Abou Haydar, Yasmina
Identifying the impact of bacterial extracellular vesicles in antibiotic stress response 46

Aftab, Nadia
Differential cultivability of isogenic Staphylococcus aureus sub-populations in different growth environments 47

Agapov, Aleksei
The impact of expression level on anti-phage defence system performance 48

Ahmed, Huda Presenter: Banzhaf, Manuel
High-throughput chemical genetic screening of 3,000 sequenced Salmonella enterica clinical isolates 49

Airoldi, Martina
E. coli resistome plasticity governs antibiotic resistance after short-term treatment with aminoglycoside 50

Allaart, Maximilienne
Lactate stereoisomers are metabolized differently in the gut microbiome 51

Alzheimer, Mona
Functional genomics of Campylobacter-host interactions in an intestinal tissue model reveals a small lipoprotein essential for flagellar assembly 52

Amend, Lena
Systematic assessment of commensal-pathogen cross-feeding in the mammalian intestine 53

Aubry, Mathilde
Intraspecies communication through peptide pheromones in salivarius streptococci 54

Ayub Ow Yong, Liyana
A recipient-based anti-conjugation factor that triggers an abortive mechanism by targeting the Type IV secretion system 55

Baland, Elisabeth
Carbohydrate degradation pathways in the human gut microbiome 56

Bancil, Yash
Using multicoloured spectral flow cytometry to dissect microbial heterogeneity and enrich for bacterial and fungal species at single-cell resolution 57

Barath, Sivaraj Presenter: Govindarajan, Sutharsan
Jumbo bacteriophages as models of ancient cellular organization 58

Barman, Niladri
Mycobacterium tuberculosis topoisomerase I is a global regulator of gene expression 59

Battista, Miriana
An experimental toolbox to elucidate the role of pneumococcal extracellular vesicles in host-pathogen interaction 60

Beamud, Beatriz Presenter: Yildiran, Eren
Breaking down barriers: determination of bacterial restricted sequences for efficient DNA delivery 61

Bellinzona, Greta
FOGS: a novel time-aware index of bacterial genome plasticity to predict emerging high-risk clones 62

Bellinzona, Greta
Harnessing structural predictions to understand host-symbiont dynamics: the case of Midichloria mitochondrii 63

Benešová, Anna
Toxic activity of colicin Js, a colicin unique by its organisation and structure 64

Benz, Fabienne
Molecular mechanisms and ecological role of type IV-A3 CRISPR-Cas in plasmid competition 65

Berthold, Dorothée
Mucin degradation and spatial organization in a synthetic gut bacterial community 66

Beste, Tristan
Spatially resolved single-molecule imaging in thick tissues: establishing cycleHCR to study infection processes 67

Birk, Marlene
An atlas of human gut microbiota secreted effector proteins 68

Birkholz, Nils
Phage anti-CRISPR control by a DNA- and RNA-binding helix–turn–helix protein 69

Blaya-Martinez, Lorena
A double-edged sword: how antibiotic treatment may promote the horizontal spread of antibiotic resistance genes in the gut 70

Bobonis, Jacob
Receptor-normalized generalist-specialist phage co-infections in marine Vibrio 71

Bognar, Bence
Advancing antibiotic combination discovery through machine learning and analytical modeling 72

Borrelli, Carolina
Polymyxin B lethality requires energy-dependent outer membrane disruption 73

Bougit, Emelyne
Unraveling depletion mechanism of the virulence gene pla in epidemic strains of Yersinia pestis. 74

Bougit, Emelyne
Use of circulating host miRNAs as biomarkers for plague diagnosis. 75

Brodmann, Maj
MtvS interacts with RNA polymerase to regulate the Francisella type V-A CRISPR-Cas system 76

Bruchhardt, Thea
A primary cell-based model reveals novel insights into Campylobacter jejuni infection of the human intestine 77

Bryant, Jack
Investigating the role of m48 metalloproteases in Escherichia coli cell envelope biogenesis 78

Brzobohatá, Hana
LEGO-Lipophosphonoxins: Tolerance, adaptation and physiological response to membrane-targeted antibiotics treatment 79

Bulvas, Ondrej
Dynamic allosteric regulation of mycobacterial IMPDH: beyond simple feedback mechanism 80

Burckhardt, Juan
Engineering gut bacteria depleted by industrialization to survive malabsorption 81

Burgaya, Judit Presenter: Galardini, Marco
Using large-scale genome sequencing of clinical isolates to identify transmission clusters, in-hospital evolution, and predict antimicrobial resistance 82

Burkhardt, Nicolas
Reduction of (p)ppGpp levels in experimentally evolved Ralstonia pseudosolanacearum promotes adaptation to both plant xylem and legume symbiosis 83

Burrichter, Anna
Understanding context dependency of microbial metabolism and ecology: an integrative approach using proteomic and metabolic modelling 84

Carcassonne, Prunelle
Identification of a novel key actor in motility regulation during Myxococcus xanthus cell division 85

Castelli, Michele
Re-examining intracellular symbioses in unicellular eukaryotes, do bacteria manipulate their hosts? 86

Casters, Yorben
Unravelling phage-host co-existence strategies 87

Cecchino, Laura
Enhancing resolution in microbial imaging and RNA detection: integrating expansion microscopy with multiplexed FISH. 88

Chiti, Elena
Unraveling the molecular mechanisms of Helicobacter pylori transition to the coccoid state using SAMMY-Seq technology 89

Chmielowska, Cora
Phages under pressure – how SPBeta-like bacteriophages are regulated by bacterial SOS response and phage-communication 90

Codemo, Loïc
Integration of Tn4430 in vivo into ColE1 plasmids is driven by recognition of a consensus sequence 91

Coluccia, Marco
Under pressure: the Rcs system supports Shigella flexneri survival in and out of host cells 92

Cornejo, Fabian
Ribosome degradation during stress in Bacillus subtilis 93

Cosi, Valentina
An RNA route to establishing the cancer-associated microbe Fusobacterium nucleatum as a model organism 94

Coullin, Killian
Comparative analyses of the oxidative stress response between saprophytic and pathogenic Leptospira species enlightens its evolution within the Leptospira genus 95

Couture, Laurence
High-throughput tools to probe Salmonella-gut microbiota dynamics 96

Croci, Carlo
Comparative genomics of UBA3830, a novel lineage of animal-gut dwelling Alphaproteobacteria 97

Daveri, Andrea
Insights in the biology of the integrative conjugative element ICEclc 98

De Bernardini, Nicola
The hidden influence of phage-host interactions on carbon dioxide methanation 99

De Vrieze, Lucas
Clostridium XIVa: friends with benefits that were late to the gut party 100

Debache, Auriane
Development of an ex vivo model to study the intratumoral microbiota 101

Debande, Lorine
SPATEs promote the survival of Shigella to the plasma complement system upon local hemorrhage and bacteremia 102

Debatisse, Kevin
Key factors governing the integron functioning and integron evolution trajectories 103

Dehaene, Riet
Evaluation of virulence in a collection of Pseudomonas aeruginosa strains 104

Dereinne, Denis
Targeting resistance mechanisms to improve class II bacteriocin efficacy against staphylococcus aureus 105

Desmet, Martin
Towards the conversion of a DD-peptidase into a beta-lactamase by directed evolution. 106

Dessartine, Margot
Microcolony formation: a shield against diverse bacterial competition strategies 107

Dessertine, Maxence
Contribution of cuep to salmonella enterica adaptation to copper/oxidative dual stress 108

Di Martino, Maria Letizia
A scalable gut epithelial organoid model reveals the genome-wide colonization landscape of a human-adapted pathogen 109

Dorado-Morales, Pedro
Conjugative-killer plasmids, a novel antimicrobial alternative 110

dos Anjos Borges, Luiz Gustavo
MetaGAM reveals spatial landscape of bacterial associations in microscale 111

Dubuisson, Lison
Deciphering the CovM-CovRS system: a novel regulatory system controlling competence in Streptococcus salivarius 112

Ehrmann, Anja
Competition and coexistence of virulent phages of E. coli in resource-limited environments 113

Emam, Elhassan Presenter: Fathi Emam, Elhassan Ali
Mycobacterial MutT1 mediated dephosphorylation of the sensor kinases reveals a new link in the regulation of the two-component signaling in bacteria 114

Fan, Michelle
Is our microbiome friend or foe? understanding the effect of antibiotics on resistant pathogens in the gut microbiome. 115

Farano, Anna Carla
The impact of bacteriophages on gut microbial communities 116

Feng, Xueyin Presenter: Gao, Beile
The architecture, assembly, and evolution of a complex flagellar motor 117

Fideli, Vincent
Engineering bacterial traps to understand and inspire next-generation antibiotics 118

Fruchard, Louna
Beyond RNA modification: a novel role for tRNA modifying enzyme in oxidative stress response and metabolism 119

Gaviria Cantin, Tania
A CRISPRi-based genetic tool for targeted gene silencing in Lacticaseibacillus rhamnosus GG 120

Geromiller, Juliana
Best enemies: how an antibiotic can save bacteria from being killed by phages 121

Gerovac, Milan
Jumbo phages control stress response via ribosome targeting 122

Ghandour, Rabea
Domesticating a new chromosome and rewiring RNA networks 123

Gialama, Dimitra
Discovery of novel antimicrobials: inhibitors of microbial functional amyloid aggregation linked to biofilm formation 124

Gil-Campillo, Celia Presenter: Domínguez San Pedro, Asier
Development of a switchable CRISPR interference platform for Haemophilus influenzae reveals growth requirements at the genome scale 125

Gillard, Justine
Tracking the transfer of native integrative conjugative elements to understand how antibiotic resistance spreads in the human gut microbiota 126

Giri, Samir
Impact of non-antibiotic treatment on antimicrobial resistance of human gut bacteria 127

Goncalves, Océane Presenter: Côté, Jean-Philippe
Trikafta prevents the emergence of high-biofilm forming small colony variants of Pseudomonas aeruginosa in a cystic fibrosis-like environment 128

Gottstein, Willi Presenter: Herrera-Domínguez, Lucía

Towards a self-running lab to characterize bacterial communities for food applications 129

Gourle, Hadrien Presenter: Verma, Jyoti
Resolving microbial genomes in complex communities at the single-cell level 130

Cancelled 131

Guedes, Maria Presenter: Aguilar, Carmen
FimH drives E. coli invasion of luminal prostate cells by binding to the prostate-specific membrane receptor PPAP 132

Guzzi, Noa
Study of the replication of an emerging megaplasmid in the pathogen Vibrio cholerae 133

Haavisto, Vilhelmiina
Development of a minimal chitin-degrading bacterial community 134

He, Yuzhang Presenter: Liu, Xue
Identification and mechanistic analysis of a new antimicrobial using multi-species CRISPRi-seq 135

Heiniger, Benjamin Presenter: Ahrens, Christian
Overcoming notorious challenges in prokaryotic genome annotation: identifying missed small proteins with proteogenomics and Ribo-seq and consolidating genome annotations 136

Hemphill, Jamia
Investigating antimicrobial activity in commensal bacterial communities in the human gastrointestinal microbiome. 137

Hernandez Ortego, Carlos
Gut bacteria degrade the danger signal extracellular ATP to hypoxanthine 138

Hernández Tamayo, Rogelio
Characterization of the Caulobacter crescentus DinG helicase 139

Herrou, Camille
Molecular basis of the activation of type IV filament machineries in bacteria 140

Hirmondó Váradiné, Rita
Prolonged stress, lasting changes: Adaptation in mycobacteria without mutations 141

Hjørungnes, Martinus
The role of two-partner secretion systems in the nitrogen fixing legume symbiont Paraburkholderia phymatum 142

Hogan, Andrew
A high-throughput platform to quantify bacterial defense against protist predation 143

Hong, Alice
Engineering the probiotic E. coli Nissle 1917 for assessment of osmotic stress in the gut 144

Hunya, Ágoston
Virulence gene content and ecological niche shape the spread of antibiotic resistance in Escherichia coli 145

Ignatov, Dmitry
Novel RNA-binding protein YebC enhances translation of proline-rich motifs in bacteria 146

Imdad, Saba
PerfringicinS, a novel circular bacteriocin produced by Clostridium perfringens with potent antimicrobial activity against Methicillin-resistant Staphylococcus aureus 147

Iwanska, Olga
Ribosomes translocation into the spore of Bacillus subtilis is highly organised and requires peptidoglycan rearrangements 148

Jagodnik, Jonathan Presenter: Guillier, Maude
30S-seq redefines the bacterial Ribosome Binding Site 149

Jancheva, Magdalena
A phage-selective trigger hints at an SOS-independent mechanism of prophage induction by oxidative stress 150

Janet-Maitre, Manon
Intracellular Acinetobacter baumannii serves as a reservoir for de novo lung infection through a ‘persist and resist’ strategy in macrophages 151

Janssen, Axel
Core essentialome dynamics in Streptococcus pneumoniae under antibiotic-induced stress 152

Jensen, Catharina
A tale of two fates: the duel for survival between Acinetobacter baumannii and Staphylococcus aureus 153

Jia, Xiu
When the river meets the sea: bacterial community dynamics after coalescence 154

Jones, Matthew
Understanding enterobacteria tolerance to an unconventional neutrophil-generated oxidant 155

Kaderabkova, Nikol
The natural reservoirs of Mobile Colistin Resistance proteins 156

Karneyeva, Karyna
FKy-1 phage: the first model for deciphering megaphage biology 157

Keck, Camille
Structural insights into a novel metabolically induced mycobacterium tuberculosis sub-cellular compartment by cryo-electron tomography 158

Khamas, Amanda Batoul
Outer membrane protein A and beyond: unraveling the molecular mechanisms of Acinetobacter baumannii virulence 159

Kim, Janie
RNA modifications in host-microbe dynamics: Vibrio fischeri-bobtail squid and MS2 phage-E. coli 160

Kim, Lili
The Phenotypic Landscape of Bacillus subtilis 161

Kim, Nayoung
Microbial cooperation between enterotoxigenic Bacteroides fragilis and pks$^+$ Escherichia coli reshapes epithelial architecture to promote colorectal carcinogenesis 162

Kiribayeva, Assel
Disrupting bacterial adhesion and biofilm formation with xylanase from Bacillus sonorensis 163

Koberská, Markéta
ABCF protein-mediated resistance shapes bacterial responses to antibiotics based on their type and concentration 164

Kok, Weine
Caveats and considerations for constructing bacterial transposon mutant libraries 165

Komlosi, Daniel Presenter: Shanks, Robert
Stick around or swim away? Identification of new regulators of the acute to chronic lifestyle transition by Pseudomonas aeruginosa 166

Koppová, Kamila
Inhibitor-specific physiological responses in solventogenic clostridia: ferulic acid, coumaric acid, and furfural effects 167

Koziy, Yulianna (Julie)
Visualising bacteriocins on living bacterial cells 168

Krähenbühl Amstalden, Martin
Transcriptional chemical genomics approach for compound-mediated regulation of virulence and antibiotic resistance in Salmonella Typhimurium 169

Krammer, Karina
Drivers and constraints of prophage persistence in natural communities 170

Kscheschinski, Bjoern
Inferring single-cell dynamics to learn from biological fluctuations 171

Kuang, Xu
Bacteriophages mobilise bacterial defence systems via lateral transduction 172

Kurowska, Anna
Evolution of the bacterial cell envelope: a role of teichoic acids in the diderm to monoderm transition? 173

Lallement, Claire Presenter: Michaux, Charlotte
Dual control of β-lactam resistance by two-component systems in Enterobacter cloacae complex 174

Lan, Freeman
Ultrahigh-throughput single-cell targeted DNA sequencing of bacterial colonies reveal highly coordinated quasi-clonal populations 175

Lanster, David
Engineering bacterial competition to control microbiomes 176

Lázár, Viktória
Exploiting the self-Induced genotoxicity of carcinogenic pathogens 177

Li Volsi, Mattia Nicolo
Functional and structural study of three sRNAs controlled by NikR and Fur in Helicobacter pylori 178

Lim, Sylvester
Ecological principles of colonisation resistance against the key pathogen Shigella sonnei 179

Lin, Jordan
In vitro genome synthesis and propagation of the prototypic crAssphage Carjivirus communis 180

Liu, Catherine
Sigma factor-associated TnpB proteins engage in RNA-guided DNA-targeting activity 181

Lopatina, Anna
Interpretable machine learning reveals a diverse arsenal of anti-defenses in bacterial viruses 182

López Rodríguez, Elena
Harnessing DGRs for nanobody evolution and optimization 183

Lourenço, Marta
Escherichia coli strains coevolution under competent or compromised immune system 184

Machacek, Stanislav
Evolutionary and environmental insights into termite pheromone biosynthesis: a structural and functional approach 185

Madhavan, Vishnu Narayanan
Salted signaling with chvig in caulobacter: who is the pepper? 186

Maire, Amandine
In Vivo CRISPRi screens reveal genetic strategies of E. coli adaptation in the gut 187

Mansour, Moïse
Streptococcus pyogenes prophage-encoded toxin-antitoxin system as a phage defence mechanism 188

Mansour, Nour
Intracellular persistence and antibiotic recalcitrance of Enterobacter cloacae across host niches 189

Marconi, Roberta
A cultivation-based approach to explore the association between coffee intake and Lawsonibacter asaccharolyticus 190

Márquez Blesa, Ana Rosa
Single-colony RNA-sequencing: a high-throughput platform for bacterial microcolony transcriptomics and microbial interactions 191

Martín Correa, María Teresa
New inhibitor of TEM-1 beta-lactamase 192

Maslov, Ivan
Stress-induced alterations in localization and mobility of functional membrane microdomains of E. coli 193

Mathis de Fromont, Jade
sRNA regulation by two-component systems in a laboratory Escherichia coli strain and a clinical isolate 194

McCallum, Giselle
Expanding the Bacteroides synthetic biology toolkit to develop an in vivo intestinal malabsorption biosensor. 195

Meng, Fanfan
Bacteria senses plant hormone salicylic acid by a novel allosteric mechanism 196

Mulkern, Adam Presenter: Galardini, Marco
A screen for resistance to sequence-based antimicrobials and the development of tools for their design 197

Mullapudi, Edukondalu Presenter: Wilmanns, Matthias
Deciphering a combinatorial jigsaw puzzle of Mycobacterial Acyl-CoA Carboxylases 198

Müller, Katharina
Unraveling the impact of protein synthesis inhibitors on bacteroides uniformis 199

Navarro Cantero, Susanna Presenter: Torrent, Marc
Precision antibiotics: targeting protein-protein interactions to combat gram-negative pathogens 200

Nedjar, Hosni
Battle for iron between Crohn's disease associated Escherichia coli and macrophages 201

Nelson, Nora
Dissecting the chemical signals that determine dietary xenobiotic metabolism in the gut microbiome 202

Ngo, Hoan Presenter: Yeom, Jinki
Priming of a signal transduction system confers full activation of virulence upon Acinetobacter baumannii 203

Niemi, Meeri
Characterisation of a novel jumbophage collection 204

Ogunleye, Adewale
High-throughput profiling of drug combinations in bacteria reveals driving principles of synergy and antagonism beyond growth inhibition 205

Olina, Anna
Phage vs. Phage: How prophages equip bacteria to resist phage infections 206

Ostermayer, Jasmin
Tus/ter determines replication direction of chromosome 2 in Pseudoalteromonas haloplanktis 207

Pak, Jumi
Increased membrane rigidity sufficient to promote antibiotic persistence in pathogenic bacteria 208

Parab, Lavisha
Prophage maintenance can have higher costs than phage resistance via cell surface modifications despite granting superinfection exclusion 209

Parkhill, Susannah

Using CRISPR interference to define evolutionary drivers and constraints in Klebsiella pneumoniae. 210

Paul, Souparno

Evaluation of Neuroprotective function of GABAergic psychobiotic strains 211

Pérez, Lucía

Functional proteomics in representative species of the human gut microbiome 212

Peruzzi, Alberto

Emptying the tank: E. coli shifts carbon metabolism into energetic overdrive to sustain growth despite antibiotics 213

Philip, Jamiema Sara

Unveiling the diversity and evolutionary dynamics of bacterial flagellar motors through genomic analysis 214

Pigeolet, Louise

Regulation network connecting cell wall integrity and competence in salivarius streptococci 215

Plum, Miro Thorsten Wilhelm

From friend to foe: how mucosal surfaces influence Klebsiella pneumoniae pathogenicity in the gut and lung 216

Pugh, Hannah

Comprehensively defining determinants of mutation rate and spectrum 217

Putz, Elizabeth H. M.

Quorum sensing control of prophage induction in Vibrio anguillarum 218

Reyes-Matte, Octavio

Surface-to-volume ratio is a species-specific trait of rod-shaped Bacillaceae 219

Rico, Juan
Expanding genetic systems programmability through host-mediated modulation of input signal dynamics 220

Rochette, Paul
Harnessing diversity-generating retroelements for directed evolution of Cas9 221

Rodriguez, Valentin
Unravelling the mechanism by which the gut commensal Escherichia coli ED1a kills neighbouring bacteria 222

Rouam el Khatab, Oussama
Mapping the interaction landscape of multi-member nasal microbiota communities 223

Roy, Gauthier
Essential gene targeting in Staphylococcus aureus by antisense oligomers 224

Said Muñoz, Natalia Presenter: Herrera Paredes, Sur
A synthetic community strategy to disentangle biotic and abiotic effects on microbial assembly 225

Sarigöz, Oytun
Revealing the metatranscriptome of polymicrobial biofilm infections in Humans 226

Schlegel, Susan
Internal expression of CDI-associated toxin-immunity pairs in Escherichia coli 227

Schorr, Eva
A phenotypic landscape of key Bacteroides species 228

Schwarzenbach, Anna
Evolving pathogen-killing bacteria as live biotherapeutics 229

Serrato-Salas, Javier Presenter: Gendrin, Mathilde
Using transient colonization to understand mosquito-bacteria interactions 230

Shreekar, Shryli Kedambadi
Surviving together: metabolic dependencies in microbial robustness 231

Sichert, Andreas
Synergistic degradation of algal polysaccharides by complementary metabolisms in microbiomes 232

Sin, Daniel Zhen Ye
Exploring arbitrium-mediated crosstalk between bacteriophages 233

Spatharas, Panagiotis
Dissecting the activation mechanism of the Retron-Sen2 anti-phage defence system 234

Strunov, Anton
Deciphering catabolic metabolic heterogeneity in comammox bacteria with spatial transcriptomics 235

Stubbusch, Astrid Presenter: Schubert, Olga
Antagonism as a foraging strategy in microbial communities 236

Stuermer, Vanessa
Microfluidic platform designs for mapping foraging strategies of protistan predators in soil-like environments 237

Sudarsan, Suresh
Transcriptional control of high cell density phenotypes 238

Sunder, Varun
Genetic determinants of pseudomonas aeruginosa internalization into the human airway epithelium 239

Sünderhauf, David
CRISPR-Cas is beneficial in plasmid competition but limited by competitor toxin-antitoxin activity when horizontally transferred. 240

Tan, Wee Boon Presenter: Chng, Shu-Sin
Primary role of the Tol-Pal complex in bacterial outer membrane lipid homeostasis 241

Tcidulko, Aglaia
Upper respiratory tract microbiome analysis of okhotsk sea bowhead whales (Balaena mysticetus) 242

Tejada Arranz, Alejandro
Phenotypic heterogeneity of Pseudomonas aeruginosa in infection-like conditions 243

Thirumal Muthu, Kannan
Utilization of lignin-derived aromatic compounds by Bacillus sp., 244

Tietze, Alexandra
Rethinking infection treatment: applying systems biology for drug combinations and host interactions 245

Tomanek, Isabella
Why is the human gut microbiome so stable? 246

Tomasek, Kathrin
OM-89 suppresses recurrent urinary tract infections by modulating the antimicrobial activity of bladder epithelial cells 247

Tsai, Chia-En
The evolutionary tradeoff between phage resistance and interbacterial competition in Salmonella 248

Vaneynde, Dries
Studying intracellular protein aggregate dynamics in escherichia coli 249

Vanhemmeseel, Chloé
Engineering a synthetic ComR biosensor: unlocking new frontiers in bacterial communication 250

Vieira, Filipe
Harnessing the Arabidopsis phytomicrobiome reveals a novel protein inhibiting Xylella fastidiosa 251

Vilhena, Cláudia
Spatial and temporal dynamics of pneumococcal cell wall under host immune response revealed by super-resolution microscopy 252

Villa, Romain
Adaptation and microbial interactions of the gut archaeon Methanobrevibacter smithii 253

Vollenweider, Vera
Pyoverdines: novel antimicrobial compounds against human bacterial pathogens 254

Walch, Philipp
Systems Approaches in Co-Infections 255

Wang, Xiaohan
SUMAT: enabling high-throughput metagenomics for deep-sea microbiology 256

Wielert, Isabelle
Pilin variation affects the gonococcal bacterial lifestyle, leading to differential gene expression involved antibiotic tolerance 257

Xu, Wenhao
Specificities of chemosensory receptors in the human gut microbiota 258

Yang, Alessio
Phages carry multiple triggers and blockers against the same bacterial defense system 259

Yang, Weiwei Presenter: Ettwiller, Laurence
A Genome-Phenomes Association Framework (MetaGPA) for Functional Discovery directly on intact environmental Microbiomes 260

Yuan, Zhi-Hui
Killing process and signal recognition of Cryptococcus neoformans through bacterial outer membrane vesicles 261

Zanon, Andrea
Synthetic soil microcosms for real-time imaging of microbial predator-prey dynamics 262

Zarrella, Tiffany
Interspecies surfactants serve as public goods enabling surface motility in Pseudomonas aeruginosa 263

Zhang, Yu
CRISPRi-seq identifies fprB as a synergistic target to enhance gallium therapy against Pseudomonas aeruginosa 264

Zhang, Zheren
Combining synthetic biology and evolution to degrade environmental pollutants 265

Zhou, Ge
High-throughput machine learning-aided prediction and characterization of klebsiella pneumoniae growth features 266