CORE

Technology Platforms at UCD Conway Institute

Leading technologies supporting research in academia and industry





INTRODUCTION

The UCD Conway core technologies facilities is the most comprehensive and advanced analysis platform for the life sciences and biomedical research in Ireland. We provide technology solutions to 21st century research questions. Our services are available to all researchers in academia & industry.

The facility not only provides access to high-end equipment, but also the technical expertise with bespoke project design and seamless analysis, across several experimental platforms. Our dedicated team of scientists and technical staff work with clients to design experiments that address their research question, taking a 'problemsolving' approach to find the 'best fit' technology solution and can assist with downstream analysis as needed. This approach has provided comprehensive solutions to challenging research questions for clients within University College Dublin, across Higher Education Institutions in Ireland, as well as academic and industry collaborators internationally. Access to the core technologies ensures rigor in experimental processes, drives scientific advances, supports publications and competitive funding applications, and delivers exceptional research training opportunities.

Our staff can be contacted at any time to discuss individual requirements and would be happy to arrange a visit to our facilities.

> Professor Helen Roche, Director, UCD Conway Institute

GENOMICS

10 X Single Cell Sequencing Illumina Sequencing Nanopore Sequencing Real Time PCR Digital PCR



Contact details:

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Director's Introduction

Genomics is one of the most exciting and fruitful areas of research in the 21st century. Genome and transcriptome sequencing can be used to identify variants associated with disease, to determine how an organism responds to disease or drug treatment, to identify organisms (e.g. in a microbiome), and to track pathogens during disease outbreaks.

We have a range of facilities for nextgeneration sequencing, including short read (Illumina) and long read (Oxford Nanopore) technologies, as well as single cell analysis (10X Genomics). We also offer high-throughput real-time and digital PCR analysis.

Our core technologies have been used in a wide range of large disease studies in humans and model organisms, to characterise disease outbreaks, and to study the role of individual cells during organ development.

We have been offering genomics solutions to academic and commercial customers for more than 20 years in a customisable range of services for each stage of the research pathway, from experimental design and strategy to final publication.

Education

Our team are involved in the delivery of both accredited graduate and continuing professional development modules to scientists involved in genomic research. For more information, go to: www.ucd.ie/conway/education/

 CNWY40090 Introduction to 'Omics' & Advanced Imaging Technologies







PCR Based Technologies

Real-Time PCR

Real-Time PCR or quantitative (qPCR) is the gold standard for accurate and sensitive quantification of specific nucleic acid target sequences in biological samples. It combines fluorescent based assays with the conventional polymerase chain reaction to simultaneously amplify target sequence and monitor its accumulation as PCR product in 'real- time'. Changes in fluorescence measured at initial amplification are directly proportional to the input amount of target and this provides the basis of subsequent quantitative data analysis.

Applications

Real-Time PCR has a wide range of applications across diverse areas of biomedical research, diagnostics and biotechnology.

These include:

- Gene expression quantification
- Micro RNA and noncoding RNA analysis
- Copy number variation (CNV)
- Drug metabolism enzyme (DME) profiling
- SNP genotyping
- · Mutation detection
- · Viral analysis

Instrumentation

The core facility operates the QuantStudio 7 Flex Real-Time PCR instrument from Applied Biosystems. This is a high throughput instrument which can detect very low discrimination between samples over a broad dynamic range. It supports a versatile and intuitive workflow with the following features:

 Interchangeable thermal cycling blocks provide flexibility to run samples in 96 well, 384 well plates or 384 microfluidic card formats.

- Optimised for use with both Taqman and Sybr Green assay chemistries with 6 excitation and emission filters allow multiple dye combinations.
- Continuous wavelength detection supports the use of multiple fluorophores in a single reaction.
- Quantstudio Real-Time PCR Software provides tools for instrument operation, data collection and analysis.
- Design and analysis software and applications allow the generation of high quality data sets from multiple run files based on different functional applications and approaches.



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Digital PCR

Digital PCR (dPCR) is a complementary technology to Real-Time PCR and many of the assays are transferable between systems. It works by partitioning a bulk PCR reaction into thousands of reaction chambers such that some receive a target copy while others remain empty. Detection of the presence or absence of the DNA target is based on whether or not amplification occurred in that partition. From this digital output, a highly precise and sensitive calculation of absolute target concentration can be derived.

Applications:

The increased precision and sensitivity of dPCR expands the boundaries of some qPCR applications and enables absolute quantification without the use of a standard curves.

These include:

- Rare mutation analysis in liquid biopsies
- Low target copy detection for pathogen & GMO screening
- Copy number variation

Instrumentation:

The Quantstudio 3D Digital PCR System from Applied Biosystems uses sealed-chip technology throughout the streamlined process. Samples are loaded onto chip with 20,000 independent reaction wells for partitioning, amplified on an integrated flat block thermal cycler and digital output read on the Quantstudio 3D System.

Expertise & Services:

The core facility offers a range of technical services and training in this area to researchers from initial experimental design through to data analysis.

These include:

- Introductory presentations
- Assay design, selection and validation
- Sample preparation protocols
- · Instrument and software training
- Data review & analysis
- Technical support









Next Generation Sequencing Technologies

The Genomics Core provides access to state of the art, multi-platform Next Generation Sequencing (NGS) based technologies. NGS has driven major advances in genomics led research over the past two decades and now routinely underpins many research studies across a variety of disciplines. We offer access to both short read (Illumina) and long read (Oxford Nanopore) NGS platforms, including a 10 X Genomics single cell sequencing system.

Instrumentation:

Illumina NextSeq Platform The Illumina NextSeq Platform delivers powerful high-throughput next generation sequencing of short reads with speed and efficiency. Utilising Illumina's proprietary sequencing-bysynthesis technology and reversible terminator chemistry, it enables the parallel sequencing of millions of DNA fragments with exceptional accuracy.

The NextSeq is easily configured, providing researchers with scalability to handle various project sizes. Based on read length and coverage needs, researchers can choose between multiple flow cell configurations. The platform is fully integrated with Illumina's BaseSpace Sequence Hub cloud, which allows streamlined run management, primary data analysis/QC and data transfer from a single source.

Applications:

A broad menu of sequencing applications is supported including, RNA-seq, exome, small whole genome, targeted resequencing.

Oxford Nanopore Technologies MinION Oxford Nanopore Technologies MinION enables high throughput long read sequencing of DNA and RNA samples in real-time. The technology revolves around a flowcell composed of an array of embedded protein nanopores. The DNA/RNA sequence is read by measuring the individual change in current exhibited by each base as it passes through the pore.

One of the main advantages of the technology is the ultra long read lengths produced, which greatly improves de novo genome assemblies, structural genomic variant and transcriptomic studies. Nanopore sequencing has been successfully used in the areas of disease surveillance, environmental monitoring and the identification of food chain pathogens. The Genomics Core offers access to ONT MinION Mk1B long read sequencing devices, which allow yields of up to 50Gb per flowcell run. Compatible flowcells contain an array of up to 500 protein pores, with the flexibility to generate short to ultra-long (>4 Mb) reads.

Applications:

The following sequencing applications are supported:

- Whole genome
- Exome
- Targeted resequencing
- RNA-sequencing (direct/cDNA)
- Metagenomics

Single Cell Sequencing – 10 X Genomics

Single cell sequencing allows genome and transcriptome analysis of individual cells, providing a highresolution view of cell-to-cell variation. This highly sensitive technology enables researchers to explore the distinct biology of individual cells in complex tissues and understand cellular subpopulation responses to environmental cues. The 10X Chromium Controller is a benchtop single cell library preparation system. The platform utilises advanced microfluidics to generate tens of thousands of single cell partitions, each containing an identifying barcode for downstream analysis. Partitioning events occur on a microfluidic chip in the presence of barcoded gel beads and oil to create GEMs (Gel Bead in EMulsion). Up to 8 samples can be run simultaneously per chip.

As many as 10,000 cells per sample are encapsulated in nano-liter scale GEMs. Final amplification and library construction is performed in bulk after GEMs are broken. Resulting libraries are compatible with Illumina sequencing platforms.

Applications:

The following applications are available,

- 3' gene expression
- Targeted gene expression (custom or panels)
- Assay for chromatin accessibility (ATAC Seq)
- Immune profiling of B and T cell receptors and 5' gene expression
- Multiomic (Gene expression + ATAC)



In addition, the following applications can be paired with gene expression assays/immune profiling,

- Identification of CRISPR perturbations
- Antibody-based feature barcoding can be used to quantify the levels of cell surface proteins



Expertise & Services:

New and potential users are encouraged to contact the Core Facility in the planning stages to discuss their individual requirements. The Genomics Core provides a range of NGS related services including,

- Advice on initial experimental planning and costs for grant proposals
- Full library preparation service
- Sequencing only service
- Comprehensive training across all NGS Instrumentation
- Initial data QC
- Ongoing technical support

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PROTEOMICS

Mass Spectrometry Resource





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Director's Introduction

Proteomics is the large-scale study of proteins, for example all the proteins in a cell or tissue analysed in a single experiment. A researcher may want to identify the molecules present in a sample that they have isolated, or to compare the relative levels of proteins in samples from healthy and diseased tissue. We can also help analyse single molecules in detail: map protein modifications like phosphorylation or methylation, or identify interacting proteins and drug binding sites.

The Mass Spectrometry Resource is a facility dedicated to biological mass spectrometry. Mass spectrometry is an analytical technique capable of accurately determining the mass, charge and chemical structures of molecules. Our instrumentation is capable of covering all aspects of modern proteomic science including quantitative proteomics, protein post-translational modifications and protein-protein interactions.

We offer the dedicated strategic support of our expert team, both before mass spectrometry (sample preparation and separation) and after (data analysis, bioinformatics) to enable our research and commercial partners to take full advantage of their results.

Education

Our team are involved in the delivery of both accredited graduate and continuing professional development modules to scientists involved in genomic research. For more information, go to: www.ucd.ie/conway/education/

- CNWY40090 Introduction to 'Omics' & Advanced Imaging Technologies
- CNWY40160
 Applied Proteomics

Mass Spectrometry Resource

The Mass Spectrometry Resource is a state-of-the-art biologic mass spectrometry facility providing access to all the necessary instrumentation for high-throughput, high accuracy protein identification, quantification and characterisation.







Instrumentation:

We use two mass spectrometry platforms:

- Thermo Scientific Q Exactive with Thermo Scientific Ultimate 3000 RSLCnano chromatography system.
 This is a hybrid ESI-LCMS instrument that combines precursor ion selection using a quadrupole with high resolution high mass accuracy (HRAM) by Orbitrap.
- Bruker timsTOF Pro mass spectrometer with Evosep One chromatography system or Bruker nanoElute chromatography system. A trapped ion mobility (TIMS) analyser can be synchronised with a quadrupole mass filter to enable the highly efficient PASEF (parallel accumulation serial fragmentation) acquisition procedure with acquisition rates of 100 Hz.

The combination of the multiple LC options and the two mass spectrometry platforms enable separation of complex mixtures of peptides, identification of peptides and their respective fragments as well as quantification based on peptide ion current. Typically, data dependent acquisition (DDA) is carried out. However, users can also avail of data independent acquisition methods (DIA).







Software Suite:

Raw data files generated by each mass spectrometer are subjected to database search with the appropriate algorithm (MaxQuant, Peaks, MSFragger, DIA-NN, Mascot).

Expertise & Services:

- Discussions on the suitability of the platform, experimental design and strategy
- Sample running service
- Access to state-of-art software suite (Peaks Studio, MaxQuant, Mascot) for protein identification (de novo sequencing and database matching), quantitation and PTM characterisation
- Custom analysis
- Mass spectrometry software training



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IMAGING

Sample Preparation Electron Microscopy Light Microscopy



Contact details:

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Director's Introduction

We focus on providing contemporary imaging technologies and knowhow to researchers in the wider Irish scientific community; both in academia and industry. Our consolidated instrumentation suite spans all aspects of light and electron microscopy as well as sample preparation and image processing and analysis facilities. We use our technical expertise to assist in the widest possible range of applications for microscopy, in advancing the development of new applications and new imaging technologies.

We work with a wide range of researchers on diverse applications from retinal disease, clinical viral diagnostics, nanoparticle-cell interaction and toxicity, pharmaceutical development to food quality control and development, and much more. We provide expert advice on translating a scientific problem in imaging into practical research plans and supporting our users until the point of publication. By adopting a problem-solving approach, we can help our clients find a microscopy solution that works for their research; simply, accurately and quickly.

Education

Our team are involved in the delivery of both accredited graduate and continuing professional development modules to scientists interested in using imaging technologies within their research. For more information, go to: www.ucd.ie/conway/education/

- CNWY40090 Introduction to 'Omics' & Advanced Imaging Technologies
- CNWY40120 Advanced Biological Imaging

Electron Microscopy

Image resolution in light microscopy is limited by the wavelength of light and is incapable of resolving structures of less than 200 nm. However, the resolution of electron microscopy limited by biological sample preparation goes beyond 1 nm. Transmission Electron Microscopy (TEM) is used to investigate ultrastructure of thin samples (limited by the penetration of electron beam): flat cells, nanoparticles, biological tissues embedded into polymers etc. Scanning Electron Microscopy (SEM) is used to investigate fine structure on surfaces of biological and non-biological objects.







Applications:

Research topics include detection of viruses for human patients, inflammation, oncology, cardiovascular biology, morphology of zebrafish retina, bacteriology, food sciences, polymer films for biosensors, nano-particle toxicity in vitro and artificial joints.

Instrumentation:

- Two transmission electron microscopes (TEM)
- One scanning electron microscope (SEM)
- Three ultramicrotomes, including one suitable for cryo-ultramicrotomy
- Fume hood, oven for EPON embedding and other TEM sample preparation instruments
- Critical point dryer, gold/carbon coater and other EM sample preparation instruments
- Light microscopes for EM sample preparation

Expertise & Services:

- Experimental strategy, technology choice and planning
- Sample preparation: TEM and SEM
- Image acquisition: TEM and SEM
- Image analysis, including EM tomography
- Training in sample preparation, imaging and image analysis



Light Microscopy

Our instrumentation suite covers the widest range of light microscopy requirements including:

Transmission light microscopy:

- Bright field
- Dark field
- Phase contrast
- Polarized light
- Differential interference contrast (DIC)



Fluorescent microscopy:

- Epi-fluorescence
- Laser confocal (single pinhole)
- Spinning disc confocal
- Fluorescence resonance energy transfer (FRET)
- Fluorescence-lifetime imaging microscopy (FLIM)
- Fluorescence recovery after photobleaching (FRAP)
- Photoactivation
- Total internal reflection
 fluorescence (TIRF)
- FRET/FLIM TIRF
 confocal microscope

Reflected light microscopy

Applications:

Research topics include oncology, dermatology, cardiology, biology of worms, insects and zebrafish as well as nano-biology. We can discuss your requirements for the imaging of native, stained or immunolabelled cells or tissue sections, time lapse imaging of live cells and Z-stack acquisition for 3D microscopy.

Expertise & Services:

- Image acquisition
- · Image analysis

Training in:

- · sample preparation
- imaging: transmission, fluorescent, confocal and live cell microscopy
- · image analysis





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FLOW CYTOMETRY

Flow Cytometry Cell Sorting Multiplexed Assay Platforms



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Director's Introduction

Flow cytometry is an incredibly efficient technique for counting and examining the physical and biological characteristics of cells and particles. The technique has many applications in humans, animals, plants and microorganisms. We provide a comprehensive service for commercial clients and academic researchers who use the technology across a wide range of studies from obesity and cancer research to nanoparticles and biofuel investigations. We work with the major cytometry manufacturers beta testing their instruments, evaluating markers and/or software (Accuri, BD, Beckman Coulter, De Novo Software) and also provide a consultancy service for companies using this technology.

What really differentiates our service is the expertise of our team in assisting with the analysis of complex results for our clients and research partners. We aim to find a tailored flow cytometry solution that works for their research. It is this expertise that also enhances the quality of our education and training programmes.

Education

Our team are involved in the delivery of both accredited graduate and continuing professional development modules to scientists interested in using flow cytometry techniques within their research. For more information, go to: www.ucd.ie/conway/education/





- CNWY40090 Introduction to 'Omics' & Advanced Imaging Technologies
- CNWY40130 Flow Cytometry Principles & Practice

Assoc. Prof. Blanco is also deeply involved in many internationally recognised educational programmes.

Flow Cytometry

Flow cytometry technology can be used to measure intrinsic cell characteristics such as autofluorescence or granularity and extrinsic cell characteristics such as DNA, internal and external receptors. This has many applications in humans, animals, plants and microorganisms with the most common applications in cell cycle, apoptosis/ necrosis, ploidy determination, immunophenotyping, protein expression and Ca2+ concentration.

Cell sorting allows the physical isolation of cell populations for further procedures such as cell culture and studies of protein expression.

Multiplexing or multiple analyte detection offers a broad picture of the cytokines involved in a certain biological process. The measurement of cytokines and other soluble factors is becoming increasingly important in the study and management of numerous diseases.

Instrumentation:

Flow Cytometry:

 Beckman Coulter CytoFLEX LX and CytoFLEX S:

These state-of-the-art benchtop analysers allow the analysis of blood or cultured cells, bacteria, algae, yeasts, microparticles and even nanoparticles like extracellular vesicles.

CytoFLEX Platform demonstrates outstanding sensitivity and reproducibility. These cytometers have the ability to reliably detect 80 nm polystyrene beads, the CytoFLEX is a trustworthy partner in your extracellular vesicle and other small particle research. Both CytoFLEX units are equipped with a 96 well plate loader station.

The CytoFLEX LX unit is equipped with six excitation wavelengths (375 nm, 405 nm, 488 nm, 561nm, 638 nm, 808 nm), and can collect 21 fluorescent markers, plus FSC and SSC.

The CytoFLEX S unit four excitation wavelengths (405 nm, 488 nm, 561nm, 638 nm), is able to collect 13 fluorescent markers, plus FSC and SSC.

Scatter of violet and red laser are also available, as well as extra sets of filters.

Cell Sorting:

• FACSAria III Cell Sorter:

This high-speed cell sorter (40,000 events/second) has 4 lasers: 488nm (blue), 561nm (green), 633nm (red) and 407nm (violet) for detection of FSC, SSC and up to 10 fluorescent parameters. It is able to sort 4 populations of cells at the same time and perform single cell cloning in well plate platforms with a 100% purity level and 95% viability.

Multiplexing:

Luminex xMAP200 & MagPix:

The bead-based assays follow the same principle as a sandwich immunoassay. Fluorescent beads are coated with antigen-specific antibodies. A mixture of coated beads is incubated with the sample. Analytes in the sample bind to the Ab coating the beads. A biotin-conjugated Ab mix is added, which binds to the analytes bound to the capture Ab. A fluorochrome binds the biotin conjugates. Our instruments differentiate the bead populations and calculate the analyte concentration in the samples being analysed. Providing a rapid, reliable, costeffective and informative solution, the main benefits of multiple analyte detection are:

- Reduced cost and labour by multiplexing
- Requires less than 50 µl of sample
- Shortened time-to-results by favourable reaction kinetics
- Gives faster, more reproducible
 results than ELISA

Flexible multiplexing in the range of 1 to 100 analytes meets the needs of a wide variety of applications such as protein expression profiling, focused gene expression profiling, autoimmune disease, genetic disease, molecular infectious disease, and HLA testing

Expertise & Services:

The flow cytometry facility provides a range of services including instrumentation, workstations, training, software for analyses as well as technical expertise and advice.

- Trained users prepare and run their own samples.
- Untrained users may avail of the sample running service and results analyses.







METABOLOMICS

Sample Preparation Mass Spectrometry -Based Metabolomics Data Processing Statistical Analysis



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Director's Introduction

Metabolomics is the comprehensive analysis of small molecules called metabolites in biological samples. It is a powerful approach to investigate alterations in metabolic pathways under different conditions.

The metabolomics core facility is based on state-of-the-art mass spectrometry for high-throughput metabolite identification and quantification. It covers a large number of related metabolites present in diverse areas of metabolism such as amino acid metabolism and lipid metabolism. Measurements can be performed on a wide variety of biofluids, tissue and cell culture samples.

We work with both commercial clients and academic researchers on diverse projects in areas such as nutrition research, metabolic diseases, food science. Our researchers offer unique expertise and advice on performing metabolomic studies from experimental design through data acquisition to data analysis and biological interpretation.



Education:

Our team is involved in the delivery of graduate and continuing professional development modules to scientists involved in metabolomic research. For more information, go to: www.ucd.ie/conway/education/

CNWY40090 Introduction to Omics

Sample preparation

The facility provides a service for sample preparation in diverse biological samples including urine, plasma, tissue, cell culture samples and food samples.

Expertise & Services:

The metabolomic core offers expertise and advice on sample preparation prior to LC-MS analysis.

The staff provide services on the following sample preparation:

- Metabolite extraction from tissue samples
- Metabolite extraction from cell pellets
- Metabolites extraction from biofluids

Mass spectrometrybased metabolomics

Our core provides targeted metabolomic platforms based on state-of-the-art mass spectrometry for high-throughput metabolite identification and quantification in the most challenging matrices.

Instrumentation:

The equipment includes one SCIEX QTRAP 6500plus mass spectrometer coupled to SCIEX ExionLC[™] Series UHPLC. This QTRAP 6500plus system features the multi-component lonDriveTM Technology like the lonDriveTM Turbo V Source and lonDrive High Energy Detector to obtain better sensitivity and greater detection ability. Data acquisition and analysis software as follows:

- AB Sciex Analyst software
- Biocrates MetIDQ software.
- Qtrap MS instrument

Expertise & Services:

We provide targeted assays to detect and quantify a large number of related metabolites present in diverse areas of metabolism such as amino acid metabolism and lipid metabolism. More than 500 metabolites from 26 compound classes can be measured with minimal sample volume. Examples of such metabolites are as follows:

- Amino acids
- · Biogenic amines
- Acylcarnitines
- · Phosphatidylcholines
- Sphingolipids
- · Triglycerides

We provide expertise in data analysis and bioinformatic analysis of metabolomics data.

Data processing and statistical analysis

The core team will process the raw data and support the primary analysis of the data. Support for multivariate data analysis and pathway analysis is provided.

Expertise & Services:

We provide a range of services and expertise related to data quality control and statistical analysis including:

- Quality checks to ensure highly robust and quantitative metabolomic data
- Provide services for univariate statistical analysis (ANOVA, ANCOVA, t-test), multivariate statistical analysis such as principal component analysis, cluster analysis and correlation analysis
- Training on the statistical analysis methods listed above and the use of relevant software and tools
- Expertise on interpretation of the results is also provided

Contact:

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RESEARCH PATHOLOGY

Immunohistochemistry Multiplex Staining Digital Pathology Image Analysis

Director's Introduction

Research pathology core technologies provide state-of-the-art automated immunohistochemistry and linked digital pathology services on frozen and formalin fixed paraffin–embedded human and animal tissue. We advise and assist on your translational tissue research project and can help select the most appropriate antibodies.

This facility also provides slide scanning systems that allows users to digitise both brightfield and fluorescent microscopy slides, review, annotate, analyse and manage the images locally or remotely via a slide management system.



Contact details: Prof. Aurelie Fabre Director of Research Pathology E: afabre@svhg.ie



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Education

Our team is involved in the delivery of both accredited graduate and continuing professional development modules to scientists involved in translational histopathological research. For more information, go to: http www.ucd.ie/conway/education/

- CNWY40090 Introduction to 'Omic' & Advanced Imaging Technologies
- CNWY40180 Introduction to Core Research Skills for Laboratory-Based Biological Scientists
- PATH40050 AI & Digital Pathology

Immunohistochemistry & Digital Pathology

The facility provides translational tissue immunohistochemistry and digital pathology including:

- Automated immunohistochemistry
- Antibody optimisation
- Single, double and multiplex staining
- Whole slide imaging
- Image analysis
- Spatial phenotyping







Instrumentation:

- Dako Autostainer Link 48
- Dako PT-Link
- Dako Hybridizer
- Leica Aperio AT2 scanner
- Akoya PhenoImager HT multispectral scanner
- Slide management system (onsite and remote)
- Image Analysis Software

Expertise & Services:

- Advice on tissue preparation
- Provision of control tissues
- Tissue and antibody optimisation
- · Automated immunohistochemistry
- Automated multiplex
 immunofluorescence
- Digital pathology
- Image annotation and quantitative/ spatial analysis

"The systematic rigour and attention to detail at the Research Pathology core ensured that our immunohistochemical staining was specific and free from artefact. This permitted quantitative morphometric analysis to be conducted to assess treatment effects. This also allowed us to correlate immunohistochemical and transcriptomic data."

Testimonial by

Assoc. Prof. Neil Docherty UCD Diabetes Complications Research Centre



ASSOCIATED CORE TECHNOLOGIES

There are many associated technologies under the management of Conway Fellows that are located either within UCD Conway Institute or on the wider UCD campus. These technologies have been secured through competitive funding applications and are available for use through a collaborative arrangement. Please contact the appropriate staff member using the contact details below:

High Content Analysis

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Atomic Force Microscopy

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