Innovate UK

Results of Competition: Finding value in complex biological data - integrated ‘omics CR&D

Competition Code: 1505_CRD1_BIOS_IOMIC

Total available funding for this competition was £1.5M from Innovate UK

Note: These proposals have succeeded in the assessment stage of this competition. All are subject to grant offer and conditions being met.

Participant organisation names	Project title	Proposed project costs	Proposed project grant
Ingenza Ltd University of Glasgow	Enhanced interpretation of metabolomics data to accelerate microbial engineering	£399,695	£315,737

Project description - provided by applicants
This project addresses a current severe limitation in the successful industrial use of engineered microbes,namely to rapidly achieve predictable, iterative improvements in productivity to establish competitive processeconomics. It combines software engineering, bioinformatics, metabolomics and high-throughput constructionof recombinant bacteria and yeast, to implement a system that will accelerate the development of engineeredstrains for next generation biosynthesis of fuel, chemicals and polymer products, manufactured fromsustainable feedstocks. The project will combine the strengths of a leading UK Industrial Biotechnology SMEand a state of the art university Polyomics facility to demonstrate a step change in the UK's capability todevelop new industrial bioprocesses.

Note: you can see all Innovate UK-funded projects here
https://www.gov.uk/government/publications/innovate-uk-funded-projects Use the Competition Code given above to search for this competition’s results

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Analytics Engines Ltd Almac Diagnostics Ltd	Bioinformatics Advanced Technology Platform (BAT Plat)	£331,897	£208,031

Project description - provided by applicants

This project will build a bioinformatics pipeline on top of the Analytics Engines big data platform enabling:diagnostic/companion diagnostic repositioning, target selection, data-driven drug discovery, data-driven drugrepositioning and pre-clinicial model system alignment.This is enabled by driving the translation of bioinformatics pipelines from ad-hoc, research-drivenenvironments into industrialised clinical processes. In order to achieve this aim, pipelines need to be fullytraceable, repeatable and scalable. Enterprise-grade technologies offering scalable storage and computationare already available, this proposal addresses the challenge of mapping bioinformatics pipelines to thesetechnologies.

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Biocatalysts Ltd EMBL - European Bioinformatics Institute	MetXtra - An Integrated High-Throughput Metagenomics Platform for Enzyme Discovery	£368,878	£256,656

Project description - provided by applicants

Only a tiny fraction (~1%) of all microorganisms can currently be grown in the laboratory and hence have theirDNA sequenced. Thus, there is a huge wealth of genetic sequence data still to be discovered fromenvironmental samples of the remaining 99% of uncultured microorganisms. The field of metagenomicsdirectly samples microorganisms living in the environment, thereby avoiding the need for laboratory culturingbefore DNA sequencing. Metagenomics projects can yield very large amounts of DNA sequence data and themajor bottleneck to exploiting this data for enzyme discovery is the actual data analysis. The objective of thisproject between Biocatalysts Ltd and EMBL-EBI is to develop a novel and unique data analysis softwareplatform, MetXtra, for the rapid and efficient identification of completely novel enzymes for IndustrialBiotechnology (IB) applications from large metagenomic DNA sequence libraries.

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Congenica Ltd University College London (UCL)	Clinical Multi-omic Solutions for Rare Diseases	£399,758	£309,990

Project description - provided by applicants

Clinical Multi-omic Solutions for Rare Disease" is a partnership between UCL Institute for Child Health and Congenica to create clinical multi-omic tools and technologies in orphan disease to accelerate understanding of these diseases, improve diagnostic yield and enable the acceleration of new precision treatment development.

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Desktop Genetics Ltd Imperial College London	CRISPR in the Wild: demonstrating model-driven epigenome editing in cancer	£399,325	£307,267

Project description - provided by applicants

Epigenome editing provides an opportunity to reverse aberrant epigenetic drivers of diseases such as cancer where epigenetic change drives tumour evolution and determines treatment success. Adapting CRISPR/Cas9 genome editing to the clinic requires the integration of large, heterogeneous biological data sets into a unified in silico cellular model suitable for vector design and analysis. We propose to integrate genome, epigenome, and transcriptome sequencing for designing epigenome modifying CRISPR (EpiCRISPR) vectors. Our software platform will map epigenetic changes associated with disease states and design EpiCRISPR libraries targeting gene regulatory elements associated with an altered epigenetic landscape to generate novel epigenome editing treatment approaches. We will utilise the drug-resistance in ovarian cancer as a test case, where clinically relevant genomic and epigenomic datasets have already been generated and there is a clinical need to improve patient outcome by overcoming drug resistance. We anticipate a tool of this caliber will allow for unparalleled insight into the function of cellular mechanisms and thus hugely impact translational omics research.

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