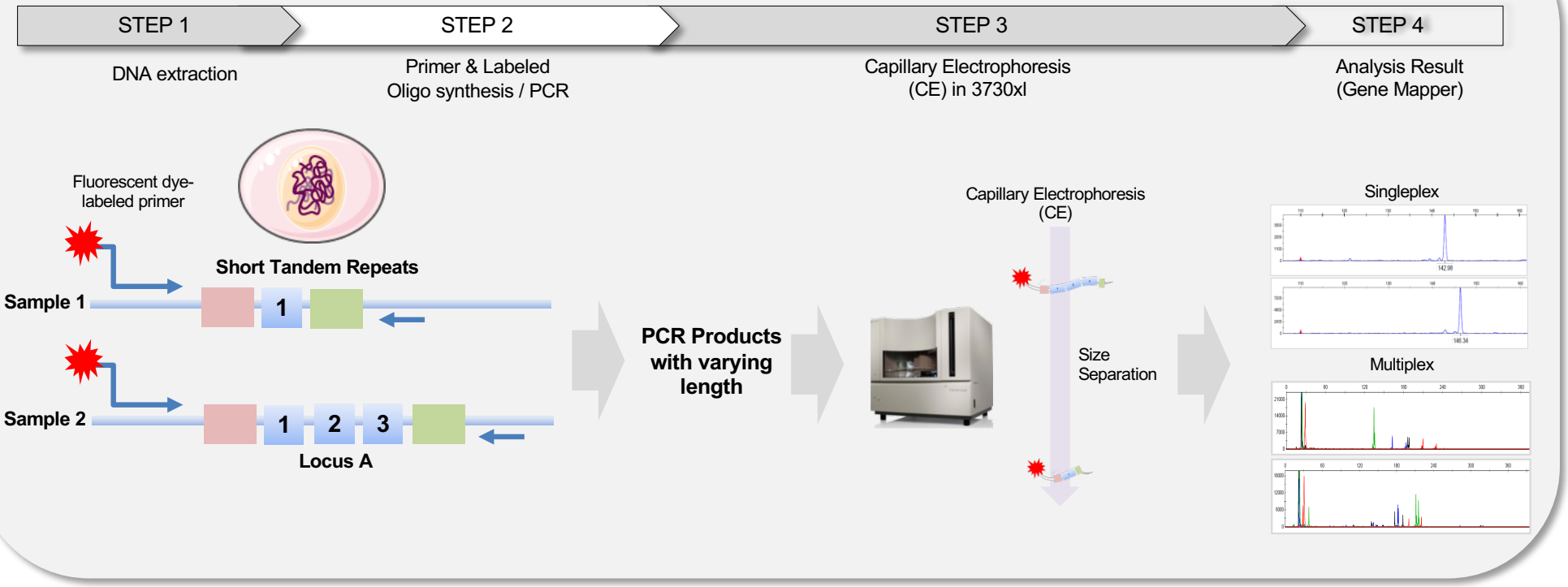
- Purified DNA or PCR product
- Amount : minimum 10 ng/sample

Using Dye

6-FAM
VIC
NED
PET
500-LIZ (500bp)



Service workflow



Microbial Identification Service

Service description

The '**Identification service**' of us is used to identify species of an unidentified subject or to classify strains by analyzing specific sequence of genomic DNA, mitochondria DNA and chloroplast DNA to be analyzed.

Service features

a. 16s rDNA microbial identification
b. Fungi 5.8s (ITS) / 18s (NS) / 25-28s (NL or NR) microbial identification

Sample requirement

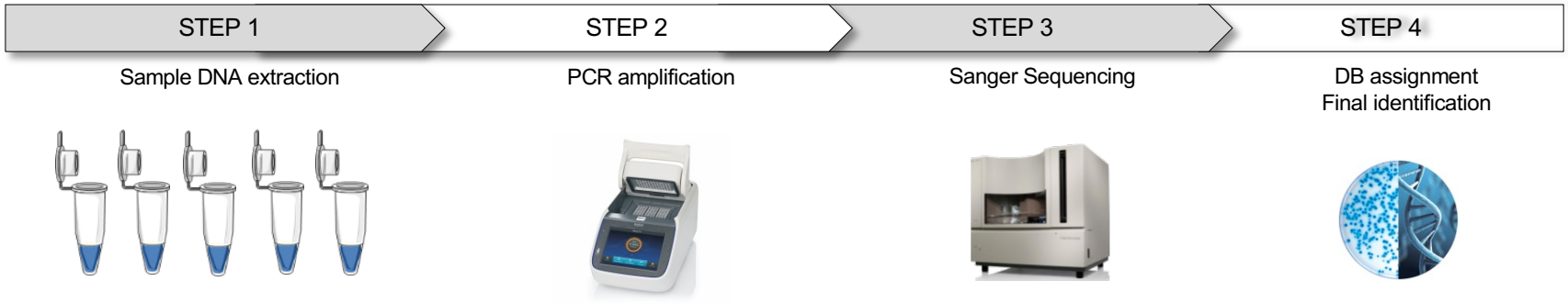
- gDNA with each tube

Type	Concentration	Volume	Purity
gDNA	≥ 30ng/ul	≥ 30ul	A260/A280: ~1.8 A260/A230: 2.0 ~2.2

Service turn-around

- 2~3 working days

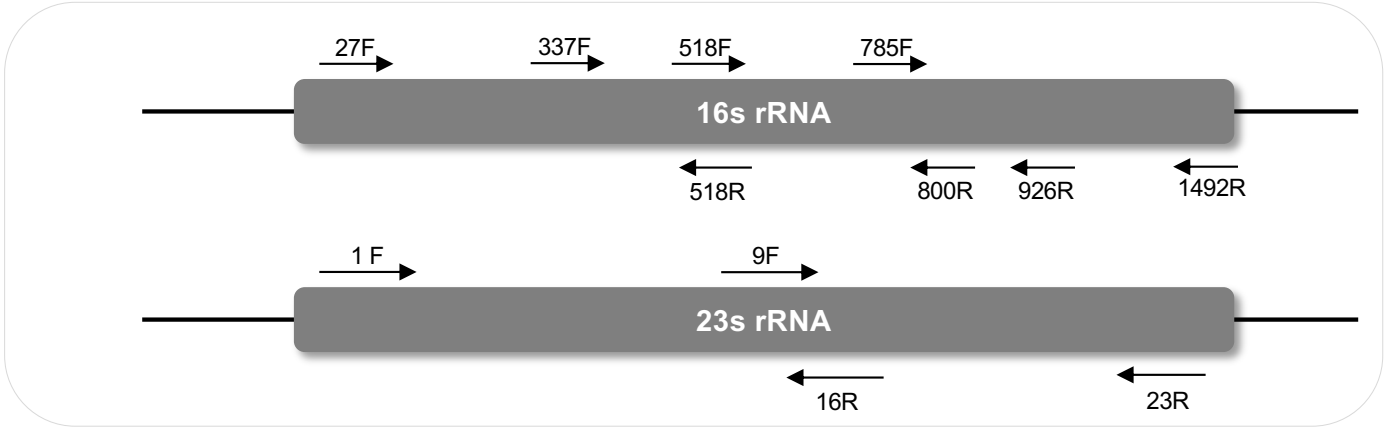
Service workflow



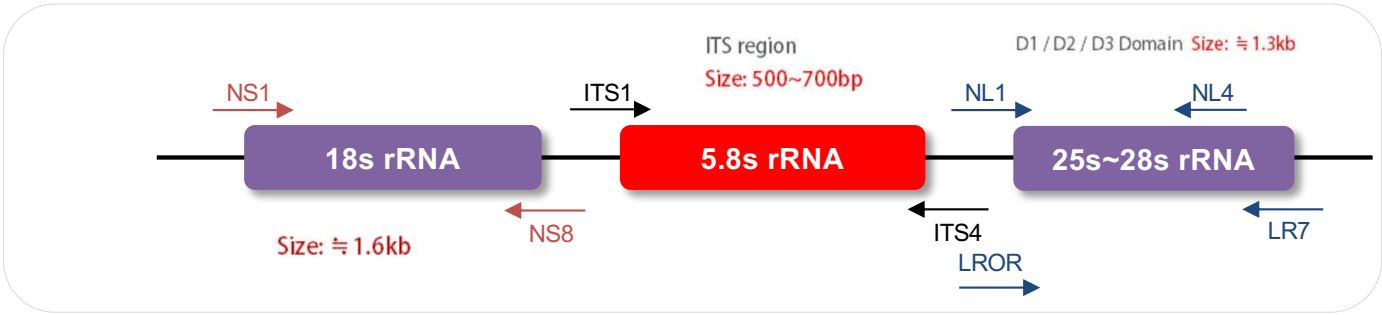
Identification Service

: Detection locus

16s rRNA
microbial identification



5.8s (ITS), 18s (NS),
25-28s (NL or LR) rRNA
microbial identification



Bisulfite Sequencing Service

Service Description

Methylation of Cytosine-Guanine (CpG) nucleotides in genome DNA is associated with gene silencing and is considered one of the most important epigenetic phenomena. CpG methylation, especially in the promoter site of a specific gene, was observed to be the earliest and most frequent change in some cancers by inducing inactivation of tumor inhibitors.

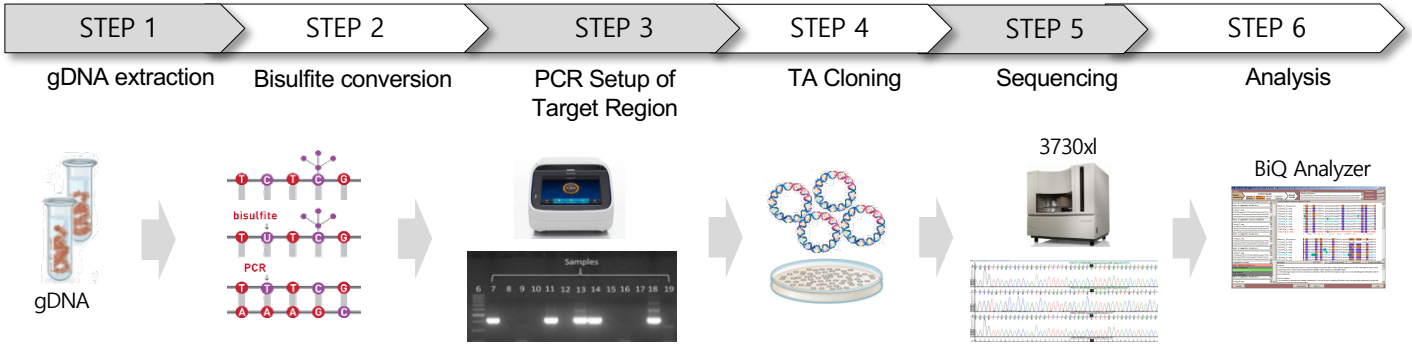
Bisulfite sequencing is a widely accepted standard method for detecting methylated CpGs through the bisulfite conversion of unmethylated cytosine.
We provides integrated services such as bisulfite processing, PCR, TA cloning, DNA sequencing, and comparative analysis for cytosine methylation.

1) Genomic DNA bisulfite conversion of unmethylated cytosines
2) Preliminary PCR setup
3) Sub-cloning of PCR products (TA Cloning)
4) Sequencing using ABI Prism™ 3730xl DNA Sequencers
5) Data analysis using BiQ Analyzer

Turnaround Time

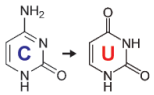
3~4 Weeks

Workflow



5′ – GA*C*CGTT*C*CAGGTCCAGCAGTGCGCT-3′

Bisulfite Conversion
Unmethylated cytosines completely changed to uracil



5′ – GACUGTTCUAGGTUUAGUAGTGUGUT-3′ → 5′ – GACTGTTCTAGGTTTAGTAGTGTGTT-3′