Precision AMR Programme at HSL
Location

- Based within the diagnostic Infection Sciences and Molecular Pathology departments at the Halo building, 1 Mabledon Place.

Microbiology (Level 3 & 4)
- Routine Bacteriology (Swabs & Urines)
- Blood Cultures
- Respiratory Pathogens (CL3)
- Tissues & Fluids
- Enteric Pathogens
- Hospital Acquired Infections
- Regional Mycology Unit
- Hospital of Tropical Diseases Parasitology

Molecular Pathology (Level 5)
- Molecular Virology (including APDU)
- Molecular Microbiology
- Molecular Parasitology
Laboratory Scientific Team

Dr Paul Grant
• Lead Clinical Scientist, Molecular Virology

Dr Alan Williams
• Lead Clinical Scientist, Molecular Microbiology

Dr Rebecca Gorton
• Lead Clinical Scientist, Molecular Microbiology

Dr Jude Heaney
• Lead Research Scientist, ADPU

Dr Vicky Enne
• Senior Research Associate, UCL

New Precision AMR Clinical Scientist Post
Exemplar Projects at HSL

**Dr Paul Grant/Dr Jude Heaney**
- WGS for detection of drug resistance in herpes simplex virus
- WGS for detection of drug resistance in HIV-1

**Dr Vicky Enne/Dr Alan Williams**
- Potential of rapid direct from sample ONT MinION sequencing for prediction of antimicrobial resistance phenotypes and strain typing
- Combining long and short-read sequencing for mapping of carbapenemase-encoding plasmids from Gram-negative bacteria: an essential tool for tracing CPE outbreaks

**Dr Rebecca Gorton**
- WGS of pneumocystis for strain relatability and resistance profiling to Septrin (Cotrimoxazole) in chronic and acute PCP
- WGS of clinically significant aspergillus isolates to determine TLR gene profiling for Azole resistance
Clinical Laboratory Facilities

- High volume DNA/RNA Extraction
- Bacteriology
- Containment Level 3
- Clinical PCR & Sequencing
New Extraction Facilities

- Support for additional DNA/RNA extraction specifically within containment level 3.
Sequencing Technology & Capabilities

New Sequencing Facilities

- Short-read
- Uni-directional
- Short-read
- Bi-directional
- Long-read
- Real time data
Led by Dr Eleni Nastouli and developed by UCLH and UCL Clinicians, Scientists & Bioinformaticians

Validated extensively using HIV and Influenza and other viral and bacterial targets

New bioinformatics framework partner with HSL for Bacterial Informatics

Collaboration with Centre for Clinical Microbiology (UCL/RFL)

Fungal Development Programme with HSL.

Open access informatics tools available through Oxford Nanopore.

Used by clinical and academic researchers across the North London Campus.
**GENOME SEQUENCING REPORT - HIV**

**UCLH - Advanced Diagnostics Pathogen Unit**  
**Report Published:** The 6 Jan 2019  
**Website:** www.uclh.nhs.uk  
**Address:** 335 Euston Rd, Bloomsbury, NW1 3BU  
**Telephone:** 020 3456 7890  
**Patient Name:** [Redacted]  
**Barcode:** [Redacted]  
**Patient ID:** [Redacted]  
**Sample Type:** [Redacted]  
**Sample Collection Date:** [Redacted]  
**Reporting Lab:** [Redacted]  
**Requester Contact:** [Redacted]

**Summary**

The specimen was positive for Human Immunodeficiency Virus-1 (HIV)  
Subtype CRF02_AG

**Drug Resistance**

**Nucleoside Reverse Transcriptase Inhibitors (NRTI)**

- abacavir (ABC): SUSCEPTIBLE  
- zidovudine (AZT): SUSCEPTIBLE  
- emtricitabine (FTC): SUSCEPTIBLE  
- lamivudine (3TC): SUSCEPTIBLE  
- tenofovir (TDF): SUSCEPTIBLE

**Non-nucleoside Reverse Transcriptase Inhibitors (NNRTI)**

- doravirine (DOR): SUSCEPTIBLE  
- efavirenz (EFV): SUSCEPTIBLE  
- etravirine (ETR): SUSCEPTIBLE  
- nevirapine (NVP): SUSCEPTIBLE  
- rilpivirine (RPV): SUSCEPTIBLE

**Protease Inhibitor**

- atazanavir/r (ATV/r): SUSCEPTIBLE  
- darunavir/r (DRV/r): SUSCEPTIBLE  
- lopinavir/r (LPV/r): SUSCEPTIBLE

**Integrase Strand Transfer Inhibitor**

- bictegravir (BIC): SUSCEPTIBLE  
- dolutegravir (DTG): SUSCEPTIBLE  
- elvitegravir (EVG): POTENTIAL LOW-LEVEL RESISTANCE  
- raltegravir (RAL): POTENTIAL LOW-LEVEL RESISTANCE

**Authorised**

**Signature** [Redacted]  
**Name** [Redacted]  
**Position** [Redacted]  
**Date** [Redacted]
# Informatics Pipelines & Data Analysis

## Validated Pathogens

<table>
<thead>
<tr>
<th>Species</th>
<th>cgMLST</th>
<th>MLST</th>
<th>Other typing schemes</th>
<th>Markers of special interest</th>
<th>Antibiotic classes</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>S. aureus</em></td>
<td>⬜️</td>
<td>⬜️</td>
<td>SCCmec, spa sequences</td>
<td>TSST-1, PVL, ETs</td>
<td>13</td>
</tr>
<tr>
<td><em>K. pneumoniae</em></td>
<td>⬜️</td>
<td>⬜️</td>
<td>-</td>
<td>ESBL, CRE</td>
<td>25+</td>
</tr>
<tr>
<td><em>E. coli</em></td>
<td>⬜️</td>
<td>⬜️</td>
<td>phylogroup</td>
<td>ESBL, CRE</td>
<td>25+</td>
</tr>
<tr>
<td><em>Enterococcus faecium</em></td>
<td>⬜️</td>
<td>⬜️</td>
<td>-</td>
<td>Vancomycin</td>
<td>25+</td>
</tr>
<tr>
<td><em>C. difficile</em></td>
<td>⬜️</td>
<td>⬜️</td>
<td>-</td>
<td>Multiple</td>
<td>25+</td>
</tr>
<tr>
<td><em>S. enterica</em></td>
<td>⬜️</td>
<td>⬜️</td>
<td>-</td>
<td>Multiple</td>
<td>25+</td>
</tr>
<tr>
<td><em>P. aeruginosa</em></td>
<td>⬜️</td>
<td>⬜️</td>
<td>-</td>
<td>Multiple</td>
<td>25+</td>
</tr>
<tr>
<td><em>N. gonorrhoeae</em></td>
<td>⬜️</td>
<td>⬜️</td>
<td>-</td>
<td>Multiple</td>
<td>25+</td>
</tr>
<tr>
<td><em>A. baumannii</em></td>
<td>⬜️</td>
<td>⬜️</td>
<td>-</td>
<td>Multiple</td>
<td>25+</td>
</tr>
</tbody>
</table>
Staphylococcus aureus

#83 - P26 - 2017-09-27 13:55

Resistance markers for the following antibiotics have been identified: Ciprofloxacin, Clindamycin [inducible], Erythromycin, Gentamicin, Isoniazid-Perfloxacin, Penicillin-tabile-Perfloxacin, Trimethoprim.

Identified resistance markers

Identified resistance markers confer a resistance level above EUCAST clinical breakpoints.

<table>
<thead>
<tr>
<th>ANTIBIOTIC</th>
<th>GENES</th>
<th>MUTATIONS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ciprofloxacin</td>
<td>Not supported</td>
<td>grA (S80I) [J231], grA (S80G) [J231], grA (S80I) + grA (S80G) [J231]</td>
</tr>
<tr>
<td>Clindamycin (Inducible)</td>
<td>emc[4][15][12]</td>
<td>Not supported</td>
</tr>
<tr>
<td>Erythromycin</td>
<td>emc[4][15][12]</td>
<td>Not supported</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>aac(3)-Ia [15][17]</td>
<td>Not supported</td>
</tr>
<tr>
<td>Isoniazid-Perfloxacin</td>
<td>nac(1)[4][18]</td>
<td>Not supported</td>
</tr>
<tr>
<td>Penicillin-tabile-Perfloxacin</td>
<td>nac(1)[4][18]</td>
<td>Not supported</td>
</tr>
<tr>
<td>Penicillin</td>
<td>nac(1)[4][18]</td>
<td>Not supported</td>
</tr>
<tr>
<td>Trimethoprim</td>
<td>dfr[A] [23][21]</td>
<td>No mutations found</td>
</tr>
<tr>
<td>Clindamycin</td>
<td>No genes found</td>
<td>Not supported</td>
</tr>
<tr>
<td>Fusidic Acid</td>
<td>No genes found</td>
<td>Not supported</td>
</tr>
<tr>
<td>Mupirocin</td>
<td>No genes found</td>
<td>Not supported</td>
</tr>
<tr>
<td>Rifampicin (Rifampin)</td>
<td>No genes found</td>
<td>Not supported</td>
</tr>
<tr>
<td>Tetacycline</td>
<td>No genes found</td>
<td>Not supported</td>
</tr>
<tr>
<td>Vancomycin</td>
<td>No genes found</td>
<td>Not supported</td>
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</table>

**Typing**

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<tr>
<td>araC</td>
</tr>
<tr>
<td>araE</td>
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<tr>
<td>grF</td>
</tr>
<tr>
<td>grk</td>
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<tr>
<td>pta</td>
</tr>
<tr>
<td>tpi</td>
</tr>
<tr>
<td>vga</td>
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</table>

**SCCMEC - TYPE IV**

<table>
<thead>
<tr>
<th>IS1272</th>
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<tbody>
<tr>
<td>ccrA1</td>
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<tr>
<td>ccrA2</td>
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</tr>
<tr>
<td>ccrA3</td>
<td>Not found</td>
</tr>
<tr>
<td>ccrA4</td>
<td>Not found</td>
</tr>
<tr>
<td>ccrB1</td>
<td>Not found</td>
</tr>
<tr>
<td>ccrB2</td>
<td></td>
</tr>
<tr>
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<tr>
<td>ccrB6</td>
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<tr>
<td>ccrC</td>
<td>Not found</td>
</tr>
<tr>
<td>mecA</td>
<td></td>
</tr>
<tr>
<td>mecC</td>
<td>Not found</td>
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</table>

**Sample Quality**

<table>
<thead>
<tr>
<th>Measure</th>
<th>Quality</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sequence depth</td>
<td>83x</td>
</tr>
<tr>
<td>Average read length</td>
<td>151bp</td>
</tr>
<tr>
<td>Fraction of core genes identified</td>
<td>98.6%</td>
</tr>
</tbody>
</table>

**References**


[3] Topoisomerase mutations that are associated with high level resistance to earlier fluoroquinolones in Staphylococcus aureus have less effect on the antibacterial activity of levofloxacin. [Link](http://www.ncbi.nlm.nih.gov/pubmed/21986499)


[7] Extended spectrum of quinolone resistance, even to a potential third generation agent, as a result of a minimum of two grA and two grB mutations. [Link](http://www.ncbi.nlm.nih.gov/pubmed/21986499)
Phylogenic Analysis (cgMLST / SNP clustering)

Reference: *Staphylococcus aureus subsp. aureus HO 5096 0412 complete genome (NC_017763.1)* [Link]
WIMP report, shown for a sample containing bacteria, viruses and fungi.
How to Access the Facility

- Email: Precision-AMR@hslpathology.com
- Email: apdu@nhs.net
- Website: www.hslpathology.com/research-development
How to Access the Facility

Sign In

Email Address

Password

Sign In

Forgot Password?
Thankyou