

**SATURDAY JUNE 22<sup>ND</sup>****E-Poster Session****12.00-14.00**Chair: Alessio Fasano, *USA***Poster Area 1****Topic 1: IMPROVING METHODS AND PROTOCOLS OF MICROBIOTA STUDIES**  
30 e-posterChair: Gianluca Ianiro, *Italy***Poster Area 2****Topic 1: IMPROVING METHODS AND PROTOCOLS OF MICROBIOTA STUDIES**  
25 e-posterChair: Carla Fiorentini, *Italy***Poster Area 3****Topic 5: MANIPULATING THE GUT MICROBIOME TO IMPROVE HEALTH**  
30 e-posterChair: Maria Vasile, *Belgium***Poster Area 4****Topic 5: MANIPULATING THE GUT MICROBIOME TO IMPROVE HEALTH**  
21 e-poster**Topic 0: THE INTERACTION OF THE HUMAN HOLOBIONT WITH OTHER BIONTS**  
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# SATURDAY JUNE 22<sup>ND</sup>

## E-Poster Session

12:00 – 14:00

Poster Area 1

Chair: Alessio Fasano, *USA*

### Topic 1: IMPROVING METHODS AND PROTOCOLS OF MICROBIOTA STUDIES

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- 20** MACHINE LEARNING FRAMEWORK FOR CLASSIFICATION OF ADENOCARCINOMA AND SQUAMOUS CELL CARCINOMA USING LUNG MICROBIOME DATASET FOR THEIR EARLY DIAGNOSIS  
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- 46** HIGH-THROUGHPUT ANAEROBIC SCREENING FOR IDENTIFYING COMPOUNDS ACTING AGAINST GUT BACTERIA IN MONOCULTURES OR COMMUNITIES  
Patrick Müller, *Germany*
- 66** IMPROVED AUTOMATED HIGH-THROUGHPUT PURIFICATION OF METAGENOMIC SAMPLES  
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- 93** IDENTIFYING PHASE VARIABLE GENES WITHIN DIFFERENT SUB-POPULATIONS OF ADMIXED HELICOBACTER PYLORI  
Ebony Cave, *UK*
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- 108** FORMALISING MEASURES OF FUNCTIONAL REDUNDANCY OF MICROBIOME COMMUNITY MODELS VIA RELATIVE ENTROPY  
Daniel Fässler, *Germany*
- 115** COMBINED ANALYSIS OF DUAL 16S RRNA AMPLICON SEQUENCES THROUGH CONCATENATION OF PAIR-END READS ENHANCED MICROBIOME DIVERSITY AND FUNCTIONAL PROFILING  
Kyoung Su Kim, *South Korea*
- 119** MBQTL: AN R/BIOCONDUCTOR PACKAGE FOR MICROBIAL QUANTITATIVE TRAIT LOCI (QTL) ESTIMATION  
Mercedeh Movassagh, *USA*

- 128** OPTIMISATION OF OXFORD NANOPORE TECHNOLOGIES IN THE OF STUDY MICROBIAL CELL-FREE DNA  
Arielle Kae Sulit, *New Zealand*
- 133** IMPACT OF REFERENCE DATABASE VERSIONS AND ANALYSIS PARAMETERS ON TAXONOMIC CLASSIFICATION OF METAGENOMIC DATA  
Car Reen Kok, *USA*
- 139** GUT BACTERIAL PROTEOME ANALYSIS USING INDIVIDUAL-SPECIFIC PROTEIN CATALOG BASED ON METAGENOME AND METATRANSCRIPTOME ANALYSIS  
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- 143** MRGM: AN ENHANCED CATALOG OF MOUSE GUT MICROBIAL GENOMES EXPANDING TAXONOMIC AND FUNCTIONAL LANDSCAPES  
Nayeon Kim, *South Korea*
- 178** A MULTIDISCIPLINARY DELPHI CONSENSUS ON THE STATE OF THE ART AND HOW TO SHAPE THE FUTURE OF MICROBIOME-BASED BIOMARKERS  
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- 193** MANOCCA, A NOVEL COVARIANCE-BASED TEST IDENTIFIES LINKS BETWEEN GUT MICROBIOME CO-ABUNDANCE NETWORK AND AGE, SEX, SMOKING STATUS AND BODY MASS INDEX  
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- 250** MULTI-TASK GAUSSIAN PROCESS-BASED ACTIVE LEARNING FOR ENHANCED TRAVELER'S DIARRHEA PREDICTION USING MICROBIOME DATA  
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Riccardo Auccello, *Italy*
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- 267** TAXONOMIC CLASSIFICATION OF METAGENOME-ASSEMBLED GENOMES WITH KMETASHOT  
Giuseppe Defazio, *Italy*

- 282** TRANSLATIONAL POTENTIAL OF SPECIFIC PATHOGEN-FREE GUINEA PIGS' AIRWAY PHYSIOLOGY AND ITS RELEVANCE FOR MODELLING OF RESPIRATORY PATHOLOGIES  
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- 283** ANTIBIOTIC TREATMENT DECREASES COUGH REACTIVITY IN CONVENTIONALLY BRED GUINEA PIG ANIMAL MODEL  
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- 293** AN OPEN-ACCESS, CLOUD-BASED PLATFORM FOR A COMPREHENSIVE ANALYSIS OF METAGENOMIC DATA  
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- 294** TAKE CARE OF THE FUNDAMENTALS – UNBIASED DNA EXTRACTION FOR REPRESENTATIVE MICROBIOME INSIGHTS  
Lisa Mahler de Sanchez, *Germany*
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Marisa Isabell Keller, *Germany*
- 316** DONOR SCREENING FOR FECAL MICROBIOTA TRANSPLANTATION WITH A DIRECT STOOL TESTING-BASED STRATEGY: A PROSPECTIVE COHORT STUDY  
Debora Rondinella, *Italy*
- 330** GENOMIC LANGUAGE MODELS FOR UNDERSTANDING THE MICROBIOME  
Balázs Ligeti, *Hungary*
- 344** DISTRIBUTION CHARACTERISTICS OF TEN DOMINANT GUT MICROBIOTA IN HEPATIC PATIENTS UNDER DIFFERENT STAGING SCORING SYSTEMS  
Pengcheng Lou, *China*
- 346** LONG-READ METAGENOMICS OF THE HUMAN SKIN MICROBIOME USING IMPROVED MICROBIAL DNA EXTRACTION METHODS  
Rina Kurokawa, *Japan*

12:00 – 14:00

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Chair: Gianluca Ianiro, *Italy***Topic 1: IMPROVING METHODS AND PROTOCOLS OF MICROBIOTA STUDIES**

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- 387** RECENT ADVANCES IN HIGH PERFORMANCE METAPROTEOMICS FOR INTERROGATING THE DYNAMIC METABOLIC ACTIVITIES OF THE HUMAN GUT MICROBIOME  
Robert Hettich, *USA*
- 390** DEEP EMBEDDINGS FOR REPRESENTING GUT MICROBIOME SAMPLES WITH VISION AND HIERARCHICAL MODELS  
Camilo Valdes, *USA*
- 391** EXPANDING THE CULTURED DIVERSITY OF THE HUMAN GUT MICROBIOME USING A NOVEL HIGH-THROUGHPUT ANAEROBIC CULTIVATION PLATFORM  
James Volmer, *Australia*
- 395** CHASING LOW BIOMASS: BUILDING EFFECTIVE AND OPTIMIZED END-TO-END WORKFLOWS FOR SKIN AND ENVIRONMENTAL SAMPLES  
Brice Le Francois, *Canada*
- 398** EVALUATION OF NANOPORE SEQUENCING FOR HIGH-RESOLUTION HUMAN GUT MICROBIOME PROFILING BY NEAR FULL-LENGTH 16S RRNA GENE AMPLICON SEQUENCING  
Dieter Tourlousse, *Japan*
- 411** CHARACTERISTICS AND CLINICAL IMPLICATIONS OF THE GUT MICROBIOTA IN DIFFUSE LARGE B-CELL LYMPHOMA – THE MICHELIN STUDY  
Christiane S. Staxen, *Denmark*
- 413** COMPREHENSIVE ANALYSIS OF OTU RELATIONSHIPS USING TIME-SERIES DATA OF A MICROBIOME CONTAINING MANY ZEROS  
Rie Masukawa, *Japan*
- 419** AN OPTIMIZED FLOW CYTOMETRY SORTING-SEQUENCING PIPELINE TO GET INSIGHTS INTO THE FUNCTIONALITY AND ACTIVITY OF MICROBIAL ECOSYSTEMS  
Valerie Goethals, *Belgium*
- 424** RAPID IDENTIFICATION AND QUANTIFICATION OF PROBIOTICS WITH PAN-GENOME ANALYSIS-BASED REAL-TIME PCR  
Joon-gi Kwon, *South Korea*

- 494** ASSESSING THE GENERALIZATION OF AI MODELS FOR UNSEEN MICROBIOME STUDY DATA  
Andre Goncalves, *USA*
- 497** STRAINER2 QUANTITATIVE SEQUENCE-BASED STRAIN TRACKING OF VE707, A DEFINED BACTERIAL CONSORTIUM FOR MULTIDRUG-RESISTANT ORGANISM (MDRO) DECOLONIZATION  
Andrea Watson, *USA*
- 527** SHORT READS VS LONG READS FOR WHOLE GENOME SHOTGUN METAGENOMIC APPLICATION  
Elisabetta Notario, *Italy*
- 531** CROCODEEL : AUTOMATED DETECTION OF WELL-TO-WELL CONTAMINATION IN METAGENOMIC DATA  
Goulet Lindsay, *France*
- 532** GENOME-WIDE ASSOCIATION STUDY OF THE GUT MICROBIOME  
Raphaël Malak, *France*
- 543** EXPLORING SPATIAL HOST-MICROBIOME INTERACTIONS IN THE MURINE INTESTINE  
Ece Kartal, *Germany*
- 547** COMPREHENSIVE LARGE-SCALE SURVEY OF PLASMIDS IN THE AUSTRALIAN HUMAN GUT MICROBIOME  
Alex Chklovski, *Australia*
- 553** DEVELOPMENT OF A SINGLE-STAGE BIOREACTOR FOR THE STUDY OF THE GUT MICROBIAL ECOLOGY IN THE ASCENDING COLON  
David Felipe Garcia Mendez, *Australia*
- 554** A COMPUTATIONAL METATRANSCRIPTOMIC PIPELINE TO INVESTIGATE HOST-MICROBE INTERACTIONS IN LOW MICROBIAL BIOMASS SAMPLES  
Icaro Maia Santos de Castro, *Brazil*
- 564** MORE METAGENOMIC PROTEIN ASSIGNMENTS, FASTER, USING UNIREF AND CLUSTERED NR  
Anupam Gautam, *Germany*
- 567** DOO DOTS: A DRIED FECAL SPOT (DFS)-BASED BIOANALYTICAL PLATFORM FOR FECAL METABOLITE QUANTITATION  
Thomas Horvath, *USA*
- 592** TOWARDS A FULLY AUTOMATED LABORATORY FOR HIGHLY REPRODUCIBLE MICROBIOME RESEARCH  
Moreno Zolfo, *Japan*

- 635** PREDOMICSAPP: A WEB APPLICATION FOR INTERPRETABLE AND ACCURATE CLASSIFICATION OF OMICS COMMENSURABLE DATA  
Gaspar Roy, *France*
- 660** INTEGRATION OF MULTI-OMICS DATA IDENTIFIED NOVEL METABOLIC PATHWAY REGULATION IN CARDIOMETABOLIC DISEASES  
Kunkai Su, *China*
- 663** A NOVEL IN VITRO APPROACH TO IDENTIFY MICROBIAL AND CELLULAR SIGNATURES OF SHORT BOWEL SYNDROME (SBS)  
Ludovica Marinelli, *Italy*

**12:00 – 14:00**

**Poster Area 3**

Chair: Carla Fiorentini, *Italy*

**Topic 5: MANIPULATING THE GUT MICROBIOME TO IMPROVE HEALTH**

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Elise Tuerlinckx, *Belgium*
- 131** VEILLONELLA MHL0042 REDUCES THE SEVERITY OF EAE BY MODULATING THE CECUM MICROBIOME  
Joon-Young Park, *South Korea*
- 135** CARROT POLYSACCHARIDE RHAMNOGALACTURONAN-I AMELIORATES STRESS-INDUCED INTESTINAL PERMEABILITY IN AN HUMAN EX VIVO COLONIC MODEL  
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- 140** STRUCTURE-DEPENDENT DEGRADATION OF MILK OLIGOSACCHARIDES BY NEWLY ISOLATED INTESTINAL COMMENSAL BACTERIAL STRAINS FROM SUCKLING PIGLETS AND RABBITS  
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- 155** THE SIGNATURE OF HOST AGING IN PERSONALIZED GUT MICROBIOME FLUXOME DATA  
Ameneh Mehrjerd, *Iran*
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- 181** THE GUT MICROBIOME ACROSS THE COLORECTAL ADENOMA-CARCINOMA SEQUENCE: A STUDY NESTED IN THE TURIN-PIEDMONT COLORECTAL CANCER SCREENING PROGRAM  
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- 195** ENGINEERING GUT MICROBIOME STRAINS THAT STABLY ENGRAFT IN PATIENTS USING A BARCODED DNA ASSEMBLY STRATEGY  
Constantin Ruprecht, *Germany*
- 214** SYNBIOTIC WITH GAC FRUIT EXTRACT SUPPLEMENTATION AS A NOVEL STRATEGY TO REDUCE SERUM TMAO IN CKD: A RAT MODEL STUDY  
Thasinas Dissayabuttra, *Thailand*
- 224** INDICATION SPECIFIC PROBIOTICS FOR HUMAN HEALTH: WHICH STRAINS FOR CHRONIC WOUNDS AND WHICH FOR BETTER SLEEP  
Ingeborg Klymiuk, *Austria*
- 236** PROBIOTICS IN THE CORRECTION OF LIPID METABOLISM  
Vasilisa Dudurich, *Russia*
- 241** ASSOCIATION OF LEISURE TIME PHYSICAL ACTIVITY WITH GUT MICROBIOTA COMPOSITION IN EARLY ADULTHOOD  
Hanna-Mari Boelius, *Finland*
- 257** ENGRAFTMENT OF VIABLE MICROBIOTA AFTER FECAL TRANSPLANTATION DRIVES CLOSTRIDIODES DIFFICILE INHIBITION  
Jose Clemente, *USA*
- 273** THE ROLE OF VSL#3 IN THE TREATMENT OF FATIGUE AND OTHER SYMPTOMS IN LONG COVID-19 SYNDROME: A RANDOMIZED, DOUBLE-BLIND, PLACEBO-CONTROLLED PILOT STUDY (DELONG#3)  
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- 278** EFFICACY OF VAGINAL SEEDING IN RESTORING BACTERIAL LOAD AND VIABILITY IN A CLINICAL TRIAL OF C-SECTION NEWBORNS AT RISK OF DEVELOPING FOOD ALLERGIES  
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- 281** ANTIDEPRESSANTS AND THE COMPOSITION OF THE GASTROINTESTINAL MICROBIOME IN WOMEN LIVING WITH FIBROMYALGIA  
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- 303** DYNAMICS OF ESBL E. COLI INTRODUCTION AND DISPLACEMENT IN THE GUT: A CLINICAL STUDY  
Leamid Laganenka, *Swiss*
- 320** LACTIPLANTIBACILLUS DSM 33464 (SMARTGUARD™), A PROBIOTIC SUPPORTING THE GUT MICROBIOTA NATURAL PROCESS OF LIMITING DAILY LEAD ABSORPTION: RESULTS FROM A CLINICAL STUDY IN YOUNG WOMEN IN MEXICO  
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- 323** IDENTIFICATION OF EXOPOLYSACCHARIDE PRODUCED BY LACTICASEIBACILLUS RHAMNOSUS IR06 IN MILK-BASED MEDIA AND ITS PROTECTIVE EFFECTS ON UVB-IRRADIATION-INDUCED SKIN DAMAGE  
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- 332** FAECAL MICROBIOTA TRANSPLANTATION REDUCES ANTIMICROBIAL RESISTANCE: BY INDUCING BACTERIOPHAGE NETWORK REMODELLING AND ENTERIC PATHOGEN REDUCTION, ENHANCING INTESTINAL BARRIER FUNCTION AND IMMUNITY  
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- 350** TETRASTIGMA HEMSLEYANUM ALTERING THE FIRMICUTES TO BACTEROIDETES (F/B) RATIO OF GUT MICROBIOTA AND EFFECT ON INFLAMMATION OF THE LIVER AND GALLBLADDER  
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- 359** THE KEY OF POLYGONATUM ODORATUM TO ALLEVIATING THE SYMPTOMS OF TYPE 2 DIABETES: GUT MICROBIOTA  
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- 368** THE INFLUENCE OF GUT MICROBIOTA COMPOSITION ON DNA METHYLATION IN PEDIATRIC QATARI CHILDREN DIAGNOSED WITH TYPE 1 DIABETES MELLITUS  
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Chair: Maria Vasile, *Belgium*

**Topic 5: MANIPULATING THE GUT MICROBIOME TO IMPROVE HEALTH**

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- 634** LONG-TERM IMPACT: BACTERIOPHAGE-DRIVEN DNA INVERSIONS SHAPE BACTEROIDES FRAGILIS FUNCTIONALITY  
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- 646** SEX-SPECIFIC EFFECTS OF BOVINE COLOSTRUM ON MICROBIOTA-GUT-BRAIN AXIS INTERACTIONS IN ZONULIN TRANSGENIC AND WILD-TYPE MICE  
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**Topic 0: THE INTERACTION OF THE HUMAN HOLOBIONT WITH OTHER BIONTS**

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- 624** WATER MICROBIOME, RESISTOME, AND SOURCES OF FECAL CONTAMINATION IN A GUINEA WORM ENDEMIC COUNTRY  
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