

Ainelo, Andres		
DarB modulates the (p)ppGpp synthetase activity of the ribosomal factor Rel by promoting ATP incorporation to the SYNTH domain		55
Airoldi, Martina		
Tackling the mechanism of species-specific drug combinations in bacteria		56
Aitmanaite, Lina		
The identification of full length CRISPR-Cas systems in metagenomic samples		57
Akduman, Nermin		
Microbiome modulators for environmental enteric dysfunction		58
Alqurainy, Nasser	Presenter: Fillol-Salom, Alfred	
A widespread family of phage-inducible chromosomal islands only steals bacteriophage tails to spread in nature		59
Alves, Ângela		
PurA, an adenylosuccinate synthetase required for <i>Listeria monocytogenes</i> intracellular lifecycle		60
Amicone, Massimo		
Evolutionary rescue theory to predict the emergence of resistance within microbial communities		61
Amoura, Ariane	Presenter: El Meouche, Imane	
Following the heterogeneity in antibiotic response and growth in a UTI model of infection		62
Anderson, Brent		
Protease processing of secreted proteins in the human gut commensal <i>Bacteroides</i>		63
Andrieu, Camille	Presenter: Ezraty, Benjamin	
<i>Salmonella Typhimurium</i> uses the Cpx stress response to detect N-chlorotaurine and promote the repair of oxidized proteins		64

Anguita, Raúl	
Exploring the use of human RNases to enhance antimicrobial peptides' action	65
Arbulu Ruiz, Sara	
Unravelling the role of bacteriocins in shaping oral biofilms	66
Arnoldini, Markus	
Quantifying the fermentation product harvest from the human gut microbiota	67
Aubert, Corinne	
A diverged transcriptional network for usage of two Fe-S cluster biogenesis machineries in the delta-proteobacterium Myxococcus Xanthus	68
Augenstreich, Jacques	Presenter: Briken, Volker
Spatio-temporal analysis of LC3 association to Mycobacterium tuberculosis phagosomes in human macrophages	69
Bager Skjerning, Ragnhild	
Expression of type II toxin-antitoxin systems is a trade-off between transcriptional initiation efficiency and promoter affinity of the TA complex	70
Baharoglu, Zeynep	
tRNA queuosine modification reprograms translation in response to antibiotics in Vibrio cholerae	71
Balgová, Tamara	
Rifampicin: stops or stimulates transcription?	72
Banta, Amy	
CRISPR tools for functional genomics in diverse bacteria	73
Barbotin, Aurélien	
Direct measurement of membrane fluidity in Bacillus subtilis using TIR-FCS	74
Basile, Arianna	
Extensive depiction of microbial metabolism improves modelling of gut communities	75

Bechon, Nathalie	
A new AVAST defense system recognizes an anti-AVAST phage protein to activate defense	76
Beckham, Kate SH	
Insights into the structural diversity of mycobacterial type VII secretion systems and mechanisms of protein translocation	77
Bernard, Célia	
Altered amino acid metabolism promotes drug tolerance through the transcriptional regulator WhiB7 in Mycobacterium abscessus	78
Besançon, Hervé	
Tailored liposomal nanotraps for the treatment of Streptococcal infections	79
Beste, Tristan	
Implementing thick-section spatial transcriptomics to investigate host-pathogen interactions	80
Binsfeld, Christoph	
Systematic characterization of drug transport regulation in Escherichia coli	81
Biswa, Bhim Bahadur	
Changes in the gut microbiome associated with domestication of mice	82
Bittremieux, Diana	
Discovery of mechanisms of interactions between bacteria and bacteriophages in the human gut microbiome	83
Boggon, Cameron	
Engineering structured polymicrobial communities using bio-sCAPA	84
Bollen, Celien	
Persister and viable but nonculturable cells are characterized by proteome-wide aggregation	85

Borah, Nabajyoti	
Molecular insights of RNA polymerase recycling by mycobacterial HeID	86
Borbora, Salik Miskat	
Altered host signaling regulates oxidative stress levels in macrophages during mycobacterial infection	87
Bornet, Elise	
Resolving morphotype-specific gene expression in Bacteroides thetaiotaomicron by single-bacterium RNA-seq	88
Brejndal, Kamilla	Presenter: Hansen, Nikolaj
A TA-associated cell envelope regulatory factor in Caulobacter	89
Brenzinger, Susanne	
The abortive infection system CBASS controls resistance and enables killing by antifolate antibiotics in Vibrio cholerae	90
Brezovska, Barbora	
MoaB2 binds to σA in Mycobacterium smegmatis and modulates its availability and stability	91
Bryant, Jack	
Dissection of Bam complex accessory subunit function in Escherichia coli	92
Brzobohatá, Hana	
LEGO-lipophosphonoxins: Mechanism of action, kinetics and interactions with Gram positive and Gram negative bacteria	93
Byers, Sally	
A group of temperate bacteriophages equip their Klebsiella hosts with potent interbacterial weapons	94
Cacace, Elisabetta	
Nitrogen cycling in the human gut microbiome across ages of life	95
Cappio Barazzone, Elisa	
Microbiota influence on Urea Cycle Disorders	96

Chanin, Rachael	Presenter: Gill, Matthew	
Microbial intragenic DNA inversions expand coding potential		97
Charbonnier, Mathilde		
Role of regulatory RNAs in the adaptation of <i>Staphylococcus aureus</i> to metal-dependent immune strategies		98
Chen, Zhuoyan		
Visualising ESX-4 membrane complex structure using single-particle cryo-EM		99
Chou, Todd		
A segmentation clock patterns cellular differentiation in a bacterial biofilm		100
Chowdhury, Aysha		
Exploiting selfish genetic elements for the discovery of new antibiotics and resistance genes		101
Condinho, Manuel		
The importance of PNPase for biofilm formation		102
Cooper, Kendal		
The cytosolic chemoreceptor McpA is part of the invasion regulon of <i>Salmonella</i> and contributes to colonization in the inflamed gut		103
Cornejo, Fabian		
Role of RNA maturation in the stress response of <i>Bacillus subtilis</i>		104
Craig, Sophie		
Discovery and characterisation of novel bacterial defence systems		105
Csorgo, Balint		
Type I CRISPR Cascade-Cas3 deletions uncover anti-phage and pro-phage factors		106
Cury, Jean		
Conservation of antiviral systems across domains of life reveals novel immune mechanisms in humans		107

Damgaard, Andreas		
Bacteriophage resistance mechanisms in clinical isolates of <i>P. aeruginosa</i>		108
Dash, Swagatika		
Does phenotypic heterogeneity in amino acid biosynthesis provide ecological benefit to soil bacteria?		109
Deaconescu, Alexandra		
Structural Basis for Bidirectional Regulation of the RpoS General Stress Response via the RssB Protein		110
Deghelt, Michael		
The outer membrane and peptidoglycan layer form a single mechanical device balancing turgor		111
Dénéreaz, Julien		
Mapping the pneumococcal genome-wide interaction network with dual CRISPRi-seq		112
Dewachter, Liselot		
The essential GTPase ObgE regulates LPS synthesis in <i>Escherichia coli</i> through a direct interaction with LpxA		113
Ding, Lili		
A bacterial receptor DIIS senses the ROS to control the lifestyle transition of <i>Xanthomonas campestris</i>		114
Do, Hackwon	Presenter: Kumaraswami, Muthiah	
A human probiotic promotes pathogen colonization by signal induction and protease production		115
Doherty, Hannah		
ChemGAPP: A package for chemical genomics analysis and phenotypic profiling		116
Dugic, Milica		
LEGO-Lipophosphonoxins: Mode of action and pore selectivity on different target membranes		117

Dupuy, Emile	
A molecular device for the redox quality control of GroEL/ES substrates	118
El Mouali, Youssef	
Prevotella copri RNA landscape in the mouse gut drives identification of an abundant regulatory sRNA in vivo	119
Figueiredo, Sandra	
Beta-oxidation: a well-kept secret of cyanobacteria	120
Focant, Charline	
Study of the biogenesis of the VirB type IV secretion system in Brucella abortus	121
Fossati, Andrea	
Next-generation interaction proteomics for quantitative Jumbophage-bacteria interaction mapping	122
Frund, Mélissa	
Investigation of the Min system in the division process of Acinetobacter baumannii	123
Fu, Beverly	
Discovery of gut microbial enzymes that produce the malodorous skatole	124
Garb, Jeremy	
Multiple phage resistance systems inhibit infection via SIR2-dependent NAD⁺ depletion	125
Garcia Pino, Abel	
Unravelling structure and dynamics of the ppGpp hydrolase SpoT during the stringent response	126
Georjon, Héloïse	
Genomic characterization of the antiviral arsenal of Actinobacteria	127
Geslain, Sandra	
Divergence of the intrinsically disordered RNase E C-terminal extension and implications for RNA degradosome composition	128

Ghandour, Rabea	
RNA-mediated regulation of <i>Vibrio cholerae</i> flagellar expression hierarchy	129
Gilep, Konstantin	
The diversity of VapD toxin-antitoxin systems	130
Giovannercole, Fabio	
The TAM complex of Bacteroidetes: a fertile ground for novel biology	131
Gitari, Joseph	
Breaking the unbreakable: using mycobacteriophage to lyse <i>Mycobacterium tuberculosis</i>	132
Goemans, Camille	Presenter: Giri, Samir
Impact of non-antibiotic treatment on antimicrobial resistance of human gut bacteria	133
Goemans, Camille	
The impact of protein synthesis inhibitors on gut microbes	134
Goncalves, Océane	
High-throughput genetic analysis finds new genes involved in twitching motility of <i>Pseudomonas aeruginosa</i>	135
Gonzalez Espinoza, Gabriela	
Crosstalk between an iron-responsive sRNA and a manganese-sensing riboswitch in <i>Staphylococcus aureus</i>	136
Goodall, Emily	
Coupling transposon insertion sequencing with reporter systems for the identification of protein coding sequences	137
Goradia, Nishit	Presenter: Wilmanns, Matthias
Structural and functional characterization of a cidal mycobacterial toxin-bacteriophage antitoxin mimic complex	138
Greter, Giorgia	
Acute and specific induction of gut-microbial metabolism disrupts host circadian rhythm	139

Gucwa, Katarzyna		
Regulatory protein of a restriction-modification system interferes with <i>E. coli</i> global regulatory networks, and reveals an unexpected link between a cryptic <i>Rac</i> prophage excision and lipopolysaccharide biosynthesis defects		140
Guedes, Maria	Presenter: Aguilar, Carmen	
UPEC forms intracellular bacterial communities and persister-like cells in prostate organoid cells dependent on FimH adhesin		141
Gürth, Clara-Marie		
Imaging microbiological samples down to molecular scale with MINFLUX nanoscopy		142
Heiniger, Benjamin	Presenter: Ahrens, Christian	
Proteogenomics identifies conserved and lineage-specific novel small proteins in clinical reference strains of <i>Mycobacterium tuberculosis</i>		143
Hemsley, Claudia	Presenter: Bergkessel, Megan	
Regulation of protein biosynthesis during growth arrest in <i>Pseudomonas aeruginosa</i>		144
Hennes, Marc	Presenter: Maier, Berenike	
Collective polarization dynamics in bacterial colonies signify the occurrence of distinct subpopulations		145
Hira, Jonathan	Presenter: Lentz, Christian	
Sorting out their differences – High-throughput phenotypic profiling of single cells and subpopulations within isogenic bacterial pathogen cell populations		146
Hochhauser, Dina		
The defense island repertoire of the <i>Escherichia coli</i> pan-genome		147
Hogan, Andrew		
Profiling cell envelope-antibiotic interactions reveals vulnerabilities to β-lactams in a multidrug-resistant bacterium		148
Hossain, Saika	Presenter: Kehl-Fie, Thomas	
The broad-spectrum metallophore staphylopine sensitizes <i>Staphylococcus aureus</i> to copper poisoning during infection		149

Huang, Han-Yi		
Investigating <i>Pseudomonas aeruginosa</i> physiological adaptation to live on surfaces		150
Husáková, Markéta		
Antimicrobial and photoantimicrobial activity of <i>Monascus</i> extracts		151
Iwanska, Olga		
The translatome of sporulating <i>Bacillus subtilis</i>		152
Iwanska, Olga	Presenter: Kovalenko, Mariia	
Tracking of cell poles during asymmetric cell division of sporulating <i>Bacillus subtilis</i> cells using fluorescent D-amino acid		153
Izert, Matylida		
Targeted Protein Degradation of <i>Escherichia coli</i> Proteins Using Clp-Interacting Peptidic Protein Erasers (CLIPPERS)		154
Janssen, Axel		
Identifying the importance of GalU in competence and transformation in <i>Streptococcus pneumoniae</i> through a CRISPRi-Seq based screening method		155
Jirat Matejckova, Jitka		
RIP-seq in bacteria – A method for identification of RNAs interacting with the bacterial transcription machinery		156
Kaderabkova, Nikol	Presenter: Mahmood, Ayesha	
Oxidative protein folding expands the mutational landscape of β-lactamase enzymes		157
Kahn, Amaranta		
Exploring a new pathway of exogenous fatty acid incorporation in cyanobacteria		158
Karneyeva, Karyna		
Target Recognition Accuracy: Exploring Type III CRISPR-Cas Systems		159

Keegstra, Johannes	
Diversity in bacterial motility strategies and endurance during nutrient limitation	160
Kim, Lili	
Phenotypic Landscape of the Gram-Positive Cell	161
Kioui, Despoina-Evgenia	
Investigation of the antimicrobial and antibiofilm potential of Lactiplantibacillus pentosus L33 against common human enteropathogens	162
Knopp, Michael	
The impact of the microbiome on the fitness of antibiotic resistant pathogens	163
Konovalovas, Aleksandras	
From nose to lungs: Unveiling the microbial landscape in Bronchiectasis patients	164
Koo, Byoung-Mo	
Dissection of Envelope Homeostasis in Bacillus subtilis Using Double-CRISPRi	165
Koumoutsi, Alexandra	
Unravelling gene function and organisation in E. coli	166
Krähenbühl Amstalden, Martin	
Influence of chemical stressors in sRNA-mediated antibiotic activity and virulence response in Salmonella Typhimurium	167
Krüger, Aileen	
Genome-wide analysis of iron- and heme-dependent regulatory networks in Corynebacterium glutamicum	168
Krupinskaite, Agne	Presenter: Stankeviciute, Jonita
Bacterial α-L-fucosidases for the synthesis of fucosylated oligosaccharides	169
Kühn, Marco	
Sensory adaptation of mechanosensing in Pseudomonas aeruginosa fine-tunes twitching motility and virulence	170

Lang, Manon	
Uridine as a potentiator of aminoglycosides through activation of carbohydrate transporters	171
Lassak, Jürgen M.	
Expansion of the genetic code with amino acids modified at the protein backbone	172
Latoch, Przemyslaw	
TimeSeqR: a comprehensive R package for integrated analysis of transcriptomic and translatomic Data from Time-Course RNAseq and RIBOseq experiments	173
Lauber, Frederic	
Biochemical insights into unique Bacteroidetes pore-forming toxins	174
Lázár, Viktória	
Antibiotic persistence in multidrug treatment	175
Le Blanc, Laure	
Bacteria adapt to mechanical confinement through morphogenetic reprogramming	176
Lensen, Arthur	
The impact of the Rac1/Rab35 dual effector MiniBar on the intracellular lifestyle of Shigella	177
Lien, Yun-Wei	
Mechanism and Regulation of Bacterial Predation via Ixotrophy	178
Liepins, Janis	
Development of laser speckle imaging method for microbial growth analyses	179
Linares Otoyá, Luis	
Quorum sensing in marine Bacteroidota	180
Lisevich, Irina	
Optimization of flagella gene expression in E. coli	181

Lopes, Inês		
Microscopy-based phenotypic profiling of infection by <i>Staphylococcus aureus</i> clinical isolates reveals intracellular lifestyle as a prevalent feature		182
López Rodríguez, Elena		
Accelerated evolution of nanobodies using diversity-generating retroelements		183
Louis, Gwennaëlle		
Characterization of envelope stress responses in <i>Bacteroidetes</i>		184
Louro, Mónica		
OMM12 biofilm community dynamics		185
Louwagie, Elen		
Pooled CRISPRi screening reveals persister formation and recovery mechanisms in <i>Escherichia coli</i>		186
Lutz, Karla	Presenter: Herz, Michaela	
Visualization of the mycobiome		187
Maire, Amandine		
Impact of genetic diversity on the fitness of <i>E. coli</i> in the healthy and inflamed gut environment		188
Maity, Ritwik		
One-Pot OMiCs Analysis for Rapid Antibacterial Mode of Action Determination		189
Marcalíková, Adéla		
A high-throughput assay for screening of virulence factor inhibitors of <i>Porphyromonas gingivalis</i>		190
Marli, Marita		
Identifying genetic factors contributing to <i>Staphylococcus aureus</i>-associated bovine mastitis using CRISPRi sequencing		191
Martyn, Jessica		
Assessment of <i>Legionella pneumophila</i> effector secretion in real time		192

McFarlane, Riley	
Investigating the contribution of RsaC to the ability of <i>Staphylococcus aureus</i> to survive manganese starvation	193
Meacock, Oliver	
A general theory of microbial interaction dependencies	194
Mediati, Daniel	
The regulatory RNA interactome of methicillin-resistant <i>Staphylococcus aureus</i> reveals genes required for virulence and antibiotic tolerance	195
Meireles, Diana	
Signals controlling the expression of the <i>Listeria monocytogenes</i> virulence regulator CadC	196
Melamed, Sahar	
Elucidating RNA-RNA interaction networks during interbacterial interactions and upon phage infection	197
Mende, Daniel	
The future of proGenomes or how to provide millions of high-quality, well-annotated genomes	198
Micaletto, Maureen	
Highly pleiotropic effects of the Pcm-dependent aspartate salvage pathway in <i>Escherichia coli</i>	199
Mikhaleva, Sofya	
Tissue-engineered organoid gut model brings a new perspective on host-microbiome-phageome interactions	200
Miksys, Algirdas	
Structural basis of type IV-A mediated CRISPR interference	201
Mongin, Grégoire	
Exploration of common mechanisms between the evolution of in vivo persistence and antibiotic tolerance in tuberculosis bacilli	202
Moreno-Fenoll, Clara	
Polar accumulation of pyoverdinin facilitates rapid exit from stationary phase	203

Moura, Ana		
Unravelling the steps involved in the cytoplasmic priming of the type VII secretion system		204
Mridha, Subham	Presenter: Kümmerli, Rolf	
A single-cell perspective on bacterial public goods production: time, space and genealogy matters		205
Mulkern, Adam		
The Impact of Genetic Background on Antimicrobial Resistance Evolution		206
Mullapudi, Edukondalu		
Structural insights into geranyl-CoA carboxylase (GCC) and Methylcrotonyl-COA carboxylase (MCC) from Mycobacterium tuberculosis		207
Müller, Janina	Presenter: Müller, Janina	
Determine phage growth parameters with a minimal model of phage-bacterial growth dynamics		208
Munnoch, John	Presenter: Hoskisson, Paul	
Chance and Necessity: Evolution guided antibiotic improvement and discovery		209
Munro, Findlay		
From famine to famine - the regulation of physiological activities in non-growing Pseudomonas aeruginosa		210
Nandy, Pabitra		
Experimental evidence of large-scale flexibility around the replication terminus of Pseudomonas fluorescens SBW25		211
Ng, Tai		
Discovery and functional characterization of B12-dependent polyiodophenol dehalogenases		212
Nguyen, Ha Ngoc Anh		
Unsaturation position in phospholipids changes cholesterol and diplopterol interaction and condensation effect		213

Niault, Théophile		
Replication coordination between <i>Vibrio cholerae</i>'s two chromosomes		214
Niault, Théophile	Presenter: Val, Marie-Eve	
Unleashing Chromosome 2 Replication in <i>Vibrio cholerae</i>: A Genome-Wide Study of RctB Initiator Binding Dynamics and Nucleoprotein Complex Formation during the Cell Cycle		215
Nicchi, Sonia		
Unraveling the roles of a secreted methyltransferase of <i>Legionella pneumophila</i>		216
Nielsen, Michelle		
Investigating the <i>C. crescentus</i> ChvIG regulon by quantitative proteomics		217
Noszka, Mateusz		
The tremendous impact of HP1021 on <i>Helicobacter pylori</i> cell physiology and response to oxidative stress		218
Offer, Ronja		
Interplay between GTP, (p)ppGpp and c-di-GMP in controlling biofilm formation by <i>Escherichia coli</i> via the diguanylate cyclase DgcE and its GTPase partner system		219
Ogunleye, Adewale		
REVIVE: Elucidating chemical cues that trigger revival from antibiotic persistence		220
Østergaard, Magnus Zimmermann		
Transposon insertion sequencing for high-throughput discovery of <i>Pseudomonas aeruginosa</i> PAO1 bacteriophage defense genes		221
Osterman, Ilya		
Phages reconstitute NAD⁺ to overcome bacterial defenses		222
Pelayo, Paula		
<i>Prevotella</i> are major contributors of sialidases in the human vaginal microbiome		223

Pham, Thuy Duong		
A <i>Klebsiella pneumoniae</i> cell-free protein synthesis system as a tool to screen natural antimicrobial compounds	224	
Piksa, Marta		
The role of bacterial lipids in the mechanism of photoinactivation	225	
Plaza, Daniel		
Pleiotropic interplay between a putative intergenic gene and a transcriptional regulator in <i>Serratia</i>	226	
Pollak, Shaul		
Public good exploitation in natural bacterioplankton communities	227	
Ponath, Falk		
Uncovering a global stress response in the early-branching species <i>Fusobacterium nucleatum</i>	228	
Poncin, Katy		
Identification and characterization of cationic bacteriocin-like peptides produced by <i>Neisseria gonorrhoeae</i> and promoting its autolysis	229	
Prentice, Jojo		
A collective defense mechanism against lytic threats in <i>Vibrio cholerae</i>	230	
Proutiere, Alexis		
Sporadic type VI secretion in 7th pandemic <i>Vibrio cholerae</i>	231	
Pugh, Hannah		
Comprehensively defining determinants of mutation rate and spectrum	232	
Pylkkö, Tuomas		
Screening for antimicrobial compounds from marine actinobacteria	233	
Qi, Qin		
Uncovering bacterial hosts of class 1 integrons in urban aquatic environments with a single-cell fusion-PCR technology	234	

Rabanal, Patricia		
Regulation of the stress-response enzyme SpoT by cellular partners		235
Rackow, Bente		
Antiphage properties of aminoglycoside antibiotics produced by Streptomyces		236
Ramirez Montoya, Maria Virginia		
A model to study microbiota-dependent mechanisms during diet-induced dysbiosis		237
Rochette, Paul		
Development of an in vivo targeted hypermutagenesis system and application to synthetic evolution of bacteriophages		238
Rosazza, Thibault		
Bacillus subtilis extracellular protease production incurs a context-dependent cost		239
Rousset, Francois		
A conserved family of immune effectors cleaves cellular ATP upon viral infection		240
Rybtke, Morten	Presenter: Sinha, Anurag	
The essential genes repertoire of enteropathogenic Escherichia coli		241
Sakenova, Nazgul		
Systematic mapping of antibiotic cross-resistance and collateral sensitivity		242
Santos Oliveira, Ana		
Strategies of Staphylococcus epidermidis biofilms to survive nitric oxide, a toxic defense molecule produced by immune cells		243
Schmidt, Silke		
The unique Legionella longbeachae capsule favours virulence and infection		244
Schniete, Jana Katharina		
Back to soil: awakening cryptic antibiotics in Streptomyces		245

Schumacher, Kilian		
Ribosome profiling reveals novel acid resistance mechanisms and small proteins in Escherichia coli		246
Sedzicki, Jarek		
Molecular landscape of the cyclic beta-1,2-glucan synthase		247
Shiver, Anthony		
A mutant fitness compendium in Bifidobacterium breve reveals molecular determinants of colonization and host-microbe interactions		248
Silas, Sukrit		
Parallelized screening of virus accessory genes reveals diverse defense and counter-defense mechanisms		249
Songailiene, Inga		
Study of multiprotein CRISPR-Cas effector and neighboring toxin-antitoxin system		250
Spratt, Madison	Presenter: Lane, Keara	
Single-cell analysis of SPI-2 gene induction reveals a dynamic, environment-tunable response		251
Srinivas, Meghana	Presenter: Kenny, John	
Metagenomics for the healthy biotransformation of milk		252
Stokar-Avihail, Avigail		
How bacterial immune systems sense phage infection		253
Su, Jinyi	Presenter: Strijbis, Karin	
Salmonella invasion at the intestinal mucosal surface: relevance of the SiiE/MUC1 pathway		254
Sulheim, Snorre		
Metabolite leakage rates are predictable from genome-scale metabolic models		255
Sullivan, Rudi		
Phenotypically profiling a Mycobacterium bovis mutant library, through a chemical-genetic screening		256

Tal, Nitzan	
Cyclic CMP and cyclic UMP mediate bacterial immunity against phages	257
Tamman, Hedvig	
Novel collection of bacteriophages infecting <i>Pseudomonas putida</i>	258
Taouk, Caroline	
Revealing processes that shape the ecosystem of <i>Prevotella</i>-dominated gut communities	259
Tesseur, Coralie	
Investigating the subcellular dynamics of the Tad pilus in a predatory bacterium	260
Tesson, Florian	
DefenseFinder: updated tool for detection and understanding of defense arsenal of prokaryotes	261
Thormann, Kai	
A conserved cell-pole determinant organizes proper polar flagellum synthesis	262
Todor, Horia	
Three bacterial DedA subfamilies with distinct functions and phylogenetic distribution	263
Tronnet, Sophie	
Extracellular ATP is a signaling molecule in gut bacteria	264
Tsai, Chia-Ni	
Investigating the mechanisms of transcriptional adaptation in <i>Pseudomonas aeruginosa</i>	265
Vaitekunas, Justas	
Promiscuity of bacterial nucleobase deaminases	266
Valenzuela, Camila	
The <i>Salmonella</i> Typhimurium effector SifA controls bacterial dormancy in epithelial cells	267

Valyi, Kezia Advanced microbiome tools for metagenomics	268
van Raaphorst, Renske Unfolding the Nucleoid of a Bacterial Predator	269
Vanková Hausnerová, Viola RIP-seq reveals novel RNAs that interact with RNA polymerase in bacteria	270
Presenter: Hnilicova, Jarmila	
Varik, Vallo Novel therapies against shigellosis	271
Vaysset, Hugo Towards the genomics-based prediction of phage-bacteria interactions	272
Velasco Gomariz, Manuel Characterisation of the small regulatory RNA AbnZ in <i>Caulobacter crescentus</i>	273
Vendrell-Fernandez, Sol Unveiling the function of a <i>Bacteroides</i> DGR-driven pilus	274
Verdegaal, Andrew Drug-microbiome-drug interaction in Parkinson's disease therapy	275
Verhaeghe, Audrey Lipopolysaccharide synthesis and traffic during growth of <i>Brucella abortus</i>	276
Vieira, Ana Interaction between the cyanobacterial strain <i>Nodularia</i> sp. LEGE 06071 and protozoa	277
Vilhena, Cláudia Characterization of mix extracellular vesicles pool after bacteria-host co-cultivation	278
Voogdt, Carlos Novel tools for making pooled and ordered transposon mutant libraries in intestinal <i>Bacteriodales</i> species	279

Walch, Philipp		
Dissecting the impact of enteric viral-bacterial co-infection on the host innate immune response and its implications for pathogenicity		280
Walker-Sünderhauf, David		
CRISPR-Cas-mediated removal of AMR plasmids is limited by presence of toxin-antitoxin systems		281
Walker-Sünderhauf, David		
Interspecific competition can drive plasmid loss from a focal species in a microbial community		282
Ward, Ryan		
Systematic Dissection of Genetic Vulnerabilities in Acinetobacter baumannii		283
Wei, Jinwei		
Plant hormone ethylene is a quorum sensing signal detected by bacterial histidine kinase BerK		284
White, Joni	Presenter: Swift, Simon	
Extracellular vesicles as a medium for cross-kingdom communication between human cells and bacteria		285
Wisniewska, Aleksandra	Presenter: Mruk, Iwona	
Molecular basis for lethal cross-talk between two unrelated bacterial transcription factors – the regulatory protein of a restriction-modification system and the repressor of a defective prophage		286
Wolfram-Schauerte, Maik		
A bacteriophage ADP-ribosyltransferase covalently links RNA chains to host proteins		287
Wons, Ewa		
Rac prophage YdaT-dependent toxicity in Escherichia coli cells – YdaT characteristics and molecular targets		288
Xu, Jingwei		
Identification, mechanistic characterization, and re-engineering of a contractile injection system		289

Yaeger, Luke		
Metabolic connections between folate and peptidoglycan pathways in <i>P. aeruginosa</i> inform the rational design of a dual action inhibitor	290	
Yang, Alessio		
Phages carry multiple triggers and blockers against the same bacterial defense system	291	
Yin, Xin		
Plant recognizes bacterial second messenger c-di-GMP and the role of plant receptor in regulating the immune response	292	
Yirmiya, Erez		
Phages overcome bacterial immunity via diverse anti-defense proteins	293	
Yong, Luoyan		
Exploring the diversity of biofilms of the <i>E. coli</i> species	294	
Yu, Takyoun		
Metabolic reprogramming confers resuscitation from antibiotic persistence in bacteria	295	
Zaatouf, Laila		
AMP mechanism of action on bacterial membranes determined by in vivo solid-state NMR	296	
Zammit, Thomas	Presenter: Tree, Jai	
Small RNAs are TRAPP'ed by a T6SS toxin-immunity complex	297	
Zannoni, Annamaria		
Dissecting stress response networks in <i>Campylobacter jejuni</i> using a chemical-genomics approach	298	
Zhao, Yansong		
Maintenance of diverse microbial communities on single-carbon-source environments	299	
Zietek, Matylda		
Sensing and modulation of cell shape by the Rcs stress response	300	