QIB EXTRA

TraDIS-*Xpress* services

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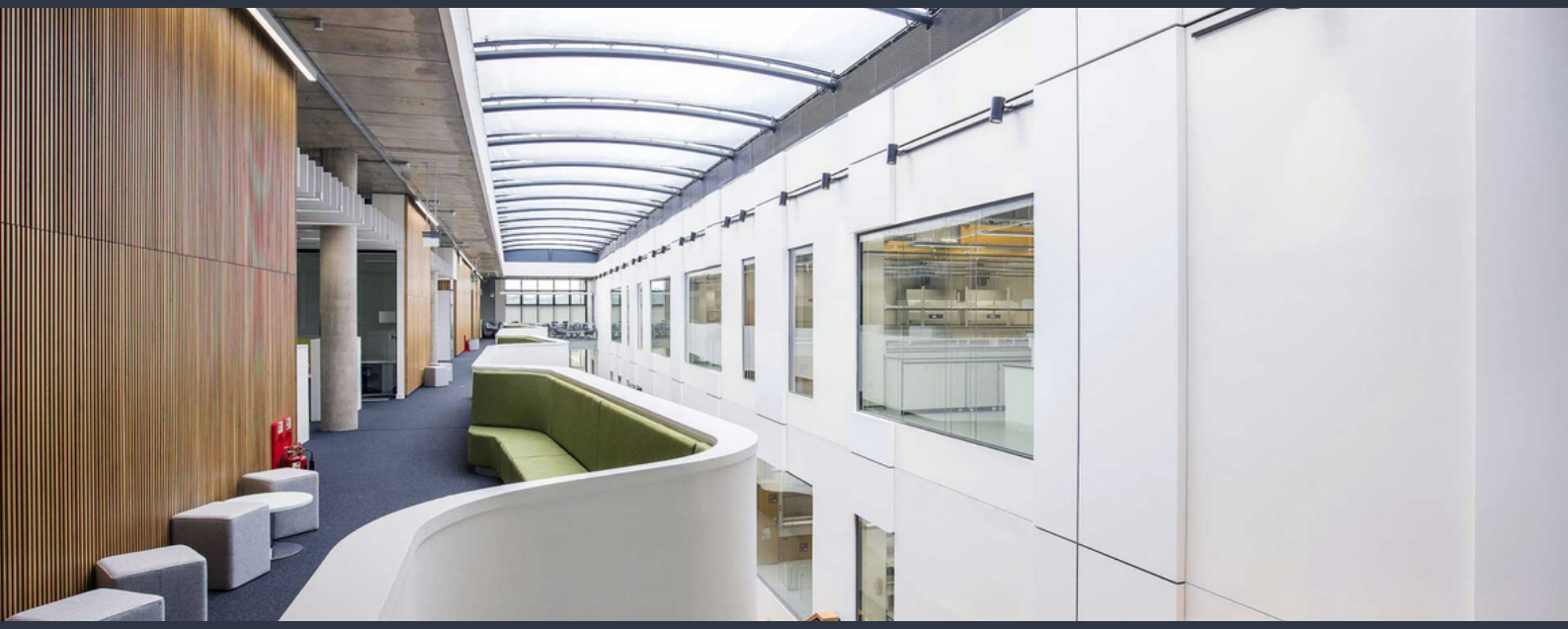
About QIB Extra



QIB Extra is an IS09001 accredited, wholly owned subsidiary, of the Quadram Institute Bioscience (QIB) that provides short and long-term, high-quality strategic and applied research. QIB Extra works with both commercial companies and academic partners around the world in the areas of gut health, food safety, nutrition, and allied sectors.

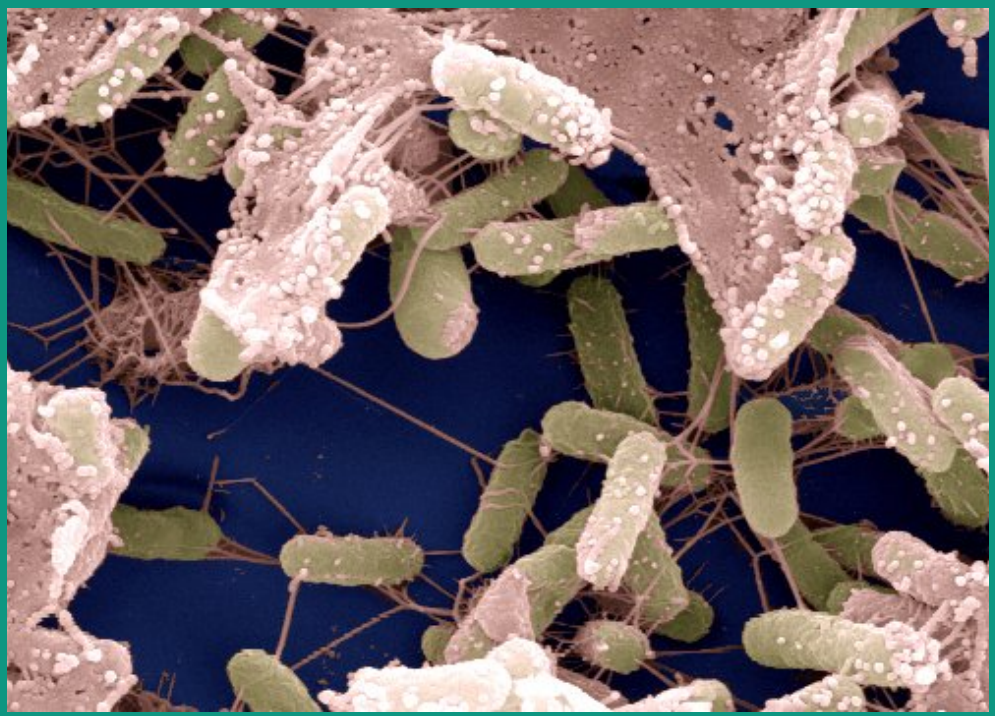
By accessing the world-leading research expertise, facilities and equipment at QIB, QIB Extra works with customers to build both highly focused and multidisciplinary projects to specific customer requirements. QIB Extra facilitates contract research delivery in a cost-effective and timely manner from the design and planning stage, through to the delivery and completion.

What is **TraDIS-*Xpress*?**

TraDIS (Transposon Directed Insertion-Site Sequencing) is a tool to assay the importance of every gene in a bacterial genome in a test condition on a single experiment.

We make highly dense libraries of unique mutants in every gene and culture these libraries under different conditions. Using next-generation sequencing approaches, we can quantify the mutants' fitness under the different conditions and identify the genes that are beneficial or harmful for survival in each condition.

What makes TraDIS-Xpress different from other transposon mutagenesis tools is our ability to measure the effects of gene expression. Outward-facing promoters are incorporated into our transposons to allow controlled and measurable expression of downstream genes. This allows investigation of how gene expression, as well as gene deletion, affects bacterial survival in a given condition. This also allows us to assay essential genes, which cannot be inactivated in conventional transposon mutagenesis approaches.



TraDIS-*Xpress*

is very versatile, here are some examples of questions it can address:

- How do antimicrobial compounds work, and how do bacteria respond to them?
- How can we make a bacterial strain increase production of a valuable protein or metabolite?
- How can we improve the fitness of a bacterial strain in a culture condition?
- How can we exploit pathways of evolution to alter bacterial behaviour and prevent bacterial colonisation and contamination?

TraDIS-*Xpress*

How does it work? A step-by-step guide behind this proven method

This brochure provides a comprehensive, step-by-step explanation of how QIB Extra's TraDIS-*Xpress* team will execute a TraDIS-*Xpress* project for commercial clients, detailing each stage of the project on subsequent pages.

By scanning this QR code on this page, you will be redirected to the QIB Extra TraDIS-*Xpress* Services webpage, which includes a video tutorial offering an in-depth explanation of how TraDIS-*Xpress* works and how this can benefit our clients.

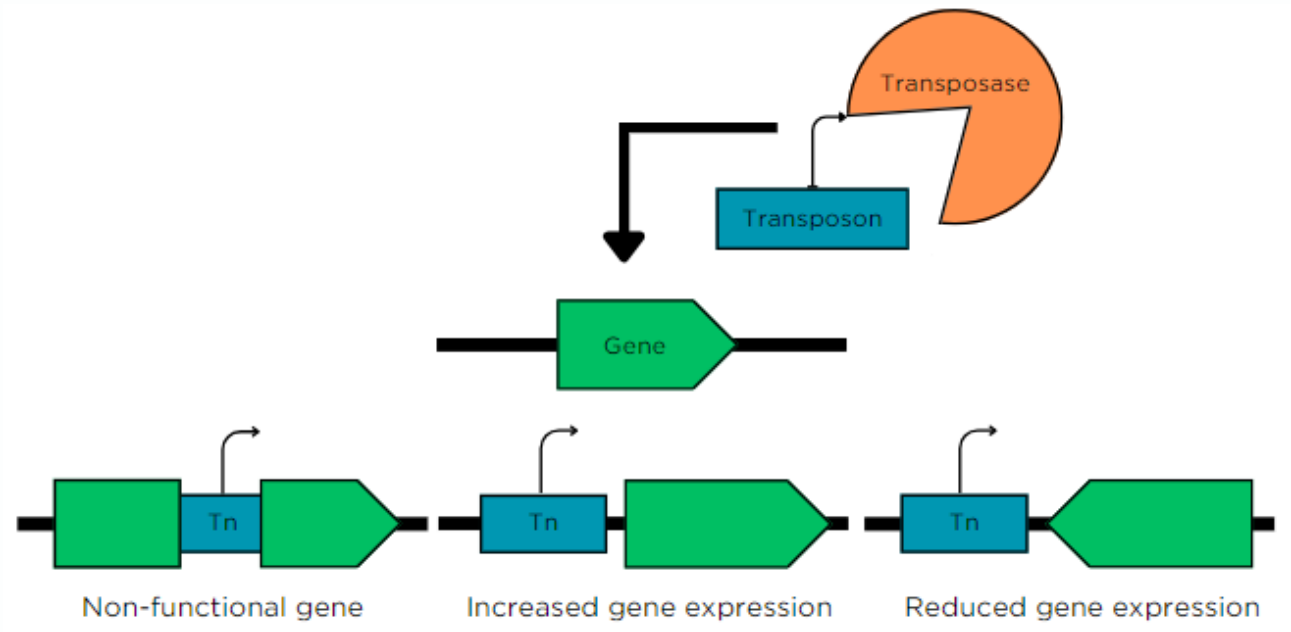
Mutant library creation

Transposons are small mobile elements that insert randomly into a genome. When inserted in the middle of a gene, the transposon interrupts transcription of the gene, inactivating its function. When we introduce a transposon to one million bacterial cells, these transposons will insert into each of these cells in a unique locus on the genome.

With TraDIS-*Xpress*, the transposon contains an outward-transcribing inducible promoter. When a transposon inserts upstream of a gene, induction of the transposon-located promoter will increase expression of the gene downstream.

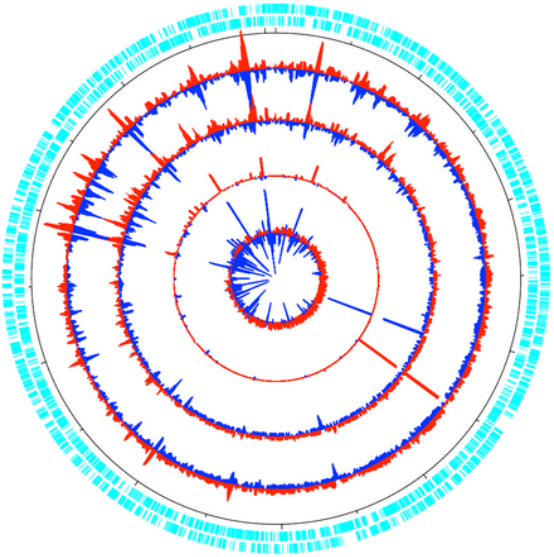
Transposons that insert downstream of a gene can increase the production of antisense mRNA, which reduces the expression of the gene. These unique mutants are pooled to create a mutant library.

We have mutant libraries in house made from *E. coli, Salmonella, Pseudomonas, Staphylococcus*, and more. Contact us to find out more about the mutant libraries we already have in house**.**



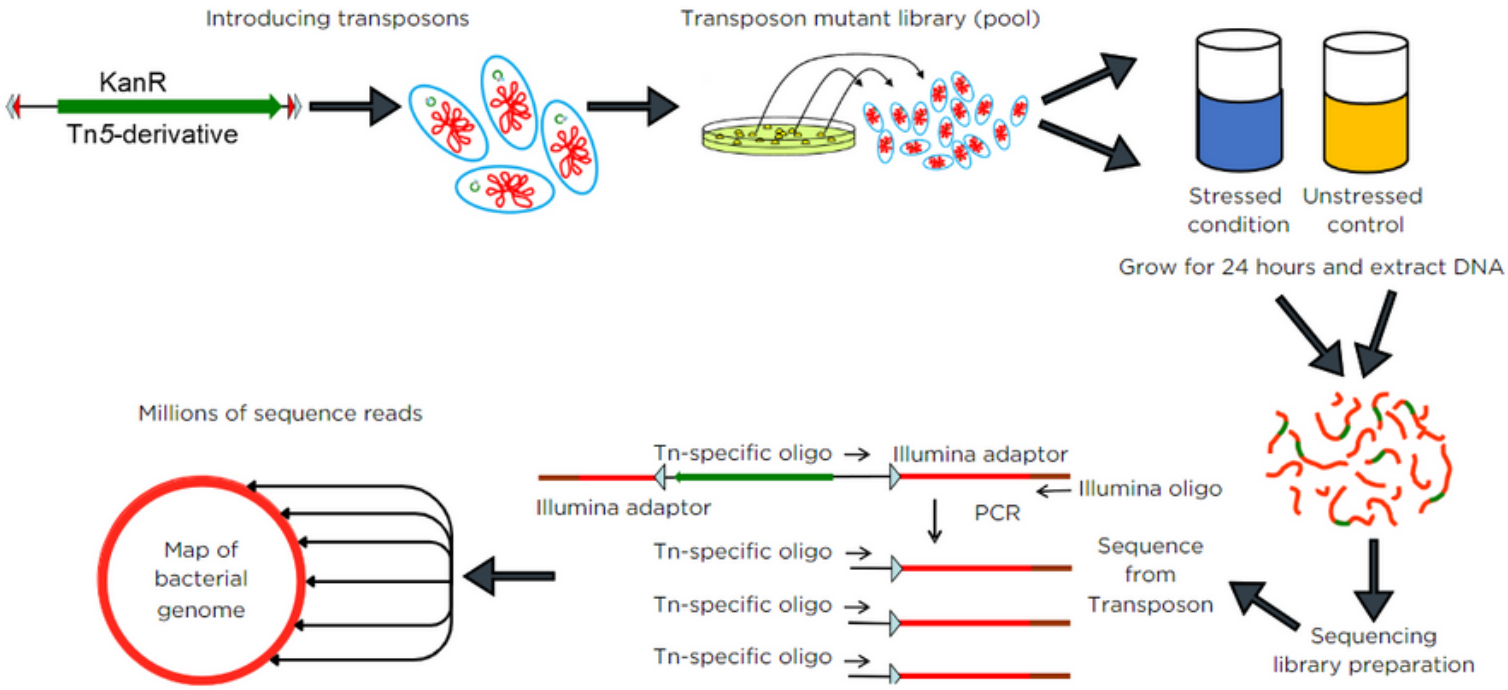
Experimental conditions and sequencing

The mutant library is grown in the experimental condition alongside a relevant control growth condition. Experimental growth conditions can be designed to best address your work.



DNA is extracted from the end population of mutants in each experimental condition. We fragment the DNA and extract only the DNA fragments containing the transposon.

Using next-generation sequencing, we read the DNA immediately downstream of the transposon to identify its location in the bacterial genome. The location and the number of reads are then mapped onto the bacterial genome.

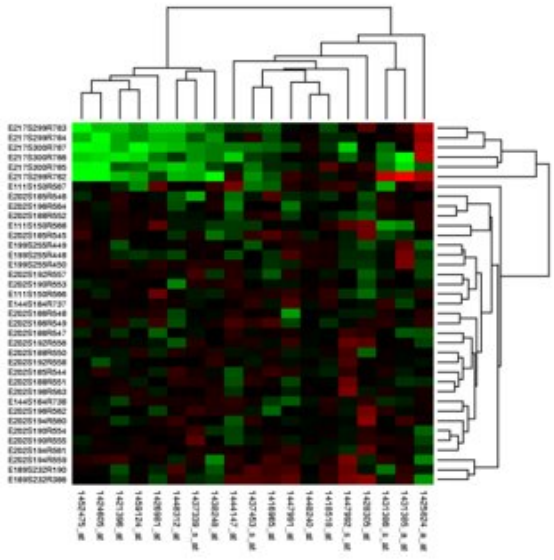


Data analysis

Software we have developed at Quadram Institute Bioscience (QIB) takes the sequencing data and produces plot files detailing the location of transposon insertions in the genome and the number of DNA fragments mapped to that location.

When more transposon insertions have mapped to a gene in test conditions relative to the control, these means inactivation of this gene by the transposon resulted in these mutants surviving and proliferating.

When no transposon insertions are found in a gene, this indicates inactivation of the gene resulted in no survival and proliferation, and therefore the function of this gene must be essential for survival.



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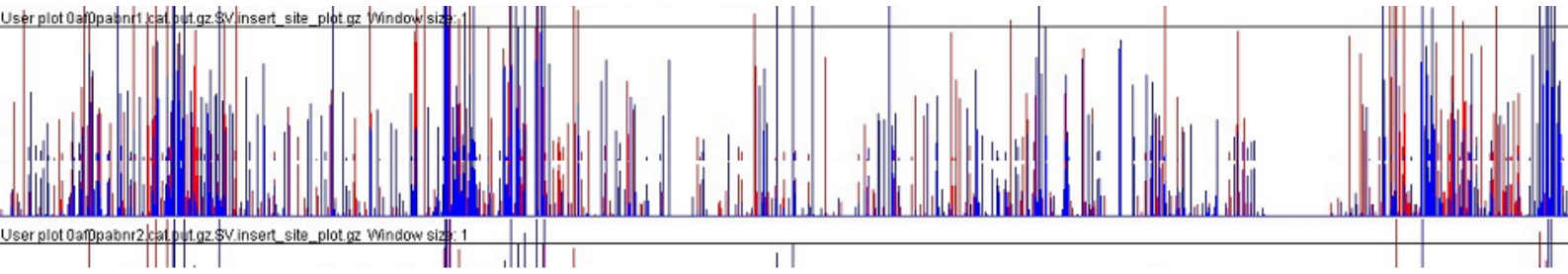

TraDIS-Xpress Team

Prof. Ian Charles OBE

Prof. Ian Charles, Director and Chief Executive Officer of Quadram Institute Bioscience, uses TraDIS-*Xpress* to study how microbes evolve, spread, and compete in the food chain. With over 40 years of academic and commercial experience, he founded biotech companies in infectious disease, including Arrow Therapeutics and Auspherix.

Prof. Mark Webber

Prof Mark Webber leads the TraDIS team and has been developing this method to study how bacterial deal with stress with a focus on antimicrobial resistance and biofilms. Webber works with multiple organisms in projects with partners from academic, public health and industry. He has published over 100 articles studying bacterial adaptation.

Dr. Keith Turner

Dr Keith Turner developed TraDIS in 2009 and TraDIS-*Xpress* in 2012. He uses TraDIS-*Xpress* to investigate antibiotic resistance and other aspects of bacterial cell biology. Turner co-founded a biotechnology company that developed new antibiotics and used TraDIS-*Xpress* to elucidate their mode of action and to predict the likelihood of resistance.

Please note that if you are reading the virtual version of this brochure, you may click on the picture of the individual to find out more detail about them.

Alternatively, please visit our webpage www.qibextra.co.uk/tradis-xpress/team to find out more about each member of the TraDIS-Xpress QIB Extra team

Dr. Muhammad Yasir

Dr Muhammad Yasir is a key figure in the development of LoRTIS and TraDIS-*Xpress*, using functional genomic tools to study bacterial survival, microbiome interactions, antibiotic resistance, and gene expression. His research has focused on gene expression regulation in human pathogens, virulence factors, and antibiotic resistance mechanisms.

Dr. Emma Holden

Dr Emma Holden applies TraDIS-*Xpress* tools to study bacterial evolution and survival. She recently completed her PhD using TraDIS-*Xpress* to study biofilm formation and antimicrobial resistance, and has experience in delivering TraDIS-*Xpress* projects for commercial partners.

Dr. Sarah Bastkowski

Dr Sarah Bastkowski is a computer scientist with expertise in computing, bioinformatics, and mathematics. She has developed new tools for analysis of TraDIS-*Xpress* data to make biological predictions from multiple data sets. She has extensive experience in algorithm development and her research focuses on antibiotic resistance evolution and microbiome data analysis.

QIB EXTRA EXPERTISE AND HOW ENGAGING WITH US CAN BENEFIT YOU

TraDIS-Xpress can be used to identify the genes and pathways that affect bacterial growth and fitness under any culture condition.

We have previously used TraDIS-Xpress to:

• Identify the mechanisms of action and synergy of antimicrobial compounds (e.g. work in collaboration with Oppilotech – Holden et al 2023, preprint on BioRxiv). Click here for more information.

• Characterise metabolic pathways that can be targeted to improve production of essential biologics

• Define potential novel targets for anti-biofilm therapeutics (e.g. new essential genes for foodborne pathogens *E. coli* and *Salmonella* have been discovered) (Holden et al 2021 Microbial Genomics, Holden et al 2022 Microbial Genomics)

• Determine how to improve resilience of probiotic bacteria in production-scale environments

An example of a completed project can be seen by scanning the QR code on this page. The link will take you to a online archive of a non-peer reviewed paper we produced for a commercial client.

WHAT QIB EXTRA CAN OFFER TO YOUR RESEARCH PROJECT?

With extensive experience in both academic and commercial environments, our team are ready to apply functional genomics tools to progress your work.

Please get in touch for more information on the mutant libraries we have in-house, the TraDIS-Xpress workflow and how we can best design experiments to best address your work.

1	2	3	4	5
CONCEPTION AND INITIATION	**DESIGN AND PLANNING**	**EXECUTION OF EXPERIMENT**	**DATA ANALYSIS**	**PROJECT CLOSING**
We meet with you to discuss how TraDIS-Xpress can benefit your work	We design experiments together to suit your needs and expectations	Experiments are carried out at the Quadram Institute by our in-house team	Data is analysed and curated by our in-house team within the Quadram Institute	Raw and analysed data are delivered to you and discussed in a follow up meeting

CONTACT US

You can contact us on our contacts page:

www.qibextra.co.uk/contact-us

Alternatively, you may call us on:

+44 (0) 1603 255001

Our team will work with you to understanding your project needs, answer your questions and provide you with a tailored project proposal that uses sound scientific principles to meet your objectives.

Over the years, we have been fortunate to work with many large and small organisations from all over the world. We believe the world-class research expertise we offer can have a real positive impact on your business and that we can deliver access to this expertise in an efficient and professional manner.

Thank you,

QIB EXTRA OFFICE TEAM

QIB Extra

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