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Poster Presentation Abstracts

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Poster Title	Livaux™ as a Prebiotic on Gut Motility: An In Silico Efficacy Analysis
Abstract	A systematic literature review is conducted to identify the molecular pathways affecting gut motility. The molecular pathways of gut motility are converted to individual mathematical models; each model is validated; and, the plurality of models are integrated with the CytoSolve® computational systems biology platform to produce an integrative model of gut motility. CytoSolve provides for the dynamic integration of molecular pathway models, in silico (through mathematical modelling on a computer), to understand synergistic effects of multi-ingredient dietary supplements on molecular pathways of biological processes. Livaux™ is a clinically proven prebiotic and was shown to boost levels of the beneficial gut bacterium Faecalibacterium prausnitzii by more than 100% in recent clinical trial by Anagenix. Combination of all the bioactive molecules at the recommended dose levels is tested in silico to elucidate the mechanism behind the beneficial effects of Livaux™ on gut motility. The results from the systematic review reveal three major biological systems that govern gut motility: 1) Mucus production; 2) Fecal bulking; and, 3) Inflammation. The results from the CytoSolve in silico modeling demonstrate that Livaux™ bioactive compounds synergistically enhance gut motility by: 1) increasing mucus production; 2) assisting fecal bulking and, 3) reducing inflammation.

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Poster Title	**PROBIOTICS: PREVENTION OF INTRA-HOSPITAL DIARRHEA IN PATIENTS USING ANTIBIOTICS THERAPY**
Abstract	**SUMMARY:** Diarrhea after hospital admission is a common finding. Patients with hospital diarrhea will have increased significantly their admission period and hospital costs. Antibiotic-associated diarrhea (Acute Diarrhea Disease) is a common adverse effect in adult patients. Acute Diarrhea Disease may cause complications such as dehydration and nutritional losses. The following antibiotics are more likely to cause Acute Diarrhea Disease: cephalosporins (cefixime and cefpodomixe) clindamycin, penicillins (amoxicillin and ampicillin), fluoroquinolone (ciprofloxacin and levofloxacin). That happens because they cause a disruption on the gut flora, selectively eliminating bacteria, which, in turn, allows the growth of fungus that produce toxins that directly irritate the bowel wall, increasing permeability and allowing toxins to be absorbed by the blood flow. **OBJECTIVE:** To investigate the number of patients in antibiotic therapy that have developed diarrhea before and after the implementation of the preventive protocol for diarrhea (involving the use of glutamine and probiotics).**METHOD**: This was a retrospective and observational trial with patients who had intra-hospital diarrhea between September and December of 2016, (before the implementation of the prevention protocol for diarrhea) and after the implementation of the same protocol, between January and July of 2017. Patients in antibiotic therapy preventively received a protein module of 10 grams of glutamine, twice a day, and a mix of probiotics with five strains: *Lactobacillus acidophilus, Lactobacillus casei, Lactococcus lactis, Bifidobacterium lactis e Bifidobacterium bifidum*, 2 grams, twice a day. **RESULTS**: Between September and December of 2016, the average number of patients with diarrhea was of 21.75/month (6.05% of admitted patients in the period). After the implementation of the protocol for diarrhea, the average number of patients with diarrhea dropped to 13.6/month (0.72% of admitted patients in the period).**CONCLUSION**: Considering the scenario laid out in this trial, we find that the implementation of the preventive protocol for intra-hospital diarrhea at Aviccena Hospital for patients using antibiotic therapy was a vital contribution to lower the incidence of the disease.

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Poster Title	PROBIOTICS: PREVALENCE ANTIBIOTIC-ASSOCIATED DIARRHEA IN A PRIVATE HOSPITAL IN THE CITY OF SÃO BERNARDO DO CAMPO, SP
Abstract	INTRODUCTION: The appearance of diarrhea in hospital is common. Patients who contract hospital diarrhea show a significant increase in their hospital stay and hospital costs. The antibiotic-associated diarrhea (ADI) is a common adverse effect arising in adult patients, the use of probiotics can manage this condition. ADI can lead to complications such as dehydration and loss of nutritional order. OBJECTIVE: To determine the number of patients on antibiotic therapy who developed diarrhea, hospital stay and days of diarrhea stay, later to propose development of preventive protocol of diarrhea and use of protein module and probiotic. METHODS: This study was retrospective and observational in patients on antibiotic therapy. Data were collected from 261 patients on antibiotics, admitted to a private hospital in the city of São Bernardo do Campo, SP, between March and April 2016. Data analysis was performed descriptively. RESULTS: The frequency of evacuation according to the gender of the patients it was observed that 67% (n = 14) of women had diarrhea, eleven were in oral nutritional therapy (TNO) and three in enteral nutritional therapy (TNE). In men 33% (n = 7) had diarrhea, where six were TNO in TNE and therefore the 21 patients (12%) had diarrhea. Antibiotic (ATB) most commonly used in patients with diarrhea in both genders was ciprofloxacin (38%; n = 8), followed by rocefin (24%; n = 5). Other Tazocin were used (9.5%; n = 2), Meropenem (4.8%, n = 1) and such associations with Dalacin rocefin (9.5%; n = 2), Meropenem with Targocid (4,8 %, n = 1), rocefin with Klaricid (4.8%, n= 1), with staficilin cirpofloxacino (4.8%, n = 1). The average number of days of diarrhea were 8 days joining both sexes, for women was the average of 5 days for those in TNO and 17 days for those in TNE. In men TNO in TNE 5 days and the average of diarrhea was 28 days. The hospital stay ranged from 6 to 31 days, six days for patients in TNO and thirty-one days for the in TNE, with the average 13 days of hospitalization. CONCLUSION: Given the whole scenario explained in this study, we conclude that the development of a protocol for the preventive management of diarrhea with probiotics for patients in early and use of antibiotic therapy would be important to reduce hospital complications, days of diarrhea and hospitalization time targeting lower financial impact for the institution.

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Poster Title	Analysis of a large-scale cohort reveals multiple lifestyle and blood markers associated with the gut microbiome
Abstract	The human gut microbiome has been found to be associated with human wellness and disease. In addition, different studies have identified specific lifestyle factors that impact the microbiome or biomarkers that are associated with its composition. However, large-scale population studies that both measure the composition of the microbiome and extensively phenotype the participants are still scarce. Here, we present a study of these relationships in 2,270 participants, comparing their microbiome composition to their dietary and lifestyle habits, bowel health, clinical laboratory tests, and medication usage. We find that the overall microbiome composition in our cohort is similar to other US-based cohorts and identify a diversity “sweet-spot” on the Firmicutes-to-Bacteroidetes axis. By applying a microbiome-specific ordination technique, we identify the major bacterial drivers of the taxonomic landscape and find that the two beneficial clades Bifidobacterium and Faecalibacterium are anti-correlated. In addition, we identify multiple factors that are significantly associated with the taxonomic composition of the gut microbiome, including cholesterol and diabetes blood markers, dietary intake and the frequency and duration of physical activity. Finally, we analyse the composition of the microbiome with respect to the usage of three broad classes of prescription medications and find that these medications have both shared and distinct impact on the composition of the gut microbiome.

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Poster Title	Computing Metabolic Routes in the Human Microbiome
Abstract	BioCyc.org is an extensive web portal for microbial genomics and metabolic pathways. BioCyc contains 13,000 microbial genomes including 929 organisms from the Human Microbiome Project. Two BioCyc databases are noteworthy as bacterial references: the EcoCyc database for Escherichia coli has been curated from 35,000 publications, and the BsubCyc database for Bacillus subtilis has been curated from 4,000 publications. In addition, the MetaCyc database is a multi-organism metabolic pathway database describing 2,600 experimentally elucidated pathways. BioCyc contains an extensive set of bioinformatics tools. Genome-related tools include a genome browser, sequence searching and alignment, and extraction of sequence regions. Pathway-related tools include a tool for navigating zoomable organism-specific metabolic map diagrams that can be painted with metabolomics and gene-expression data, and a new Omics Dashboard for interactive exploration of omics datasets. The new multi-organism metabolic route search (MORS) tool enables the user to explore biochemical conversions among metabolites that are accomplished by multiple microbiome organisms. To specify a route search problem the user provides a starting and an ending metabolite of interest, and a set of organisms. The organism set could span just a handful of named BioCyc organisms, or it could include hundreds of organisms, such as from the pre-defined gut microbiome set within BioCyc. The route-search tool then computes a set of optimal routes connecting the starting and ending compounds. Each route is a linear sequence of reactions that converts the starting compound to the ending compound. An optimal route minimizes the number of reactions used while maximizing the number of atoms from the starting compound that are incorporated into the ending compound. The set of reactions from which the routes are computed is the union of all reactions in the metabolic networks of the selected organisms -- all reactions in those organisms are assumed to be accessible, independent of transport considerations.

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Poster Title	Use of Flow Cytometry to assess the health of probiotic *Bacillus* endospores
Abstract	*Bacillus* endospores are ideal for inclusion in commercial probiotic formulations due to their resistance to environmental stress and relative metabolic dormancy. However, accurate methods to evaluate endospore health and metabolic state are lacking. We previously demonstrated that flow cytometry, in conjunction with DNA-binding dyes, can accurately enumerate populations of live, injured and dead vegetative bacterial cell. In the present study, we used flow cytometry to assess various industrially-relevant properties of endospores. Various dye systems were used with flow cytometry to characterize "healthy" (defined as dormant and heat-stable), "injured" (defined as damaged and heat-labile, prematurely germinated or both) and dead spore populations. Cell sorting was subsequently employed to isolate these populations to confirm their properties empirically. The results will help guide the development of spore-specific flow cytometry-based assays to evaluate formulations and manufacturing processes of probiotics containing endospores.

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Poster Title	Cross Contamination Control: from DNA Extraction to Sequencing
Abstract	Sequencing projects suffer from lack of controls that can be used in every step of analysis: from DNA extraction to sequencing. Sample swapping or sample-to-sample contamination can occur during any of these steps, but without *a priori* knowledge of the samples, one cannot discern contamination or similar profiles. To mitigate this issue, we have designed a barcoded DNA molecule encapsulated in a simulated cell membrane to serve as a cellular spike-in control. The average size of the encapsulated cross-contamination control was 8 ± 2 µm in diameter as measured via dynamic light scattering. To measure the efficiency of DNA encapsulation, the capsule was dissolved, and DNA load was measured by UV absorbance at 260 nM, demonstrating 85% encapsulation efficiency. DNA was extracted from the encapsulated cross contamination control by Qiagen's DNeasy PowerSoil Kit and amplified using 16S primers. An Agilent Bioanalyzer High Sensitivity Chip demonstrated that amplification occurred and produced the appropriate size amplicon product, 200 bp. A soil sample was then spiked with an encapsulated cross-contamination control and processed for amplicon sequencing. Both the soil microbes and the cross-contamination control amplified based on the different amplicon sizes: 16S = ~600 bp, the control = 200 bp and were sequenced. The unique capabilities of the spike in control enable use at the time of sample collection prior to any sample processing to identify sample swaps or contamination during all processing steps from sample to sequencing. This cross-contamination control can either be flanked with the specific primer binding sites to have the barcode amplify during an amplicon sequencing protocol, or no primer binding sites for use in whole genome sequencing protocols. A set of 384 different barcoded cross contamination control spike-ins could be synthesized to enable multiplex processing of 384 samples, a common practice in amplicon sequencing.

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Poster Title	Phenobiome: genomics-based predictive phenotype profiling of the human gut microbiome
Abstract	High-throughput genomic and metagenomic sequencing revolutionized exploration of microbial communities colonizing various sites of the human body. Amassing genomic studies begin to uncover complex associations of human microbiome with pathological conditions, immune status and response to diet and therapeutic treatments. We developed the PhenoBiome pipeline enabling prediction and comparison of metabolic properties for microbial communities based on their phylogenetic composition. Using subsystems-based metabolic reconstruction methodology (implemented in SEED/RAST environment) we infer phenotypic features (nutrient requirements, utilization capabilities, metabolite production) directly from microbial genomes. The obtained collection of binary metabolic phenotypes for ~2,300 reference bacterial genomes representing human gut microbiota was used in two-stage pipeline for prediction of phenotypes in 16S RNA samples. Stage 1 module determines taxonomic composition of input samples using QIIME2 or BION (kindly provided by Niels Larsen, Denmark) and 16S databases (NCBI, RDP). The Stage 2 module calculates the matrix of predicted community phenotypes normalized by species abundance for each sample and each metabolic feature. It uses a three-level taxonomic mapping procedure and computes averaged phenotype indices at the levels of species, genus and family for probabilistic assessment of metabolic features of those taxonomic entities that cannot be mapped to presently available reference genomes. In the output PhenoBiome produces Community Phenotype Indexes (CPIs) for each phenotype - a probabilistic estimate of a fraction of cells in the community having this phenotype (on the scale 0 – 100%). The vector of all CPIs can be used as unique Community Phenotype Signature (CPS). This approach was developed, optimized and applied to the analysis of samples from the Human Microbiome Project and American Gut Project. We calculated CPIs for >80 metabolic phenotypes. The obtained CPS for large data sets of human gut microbiota from various will enable computing different types of intra-sample, cross-sample and cross-group correlations including the analysis of metadata.

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Poster Title	Novel tools to investigate microbiome of air spaces
Abstract	Microbiome of various air spaces remains a largely unexplored territory. One of the main reasons is the lack of suitable tools to capture enough airborne biomass for microbiome investigations. To address this challenge, we have developed and tested two novel sampling technologies to capture airborne microorganisms. The first device is a self-contained, battery-operated, personal electrostatic bioaerosol sampler (PEBS). PEBS is a two-stage electrostatic precipitator consisting of a novel wire-to-wire charger and a dual half-cylinder collection chamber. Once the incoming particles are charged, they are collected on a removable stainless steel plate coated with superhydrophobic substance and then eluted into the liquid medium. The utilization of novel wire-to-wire charger design results in very low ozone production (<10 ppb) allowing its application as a personal sampler. The sampler has shown very good performance when capturing and preserving bacterial and fungal particles in laboratory and field studies. In another project, we developed a Rutgers electrostatic passive sampler (REPS). This device is small and lightweight – it fits into a standard 50 mL tube - and captures airborne microorganisms without external power or air movers. It utilizes unique properties of electroactive films to collect airborne microbial agents electrostatically. The use of flexible, thin films to collect airborne microbes allows customizing the sampler design for various air spaces and for taking samples at wide spatiotemporal scales. Air samples collected by both devices can be used to analyze microbiome of air spaces.

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Poster Title	Comparative genomics analysis reveals genetic differences between two strains of *Lactobacillus fermentum* with divergent physiological effects
Abstract	Probiotics are microorganisms that confer health benefits on their hosts. However, it has been recognised that such beneficial effects are often strain-specific and claims for one strain cannot be readily transferred to another. Although *Lactobacillus fermentum* is a probiotic microorganism generally associated with positive effects on gastrointestinal health, two strains of *L. fermentum*, AGR1485 and AGR1487, exhibit different effects on intestinal barrier function and vary in their tolerance towards bile. In model systems, the integrity of tight junction formation was shown to be weakened in the presence of ARG1487 which induced a pro-inflammatory response characterised by increased numbers of macrophages and lymphocytes, and strain-associated changes in gene expression patterns in colon tissue. To better understand the source of phenotypic variation between these two strains, a comparative genomic analysis was undertaken. Chromosomal DNA of AGR1485 and AGR1487 was sequenced and assembled. With 2.23 Mbp, the genome of AGR1485 was 0.28 Mbp larger than that of AGR1487. Annotation and manual curation of the draft genomes and subsequent comparative analyses highlighted specific features unique to each strain, with AGR1485 having 351 and AGR1487 150 strain-specific genes. Of those, AGR1485 harbours genes associated with a nitrate reductase/molybdenum co-factor biosynthesis cluster, while AGR1487 features unique genome loci involved in modulating the makeup of the bacterial cell wall via the chromosomal insertion of a unique N-acetylglucosamine synthase gene and a surface polysaccharide O-acyltransferase gene. Interestingly, the corresponding gene loci have been respectively replaced with transposase genes in AGR1485 and AGR1487. We hypothesise that such variations in the metabolism of AGR1485 or the surface makeup of AGR1487 are contributing factors to their differential effect on tight junctions. These initial analyses have highlighted marked differences between these *L. fermentum* strains and a more detailed investigation may provide further insights into the genetic basis that transforms a probiotic strain with beneficial effects into a “bad neighbour” with undesirable traits.

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Poster Title	Metabolomics reveals biochemical mechanisms of functional gastrointestinal disorders
Abstract	Irritable Bowel Syndrome (IBS) is a functional gastrointestinal (GI) disorder characterised by chronic or recurrent abdominal discomfort. Metabolomics profiling can provide biochemical fingerprints which, when interpreted onto biochemical networks, can assist with understanding the underlying mechanisms of diseases and phenotypes. In a case-control study, we aimed to identify microbial and host factors using metabolomics profiling to provide mechanistic insights into functional GI disorders, increasing the predictability of phenotypes for use in nutrition intervention studies. Individuals with functional GI symptoms (cases) or asymptomatic (controls) undergoing colonoscopy were recruited and a subset of 200 plasma samples were measured using three high resolution LC-MS metabolomics methods to detect polar and semi-polar metabolites and the lipidome, yielding 491 polar, 458 semi-polar and 768 non-polar (lipid) metabolite features respectively for multivariate analysis. Significant metabolites were identified using in-house and online databases while biochemical networks were constructed via Metscape. Plasma metabolomics profiles differed significantly between the IBS phenotypes and the control subjects, with major perturbations observed in amino acid, bile acid and lipid metabolism, and this highlighted key metabolic pathways, including microbial related pathways, for further investigation. We have successfully shown that metabolomics can detect and determine differential metabolites and pathways affected between phenotypes and next steps include applying a systems biology approach to a larger cohort size to identify key pathways and biomarkers.

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Poster Title	The microbiome and Irritable Bowel Syndrome: Insights from the Christchurch COMFORT cohort
Abstract	Irritable Bowel Syndrome (IBS) is a functional gastrointestinal (GI) disorder featuring chronic or recurrent abdominal discomfort, usually with changes in GI habit. However, the mechanisms responsible for IBS are poorly understood. Although alterations in the GI microbiome has been implicated in IBS, there is a lack of consensus on what the exact role of the microbiome is, and how it changes, in IBS. To gain a better understanding of the link between the microbiome and IBS, we undertook shotgun metagenomic sequencing of faecal samples from a case-control study. The overall aim of the study was to identify microbial and metabolomic factors that provide mechanistic insights into functional GI disorders and increase the predictability of phenotypes for use in nutrition intervention studies. Faecal samples from 200 individuals with functional GI symptoms (cases) or those that were asymptomatic (controls) were shotgun sequenced using the Illumina NextSeq platform. Taxonomic classifications were determined using Metaxa2 and the SILVA 128 database. Gene functions were assigned by alignment of sequences against a protein reference database using DIAMOND and functional classification using MEGAN. Bacterial genera that discriminated case-controls from IBS groups included *Faecalibacterium*, *Blautia*, *Roseburia*, and *Eubacterium*, which were relatively more abundant in certain IBS subtypes. For example, *Faecalibacterium* was relatively more abundant in individuals presenting with constipation associated IBS (IBS-C), while *Blautia* was more prominent in those with the diarrhea form of IBS (IBS-D). Gene functions that best separated groups included those related to carbohydrate metabolism (higher in IBS compared to case-controls), protein metabolism, and virulence factors. Our results suggest that carbohydrate fermentation by the microbiome may be an important factor in IBS.

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Poster Title	Evaluation of Methods for Simultaneous Extraction and Purification of Fungal and Bacterial DNA from Vaginal Swabs
Abstract	Background: The interactions between bacteria and fungi in the human vaginal microbiome are fundamental to the concept of health and disease. The means by which the microbiota and mycobiota interact is still poorly understood and further studies are necessary to properly characterize this complex ecosystem. The aim of this study was to select a DNA extraction method capable of recovering high quality of fungal and bacterial DNA from a single vaginal swab. Methods: 11 female volunteers (≥20 to < 55 years old) self-collected vaginal swabs in triplicate. Three commercial extraction kits: Masterpure Yeast Purification kit (Epicenter), PureLink™ Microbiome DNA Purification kit (Invitrogen), and Quick-DNA™ Fecal/Soil Microbe Miniprep kit (Zymo) were evaluated on the ability to recover fungal and bacterial DNA simultaneously. The performance of each extraction kit was compared on the basis of DNA yield and purity (NanoDrop®), bacterial DNA extraction efficiency from swabs spiked with two different species of bacteria (qPCR) and the community richness of bacterial (16S rRNA - V3-V4 region) and fungal (ITS1) microbiota composition (Illumina MiSeq amplicon sequencing). Results: The quantity of extracted DNA was significantly higher with the Epicenter kit (yield). The absorbance ratio at 260/280 nm was similar for both Epicenter kit and Zymo kit while considerably lower for Invitrogen kit (purity). qPCR results showed that both Epicenter kit and Zymo kit were uniformly efficient when extracting bacterial DNA from the two selected target bacteria. Overall, all 3 kits displayed similar bacterial microbiota profiles for the top 20 OTUs; however, the Zymo kit showed more species richness. The fungal mycobiota was only consistently obtained with the Epicenter kit. Conclusion: In the present study, the Masterpure Yeast purification kit (Epicentre) proved to be the only good candidate for purification of high quality fungal and bacterial DNA simultaneously. These findings have potential benefits that could be applied in future vaginal microbiome research. Whilst the use of a single extraction method would lessen the burden of multiple swab sampling, decrease laboratory workload and off-set costs associated with multiple DNA extractions, thoughtful consideration must be taken when selecting an extraction kit depending on the desired downstream application.

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Poster Title	The COMFORT cohort: Identifying biomarkers relevant to functional gastrointestinal disorders
Abstract	The links between food, gastrointestinal function and comfort, and mental well-being are at the forefront of nutritional research. Irritable Bowel Syndrome (IBS) is a functional gastrointestinal disorder characterised by chronic or recurrent abdominal discomfort mostly associated with changes in gastrointestinal habit in the absence of a detectable organic cause. Several central and peripheral mechanisms initiate perturbations in gastrointestinal motor and sensory functions and lead to IBS symptoms. Accurately measuring peripheral molecules, and understanding associated pathway dysfunctions and altered tissue metabolism, is important to better define these disorders. The Christchurch COMFORT cohort has been established to investigate mechanisms for gastrointestinal relief and improved transit. In a case-control study, individuals with functional gastrointestinal disorders (cases; functional constipation (FC), functional diarrhoea (FD), IBS – constipation (IBS-C), IBS – diarrhoea (IBS-D)) and asymptomatic controls undergoing colonoscopy were recruited to better characterise these disorders. A total of 320 participants have been recruited to date. Demographics, symptom scores, psychological scores and dietary intake were recorded using five questionnaires: • 'Modified Hunter New England' (ModHNE) – an amalgamation of: - Rome IV diagnostic criteria questionnaires - 12-Item Short Form Survey (SF-12) - Medical History Questions - Hospital Anxiety and Depression Scale (HADS) - Demographics • Economic Living Standards Index (ELSI) – Short form • Structured Assessment of Gastrointestinal Symptoms (SAGIS) • Diet Diary and Live Symptoms Score (FAST) • Patient-Reported Outcomes Measurement Information System (PROMIS) Metabolomics of biological samples, shotgun metagenomics sequencing of faecal samples, and quantification of plasma neurotransmitters and bacterial metabolites were carried out to identify microbial and host factors linked with, and gain mechanistic insights into, functional gastrointestinal disorders. A summary of the questionnaire and biological data obtained from the COMFORT cohort will be discussed in relation to a systems nutrition approach to identify key pathways and biomarkers relevant to functional gastrointestinal disorders.

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Poster Title	Comparison of Different Broth Brands of de Man, Rogosa and Sharpe MRS (with different Peptone source) for Effectiveness of Lactic Acid Bacteria Strain J19 (*Enterococcus faecium*) to Reduce *Listeria monocytogenes*.
Abstract	**Objective:** Lactic Acid Bacteria (LAB) produce a variety of anti-listeria antimicrobial compounds such bactericidal proteins, termed bacteriocins. *Listeria monocytogenes* is a pathogen that is ubiquitous in nature, which is commonly associated with food processing environments. The objective of this study is to compare how different peptone sources in De Man, Rogosa & Sharpe (MRS) broth affect the effectiveness of LAB strain J19 (*Enterococcus faecium*) to reduce *L. monocytogenes*. **Methodology:** Two MRS brand products were evaluated for reduction of *L. monocytogenes* in: Brand A (meat peptone) and Brand B (casein peptone). A control of *L. monocytogenes* was inoculated into each brand and had no added J19. In addition, a treatment of each broth was co-inoculated with *L. monocytogenes* and J19.The samples were incubated at 37°C for each 0, 6, 12, 24, and 48-hour time points. Each experiment was replicated four times and enumeration of *L. monocytogenes* was evaluated on Oxford (MOX) agar and LAB J19 on MRS agar. **Results:** At 12 hours, *L. monocytogenes* in both groups of controls grew to approximately $\log_{10}$ 8.00 CFU/ml. The J19 strain effectively reduced *L. monocytogenes* at a statistical significant ($p < .05$) level in comparison to the controls at time point six hours in Brand A. In addition, the J19 strain performed better in Brand A and reduced *L. monocytogenes* to undetectable levels after 12 hours. The MRS Brand B treated with J19 did not fully inhibit *L. monocytogenes* until 48 hours. **Significance and implications of results:** Ingredient composition can influence the inhibitory activity of LAB against pathogens. These results suggest, brand of MRS and specifically peptone source could be a difference in 1 to 2 logs, which is equivalent to 90 to 99% more reduction of pathogen.

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Poster Title	Gut Microbiome and self-reported measures of mental health
Abstract	Background: Evidence suggests that shifts in the gut microbial communities (GMC) may contribute to mental health functioning via central nervous system signalling pathways, although the nature of the gut-brain interactions remains poorly understood. Previous research has shown that neuroinflammatory pathways may play a role in the etiology of depression, with depressive symptoms underlined by increased levels of proinflammatory cytokines. Thus, the current study aimed to examine the relationship between self-reported measures of mental health (depression, happiness, and stress), the gut microbiome which was measured in stool, and circulating concentrations of inflammatory biomarkers (IL-6, IL-8, CRP) in a cross-sectional study of 1,874 individuals participating in a wellness program in the United States. Methods: We applied a permutation-based approach to assess differences in overall GMC structure across mental health measures. Indicator species analysis was used to examine potential taxa-level differences between groups. Causal mediation analysis was used to measure the impact of inflammation on the association between GMC and mental health measurements. Results: We found overall GMC differences between depressed and non-depressed individuals, as well as between individuals grouped by stress and happiness levels. Indicator species analysis identified several taxa associated with depression and low levels of happiness. Circulating concentrations of CRP and IL-6 were associated with depression, higher levels of stress, and lower levels of happiness, although these inflammatory markers did not mediate the association between GMC and mental health. Conclusion: Findings from the study showed that there maybe be overall microbiome and taxa-specific differences between individuals with mental health outcome related to depression and stress. Moreover, these associations were not mediated by inflammatory cytokines CRP and IL-6, suggesting alternative pathways may exist.

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Poster Title	Flexible Panel-Based Solutions for Pathogen Detection using Spatial Multiplexing on Nanofluidic qPCR Platform (TaqMan™ OpenArray™)
Abstract	Although a gold standard for testing, culture-based approaches to pathogen detection lack sensitivity, specificity, take a long time to get an answer, and can often miss fastidious or hard to grow pathogens. Majority of on-market molecular pathogen detection tests available on the market are costly, lack flexibility to regional needs, not scalable, and cannot be customized to develop clinically relevant tests for the populations laboratories are testing. Applied Biosystems' range of flexible-content pathogen detection solutions allow laboratories the freedom to run fixed or custom panels of qualified and validated assays that deliver specific, sensitive, low-cost and scalable solutions for some of the most common commensal and pathogenic microbes globally – allowing laboratories to get the most answers from their pathogen detection tests the first time around. With the combination of trusted Applied Biosystems products, including TaqMan assays (offering > 10 Million assays) – delivering highly reproducible sensitive and specific answers needed for pathogen detection analysis – along with the QuantStudio range of real-time PCR systems, we have developed a growing menu of flexible-content pathogen detection solutions that meet the ever-changing needs of clinical laboratories running infectious disease testing. Our end to end commercial solutions include qPCR panels for Vaginal Microbiota, Urinary Tract Microbiota and Respiratory Tract Microbiota. Additional we also provide customized panels to meet any commensal and pathogenic microbial detection need.

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Poster Title	A novel non-enzymatic hydrolysis for customized efficient production of natural plant-derived prebiotics
Abstract	There is recent scientific evidence outlining the prebiotic activity and added health benefits of AXOS, β-glucan and XOS in human nutrition and skin health. Economically efficient methods of production of AXOS, β-glucan and XOS can be achieved by deriving them from agricultural and food processing side-streams. In the study we show the process of using IONZYMES, Embion's range of proprietary processing aids, for selectively hydrolysing the biomass matrix of a variety of plant residues towards the production of AXOS, β-glucan and AXOS. Specifically, corn stover, corncob, and brewers' spent grain were evaluated. The results demonstrated the ability to: (a) produce AXOS and XOS with variable Degree of Polymerisation (DP), while minimizing the production of monomeric sugar; (b) alter the DP profile by tuning the process parameters; (c) preferentially hydrolyze hemicellulose but can also act on cellulose. The desired product is obtained within the short reaction time (30 min-2 hours) with a high purity without any additional purification step (70-85 wt% purity)

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Poster Title	CMiST Microbial Isolation Facility: Rapid Establishment of Bacterial Species Libraries From Clinical Samples Using MALDI-TOF Identification
Abstract	The Center for Microbiome Sciences and Therapeutics (CMiST) at the University of Washington Seattle offers a suite of technologies to academic and industry partners to facilitate the development of microbiome-based therapies. Here we describe bacterial isolation methodology coupled to MALDI-TOF biotyper identification that enables the rapid establishment of bacterial libraries from clinical samples. This methodology has been applied to stool samples from obese adolescents and colon biopsy samples from individuals screened for colorectal cancer. The species isolated predominantly belong to the Bacteroides and Bifidobacteria genera and include those previously associated with progression to diabetes or colorectal cancer. Further experiments show that prior freezing of samples reduced the total yield of bacteria recovered, and disfavoured the recovery of Bacteroides species. On-going work is focused on comparative genetic and functional analysis of clinically relevant strains, and on adapting MALDI-TOF technology to identify pathology-associated microbial traits.

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Poster Title	Developing standards for the analysis of the gut microbiome
Abstract	Developments in Next Generation Sequencing technologies have facilitated the rapid expansion of the microbiome field. Microbiome studies commonly consist of the same core steps; a platform-specific library preparation (which may be preceded by a 16S rRNA amplification step), sequencing via a NGS technology, and data analysis through either a previously published or in-house bioinformatic pipeline. Despite this common framework underpinning nearly all microbiome studies, variations across the materials and methodologies employed to perform each key processing step, have been demonstrated to cause significant variations in results. Currently, there are no internationally accredited microbiome standards for use in the analysis of the gut microbiome. NIBSC generates and supplies 95 % of the World Health Organisation International Standards (WHO IS) and reference materials. The goal of this work was to develop two microbiome DNA reference standards for the standardisation of downstream (post-extraction) gut microbiome analytical steps. It is our intention that these will undergo a collaborative study for endorsement as a WHO IS and subsequently be made available to the scientific community. Here, we outline the generation of the two 18-strain mock communities for use as microbiome standards, assess their composition in comparison to all microbiome run controls which are currently publicly available, and perform a comprehensive analysis via Shotgun Metagenomic sequencing to evaluate how accurately prevailing methodologies reconstruct the composition of the standards. Our results demonstrate that shotgun sequencing can accurately detect and identify all species present in both an even-composition standard and a standard with bacteria differing in concentration by two-log fold. However, variations in bioinformatic protocols impacted the taxonomic reconstruction of the microbial community present. This data suggests that the NIBSC Gut Microbiome DNA Standards will allow users to accurately benchmark protocols to ensure they are fit for purpose (i.e. to analyse the gut microbiome) facilitating commutability between studies.

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Poster Title	Pre-Sequencing, Sequencing and Post-Sequencing considerations for Applied Metagenomic Sequencing
Abstract	Shotgun metagenomic sequencing is rapidly adopted by the biomedical community for preclinical and clinical research. Benefits of metagenomic sequencing include a highly accurate, unbiased, and culture independent characterization of microbial communities. However, despite the positive impact of metagenomic sequencing on microbiome research, many laboratories are challenged by the method's disruptive effect on traditional Next-Generation Sequencing (NGS) practices and by the complexities inherent to establishing a robust and standardized NGS workflow. Metagenomics is uniquely sensitive to the introduction of bias along almost every step of the workflow which can impact accuracy, precision, and comparability between studies or even samples. In this presentation we shed light on failure-modes and present mitigation strategies employed at the CosmosID NGS Service Laboratory along the three workflow phases: Sample preparation: The various laboratory methods employed for sample collection, preservation, nucleic acid isolation and preparation of sequencing libraries need to avoid laboratory contamination and control the introduction of bias or variability. Quality control practices and the use of internal standards and controls is an important part of this phase. Sequencing: Differences in data quality, read length and depth, as well as distinct error profiles among the various NGS platforms must be carefully considered as they otherwise affect consistent and accurate data interpretation. Data interpretation: Metagenomics data analysis poses a huge data and informatics challenge. A myriad of published algorithms explore different approaches for deconvoluting the valuable biological signals from bias and error introduced during sample preparation and sequencing. While the clinically informative and actionable unit in microbiology is a strain, not a species, most available methods fail at sub-species level resolution. Therefore, the choice of algorithms and databases has a significant impact on the fidelity and actionability of the analysis outcome.

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Poster Title	Development of a Selective Medium for the Isolation and Enumeration of Lactobacillus bulgaricus
Abstract	Lactobacillus delbrueckii ssp. bulgaricus is an industrially important organism that is widely used in dairy industries, particularly in yogurt production. L. bulgaricus is mandatory for traditional yogurt, has several health benefits and also meets the prerequisites for probiotic bacteria. Currently, the standard medium, de Man, Rogosa and Sharpe (MRS), is insufficiently selective for the L .bulgarcius species and also produces inaccurate quantitative results. Consequently, there is a need for a reliable medium for the differential enumeration of L. bulgaricus. Thus, the objective of this study was to develop an agar medium for the differential isolation and enumeration of L. bulgaricus. A modified, reinforced clostridial medium (mRCM) was developed by adding 0.025% CaCl2, 0.01% uracil, 0.2% Tween 80, 0.5% fructose, 0.5% dextrose, 1% maltose and 0.25% pyruvate to RCM. The addition of 0.04% aniline blue dye to the mix contributed to an improved morphology and differentiation of L. bulgaricus colonies from the mixed yogurt culture. Cell recovery and bacterial counts of L. bulgaricus in tested yogurt brands using mRCM-BLUE were higher than those in the standard MRS medium as mRCM-BLUE largely inhibited the growth of other bacterial species (Streptococcus thermophilus, Lactobacillus acidophilus, Bifidus and Lactobacillus reuteri) present in the yogurt. Our results thus suggest that mRCM-BLUE could be recommended as a selective agar medium for the isolation and enumeration of L. bulgaricus.

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Poster Title	Circadian Rhythms, Gut and Brain Microbiomes
Abstract	Current research has shown that gut microbiomes have a 24-hour circadian rhythm. While the overall rhythm of the body is reliant on the circadian clock set by the Suprachiasmatic Nucleus (SCN) of the hypothalamus in the brain, multiple compartments in the body – such as the gut microbiome – have local, peripheral clocks that have complex and interconnected processes regulating the overall health of the host. Daily activities such as food intake patterns, sleep, exercise and medications affect gut health, which in turn impact sleep-wake cycles, hormone levels and overall metabolic processes. Just like the gut plays a critical role in the state of the mind, stress levels and brain health can alter the microbial balance of the gut, interrupting digestive processes and resulting in greater susceptibility to infections. This information suggests a role for the importance of timing the for collection for fecal samples for the analysis of microbial diversity as part of clinical trial outcomes. When conducting clinical trials for functional foods and dietary supplements, there is a need to rethink current concepts of testing times with regards to anything that will affect the gut microbiome, such as stool samples, saliva samples and skin scrapings due to the additional presence and interaction of nasal and skin microbiomes. In addition, there is thought-provoking information concerning the existence of a brain microbiome. With regards to the SCN in the hypothalamus and its regulation by the hormone melatonin in setting the internal pace of the body, the current research provides immense applications for the supplement industry in the 21st century. Further questions beg to ask whether there are oral circadian rhythms of the oral microbiome, and whether they are connected to the gut, nasal and skin microbiomes.

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Poster Title	Gut feeling: function based microbiome research
Abstract	In spite of a rising awareness of gut microbiota impact on multiple health issues, most of the studies are focused solely on taxonomic differences, without even trying to explain the underlying mechanisms. Moreover, recent studies on checkpoint inhibitor cancer therapies proved their dependency on gut microbiota content, yet no specific species were commonly identified to play a key role in the response to treatment. Nevertheless, those discoveries have opened a novel segment of the Next Generation Probiotics (NGP) market. During this talk, Ardigen will present the BiomeScout algorithm: a novel approach to metagenomic research that puts a function as a key entity. Additionally, Ardigen is developing BiomeSeer and BiomeBrewer, two complementary algorithms: a strain phenotype predictor and probiotic cocktail optimiser. Combined, our technologies form a NGP Discovery Platform “BiomeForte” that will provide user with an end to end design of beneficial bacterial composition, defined by its functional importance.