



Health Protection Agency
Microbiology Services Colindale

**DEPARTMENT FOR BIOANALYSIS AND
HORIZON TECHNOLOGIES**

USER MANUAL

CONTAINS INFORMATION ON BIOANALYTICAL SERVICES

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INTRODUCTION

The Department for Bioanalysis and Horizon Technologies (DBHT) is formed of the Molecular Identification Service Unit (MISU), the Genomic Services Unit (GSU), Applied and Functional Genomics Unit and Proteomics Unit.

MISU provides a specialist identification service for atypical bacteria, difficult to isolate and emerging pathogens detected in culture negative clinical samples and isolates. Over 1000 species are identified using comparative sequence analysis of 16S ribosomal DNA sequences. Additional specialised tests are required for pathogens that belong to a closely related species that have almost identical 16S ribosomal DNA composition. The Unit provides three tests to identify species within the genus *Bacillus* and the unit processes anaerobic pathogens which are difficult to isolate from clinical samples and characterise by phenotypic tests in most frontline laboratories.

Specialist identification is based on 16S ribosomal DNA sequence analysis of bacterial isolates and clinical samples which are received from Health Protection Agency, National Health Service, private and commercial laboratories throughout the UK and overseas. MISU's role is to receive and process isolates and clinical samples. Biomass for DNA extraction is obtained and target genes are amplified by PCR. PCR products are cleaned up and are submitted for Sanger sequencing or specific pyrosequencing. Identification is achieved by comparing sequence similarity (homology) between the sample PCR product sequence and reference sequences of bacterial species provided by online databases as well as internal DBHT databases, after which a final report is sent to the customer. All clinical samples are archived and all isolates received are sub-cultured and archived. DBHT also has a strong research and development commitment to improve methods of microbial identification and has active programmes in proteomics and mass spectrometry applications.

The Genomic Services Unit provides generic nucleic acid sequencing and fragment sizing services. The unit receives nucleic acids, plasmids, PCR products and bacterial samples (non ACDP3) from customers both within Colindale and across the HPA. Samples are processed based on specific protocols and service type selected by customers from a list in both the user manual and a memorandum of understanding provided to each customer. Sequence and fragment sizing data are checked by Genomic Services against internal standards and quality scores before electronically notifying and reporting the results to allow customers to analyse their own data. In the cases of services requiring customers to submit bacterial cultures for extraction of nucleic acids material prior to sequencing or sizing the service is organised and agreed prior to direct submission of the samples to GSU.

The Department has a strong research and development commitment to improve methods of sequence-based microbial identification and genotyping and has active programmes specialising in Proteomics and mass spectrometry applications in microbial detection and biomarker discovery. Genomic research is organised to address high throughput analysis, resequencing, microarray and other hybridisation and rapid detection approaches. Established approaches are published and shared with reference and specialist laboratories across the HPA through training, workshops and provision of assay and test development and transfer to HPA Laboratories.

CONTACT DETAILS

Department for Bioanalysis and Horizon Technologies

Bioanalytical Services:

1. Molecular Identification Services Unit

Address	Microbiology Services Colindale 61 Colindale Avenue London NW9 5HT	DX Address	HPA Colindale SRMD (MISU) DX 6530001 Colindale NW
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Telephone	020 8327 7869
Fax	020 8327 7870
Email	MISU-Services@hpa.org.uk
Internet	http://www.hpa.org.uk/cfi/misu

2. Genomic Services Unit

Address	Microbiology Services Colindale 61 Colindale Avenue London NW9 5HT	DX Address	HPA Colindale SRMD (GSU) DX 6530001 Colindale NW
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Telephone	020 8327 7772
Fax	020 8327 7870
Email	AFGU@hpa.org.uk
Internet	http://www.hpa.org.uk/cfi/afgu

The Department provides all services under a joint Service Management Team that co-ordinates service delivery, development and introduction of services within the Department. This includes optimisation and validation of customer assays and support of reference and specialist services. The Services Management team is made up of Head of DBHT and Heads of Units within the Department.

1. Molecular Identification Services Unit

Unit Head	Professor Haroun Shah (PhD, FRCPath)
Deputy Unit Head	Dr Julie Logan (PhD)
Laboratory Manager	Paul Laidler (B.Sc C.Sc F.I.B.M.S D.M.L.M.)

PRELIMINARY IDENTIFICATION OF ISOLATES MUST BE UNDERTAKEN BY THE SENDING LABORATORY AND RECORDED ON THE REQUEST FORM. DO NOT SEND SUSPECTED CONTAINMENT LEVEL 3 BACTERIAL PATHOGENS. MISU DOES NOT OFFER A SERVICE FOR THIS CLASSIFICATION OF ORGANISM.

The Molecular Identification Services Unit specialises in the identification of atypical and rarely isolated bacteria using comparative sequencing of targeted genes as the basis for characterisation from pure cultured isolates and detection of bacteria in clinical samples from normally sterile sites. MISU provides a service for amplifying and sequencing a universal ribosomal RNA gene (16S rDNA) present in all bacteria. This results in the generation of a DNA sequence that is compared to thousands of other similar sequences held in genetic databases. Comparative analysis using established algorithms provide a similarity score for each sequence which is calculated and used to determine which species/ group/genus the sequence is identified as.

MISU accepts samples sent from:

- Within HPA Microbiology Services Colindale
- ALL HPA Microbiology Service Laboratories
- Reference laboratories, NHS and private laboratories within the UK
- By arrangement from commercial laboratories

Laboratory Opening times

Core working hours: Monday – Friday 09:00-17:30

Clinical advice is not available in this Department

Sample Transportation

To ensure that specimens are processed as rapidly as possible, the unit name (MISU) should be clearly identified on the address label.

Specimens sent by post or by courier must be in a sealed container, surrounded by sufficient absorbent material to take up any leakage in the event of damage during transit, sealed in a plastic bag and placed in an approved outer container which meets current postal or other transport regulations. The request form must be packaged separately from the sample. HPA guidance on the transport of infectious substances can be found at:

<http://www.hpa.org.uk/PackingSamples>

Sample Submission Guidelines

The MISU request form (M1) can be obtained from <http://www.hpa.org.uk/SRMTests>.

The request form is self explanatory but essential information must be completed including name and address of sending laboratory, patient's name, age, date of birth (human isolates), isolate details, date specimen was collected plus any relevant clinical information.

Failure to supply appropriate information may result in a delay in processing or sample rejection. If you are unsure of how to fill out the request form, please contact the unit for guidance or see:

http://www.hpa.org.uk/web/HPAweb&HPAwebStandard/HPAweb_C/1204100439590

MISU submissions regarded by the sending laboratory as urgent should be notified to the relevant unit by telephone. See contact details on page 27.

Sample Rejection

Samples may be REJECTED if:

- Form **NOT** completed satisfactorily with the minimum data set of:
Senders address and contact details
At least two of the following 3 unique identifiers:
Patient name or number
Patient date of birth
Sender's reference
Relevant clinical information and/or, if a culture or a specimen for confirmatory testing, the sender's presumptive ID and lab results is absent.
NB. If samples are a) for surveillance studies b) food or environmental samples c) from non-human subjects these can still be sent however, identifiers and data appropriate to the sample type must be provided.
- Packages marked as SHIPPING CATEGORY A and/or UN2814
- Specimens in unsafe/non-regulation packaging, e.g. envelope, packaging without any shipping category labelling to indicate contents.
- Packages where the request form cannot be seen once the outer transport package has been opened (i.e. form omitted or enclosed with specimen).
- Packages with mix of Hazard Group 2 and Hazard Group 3/4 specimens.
- Broken or leaking primary specimen container, or package with damage to secondary container.
- Sample received in unusual container or format e.g. culture on a plate, a syringe/needle.
- If a Reference Laboratory Referral form is used, the form submitted is not the current version, or is an incorrect form for the request.
- A specimen, or specimens, from the same patient is sent with more than one Referral Form, i.e. for different pathogen investigations.
- Type of specimen not recorded or specimen type doesn't match that expected for the request e.g. sputum for Flu strain typing.

- Clinical information or travel/contact history suggests potential for a different infection to that indicated by presumptive ID or test request.

Compliance with the Human Tissue Act

Submitting tissue samples from deceased people

Microbiology Services Colindale is licensed by the Human Tissue Authority (HTA) (Licence number 12459) to store tissues from deceased people for scheduled purposes. Post mortem samples are submitted to Microbiology Services Colindale by coroners or pathologists for examination to help them determine the cause of death.

Obtaining consent to remove, store and use human tissues for a scheduled purpose is one of the underlying principles of the Human Tissue Act. Microbiology Services Colindale receives post-mortem samples from Coroners' post-mortems or from NHS establishments across the UK and therefore we are performing the examination under the authority of the coroner. Unless consent has been obtained or the coroner has requested that samples are retained for further testing, samples are disposed of within three months of the initial test being performed.

When tissue samples from deceased people are received at Microbiology Services Colindale they are retained securely and confidentiality is maintained in compliance with [Caldicott principles](#) as are all samples received at this centre. It is normal practice for tissue samples from the deceased to be disposed of in the same way that all other clinical samples we receive at Microbiology Services Colindale are disposed of. However, we will adhere to any specific requirements regarding disposal or returning tissue samples if requested by the sending coroner or pathologist.

Delay in turnaround times/Factors known to affect the tests or results.

The identification of microorganisms may be delayed as a result of the following:

- Inappropriate or incorrectly completed request forms.
- Slow growing fastidious organisms.
- Tough cell wall and extra cellular polymeric material may hamper DNA extraction thus additional lengthy extraction procedures may be required.
- Spore-formers may spread and mask colonies so that repeated sub-culture may be required.
- Cultures in which there is a preponderance of spores over vegetative cells so that DNA yield may be poor and require further processing.
- Organisms that possess DNA that is difficult to sequence and may require repeating using other methods.

Reporting of results

All results are reported back to the sending laboratory on completion of tests.

Policy on Faxing and Emailing Reports Containing Patients' Data

The following guidelines are prepared having taken into account the Code of Practice on reporting patients' results by fax prepared by the Department of Health and Caldicott recommendations.

It is HPA-Cfl policy that reports containing patients' data should **not** be sent by fax or email.

Emails cannot be relied on to guarantee security of patients' data because they can be intercepted by a third party en route.

In **exceptional** circumstances it may be necessary to send a result by fax but not by email. In this case, the following conditions must be adhered to after telephone discussion with the Laboratory.

- The report must be sent to a "safe-haven" fax machine. This means that, if the location is in general use, consideration must be given to ensuring that unauthorised personnel are unable to read reports, accidentally or otherwise. Also, the room housing the fax machine must be kept in a secure location which is locked if it is likely to be unattended at the time the fax is sent.
- Assurance must be sought from the intended recipient of the faxed report, preferably in writing, that the receiving fax machine is a "safe-haven".
- Measures must be taken to minimise the risk of mis-dialling, either by double-checking numbers or having frequently used numbers available on the fax machine's memory dial facility.
- Confirmation must always be sought from the intended recipient that the fax is expected and has been received.

Turnaround Times

The expected turnaround time is within 14 days from receipt of sample.

DETAILS OF KEY SERVICES OFFERED

1. ATYPICAL AND RARELY ISOLATED AEROBIC/CAPNOPHILIC/ANAEROBIC STRAINS

Atypical isolates are strains with phenotypic or physiological profiles deviating from the majority of strains belonging to the same genus or species (i.e. catalase test, oxidase or sugar fermentation) which affects the ability of the laboratory where it has been isolated to accurately confirm its identity. Laboratories may also seek confirmatory testing since the phenotypic tests currently in use target groups of known clinically significant organisms and may not confirm the identity of emerging and unusual infectious agents.

2. BACTERIAL TAXA WHICH ARE DIFFICULT TO IDENTIFY TO A SPECIES LEVEL

Such species because may have high genetic similarity or paucity in differentiating phenotypic tests resulting in mis-identification. Specifically, aerobic actinomycetes, aerobic spore-formers (*Bacillus* species) and anaerobic bacteria (mainly non-fermentative species).

Aerobic Actinomycetes

NOTE: SOME *MYCOBACTERIUM SPP.* ISOLATES ARE SIMILAR IN MORPHOLOGY TO AEROBIC ACTINOMYCETES, IF THE ISOLATE IS SUSPECTED TO BE A MYCOBACTERIUM SPECIES BASED ON PRELIMINARY TESTS OR CLINICAL ASSESSMENT THEN IT IS NOT ACCEPTED FOR THIS SERVICE AND SHOULD BE REFERRED TO THE HPA MYCOBACTERIUM REFERENCE LABORATORY.

Organisms collectively grouped under the broad category “aerobic, gram-positive with/without branching filaments form a very diverse collection of ill-defined genera and species. Often referred to as the ‘non-TB mycobacteria complex’, ‘*Nocardia* complex’, ‘*Rhodococcus – Gordonia – Tsukamurella – Corynebacterium* complex’ etc., they may be seen in pathology specimens and are often highlighted by the presence of sulphur granules. The taxonomy of this group has been actively investigated over the last 20 years but is still in a state of flux. Their poor phenotypic identification is often compounded by their slow and poor growth.

Aerobic Spore Formers (*Bacillus* species)

NOTE: SUPECTED *BACILLUS ANTHRACIS* ISOLATES ARE NOT ACCEPTED BY THE SERVICE AND SHOULD BE SENT TO HPA SPECIAL PATHOGENS REFERENCE UNIT.

Species of the genus *Bacillus* produce spores and require aerobic growth conditions. They comprise over 200 species that inhabit most environments. While particularly significant as food-borne contaminants, these organisms are arguably the most

ubiquitous in nature. Conventional methods may be very tedious and indeterminate in separating them into species, and they tend to be clustered within groups and subgroups based on phenotypic tests and morphological properties.

Molecular methods are more accurate in distinguishing between genetically related groups. MISU provides a 16S rDNA based identification which separates the majority of species, however, two main groups linked to human infections known as *B. subtilis* and *B. cereus* groups require additional tests to sub-divide them into species. By sequencing additional gene targets within each of these groups, higher resolution identification can be obtained. For this purpose, the service provides tests based on *dnaX* and *gyrB* sequencing to speciate these groups.

Anaerobic Bacteria

NOTE: SUSPECTED FOOD-BORNE ANEROBIC SPORE-FORMERS (INCLUDING CLOSTRIDIUM BOTULINUM ARE NOT ACCEPTED BY THIS SERVICE) AND SHOULD BE SENT TO THE HPA FOOD-BORNE REFERENCE UNIT.

Anaerobic bacteria require specialist isolation and culturing conditions to avoid oxygen contamination that may result in the loss of bacterial viability. Additionally, several species are non-fermentative and difficult to identify using standard phenotypic tests. MISU provides a specialist service for the identification of isolates of anaerobic bacteria based on comparative 16S rDNA sequencing.

3. CULTURE NEGATIVE CLINICAL SAMPLES

MISU provides a specialist service for the detection and identification of bacteria in clinical samples from normally sterile samples. Suitable sample types include tissue (e.g. native heart valves), paraffin-embedded tissue, non-pipettable liquids (e.g. pus) and liquids/fluids (e.g. blood, CSF, blood culture fluid). Unsuitable samples from non-sterile sites include samples in direct contact with skin or mucous membranes and samples in direct connection to the intestine.

Samples should be transported in a sterile container (e.g. universal) without additives. Please place sample into sterile universal and do not add any additional water, buffers or preservatives. Sterile water or PBS might be contaminated with DNA from pseudomonas and pseudomonas like bacteria.

The amount of material must be adequate to maintain maximum sensitivity. In general we recommend 200 µl or more for liquid material (no more than 1 ml to be supplied) and a "finger nail" for solid samples ~ 1.0 cm³, selecting the most necrotic diseased area for testing. Please do not submit excess sample material, as this may result in your sample being quarantined or rejected. For blood culture medium, remove 200 µl to 1,000 µl of fluid using aseptic technique to a sterile universal. For paraffin embedded tissues supply 3-5 mm of solid block or 4-10 shavings in a sterile container.

OUTCOME OF IDENTIFICATION TESTS

- The investigation/surveillance of emerging and novel pathogens, which may be associated with a variety of acute and chronic infections.
- Identifying atypical isolates that fail identification by conventional methods.
- Confirmation of identification of actinomycetes, anaerobic isolates and *Bacillus* strains.
- Identification of bacteria detected in samples from normally sterile sites.

2. Genomic Services Unit

Unit Head
Laboratory Manager

Dr Catherine Arnold (PhD)
Paul Laidler (B.Sc C.Sc F.I.B.M.S D.M.L.M.)

Key Services

1. DNA SEQUENCING SERVICE

GSU offers various levels of DNA sequencing of PCR fragments and plasmids for laboratories of Microbiology Services Colindale and other centres within the HPA. DNA sequencing is performed on Applied Biosystems' capillary sequencers, providing up to 800 bases read length depending on the quality of the DNA template and primer supplied.

GSU will provide single read sequencing of PCR products or plasmid DNA based on dideoxy Sanger sequencing using ABI Genetic Analyser capillary platforms (3730 and 3130XL) at the HPA Microbiology Services Colindale. Normal service will be provided between 09.00 to 17.00 hrs, Monday to Friday (excluding bank holidays). An out-of-hours emergency support will be available.

GSU agrees to provide the following services:

- S1: Reaction-ready samples (DNA and primer) for sequencing.
- S2: Purified DNA samples in 96-well plate for sequencing and primers (maximum 2 per plate) to be added by GSU.
- S3: Reaction-ready single samples in microtubes for sequencing.
- S4: DNA for clean-up followed by sequencing using up to 2 primers per plate):
 - (A) Provided in 96 well plate
 - (B) Single reactions
- S5: PCR clean-up only (Using Agencourt AMPure magnetic beads)
- S6: Urgent samples as:
 - (A) Reaction-ready samples for sequencing
 - (B) Template DNA for clean-up and sequencing
- S7: Emergency out-of-hours service
- S8: Short read sequencing (≤ 500 bp read length)
 - (A) Reaction-ready samples (DNA and primer) for sequencing
 - (B) Purified DNA samples in 96-well plate for sequencing and primers (maximum 2) to be added by GSU
 - (C) DNA for clean-up and sequencing using up to 2 primers per plate
- S9: Batch short-read reaction-ready samples for sequencing
- S10: Whole genome gap filling and finishing service

S1: Reaction-ready samples (DNA and primer mixed) for sequencing

Customer will:

- Provide cleaned DNA product or plasmid with sequencing primer added to each sample in MicroAmp Optical 96-well semi-skirted reaction plates (MicroAmp Optical Plates: CFI Stores item number KHA100791.T). DNA must

be purified using a method compatible with dideoxy sequencing and there can be a maximum of 94 samples/plate.

- GSU staff can provide recommendations with regards to clean-up procedure.
- Add samples to the wells except for positions **G12** and **H12**; these are for sequencing controls only and will be added by GSU.
- Provide a total of 6 µl volume of reaction mix (in molecular biology grade water, not EDTA) containing 5 picomole of primer and **x** nanograms (Table 1) of cleaned-up DNA.
- Log onto HPA Sequencing Service electronic submission via <https://hpasequencingervices.genesifter.net> and place a sequencing order including the cost centre or project code to which the work will be charged.
- Have an option of sending twice the reaction volume (i.e. total volume of 12 µl containing 10 picomole primer and double amount of DNA). This will allow GSU to provide a rapid repeat service if required.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked “GSU Customer fridge”. The worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.
 - ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

GSU will:

- Report the sequencing data electronically to partners within 48 hours of GSU receiving the samples.
- Quality control the sequencing data by processing sequencing pGEM controls on each plate and obtain a minimum of 850 bp read length (Phred 20 quality).
- Automatically repeat reactions (if partner submits 2 x reaction volume) in the event that the sequence of our pGEM controls are less than 850 bp in length or all of the sequencing reactions provided by the partner fail. This will reduce the turn-around-time and need for sample re-submission by partners. The results will be available electronically for partners within 12 hours of repeat run.

Table 1. Recommended concentrations of DNA for Sequencing

Template	Quantity of DNA
PCR Product	
100-200 bp	1-3 ng
200-500 bp	3-10 ng
500-1000 bp	5-20 ng
1000-2000 bp	10-40 ng
>2000 bp	40-100 ng
Other DNA	
Single stranded DNA	50-100 ng
Double stranded DNA	200-500 ng
Plasmid <10 Kb	100-300 ng
Plasmid >10 Kb	100-300 ng + 20ng for each additional 1kb

Large DNA (BACs, PACs, YACs, phage, cosmids and fosmids)	0.5-1.0 µg
Bacterial genomic DNA	2-3 µg

S2: Purified DNA samples in 96-well plate and primers (maximum 2) to be added by GSU

Customer will:

- Provide samples in MicroAmp Optical 96-well semi-skirted reaction plates (MicroAmp Optical Plates: CFI Stores item number KHA100791.T). A maximum of 94 samples/plate and a maximum of 2 primers per plate
- Add samples to the wells except for positions **G12** and **H12**; these are for sequencing controls only and will be added by GSU.
- Provide a total of 5 µl volume in each well containing **x** nanograms (Table 1) of cleaned-up DNA (in molecular biology grade water, not EDTA).
- Provide 200 µl of each primer at 5 pmol/µl.
- Log onto HPA Sequencing Service electronic submission via <https://hpasequencingervices.genesifter.net> and place a sequencing order including the cost centre or project code to which the work will be charged.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked “GSU Customer fridge”. The worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.
 - ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

GSU will:

- Add 1 µl of the sequencing primer to each well, up to a maximum of 2 primers per plate.
- Report the sequencing data electronically to partners within 48 hours of GSU receiving the samples.
- Quality control the sequencing process by the inclusion of 2 sequencing pGEM controls on each plate and obtain a minimum of 850 bp read length Phred 20 quality).

S3: Reaction-ready single samples in microtubes.

Customer will:

- Provide microtubes containing a total of 6 µl volume of sample (in molecular biology grade water, not EDTA) containing 5 picomole of primer and **x** nanograms (Table 1) of cleaned-up DNA or plasmid.
- Log onto HPA Sequencing Service electronic submission via <https://hpasequencingervices.genesifter.net> and place a sequencing order including the cost centre or project code to which the work will be charged.
- Deliver the samples to level 2 Zone D and place inside the refrigerator marked “GSU Customer fridge”. The worksheet attached to the refrigerator must be completed to ensure the samples are processed with the priority of when they were submitted.

GSU will:

- Report the sequencing data electronically to partners within 48 hours of GSU receiving the samples.
- Quality control the sequencing process by the inclusion of 2 sequencing pGEM controls on each plate and obtain a minimum of 850 bp read length Phred 20 quality).

S4: DNA for clean-up and sequencing

Customer will:

(A) Samples in 96-well format

- Provide samples in MicroAmp Optical 96-well semi-skirted reaction plates (MicroAmp Optical Plates: CFI Stores item number KHA100791.T). A maximum of 94 samples/plate.
- Add samples to the wells except for positions **G12** and **H12**; these are for sequencing controls only and will be added by GSU.
- Provide a minimum of 10 µl of unpurified DNA in each well. All wells must contain the same volume and the volume must be specified on the requisition form.
- Provide a minimum of 200µl of each primer at 5 pmol/µl (maximum of 2 primers per plate).
- Log onto HPA Sequencing Service electronic submission via <https://hpasequencingervices.genesifter.net> and place a sequencing order including the cost centre or project code to which the work will be charged.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked “GSU Customer fridge”. The worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.
 - ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

(B) Single Samples

- Provide the sample in microtubes or 96-well semi-skirted reaction plate (CFI Stores item number KHA100791.T).
- Provide a minimum of 10 µl of unpurified DNA and specify the volume on the form. All tubes/wells must contain the same volume and the volume specified on the requisition form.
- Provide a minimum of 200µl of each primer at 5 pmol/µl (maximum of 2 primers per plate).
- Log onto HPA Sequencing Service electronic submission via <https://hpasequencingervices.genesifter.net> and place a sequencing order including the cost centre or project code to which the work will be charged.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked “GSU Customer fridge”. The worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.
 - ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

GSU will:

- Purify the PCR products using magnetic beads (Agencourt AMPure) on the Biomek NxP robot (Beckman) and re-suspend the samples in 40 µl nuclease free water.
- Add 1 µl of the sequencing primer to each well, up to a maximum of 2 primers per plate.
- Report the sequencing data electronically to partners within 60 hours of GSU receiving the samples.
- Quality control the sequencing data by processing sequencing pGEM controls on each plate and obtain a minimum of 850 bp read length (Phred 20 quality).

S5: PCR Clean up (Colindale based Customers ONLY)

Customer will:

- Provide PCR samples for purification in MicroAmp Optical 96-well semi-skirted reaction plates (MicroAmp Optical Plates: CFI Stores item number KHA100791.T). A maximum of 96 samples/plate.
- Provide a minimum of 10 µl or a maximum of 50 µl of unpurified PCR product in each well. All wells must be of uniform volume and the volume and the number of samples specified on the request form.
- Log onto HPA Sequencing Service electronic submission via <https://hpasequencingervices.genesifter.net> and place a sequencing order including the cost centre or project code to which the work will be charged.
- Deliver the samples to level 2 Zone D and place inside the refrigerator marked "GSU Customer fridge". The worksheet attached to the refrigerator must be completed.

GSU will:

- Purify the DNA using magnetic beads (Agencourt AMPure) on the Biomek NxP robot (Beckman) and re-suspend the samples in 40 µl nuclease free water.
- Provide the purified PCR samples within 24 hrs of receipt and notify the customer by email. The purified samples will be stored in the fridge in level 2 Zone D for collection.

S6: Urgent samples

- Priority of service maybe required for samples needing rapid turnaround time. This service will be provided through customer request and prior discussion with GSU.

(A) *Reaction-ready samples for sequencing*

Partners will provide samples as described in S1.

GSU will:

- Report the sequencing data electronically to partners within **12 hours** of GSU receiving the samples.

(B) *Template DNA for clean-up and sequencing*

Customer will provide samples as described in S4.

GSU will:

- Report the sequencing data electronically to partners within **14 hours** of GSU receiving the samples.

S7: Emergency Out of Hours Service

- GSU will provide emergency out-of-hours sequencing for samples submitted by the partner. A request for this service should be placed by communicating with the on-call GSU staff. Contact is by telephone on 07766421765 at least two hours prior to sample submission.
- An early indication of when the samples are expected for sequencing will allow better co-ordination and a faster response by GSU.
- Results for urgent reaction-ready samples (S1) will be reported within 10 hours of GSU receiving samples.
- Samples submitted for clean-up and sequencing (S4) will be reported within 14 hours of GSU receiving samples.
- Results will be delivered to partners electronically.
- Out-of-hours emergency response will be charged on a minimum of 10 samples per call.

S8: Short read sequencing (≤ 500 bp read length)

(A) Reaction-ready samples (DNA and primer) for sequencing

Customer will:

- Provide cleaned DNA product or plasmid with sequencing primer added to each sample in MicroAmp Optical 96-well semi-skirted reaction plates (MicroAmp Optical Plates: CFI Stores item number KHA100791.T). DNA must be purified using a method compatible with dideoxy sequencing and there can be a maximum of 94 samples/plate.
- Add samples to the wells except for positions **G12** and **H12**; these are for sequencing controls only and will be added by GSU.
- Provide a total of 6 μ l volume of reaction mix (in molecular biology grade water, not EDTA) containing 5 picomole of primer and **x** nanograms (Table 1) of cleaned-up DNA.
- Log onto HPA Sequencing Service electronic submission via <https://hpasequencingervices.genesifter.net> and place a sequencing order including the cost centre or project code to which the work will be charged.
- Have an option of sending twice the reaction volume (i.e. total volume of 12 μ l containing 10 picomole primer and double amount of DNA). This will allow GSU to provide a rapid repeat service if required.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked "GSU Customer fridge". The worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.
 - ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

GSU will:

- Report the sequencing data electronically to partners within 48 hours of GSU receiving the samples.
- Quality control the sequencing data by processing sequencing pGEM controls on each plate and obtain a minimum of 550 bp read length (Phred 20 quality).
- Automatically repeat reactions (if partner submits 2 x reaction volume) in the event that our internal controls are less than 550 bp in length *or* all of the

sequencing reactions provided by the partner fail. This will reduce the turn-around-time and need for sample re-submission by partners. The results will be available electronically for partners within 12 hours of repeat run.

(B) Purified DNA samples in 96-well plate for sequencing and primers (maximum 2) to be added by GSU

Customer will:

- Provide samples in MicroAmp Optical 96-well semi-skirted reaction plates (MicroAmp Optical Plates: CFI Stores item number KHA100791.T). A maximum of 94 samples/plate and a maximum of 2 primers per plate
- Add samples to the wells except for positions **G12** and **H12**; these are for sequencing controls only and will be added by GSU.
- Provide a total of 5 µl volume in each well containing **x** nanograms (Table 1) of cleaned-up PCR product (in molecular biology grade water, not EDTA).
- Provide a minimum of 200 µl of each primer at 5 pmol/µl.
- Log onto HPA Sequencing Service electronic submission via <https://hpasequencingervices.genesifter.net> and place a sequencing order including the cost centre or project code to which the work will be charged.
- Deliver the samples to level 2 Zone D and place inside the refrigerator marked "GSU Customer fridge". The worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.

GSU will:

- Add 1 µl of the sequencing primer to each well, up to a maximum of 2 primers per plate.
- Report the sequencing data electronically to partners within 48 hours of GSU receiving the samples.
- Quality control the sequencing data by processing sequencing pGEM controls on each plate and obtain a minimum of 550 bp read length (Phred 20 quality).

(C) DNA for clean-up and sequencing in 96-well format

Customer will:

- Provide samples in MicroAmp Optical 96-well semi-skirted reaction plates (MicroAmp Optical Plates: CFI Stores item number KHA100791.T). A maximum of 94 samples/plate.
- Add samples to the wells except for positions **G12** and **H12**; these are for sequencing controls only and will be added by GSU.
- Provide a minimum of 10 µl of unpurified DNA in each well. All wells must contain the same volume and the volume must be specified on the requisition form.
- Provide a minimum of 200µl of each primer at 5 pmol/µl (maximum of 2 primers per plate).
- Log onto HPA Sequencing Service electronic submission via <https://hpasequencingervices.genesifter.net> and place a sequencing order including the cost centre or project code to which the work will be charged.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked "GSU Customer fridge". The

worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.

- ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

GSU will:

- Purify the PCR products using magnetic beads (Agencourt AMPure) on the Biomek NxP robot (Beckman) and re-suspend the samples in 40 µl nuclease free water.
- Add 1 µl of the sequencing primer to each well, up to a maximum of 2 primers per plate.
- Report the sequencing data electronically to partners within 60 hours of GSU receiving the samples.
- Quality control the sequencing data by processing sequencing pGEM controls on each plate and obtain a minimum of 550 bp read length (Phred 20 quality).

(D) Single Sample for DNA clean-up and sequencing

- Provide the sample in microtubes or 96-well semi-skirted reaction plate (CFI Stores item number KHA100791.T).
- Provide a minimum of 10 µl of unpurified DNA and specify the volume on the form. All tubes/wells must contain the same volume and the volume specified on the requisition form.
- Provide a minimum of 200µl of each primer at 5 pmol/µl (maximum of 2 primers per plate).
- Log onto HPA Sequencing Service electronic submission via <https://hpasequencingervices.genesifter.net> and place a sequencing order including the cost centre or project code to which the work will be charged.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked "GSU Customer fridge". The worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.
 - ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

GSU will:

- Purify the PCR products using magnetic beads (Agencourt AMPure) on the Biomek NxP robot (Beckman) and re-suspend the samples in 40 µl nuclease free water.
- Add 1 µl of the sequencing primer to each well, up to a maximum of 2 primers per plate.
- Report the sequencing data electronically to partners within 60 hours of GSU receiving the samples.
- Quality control the sequencing data by processing sequencing pGEM controls on each plate and obtain a minimum of 550 bp read length (Phred 20 quality).

(S9) Batch Short-read reaction-ready samples (DNA and primer) for sequencing

Customer will:

- Provide reaction-ready reactions with sequencing primer added to each sample in MicroAmp Optical 96-well semi-skirted reaction plates (MicroAmp Optical Plates: CFI Stores item number KHA100791.T). DNA must be purified

using a method compatible with dideoxy sequencing and there must be 94 samples/plate.

- A minimum of 5 plates must be submitted.
- Add samples to the wells except for positions **G12** and **H12**; these are for sequencing controls only.
- Provide a total of 6 µl volume of reaction mix (in molecular biology grade water, not EDTA) containing 5 picomole of primer and **x** nanograms (Table 1) of cleaned-up PCR product.
- Log onto HPA Sequencing Service electronic submission via <https://hpasequencingervices.genesifter.net> and place a sequencing order including the cost centre or project code to which the work will be charged.
- Have an option of sending twice the reaction volume (i.e. total volume of 12 µl containing 10 picomole primer and double amount of DNA). This will allow GSU to provide a rapid repeat service.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked “GSU Customer fridge”. The worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.
 - ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

GSU will:

- Report the sequencing data electronically to partners within 10 working days of GSU receiving the samples.
- Quality control the sequencing data by processing sequencing pGEM controls on each plate and obtain a minimum of 550 bp read length (Phred 20 quality).
- Automatically repeat reactions (if partners submits 2 x reaction volume) in the event that our internal controls are less than 550 bp in length *or* all of the sequencing reactions provided by the partner fail. This will reduce the turn-around-time and need for sample re-submission by partners. The results will be available electronically for partners within 12 hours of repeat run.

S10: Whole genome sequencing and finishing

- For details and pricing please contact Genomic Services Unit (afqu@hpa.org.uk or x 7772).

Service Turnaround time:

Service No.	Service Type	Turn around time
S1	Reaction-ready samples (DNA+Primer)	48 hrs
S2	Purified DNA samples in plate and GSU to add primers (maximum of 2 primers/plate)	48 hrs
S3	Reaction-ready single samples in microtubes	48hrs
S4-A	DNA Clean-up and sequencing of samples in 96 plate-format	60 hrs
S4-B	DNA Clean-up and sequencing of single samples	60 hrs

S5	PCR purification ONLY using Agencourt AMPure beads (Samples provided in 96-well plates)	24 hrs
S6-A	Urgent reaction-ready Samples	10 hrs
S6-B	Urgent clean-up and sequencing samples	12 hrs
S7-A*	Emergency out of hours service – reaction ready	10 hrs
S7-B*	Emergency out of hours – DNA clean up and sequencing	12 hrs
S8-A	Short-read reaction ready	48 hours
S8-B	Short-read samples in plate and GSU to add primers	48 hours
S8-C	Short-read template clean-up and sequencing in 96 well format	60 hours
S8-D	Short-read template clean-up and sequencing for single samples	60 hours
S9	Batch short-read reaction ready	10 days
S10	Whole genome gap filling and finishing	On request

* **Please note:** All out of hours emergency requests will be charged at a minimum of 10 samples.

Policy on repeat reactions

- If a reaction has not passed the standard quality check and the pGEM control has not passed the quality check, the reaction will be repeated.

2. Fragment Sizing and Analysis service

GSU will provide DNA-based fragment analysis services listed below, using the ABI Genetic Analyser capillary platform (3730) at HPA Microbiology Services Colindale. The ABI 3730 instruments are spectrally calibrated to run filter set G5 and detect five fluorescent dyes (DS-33 set). The five dyes are 6-FAM (blue), VIC (green), NED (yellow), PET (red) and LIZ (orange: size standard).

Normal service will be provided between 09.00 to 17.00 hrs, Monday to Friday (excluding bank holidays).

A. Fluorescent Amplified Fragment Length Polymorphism

GSU provides fluorescent amplified fragment length polymorphism (FAFLP), a high-resolution whole genome methodology used as a rapid tool for cost-effective analysis of genetic diversity within bacterial genomes. It is useful for a broad range of applications including identification and subtyping of microorganisms from clinical samples, for identification of outbreak genotypes, for studies of micro and macro-variation, and for population genetics.

B. Fragment Separation Service

GSU provides a fragment-based separation on Applied Biosystems' capillary sequencers. The fragments can be labelled with any of the four dyes listed: 6-FAM (blue), VIC (green), NED (yellow), and PET (red). Depending on the size of the products, a 600 bp (LIZ600) or a 1200 bp (LIZ1200) size standard labelled with the 5th dye LIZ is used for sizing the fragments.

Services provided for fragment analysis:

- F1-A FAFLP process from bacterial DNA (for existing Customers only until 31 January 2011)
- F1-B FAFLP process from bacterial isolates (for existing Customers only until 31 January 2011)
- F2 Full comparative FAFLP analysis
- F3 Ready-to-run FAFLP reactions for electrophoretic separation
- F4 Ready-to-run reactions for electrophoretic separation
- F5 PCR reactions for electrophoresis separation requiring pre-processing by GSU
- F6: Urgent samples out-of-hours

All results are provided as raw data files (.fsa format) except for Service F2.*

F1: FAFLP process

(A) FAFLP from Bacterial DNA

Customer will:

- Please provide bacterial DNA samples in 96-well reaction plates (maximum of 94 samples/plate).
- Add samples to the wells except for positions G12 and H12; these are for FAFLP controls only.
- Provide a minimum of 10 µl suspension of ~500 ng of high quality DNA in molecular biology grade water.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked "GSU Customer fridge". The worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.
 - ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

(B) FAFLP from Non-HG3/4 bacterial cultures on solid agar medium

- Provide 24 hour notice for bacterial culture submission and declaration of risk-group status, bacterial genus, culture conditions, and medium used for the growth.
- Provide Non-HG3/4 bacterial cultures submitted as a single strain on solid agar plates of mid log phase growth i.e. fresh culture.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Please contact GSU to arrange for an internal transfer of cultures to DBHT.
 - ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

AND

- Complete Fragment Analysis Service request (**BW0155**) and send it electronically to afgu@hpa.org.uk.
- Provide GSU with the cost centre or project code and Task number to which the work will be charged.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked "GSU Customer fridge". The

worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.

- ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

GSU will:

- Extract DNA from cultures (where required).
- Perform FAFLP process from DNA samples.
- Undertake FAFLP process using two enzymes (selected and agreed with the partner) as outlined in SOP B13021.
- Quality control the data by processing *E. coli* K12 strain MG1655 DNA on each plate as a control and analyse the fragments generated using Peak Scanner/GeneMapper software for signal strength, quality of size standard peaks and comparison of control K12 fragment data with expected sizes.
- Report the fragment data for Service F1-A as *.fsa files electronically to partners within 5 working days of GSU receiving the DNA samples (if samples received by 10 am). The protocol requires two consecutive days to meet the 5 working days turn around times.

OR

- Report the fragment data for Service F1-B as *.fsa files electronically to partners within 6 working days of GSU receiving the bacterial cultures.

F2 Full comparative FAFLP analysis

This service is exactly the same as service F1 except

GSU will additionally:

- Provide FAFLP results as comparative data between the different isolates in the format of number of fragment differences between the different isolates and a written report. The comparative data will be provided in an Excel spreadsheet. The report will be sent in 10 working days from GSU receiving the samples for analysis.

F3 Ready-to-run FAFLP fragment separation

Customer:

- Provide ready-to-run FAFLP reactions in MicroAmp Optical 96-well semi-skirted reaction plates (maximum of 94 samples/plate) [CFI Stores item number KHA100791.T].
- Provide a total volume of 11.5 µl reaction-mix containing 1 µl of appropriately diluted FAFLP PCR reaction, 0.5 µl of LIZ-labelled size standard [ABI] and 10 µl of HiDi formamide [ABI item number 4311320].
- Specify the LIZ-labelled size standard used on the request form.
- Add samples to the wells except for positions G12 and H12 (when submitting > 46 samples); these are for FAFLP controls only. If the number of samples is ≤ 46, the samples should be placed in alternate columns of the 96-well plate, starting from Column 1, 3, 5, etc (leaving wells G11 and H11 empty) **OR** 2, 4, 6, etc (leaving wells G12 and H12 empty) and fill the sample sheet accordingly.

- Complete FAFLP request form (**BW0155**) and send it electronically to afgu@hpa.org.uk
- Provide GSU with the cost centre or project code and Task number to which the work will be charged.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked “GSU Customer fridge”. The worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.
 - ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

GSU will:

- Subject each sample to heat denaturation and run fragment-based separation on the ABI Genetic Analyser capillary platform (3730).
- Quality control the data by running LIZ-labelled size standard as control and analyse the fragments generated using Peak Scanner/GeneMapper software for signal strength & quality of peaks and check signal strength of samples.
- Report the fragment data as *.fsa files electronically to partners within 48 hrs of GSU receiving the ready-to-run samples.

F4 Ready-to-run polymorphic size-based DNA fragment separation

Customer will:

- Provide ready-to-run reactions in MicroAmp Optical 96-well semi-skirted reaction plates (maximum of 94 samples/plate) [CFI Stores item number KHA100791.T].
- Provide a total volume of 11.5 µl reaction-mix containing 1 µl of appropriately diluted FAFLP PCR reaction, 0.5 µl of LIZ-labelled size standard and 10 µl of HiDi formamide [ABI item number 4311320].
- Specify the LIZ-labelled size standard used on the request form.
- Add samples to the wells except for positions G12 and H12 (when submitting > 46 samples); these are for GSU controls only. If the number of samples is ≤ 46, the samples should be placed in alternate columns of the 96-well plate, starting from Column 1, 3, 5, etc (leaving wells G11 and H11 empty) **OR** 2, 4, 6, etc (leaving wells G12 and H12 empty) and fill the sample sheet accordingly.
- Complete FAFLP request form (**BW0155**) and send it electronically to afgu@hpa.org.uk
- Provide GSU with the cost centre or project code and Task number to which the work will be charged.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked “GSU Customer fridge”. The worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.
 - ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

- Submit should be received by GSU before 16:00 hrs to allow same day processing. (The fluorescence of the fluorophores in the reactions can decrease significantly if the samples are left in formamide for longer periods).

GSU will:

- Subject each reaction sample to heat denaturation and run for fragment-based separation on the ABI Genetic Analyser capillary platform (3730).
- Quality control the data by running LIZ-labelled size standard as control and analyse the fragments generated using Peak Scanner/GeneMapper software for signal strength & quality of peaks and check signal strength of samples.
- Report the fragment data as *.fsa files (or as previously agreed with the partner) electronically to partners within 48 hrs of GSU receiving the ready-to-run samples.

F5 PCR reactions for electrophoretic separation requiring GSU pre-processing

Customer:

- Provide PCR reactions in 96-well plates MicroAmp Optical 96-well semi-skirted reaction plates (maximum of 94 samples/plate) [CFI Stores item number KHA100791.T].
- Add samples to the wells except for positions G12 and H12 (when submitting > 46 samples); these are for GSU controls only. If the number of samples is ≤ 46, the samples should be placed in alternate columns of the 96-well plate, starting from Column 1, 3, 5, etc (leaving wells G11 and H11 empty) **OR** 2, 4, 6, etc (leaving wells G12 and H12 empty) and fill the sample sheet accordingly.
- Provide a minimum of 10 µl PCR reaction and specify the dilution required for electrophoresis.
- Specify the LIZ-labelled size standard to be used for sizing on the request form (**BW0155**).
- Complete FAFLP request form (**BW0155**) and send it electronically to afgu@hpa.org.uk
- Provide GSU with the cost centre or project code and Task number to which the work will be charged.
- Delivery of samples for processing:
 - ❖ For Customers within Colindale site: Deliver the samples to level 2 Zone D and place inside the refrigerator marked “GSU Customer fridge”. The worksheet attached to the refrigerator must be completed to ensure samples are processed with the priority of when they were submitted.
 - ❖ For Customers external to the Colindale site: Send the samples via Hays DX to: HPA Colindale, CFI (GSU), DX 6530001, Colindale NW.

GSU will:

- Dilute the PCR reactions (as agreed with the customer during validation process) and add the required HiDi formamide and appropriate LIZ-labelled size standard to each sample well.

- Subject each reaction sample to heat denaturation and run fragment-based separation on the ABI Genetic Analyser capillary platform (3730).
- Quality control the data by running LIZ-labelled size standard as control and analyse the fragments generated using Peak Scanner/GeneMapper software for signal strength & quality of peaks and check signal strength of samples.
- Report the fragment data as *.fsa files (or as previously agreed with the partner) electronically to partners within 48 hrs of GSU receiving the ready-to-run samples.

F6: Urgent samples, out-of-hours (for service F3 & F4 only)

This service is exactly the same as service F3 & F4 except

Customer will:

- Contact GSU during working hours on DECT 7772 and out-of-hours on 07766421765 as soon as fragment analysis is identified as a requirement. An early indication of when the samples are expected for urgent fragment analysis will allow better co-ordination and a faster response by GSU.

GSU will:

- Report the fragment analysis data electronically to partners within **4 hrs** of GSU receiving the samples.

Urgent, Emergency and Out-of-Hours Service

- GSU will provide urgent fragment analysis service for **ONLY** ready-to-run reactions (Service F3 and F4).
- Results for **urgent** ready-to-run samples (F3 and F4) submitted between **09.00 and 17.00 hrs** will be reported within **12 hours** of GSU receiving samples.
- **Out-of-hours** emergency samples will be reported within **4 hrs** of GSU receiving samples.
- The processing of urgent samples will commence within 2 hours of notification.
- Results will be delivered to partners electronically.
- Out-of-hours emergency response will be charged on a minimum of 10 samples per call.

LIST OF CONTACTS

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MISU Service enquiry telephone number 020 8327 7869

Email: MISU-Services@hpa.org.uk

GSU Service enquiry telephone number 020 8327 7772

Email: AFGU@hpa.org.uk

Complaints/Comments

Please telephone or email the appropriate unit head who will initiate our internal complaints procedure.

We welcome comments on how we can improve the provision of these services. Please see contact details above.