

## GDC Projects

ID	title	keywords	organism
1067	ecDNA of acetogenic bacteria	whole genome sequencing, transcriptomics, Illumina, Nanopore	Acetogenic bacteria
1066	Beech genetic monitoring	genetic monitoring, European beech, population genomics	Fagus sylvatica
1065	Amplicon sequencing of chemotactic bacteria	amplicon sequencing, low-input DNA extraction	bacteria
1062	High throughput genotyping in Alpine ibex follow-up	capra ibex, amplicon, sequencing, MHC, population structure	Capra Ibex
1061	Microbial community analyses of peatlands in Sweden	metagenomics, amplicon sequencing, metatranscriptomics, microbial community analysis	Environmental sample
1060	Microbial diversity in Swiss agricultural fields	Microbes, Agriculture, MiSeq	Agroscope & Universität Zürich
1059	Range-wide Whole Genome Sequencing in European beech (Fagus sylvatica) and other beech species	whole genome sequencing, demographic history, expansion load, gene-environment association, genomic prediction, GWAS	European beech (Fagus sylvatica L.) and other beech species
1058	Metabarcoding of riparian spider gut content	cross-ecosystem linkages, spider, aquatic subsidies	riparian spiders
1057	Oxford Nanopore Technology for microbiome	microbiome, Oxford Nanopore Technology	soil microbiome
1056	ARTFUL	Metagenomics, Nanopore, Antimicrobial Resistance, Environmental DNA, Lake	Microbial communities of aquatic environments
1055	AMF response to pesticide application and the impact of preliminary maize seed coating on plant biomass and AMF root colonization.	AMF, Pesticide, Herbicide, Maize	Zea mays, Rhizogloimus irregulare, Claroideogloimus claroideum, Funneliformis mosseae
1054	Ecological genetics of wild carnations	Adaptation, Natural selection, Genetic variation, Rapid radiations, Climate change	Dianthus (Caryophyllaceae)
1053	Zymo Halo Project	GWAS, Fungal pathogen	Zymoseptoria tritici
1052	Molecular Plant Breeding - General lab activities	Quality and quantity check of nucleic acids, sequencing, ddRAD libraries	Plants

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<b>1051</b>	Miseq Sequencing for the Plant-Soil Interactions group	Miseq	Bacteria, Fungi, AMF, Eukaryonts
<b>1050</b>	2ndFOR chronosequence	chronosequence, tropical	fungi, bacteria
<b>1049</b>	Defensive symbiosis in the wild 2: The influence of temperature on symbiont prevalence and the basis of defense specificity	aphids, adaptation, coevolution, Hamiltonella defensa, host-parasite interactions, parasitoids, resistance, symbiosis, temperature, toxin genes	Aphis fabae, Hamiltonella defensa, Lysiphlebus fabarum,
<b>1048</b>	Mechanisms underlying the success and impacts of range expanding species in mountains	bead ruptor, range-expanding, plant species, plantecology	plants
<b>1047</b>	L.stagnalis ddRAD	ddRAD	L.stagnalis
<b>1046</b>	Viral dsRNA sequencing from yeast isolates	sequencing	Virus/yeast
<b>1045</b>	PHP Diagnostik Metabarcoding	phytopathology, mycobiome, forest health	Fungi
<b>1043</b>	eDNA standardised sampling protocol	DNA samples, Extraction, Sequencing, Biodiversity analysis	ETH
<b>1042</b>	DNA extraction and genetic profiling of Radix and trematode species	Radix, trematode, parasite	Radix spp., trematodes
<b>1041</b>	DNA extraction and genetic profiling of Radix and trematode species	Radix, trematode, parasite	Radix spp, trematodes
<b>1040</b>	Bacterial interactions in nasal microbiomes	16S amplicon sequencing, microbiome, DNA extraction, PCR	Staphylococcus aureus
<b>1039</b>	External Projects (separate fundings)	Miseq, External, Sequencing, Agroscope	Soil and Root Samples for div. Sequencing
<b>1038</b>	OakID ,Ä Hybridization and introgression in white oak species (Quercus spp.)	quercus, oaks, hybridization, introgression, adaptation	Quercus ssp
<b>1037</b>	Life Cycle of Aerobic Granular Sludge	Aerobic Granula Sludge, Nitrifiers, Life Cycle, Breakage &	microbiota

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1036	Next-generation targeted small-molecule drug conjugates from DNA-encoded chemical libraries	DNA encoded chemical library, protein engineering, small molecule, drug discovery	proteins purified from CHO and E. coli
1035	Greenfjord - Assessing the accuracy of the eDNA signal measured across the fjordic ecosystem in South Greenland with established knowledge of ecology	eDNA, arctic, metabarcoding	bacteria and eukaryotes
1034	SLOOP: Sleep, development, gut microbiota	16S, infant, gut microbiome, neurodevelopment, sleep regulation	Infant stool
1033	EVO Plant	stomata, evolution	Cyperus species
1032	Microbiome analysis of banana	microbiome, banana crop, soil, organic matter	Instituto Canario de Investigaciones Agrarias
1031	Most effective organic matter for banana cultivation	banana, microbiome, fertilizer, organic mater	soil microbiome
1030	Investigation into the diversity of cell-cell associations and non-standard life using metagenomics and cryogenic electron microscopy	CPR, metagenomics, qPCR, cryo-EM	Patescibacteria
1029	Synthetic communities and microbiome complexity from field isolates	microbiome, fungi, bacteria	Bacteria and fungi
1028	Evolutionary Genomics of Lake Victoria Cichlid fishes	NGS sequence, QTL, eQTL, Whole Genome sequence	Cichlid fish
1027	Monitoring the effects of forest loss and restoration on faunal communities with environmental DNA	eDNA, CRISPR, monitoring, species	water samples with eDNA
1026	STIDirect	sti, genome sequencing	chlamydia trachomatis
1025	ACTNOW	Marine biodiversity, Marine protected area, eDNA, invasive species	ETH Zurich

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1024	The divergent roles of mono- and biallelic Trp53 mutations in leukemogenesis	RNA, Tapestation	mouse
1023	tRNA extraction from chloroplasts	RNA	Nicotiana benthamiana, Adiantum capillus-vaeneris, Cuscuta campestri
1022	Bedretto_deepcarbon_microorganisms	Groundwater, Carbon cycling, Sulfur cycling, Subsurface, microbial communities	Bacteria
1021	Understanding the mechanisms underlying IPI-549 treatment in lipedema	RNA integrity, Tapestation	Isolated RNA from human patient samples
1020	Agrometrics	eDNA, soil, earthworms, insects, agriculture	insects
1019	MaLeFiX Swiss Rivers	eDNA, freshwaterfish	freshwater fish
1018	Grundlagen für ein regionales Vernetzungskonzept „Äi populationsgenetische Analyse des Skabiosen-Schneckenfalters (Euphydryas aurinia aurinia) im Raum Zürichsee/Linthebene	ddRADseq, Raupen, Populationsgenetik, Vernetzung, Lebenszyklus	Euphydryas aurinia aurinia
1017	Identifying genetic factors in Salmonella Typhimurium for gut colonization.	BarSeq, WISH tags, Salmonella, Gut Colonization, gene fitness	Salmonella Typhimurium
1016	Exploring the soil virome's impact on microbial communities across management practices	metagenomics, metatranscriptomics, viromics, microbial ecology	Microbiomes (Environmental)
1015	Fish Welfare Assessment: development of innovative tools for the field	fish welfare, Danio rerio, Cyprinus carpio, Oncorhynchus mykiss	fish
1014	Identification of new proteins involve in starch granule initiation	starch, next generation sequencing, DNA extraction	Arabidopsis

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1013	Influence of cell size on cell physiology	Yeast, <i>S. cerevisiae</i> , Size mutants, WHI3, WHI4, petite	<i>S. cerevisiae</i>
1011	CRISPR/Cas-based methodology offers a promising approach for generating extensive phosphomutant libraries in yeast	TapeStation	Yeast, <i>E. coli</i>
1010	The <i>Patella caerulea</i> genome	<i>Patella</i> , limpet, reference genome, PacBio HiFi, assembly, annotation	limpet <i>Patella caerulea</i>
1009	WISE	Wastewater-based epidemiology, Respiratory viruses, Amplicon-based sequencing, Nanopore	Respiratory viruses
1008	PSM Bodenwirkung	pesticides, vineyards, microbiome	Prokaryotes, Fungi
1007	Sex determination: <i>Lepidium</i> and <i>Ecballium</i>	<i>Lepidium solandri</i> , <i>Ecballium elaterium</i> , Sex determination, Genome Assembly	<i>Lepidium solandri</i> and <i>Ecballium elaterium</i>
1006	Multimodal Intracellular Sub-Cellular Resolution Interfacing Arrays in CMOS	Single Cell Analysis, DNA Sequencing, Cell to Cell Interaction	Lung cell, T cell
1005	Adventisol	ITS sequencing, Pacbio, fungal communities	soil
1004	Effects of stressors on biofilm's community composition	Biofilm, community composition, stressors	Biofilm communities (algae and bacteria)
1003	Microbial diversity and function in river networks	Microbial, Diversity, Ecosystem, Function, Environmental DNA, freshwater	Bacteria
1002	Molecular basis of transient versus persistent neurobehavioral effects in zebrafish larvae	zebrafish, neurotoxicity, transient vs persistent effects, molecular markers	zebrafish ( <i>Danio rerio</i> )
1001	Life without a cell wall	L-Forms, Transcription, Antibiotic Tolerance, Antibiotic Resistance	<i>Listeria Monocytogenes</i>
1000	GDC general	lab	all

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999	Rubisco Quantification in marine phytoplankton cells using ELISA kit	Rubisco, ELISA, Microalgae	Phytoplankton
998	SURI BioTech, developing precision probiotics for early life	microbiome, probiotics, infant health	Propionibacterium and Bifidobacterium spp.
997	HealthyStart: the detection of cereal seed- and soil-borne diseases	qPCR, Cereal diseases, Tilletia, Ustilago, Microdochium	Fungal disease of Cereals
995	Application of the CRISPR-eDNA technology to marine mammal monitoring	eDNA	Ecosystems and Landscape Evolution group
994	Microbiota Vault	KingFisher Flex	NA
993	Biodiversity and biogeography of soil protists in continental and oceanic islands	testate amoebae, PacBio, metabarcoding, soil, eDNA, biogeography	Hyalospheniidae
992	Parasitoid adaptation to symbiont-conferred resistance II	ddRAD sequencing, parasitoids, coevolution, aphids, endosymbionts, QTL, adaptation, defense	Lysiphlebus fabarum
991	Legionome	Legionella, 16S rRNA, Pangenome	Legionella spp.
990	Measuring cell growth using luminescence for determining pharmacodynamics	Antibiotic, Luminescence, Growth curve, Kill curve	Escherichia coli
989	Biotic and Abiotic	georespiration, carbon cycle, oxidative weathering	lithic archaea and bacteria (16S rRNA) + fungi
988	Yeast-MHCII Display	Yeast-MHCII Display, Plasmid sequencing, Peptide library	Yeast ( <i>Saccharomyces cerevisiae</i> )
987	Development of advanced sensing platforms for water, sanitation, and hygiene (WASH)-oriented transmission of infectious diseases and antibiotic resistance	Nanopore Sequencing, Environmental Monitoring, Antibiotic resistance, Infectious diseases	Pathogens
986	RADS Lucadendron species	Lucadendron, RADS	Lucadendron sp.

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985	Metal pollution in freshwater sediments as a driver for microbial biodiversity loss	bacterial communities, freshwater sediments, biodiversity loss, metal pollution, climate change	bacteria
984	Vortex 4D	Fluorophors, ssDNA	no organism / in vitro nucleic acids & biological fluid
983	Detecting rare mammals in Switzerland via eDNA	eDNA, CRISPR/Cas, mammals, biodiversity monitoring	Various fish/mammal/amphibian species (via eDNA)
982	BIOSCAN: Tracing patterns from life	pacbio, eDNA, mitochondrial genomes, long range amplification	Vertebrates
981	Testing the cleanliness of clean rooms	low biomass, contamination	Environmental and Caulobacter vibrioides
980	Expanding the fish invitrome for animal-free prediction of chemical toxicity in fish	Invitrome, fish cell line, ecotoxicology, RNAseq, transcriptome	Danio rerio, Oncorhynchus mykiss
979	Conservation genomics of the European grayling <i>Thymallus thymallus</i>	grayling, re-sequencing	<i>Thymallus thymallus</i>
978	Microbiome analysis of guest PhD student from University of Catania at FiBL	Plant-microbiome interaction	Bacterial and fungal sequences originating from root samples
977	Mobile Organic Biofilm for Granulation	aerobic granular sludge, wastewater treatment, mobile organic biofilm	mixed community of environmental bacteria
976	Conservation genomics of the freshwater mussel <i>Anodonta anatina</i>	Genomics, Conservation, Reference genome, population genomics, freshwater mussel	Freshwater mussel <i>Anodonta anatina</i>
975	Chromatin configuration in different <i>Z. tritici</i> strains	<i>Zymoseptoria tritici</i> , chromatin configuration, Hi-C	UniversitV© de NeuchVctel
974	Airborne eDNA	qPCR, fungal plant pathogens, environmental DNA, airborne	fungi
973	Genome structure of plant pathogens	Hi-C, Fungi, Histone methylation ChIP-seq	<i>Zymoseptoria tritici</i>
972	Is toxin production beneficial for cyanobacteria?	cyanobacteria, toxin production, HMW DNA	Eawag

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971	Reference genome for Potamopyrgus antipodarum	Genome	Potamopyrgus antipodarum
970	Hydro Project - Luca Carraro	eDNA, Library, Illumina, Nova Sequencing, Functional Genomics Center	river eDNA
969	Characterization of the stereochemistry of PS linkages by Oxford Nanopore sequencing	modification, phosphorothioate, nanopore, stereoisomer	not specific/human
968	Aneuploid detection by sequencing	Aneuploidy, Illumina sequencing, Tape station, polyploidy, arabidopsis	Arabidopsis arenosa and Arabidopsis thaliana
967	3D-Omics: investigating pathogen-synbiotic-gut microbiota interactions in vitro	in vitro, gut microbiota, spatial microbial interactions, pathogen, probiotics	bacteria
966	Investigating recombination rate variation and polyploidisation in Dianthus sylvestris populations	Recombination, Polyploidisation, Outlier analyses	Dianthus sylvestris
965	Optimization of small RNA-seq ligation efficiency	small RNA, adapter ligation	Homo sapiens
964	Investigating recombination rate variation and polyploidization in Dianthus Sylvestris	Recombination, selection, polyploidization	Dianthus sylvestris
963	Microbiota Vault	Microbiota, conservation, intestinal, human	Bacterial communities and stool samples
962	Aquatic and terrestrial arthropod community dynamics in the urban matrix	Urban, Environmental DNA, Arthropods, Local/landscape filters	Environmental DNA
961	Environmental DNA (eDNA) analysis for monitoring of wildlife species in the mountains of Bhutan	eDNA, CRISPR, wildlife monitoring	various mammal species (DNA from water samples)
960	Connecting genome-wide landscapes of DNA oxidation with multiple aging mechanisms in human blood	aging, DNA damage, DNA oxidation, DNA methylation, aging clock	Homo sapiens



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958	Evolvability potential and constraints of a major wheat pathogen	epigenomics, transposable elements, Zymoseptoria tritici, evolvability, genomics	Zymoseptoria tritici
957	Investigating the distribution of sharks in Shark Bay, Australia using environmental DNA and their influence on dolphins	eDNA, Sharks	Sharks
956	Genomics of edaphic adaption, ecological speciation and sex system evolution in the <i>Silene acaulis/exscapa</i> complex	Evolutionary history, Sex chromosome evolution, genomics	<i>Silene acaulis</i> , <i>Silene exscapa</i> , <i>Silene cenisia</i>
955	COMMON-RING ,Ä Integrating evolutionary responses to improve predictions of species distributions using tree rings from European common gardens	Common gardens, dendrochronology, genomics, local adaptation, phenotypic plasticity, species distribution models, forest trees	<i>Quercus petraea</i> 25 plant species covering land plant lineages. For example, <i>Arabidopsis thaliana</i> , <i>Solanum lycopersicum</i> , <i>Anthoceros agrestis</i> , <i>Ginkgo biloba</i> , <i>Physcomitrella patens</i> .
954	EvoGuard	RNA sequencing, qPCR	
953	The city,Äs wild side: monitoring and space use of urban mammals	eDNA, mammals, urban, monitoring, wildlife	various mammals from Switzerland (eDNA samples)
952	Fish-EC consumables	Consumables	Fish
951	WISH-Tag sequencing	Amplicon sequencing, WISH-Tags, At-LSPHERE	At-LSPHERE
950	Primary and Acquired Resistance to Targeted treatment in BRAFV600E-mutated metastatic Colorectal cancer (PARTACER-Suisse)	Organoid, Colorectal cancer, BRAF	UniversitÄtsspital ZVrich (USZ)
949	Optistress	NR3C1, FKBP5, saliva, Oragene	Humans

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948	Harnessing microbial defluorination potential to predict chemotherapeutic toxicity	Metagenomics, Microbiome	several gut microbiome strains
947	Conservation genomics of <i>Phengaris alcon</i>	<i>phengaris alcon</i> , conservation genomics, RAD sequencing	<i>Phengaris alcon</i>
946	BlackGoesGreen - Soil biology	microbiome, soil, amplicon sequencing, biochar	Soil microbiome
945	Copy number analysis in transgenic <i>Arabidopsis</i>	DNA extraction, <i>Arabidopsis</i>	<i>Arabidopsis thaliana</i>
944	MAGIC	ecological genomics, forest, fungus, tree, association models, landscape genomics	<i>Fagus sylvatica</i> , <i>Cenococcum geophilum</i>
943	IL-6 detection	IL_6 detection	lung cell
942	From starch biosynthesis to chloroplast development: neofunctionalization of Branching Enzyme 1	plastids, intron splicing, translation	<i>Arabidopsis</i>
941	MOB response to autumnal lake mixing - Methylo troph analysis	Methanotrophs, Methylo trophs, bacterioplankton, freshwater lakes, syntrophy	Methanotrophs, bacterial communities
940	hnRNP K RNAseq investigation	RNAseq, CRISPR, Genetic Screen	human cell lines
939	The potential role of development in limiting genetic diversity in multicellular aggregates	microbiology, social selection, myxobacteria, development, genetic variability	Myxobacteria
938	Reef Continuity	RADseq, metagenomics	Marine Fishes
937	Fish ancient DNA	Ancient DNA, diversification, paleogenomics, paleogenetics, formalin, museomics, sedaDNA	teleost fish

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936	Adaptive and demographic history of <i>Dianthus sylvestris</i>	Population genetics, Ecological genetics, Adaptation, Climate change, Demographic inference	<i>Dianthus</i>
935	Nucleotide-resolution mapping of temozolomide-induced DNA modification	DNA damage, illumina sequencing, temozolomide	<i>Homo sapiens</i>
934	Testings, consumables	Consumables, Stock, Testing	Plants and animals so far
933	Exploring the potential of eDNA ex situ metabarcoding coupled with Nanopore Technologies to identify and age fish larvae	eDNA, Metabarcoding, Nanopore, MinION, Age estimation, Identification	MARBEC - ETHZ
932	Comparison of different 16S Sequencing approaches and targeted analysis by qPCR for determination of <i>C. difficile</i> in human fecal samples	microbiome, NGS	human
931	Arctic Greening Plant-Microbe interactions	Arctic Greening, Microbial Communities, Climate change, Tundra Ecosystems	Microbial communities
930	The ecology of the collared flycatcher ( <i>Ficedula albicollis</i> ) in Ticino	<i>Ficedula albicollis</i> , Ecology, eDNA	<i>Ficedula albicollis</i>
929	Cichlid genomes	population genomics, evolution, bioinformatics	Cichlid fish
928	Phylogenetics of of the <i>Dianthus</i> radiation	phylogeny, target capture	<i>Dianthus</i>
927	Methylation patterns of coral reef fish larvae	eDNA, MinION sequencing, methylation, fish larvae, age estimation	eDNA from <i>Dicentrarchus labrax</i> larvae
926	Wild-Tomato Genome Diversity Project	population genomics, linkage mapping, wild tomatoes, DNA quantitation, 96-well format	Wild tomatoes ( <i>Solanum</i> sect. <i>Lycopersicon</i> )
925	Understanding metacommunity structure of vernal pools in Southern France	eDNA, metacommunity structure	vertebrates and invertebrates

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924	Iron and vaccine-preventable viral diseases - an experimental study	Iron deficiency, vaccines, women of reproductive age	Human -> blood analysis
923	HealthFerm	healthferm, fermented	multiple food grade MO
922	microNASA	16S amplicon sequencing	Bacteria
921	Swiss charr diversity	Salvelinus, charr, speciation, hybridization	Salvelinus sp.
920	Sepsis Identification based on Mit. DNA	Sepsid, Sanger-Sequencing, COII, COI, CytB	Dung Flies (Sepsids)
918	Understanding metacommunity structure of vernal pools in Southern France using eDNA	eDNA, biogeochemistry, vernal pool systems	eukaryotes Chlorella vulgaris, Chlorella pyrenoidosa, Auxenochlorella protothecoides, Glycine max, Pisum sativum
917	DNA and RNA quantification in microalgae biomass	DNA-N, RNA-N, microalgae	
916	XPRIZE Rainforest	eDNA, biodiversity, drones, XPRIZE	plants and animals
915	Repeated adaptation in wild carnations	adaptation, convergent evolution, population genomics, selection, environmental stress, Dianthus	Dianthus
914	Corbicula	Corbicula	Corbicula
913	Application of CRISPR/Cas9 system to study sugar transporter genes in Barley protoplast	gene expression, sugar transport, protoplast	Barley plant
912	Altering microbe-induced stomatal closure to restrict foodborne diseases of leafy greens	Silencing, Arabidopsis thaliana, Cloning	A. thaliana
911	Diplocarpon coronariae	Nanopore Full-genome sequencing, Ascomycete, Diplocarpon coronariae	Diplocarpon coronariae
910	Plastic Particles in Arctic sea ice: Pollution burdens in a changing climate	plastic contamination, climate change, polar seawater	ETH ZV <sup>o</sup> rich
909	SHIFTeDNA	fish, edna, museum, range shift	fish
908	Cassava Source Sink improvement	Cassava, Genome engineering, Starch, Source-sink relationship	Cassava - Manihot esculenta

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907	Wales - fungal inoculation	soil inoculation, restoration, carbon capture	fungi
906	Analysis of DNA strand breaks in plasmids after irradiation with nanoparticles	nanoparticles, plasmids, radiotherapy, gel electrophoresis, DNA strand breaks	Nanoparticle Systems Engineering Laboratory, D-MAVT, ETH
905	Within-host dynamics of Escherichia coli strains in the human gut	Escherichia coli, Amplicon sequencing, Barcoding	Escherichia coli
904	Genetic Diversity of Extinct Alpine Whitefish	aDNA, alpine whitefish	Alpine Whitefish
903	The role of parental care on skin microbiome transmission in a poison frog	Skin microbiome, parental care, poison frogs	Poison frogs, bacteria
902	Pollen use by Bombus spp. across an elevation gradient	Climate change, Pollination, Bombus, DNA metabarcoding	Bombus spp. and associated food plants (many families)
901	Environmental DNA analysis of water from mining impacted rivers in Japan	environmental DNA, macroinvertebrate, mining pollution, environmental assessment, community structure	Invertebrate
900	Transcription factors modulating enzymatic activity of b-glucoocerebrosidase	neurodegeneration, Parkinson's disease, enzymatic activity, CRISPR activation, Screening, transcription factors	human
899	Prebiotics increase iron absorption from wheat-based instant cereal: stable iron isotope studies in Kenyan infants	IDA, FIA, Gut Microbiota, Prebiotic, Danone, Iron	Gut Bacteria
898	Novel GABA-producing bacterial consortia to investigate the role of the gut microbiota in the food-gut brain axis	GABA, Bacterial community composition, 16s rRNA seq	FBT
897	Environmental DNA analysis of water from mining impacted rivers in Japan	eDNA, mining impacts, biodiversity, Japan	metazoan eukayotes
896	Distribution and diet of the Eurasian scops owl (Otus scops) in Ticino	eDNA, amplicon sequencing, Otus scops	Eurasian scops owl (Otus scops)

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895	McrA gene abundance and expression in a peat depth profile	methanogenesis, pmoA, mcrA, peatlands	Peat soil micro-organisms
894	Soil Metagenome Library Generation	Sonicator, Library Generation, gDNA fragmentation	Soil Microbiome, Myxococcus xanthus
893	Quality control of CRISPR-edited rainbow trout genomic DNA	Oncorhynchus mykiss, CRISPR/Cas9, RTgutGC, AMPs, RNPs	Oncorhynchus mykiss
892	Sociogenomics of cooperative myxobacteria	Phylogenomics, Assembly, Population genomics, NGS data analyses, Read mapping	Myxococcus xanthus
891	Diversification in spatial networks	e-coli, spatial networks, modularity, evolution	e-coli
890	Spatial in vivo mechanomics of bone adaptations	single cell sequencing, transcriptomics, 10X genomics, Visium	Mouse
889	Does CRISPR-Cas block the spread of plasmids?	plasmids, CRISPR-Cas, evolutionary ecology, experimental evolution	Escherichia coli
888	Non-invasive delivery of siRNA to the brain	siRNA, drug delivery, CNS, RT-PCR	Mouse, rat
887	Cultures Across Cultures	microbiome, fermented foods, amplicon library prep, shotgun metagenomics prep	Communities of Bacteria and Yeast from foods
886	Advancing species knowledge, distributions and monitoring solutions for endemic tropical fish fauna using environmental DNA (eDNA)	fish, Iguidi River, Benin, eDNA	fish, crustaceans
885	ETH4D Benin eDNA	eDNA, Benin, fish	Fish
884	ETH4D Benin eDNA	eDNA, Benin	Fish
883	Effect of nematodes on evolved bacteria	nematode, qPCR, M.xanthus, predator-prey	Myxococcus xanthus

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882	Iron and vaccine-preventable viral disease - an experimental study	iron deficiency anemia, intravenous iron treatment, vaccine response, immune system	
881	Investigation of protists-Legionella interactions in potable water systems	Legionella, Protists, Hosts, Amoebae, Screening, Potable water	eukaryotes and bacteria
880	EcolImpact_metagenomes	biofilm, organic pollutants, biotransformations, metagenomes	periphyton
879	Microbiome Restoration	Mexico	Fungi and Bacteria
878	Tintenstrich communities in Switzerland	Cyanobacteria, Tintenstrich communities, Lichen, Cyanotoxins	Bacteria
877	Adaptation to novel climates in <i>Lactuca serriola</i>	climate change, draough stress, evolutionary response	<i>Lactuca serriola</i>
876	Meiotic adaptation to genome duplication in <i>Arabidopsis arenosa</i>	arenosa	<i>Arabidopsis arenosa</i>
875	Biofair	Climate change, fungal community, bacterial community, farming practices, wheat agrosystem	Soil bacteria and fungi
874	Characterization of sex chromosomes and sex determination in <i>Cycas revoluta</i>	<i>Cycas revoluta</i> , sex chromosomes, RNAseq, ddRADseq	<i>Cycas revoluta</i>
873	Understanding gene expression changes changes in PIF4 promoter mutated plants	gene expression, pif4, thermotolerance, arabidopsis thaliana	arabidopsis thaliana
872	Development of bacteriophage-based antimicrobials	bacteriophage, bacteria, PCR	bacteriophages, <i>E. coli</i>
871	How can organic matter-rich fertilizers increase Zn, but not Cd, in wheat grains?	wheat, biofortification, trace elements	Wheat
870	ACORN	Quercus, White oaks, Drought adaptation, Common garde experiments	Quercus spp

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869	Lakes Thun and Brienz whitefish radiation	Coregonus spp, lake Thun, lake Brienz, lake Constance, RAD, population structure, species delimitation, adaptive radiation	Coregonus spp
868	Greenland sticklebacks genomics	stickelback, Greenland, evolutionary genomics, eco-evo feedback	three-spined stickleback <i>Gasterosteus aculeatus</i>
867	Antimicrobial resistance in fresh produce	Antimicrobial resistance, fresh produce, plasmidome	Bacterial plasmid from unknown hosts
866	Epigenetics in freshwater bivalves	epigenetics, invasive species, pollution	<i>Dreissena polymorpha</i> , <i>Corbicula fluminea</i> , <i>Unio elongatulus</i>
865	Epigenomics in freshwater bivalves	epigenomics, bivalves, pollution	<i>Dreissena polymorpha</i> , <i>Corbicula fluminea</i> , <i>Unio elongatulus</i>
864	Sex determination in invasive mussels	sex chromosome, invasive species, bivalve	the quagga mussel <i>Dreissena bugensis</i>
863	SNF project: Unraveling the molecular mechanisms of trace contaminant biotransformation from wastewater to natural surface waters	Biotransformation, Wastewater Treatment Plant, Activated Sludge, Surface Water Biofilm, Trace Organic Contaminants	Activated sludge, surface water biofilm
862	Unraveling the molecular mechanisms of trace contaminant biotransformation from wastewater to natural surface waters	DNA extraction, Biotransformation, trace organic contaminants, wastewater treatment plants, natural surface water	Activated sludge
861	Transcriptome analysis of <i>Brassica nigra</i> under different priming conditions	priming, plant defense, transcriptome analysis	<i>Brassica nigra</i>
860	<i>Epichloe</i> Adaptation Genomics	<i>Epichloe</i> , Fungi, Genomics, Plant pathogens	Fungi
859	SOLACE	agriculture, microbiome	soil, plants
858	Phylogenetics of <i>Dianthus carthusianorum</i>	<i>Dianthus</i> , Herbarian, ddRAD, WGS data	<i>Dianthus carthusianorum</i>
857	Genetic Modularity	population graph, e-coli, whole-genome-sequencing	<i>E. coli</i>



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856	Single cell ribosomal sequencing in mouse models of Alzheimer's disease	Alzheimer's, sequencing, Ribo-seq	Mouse
855	Sleep Cry 2022+	sleep, gut, infants, crying	microbiota
854	Comparison of supra and subglacial microbial communities	Glacier, Otemma, MSc thesis	University of Lausanne
853	GradCatch-Using natural environmental GRADients to decipher the adaptation of soil microbial Communities to climATe Change	Climate change, Greenhouse gases, microbial communities	Bacteria, Archaea, Fungi
852	SimplexDNA (ETH spin off)	environmental DNA, metabarcoding, illumina, qPCR, library preparation	Kind of the whole tree of life
851	Physiological adaptation of E. coli to nutrient fluctuations	Bacteria, physiology, transcriptome	E. coli
850	Genomics of adaptation of Atriophallophorus winterbourni	pool-seq, genomics, adaptation	Atriophallophorus winterbourni
849	Eco Consumables	eco consumables	The Tree of Life
848	Genomic tools to assess within- and between-species diversity in grassland plants	grasslands, genetic diversity, plant biodiversity	Grassland plants
847	The evolution of floral traits in a heterogeneous environment -Continuation of the project p416 -	Flower evolution, gender specific selection, disease transmission	Dianthus carthusian-rum
846	Investigating Chromatin Architecture in Arabidopsis arenosa	ATAC-seq, RNA-seq, Arabidopsis, enzymes, kits	Arabidopsis arenosa
845	soil metagenome NI	soil microbiome, nitrification inhibitors	soil bacetria
844	Targeted Sequencing of circulating tumor DNA through CAPP-seq.	circulating DNA	human
843	Biogeochemical analysis of Methanogens in Lake Rotsee sediment	Methane, Methanogens, Methanotrophs, qPCR, Sequencing	Methanogens, Methanotrophs

ID	title	keywords	organism
842	EMS Suppressor Screen for ops opl2	phloem, DNA extraction, whole genome sequencing, genetic screen	Arabidopsis thaliana
841	PaCMan 2, POMP 2, POMP 3	hydroponics,plants,space	-
840	Replacement p463	library preparation, Caribbean tropical fish, ddRADseq	Fish
839	TEs in Brachypodium	TEs, natural selection, environmental effects	Brachypodium distachyon
838	Mesocosm selection experiment	stickleback, selection	Threespine stickleback
837	Dinobryon single cell	single cell, genome assembly	Dinobryon ( <a href="https://en.wikipedia.org/wiki/Dinobryon">https://en.wikipedia.org/wiki/Dinobryon</a> )
836	Microbiome Lighthouse	microbiome, organic agriculture, rhizosphere, phyllosphere	soil, plants
835	METALink	local adaptation, heavy metal tolerance	Arabidopsis halleri
834	Adaptation to climate change in Lactuca serriola	Climate change adaptation, RAD-seq	Lactuca serriola
833	Genomics of p.antipodarum/parasites	Host-parasite interaction, genomics	Potamopyrgus antipodarum
832	Iron absorption from an iron-fortified follow-up formula with and without the addition of a synbiotic or human milk oligosaccharides: a stable isotope study in 10, 14 month-old Thai children	qPCR, beneficial bacteria, enteropathogenic bacteria	Bacillus cereus, Clostridium difficile, Clostridium perfringens, EHEC, EPEC, ETEC, Salmonella spp., Staphylococcus aureus, Lactobacillus reuteri.
831	Overcoming Hard Limits of Thermal Adaptation	experimental evolution, thermal adaptation, evolutionary rescue	Pseudoalteromonas haloplanktis
830	Nectary starch and nectar production in the Brassicaceae family	Nectar, Starch, Nectary starch, Arabidopsis, Brassicaceae, Genetics	Arabidopsis thaliana
829	Arabidopsis - F. oxysporum interaction in pH-regulation mutants	Quality control of RNA-Seq Libraries	Arabidopsis thaliana and Fusarium oxysporum
828	in-situ incubation experiments of glacial fed stream biofilms	qPCR	archaea, bacteria, eukarya
827	Evolution, conservation, and reproduction of Potentilla leucopolitana P. J. M. V. and Potentilla praecox F. W. Schultz	conservation genetics, botany, hybridisation, polyploidy, aDNA, rosaceae	Potentilla leucopolitana, Potentilla praecox, Potentilla argentea, Potentilla heptaphylla, Potentilla verna

ID	title	keywords	organism
826	Exploring the impact of past climatic change on the genetic diversity of Swiss mountain forests: combining paleoecological and paleogenetic approaches	ancient DNA,genetic diversity, Larix decidua, subfossil tree remains	Larix decidua
825	Microbial community analysis of faecal sludge samples from Lusaka, Zambia	dewaterability, faecal sludge, anaerobic storage	bacteria
824	Microterroir	DNA extraction, KingFisher	Microbiota
823	Comparative directed evolution of proteins with different temperature adaptations	Directed evolution, Long-read sequencing, deep mutational scanning, protein evolution	Escherichia coli
822	Microbial communities of aquatic and terrestrial isopods	gut microbiome, isopods, diet, bacteria,f ungi	isopods
821	Asellus aquaticus symbionts	Asellus aquaticus, Symbionts	Asellus aquaticus
820	BIO205 UZH-Blockcourse	mtDNA sequencing, microsatellites	Homo sapiens & Pongo pygmaeus
819	Microbial communities in the sediments of Lake Rot	Microbial communities, 16S rRNA genes, qPCR, Next generation sequencing	Bacteria and Archaea
818	Influence of disturbance on members of the Phialocephala fortinii s.l. - Acephala applanata species complex (PAC)	Disturbance, Phialocephala fortinii, Conifers, Endophytes	Phialocephala fortinii, Acephala applanata
817	Identification of quantitative trait loci (QTL) for ecological traits in diploid populations of Arabidopsis arenosa.	Arabidopsis arenosa, QTL mapping, Flowering time, Ecological genetics, ddRAD-sequencing	Arabidopsis arenosa
816	Wheat powdery mildew population genetics	Genomics, Wheat powdery mildew, Population genetics	Blumeria graminis
815	EcoImpact 2 - ARA Muri	gene expression, pipetting robot	Rainbow trout (liver tissues)
814	Biodiversity is in the air ,À Biodiversity monitoring through the metabarcoding of air-borne eDNA	metabarcoding, eDNA, Insects, Biodiversity, Monitoring	airborne environmental DNA
813	Microbial community responses to phosphorus and nitrogen inputs in the organic soil horizons of two contrasting temperate beech forests	T-RFLP, phoD, nutrient addition, organic soil horizon, microbial P cycling	T-RFLP data (16S rRNA, ITS, phoD, acpA)

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812	Monitoring the molecular responses of fish cell lines exposed to micropollutants as an alternative to the sampling of fish	fish cell lines, gene expression, water samples, biomarker genes, positive control	Eawag
811	Genetic basis of stomatal aperture in Arabidopsis	Arabidopsis, GWAS, S tomata	Arabidopsis thaliana
810	Gene expression analysis Rainbow trout cell line	qPCR, pipetting robot, 384 well plates	Rainbow trout gill cell line - RTgill-W1 (Oncorhynchus mykiss)
809	Metabarcoding of Italian fishes - in-silico approach to determine intraspecific signals derived from different universal fish primers.	eDNA, metabarcoding, in-silicoPCR	Fish
808	Quantifying mRNA barcoding efficiency	qpcr, sybr, lightcycler	fixed Salmonella enterica nucleic acids
807	Global Drivers of Plant-Associated Microbial Communities: Consequences for Forest Diversity	microbiome, soils, forest, environmental sequencing, metabarcoding	Fungi, bacteria (Environmental sequences)
806	GLEE	phytoplankton, ecology, evolution, resource competition	phytoplankton
805	Herkunft und Anpassung der Eichen auf Reliktstandorten (AQUAREL)	landscape genomics, local adaptation, forest genomics	Quercus petraea
804	Multipotency of human neural crest stem cells	scRNA-seq, neural crest	Human
803	Using CRISPR-Cas for species identification in environmental DNA	CRISPR, environmental DNA, Cas13	Salmon trutta
802	DNA Analysis of Pollen Carried by Honeybees	Pollen, genetic fingerprinting, honeybees, biodiversity, citizen science, artificial intelligence	Flowering plants
801	RNA quality check for Spatial Transcriptomics/RNAseq	RIN value, RNA	RNA from mouse tissue/ RNA from mouse cells
800	Population Genetics of L. minor in Switzerland	Lemna minor, ddRAD, genetic diversity, population genetics, duckweed, plant population ecology	Lemna minor (common duckweed or lesser duckweed)
799	Algae virus coevolution	rapid adaptation, host virus coevolution, multiple stressors	Chlorella algae, Chlorovirus

ID	title	keywords	organism
798	Genetic study of stone crayfish ( <i>Austropotamobius torrentium</i> ) in Switzerland	stone crayfish	
797	EpiPop	DNA methylation, Epigenetic diversity, <i>Arabidopsis thaliana</i>	<i>Arabidopsis thaliana</i>
796	Impact of early life trauma on immune reactivity	early life trauma, immunity	Laboratory of Neuroepigenetics (UZH/ETHZ)
795	Influence of Microplastics and Freshwater Snow Heteroaggregation on Particle Settling Rates in the Freshwater Environment	microplastics, freshwater snow, settling, heteroaggregation	ETH Zurich
794	Genetic basis of mycorrhization traits in <i>Pisolithus microcarpus</i>	ectomycorrhizal fungi, experimental evolution, genome-wide association study, genomics, symbiosis	<i>Pisolithus microcarpus</i>
793	Trade off between drought and frost adaptation in swiss tree seedlings	drought resistance, osmometer, centrifuge	ETHZ
792	Organic selenium and sulfur in soils and peatlands	Metabolomics, Selenium, Sulfur, Soil, SOM, DOM, Geochemistry	None
791	Metatranscriptomics of deep buried lake sediment microbiota	metatranscriptomics, sediment microbial communities, microbial dormancy, microbial ecology	freshwater sediment microbial communities (very high diversity, large fraction of previously unsequenced, uncultured microorganisms)
790	<i>Abies alba</i> linkage map	linkage map, genome assembly, SSR, NGS, capture probes, <i>Abies alba</i> , controlled cross	WSL
789	Towards building microbial consortia for pest control: exploring adaptation to insect hosts and intraspecific diversity of pathogenicity and competition traits in insecticidal pseudomonads	Insecticidal pseudomonads, Biological pest control, Experimental evolution	<i>Pseudomonas protegens</i> CHAO
788	Microbial community composition of biofilms on rocks and sediments in an Background Alpine glacial floodplain system	microbial biofilms, glacial floodplains, subglacial ecosystems, community composition, qPCR, miseq, ecological succession, global warming	Prokaryotes, Eukaryotes, Archaea
787	The role of peripheral glia in squamous cell carcinoma	peripheral glial cells, skin, tumorigenesis	<i>Mus musculus</i>

ID	title	keywords	organism
786	Transcriptomic analysis of the <i>Lolium multiflorum</i> ,À <i>Xanthomonas translucens</i> pv. <i>graminis</i> interaction	RNA seq, qRT-PCR	ETH Zurich
785	Release Kinetics of Fluorescent Dyes in Nanocapsules	release kinetics, Cy5, Texas Red, microplate reader	nanocapsules
784	Unlocking Epigenetic Variation to Breed Sustainable Crops in a Changing Climate	Epigenetic variation, <i>Arabidopsis thaliana</i> , transgenerational stability, plant breeding, DNA methylation	<i>Arabidopsis thaliana</i>
783	Microbial communities in the deep thermal waters of Lavey-les-Bains	Deep Life, Thermal Waters, Microbial Communities	Bacteria and Archaea
782	Experimental floods and habitat fragmentation shape spatio-temporal genetic diversity patterns of an amphipod population in a regulated alpine river	Experimental floods, population dynamics, microsatellites	<i>Gammarus fossarum</i>
781	Orang-utan genomics in an evolutionary and conservation context	Pongo sp., Orang-utan, Population Genomics, Ancient DNA, Non-invasive Sampling	Pongo
780	Molecular relationships between nutrition, metabolism and the epigenome	Quality Control of libraries	Mouse <i>musculus</i>
779	<i>Chlorella</i> -bacteria co-cultivation	microalgae, co-cultivation, microbial communities, transcriptomics	<i>Chlorella vulgaris</i> , 224 different bacterial strains
778	METALink: Linking environmental, genomic, and phenotypic information to study the adaptation of <i>Arabidopsis halleri</i> to metal-polluted soils	<i>Arabidopsis halleri</i> , soil contamination	<i>Arabidopsis halleri</i>
777	Nutrient dynamics in soilless system	aquaponic, hydroponic, bioponic, lettuce, tilapia, nitrogen, community analysis, metagenome	bacteria, archaea, funghi, <i>Oreochromis niloticus</i> , <i>Lactuca sativa</i>
776	The alpine resistome	16SrRNA, shotgun sequencing, antibiotic resistance gene, metagenomics, cheese, environment	Bacteria
775	Evolution of a synthetic bacterial community	evolution, mutations, cross-feeding, microbial communities, nutrient limitation	<i>Escherichia coli</i>

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774	Identification of post-transcriptional regulatory mechanisms in parvalbumin positive basket cells by miRNA-138-5p	gene expression	mus musculus
773	The role of bacteriophages in the spread of antimicrobial resistance	bacteriophages, antibiotic resistance, qPCR	bacteriophages and bacteria
772	Determining the molecular mechanism by which acylfulvene derivatives and TC-NER cause DNA breaks	DNA damage sequencing, GLOE-Seq, DNA lesions, DNA breaks	Homo sapiens
771	CFTR NGS	cystic fibrosis, peanut allergy, CFTR	Homo sapiens
770	Investigating ecology of gut bacterial communities using in vitro PolyFermS	Gut microbiota, community ecology, 16S metabarcoding, sequencing, spacial organization, stability	Microorganisms of human gut
769	Immune Stimulation in MSUS	MSUS, immune system, immune stimulation	Mouse
768	Darwin Finches	local adaptation, selection, biodiversity	Geospiza Fuliginosa, Geospiza Fortis, Geospiza Magnirostris
767	Magnetic particle separator-based DEL selections	magnetic particle separator, affinity-based selections, DNA-Encoded Chemical Libraries	n/a, selections against purified proteins
766	PREFER Prebiotic GOS and lactoferrin for beneficial gut microbiota with iron supplements in Kenyan infants	gut microbiota, infants, iron	DNA from gut bacteria
765	Lab course Biogeochemistry 2021	Course	Environmental methane oxidizing bacteria
764	Density-dependent predation	predation, density-dependence, qPCR, environment-dependent predation	Myxococcus xanthus
763	Plant-Microbe interactions	plant microbiomes	mostly Arabidopsis thaliana
762	Unravelling the molecular mechanisms underlying the superior performance of grass stomata	gene expression, guard cells, plant physiology, stomata, starch metabolism	Hordeum Vulgare
761	Consequences of chitin degrader identity on community composition of cross-feeders	Microbial ecology, Community Composition, Chitin degradation, 16S	Marine Microbial consortia (Bacteria)

ID	title	keywords	organism
760	AK02 - 16S rRNA profiling of synthetic communities on <i>A. thaliana</i> GNSR mutants	microbiome, 16S rRNA gene sequencing, community profiling, microbiota, synthetic communities, plant immunity	<i>Arabidopsis thaliana</i> , synthetic bacterial community (SynCom-137)
759	Molecular identification of Malagasy rosewoods	conservation biology, SNP, <i>Dalbergia</i>	<i>Dalbergia</i> spp.
758	AmphiWell	environmental DNA, metabarcoding, groundwater ecology	<i>Niphargus</i> sp.
757	Wheatear Popgen	Population genomics, evolution	genus <i>Oenanthe</i> and relatives
756	ICP Forest Microbiome Analysis	microbiome, DNA sequencing, metagenomics, metabarcoding	mixed soil fungal communities.
755	GenWood vç,ç",Áú Exploring the genomic basis of wood anatomy	dendrochronology, forest genomics, local adaptation	<i>Picea abies</i>
754	DNA methylation in ESR1, ESR2, GPER	DNA methylation	Humans
753	Identification of new starch granule initiation mutants	DNA-extraction for NGS	<i>Arabidopsis thaliana</i>
752	Relative quantification of species within a community	taxonomic markers development	list of reference organisms
751	Using Environmental DNA to analyse fish diversity in the Shark Bay	environmental DNA, Shark Bay, metabarcoding, fish, biomonitoring	Actinopterygii
750	Quantification of <i>Myxococcus xanthus</i> and <i>Zymoseptoria tritici</i> by qPCR	biocontrol	<i>Myxococcus xanthus</i> , <i>Zymoseptoria tritici</i>
749	The role of genomic diversity and associated mycorrhizal communities in the response of European beech to extreme drought events (BeeGees)	drought response, whole-genome sequencing, beech, ectomycorrhiza, SNPs	<i>Fagus sylvatica</i> , <i>Cenococcum geophilum</i>
748	Hiwi Envir. Microbio.,	microbiology, functional genes	<i>mcrA</i> , <i>pmoA</i> , <i>amoA</i> communities
747	Development of sleep regulation a window of opportunity for fostering healthy development	sleep regulation, gut microbiome, infants	human gut bacteria
746	Antibiotic resistance encoded on prophages	prophages, whole genome sequencing, antibiotic resistance	<i>E. coli</i>



ID	title	keywords	organism
745	Biodiversity and microbial community composition of the Val de Roseg glacier floodplain	Biodiversity, Community composition, Glacier floodplain, metabarcoding, 16S-RNA/18S-RNA	unknown prokaryotes and eukaryotes determined in the project
744	Myvatn stickleback genomics	whole genome sequencing, <i>Gasterosteus aculeatus</i> , landscape genomics, sex-biased dispersal	<i>Gasterosteus aculeatus</i>
743	Altering microbe-induced stomatal closure to restrict foodborne diseases of leafy greens	Pattern Triggered Immunity, <i>Salmonella enterica</i> , Lettuce, Stomata	<i>Arabidopsis thaliana</i> , <i>Lactuca sativa</i>
742	Clupini genotyping	SNP, phlogeny	<i>Colletotrichum lupini</i>
741	Ploidy of <i>Asellus aquaticus</i>	<i>Asellus aquaticus</i> , freshwater isopod, ploidy, sexual reproduction, clonal reproduction	<i>Asellus aquaticus</i>
740	Fungal Endophyte Diversity on <i>Pinus mugo/montana</i>	Bachelor Thesis, PCR, DNA extraction	various Fungi, <i>Pinus mugo</i>
739	<i>Antiversa</i>	antibiotic resistance expression and spread	streams and soils microbes
738	Soil microbial responses to climate warming	Climate change ecology; microbial ecology; biogeochemistry; carbon cycling.	Soil microbial bacteria, fungi and archaea
737	EcoImpact_Macroinvertebrates_2.0	metabarcoding, COI, macroinvertebrates, diversity	-
736	Biodiversity assembly in blue and green ecosystems: speciation versus immigration	Biogeography, macroevolution, Alps	Angiospermae, Lepidoptera, Amphipoda, and multiple lineages of fish
735	Effect of Tesaglitazar on Neuronal Cultures	gene expression	<i>homo sapiens</i>
734	LeCo project - Environmental factors affecting <i>Legionella</i> growth	Microbial ecology	<i>Legionella</i> spp. and drinking water microbial community
733	Ontogenetic development and the rise and fall of sympatric species diversity	Evolution, speciation, disruptive selection, ontogeny	NA
732	LeCo project - Ecology and microbial interactions of <i>Legionella</i> in building plumbing systems	Microbial communities, 16S amplicon sequencing, miSeq, Whole Genome Sequencing	<i>Legionella</i> spp. - Microbial communities
731	Life in the Bedretto Underground Laboratory	16S, groundwater, exploratory analysis	environmental

ID	title	keywords	organism
730	Identification of environmental factors selecting for toxic cyanobacteria	cyanobacteria, toxins, toxic genes, algal blooms, non-ribosomal peptide synthase, diversity	cyanobacteria / phytoplankton
729	MicSys (SNF_Amplicon)	Long-term trial, amplicon sequencing, farming system, microbiome	soil microbiome
728	Biomarkers for effect-based monitoring of water quality with brown trout	Gene expression biomarkers, Ecotoxicology, Biomonitoring	Salmo trutta
727	Uncovering cryptic diversity in Swiss wild bees	conservation biology, wild bees, Illumina, amplicon sequencing	Wild bees
726	Functional validation of GWAS via genetic engineering (CRISPR-Cas9) in <i>B. distachyon</i> .	Agrobacterium-mediated transformation, <i>Brachypodium distachyon</i> , CRISPR/Cas9 system	<i>Brachypodium distachyon</i>
725	Characterization of auxotrophic members of the <i>Arabidopsis thaliana</i> leaf microbiota	Auxotrophy, microbiology, coculture, crossfeeding	40 bacterial species
724	BeneComb	biocontrol	nematode <i>Steinernema feltiae</i>
723	Rapid adaptation of a major wheat pathogen to dynamic host and fungicide environments during a single epidemic season	wheat pathogen, evolutionary biology, adaptation, fungicide resistance, <i>Zymoseptoria tritici</i>	<i>Zymoseptoria tritici</i>
722	Stump tail defect in boars	stump tail defect, genotyping, DNA fragment analyzer	pig
721	Runs of homozygosity and genetic load as indicators of fitness	Genetic diversity, genomic data, runs of homozygosity, inbreeding, genetic load	<i>Dianthus silvestris</i> , <i>Dianthus carthusianorum</i> [+ 5 species from the genetic diversity monitoring]
720	Pilot study for a Genetic diversity Monitoring in Switzerland	genetic diversity, conservation genetics, reference genomes	<i>Melitaea diamina</i> , <i>Eriophorum vaginatum</i> , <i>Emberiza citrinella</i> , <i>Bufo calamita</i> , <i>Dianthus carthusianorum</i>
719	Adaptive genetic diversity and phylogeography	genetic diversity monitoring, ecological genomics, SNPs, WGS	<i>Silene</i> spp. and 5 species of the GenDiv monitoring project
718	Changes in genetic diversity during the 20th century	conservation biology, population genetics, genetic diversity, herbarium, genetic erosion, demography, simulation	<i>Dianthus sylvestris</i> , <i>Arabidopsis halleri</i> , <i>A. lyrata</i> , <i>A. arenosa</i> , <i>A. thaliana</i> , <i>Arabis alpina</i> , <i>Silene exscapa</i> , <i>S. acaulis</i> , <i>Eriophorum vaginatum</i>

ID	title	keywords	organism
717	Exploring toxicological response pathways by inter-individual variation	behavior, zebrafish, toxicology, molecular mechanisms	Zebrafish
716	Global measure of biodiversity by understanding biogeochemical cycling of environmental DNA in lakes	conservation, biodiversity, monitoring, eDNA	plants and animals
715	Phage lysis timing dynamics	viral threshold dynamics, evolution, noise optimisation	E. coli
714	Age estimation based on DNA methylation patterns in Indo-Pacific Bottlenose Dolphins ( <i>Tursiops aduncus</i> )	Anthropology, CpG, methylation analysis	<i>Tursiops aduncus</i>
713	Soil microbial diversity and stability as regulators of nitrogen cycling and agricultural sustainability	Nitrogen, functional gene, gene expression	Soil microbiome
712	Yeast extract for gut microbes and colonic microbiota	Modulation gut microbiota	human proximal colon microbiota (DNA)
711	Community and population phytoplankton genetic diversity in response to nutrient addition and foundation species	community turnover, genetic turnover, 18s, 16s, ITS2, rpoC1	phytoplankton, <i>Synechococcus</i> , <i>Lagerheimia</i>
710	Multispecies experiment evolution	ecology, evolution, microbial communities	<i>Myxococcus xanthus</i> , <i>Pseudomonas fluorescens</i> , <i>Escherichia coli</i> , <i>Sphingobium yanoikuyae</i>
709	Phage Display For Multispecific Discovery	Antibody, phage display, discovery, library	M13 Filamentous Phage, E.coli Bacteria
708	Influence of spatial and temporal separation on population structure of the European cockchafer and its main fungal pathogen	Genetic structure, populations, spatial and temporal separation, SNP	<i>Melolontha melolontha</i> , <i>Melolontha hippocastani</i> , <i>Beauveria brongniartii</i>
707	Comparative genomic analysis between psychrophilic and mesophilic bacterial species	psychrophilic species	bacteria / Microorganisms
706	Plasmid stability	plasmid, evolution	<i>Escherichia Coli</i>
705	Microbial Diversity and Dynamics in a Circular Water Recycling System for Domestic Washing Machines	16S Amplicon Sequencing, Microbial Diversity, Washing Machine	Bacteria / Microorganisms
704	A_lyrata_ONT_Amplicon_seq_analysis	Oxford Nanopore, amplicon, selfing	<i>Arabidopsis lyrata</i>

ID	title	keywords	organism
703	FISHEC Shared Bioinformatics Resources	fish, ecology, evolution	fish
702	Response of a cold-adapted bacterium to temperature changes	gene expression	Pseudoalteromonas haloplanktis
701	Ecological and Evolutionary Genomics in Greenlandic Stickleback	eco-evolutionary dynamics, population genomics, genomic divergence	Gasterosteus aculeatus, Leptodiaptomus minutus, Salvelinus alpinus
700	Role of GPR35 in intestinal inflammation	IBD, GPR35, colitis, SNP, microbiota	Bacteria
699	Experimental assessing the evolution and spread of antibiotic resistance in a simulated hospital environment.	evolution, antibiotic resistance	Escherichia coli
698	The Asellus triangle: the host, the microbiome, and global change	Adaptation, gut microbiome, stress, micropollutants, temperature	Asellus aquaticus
697	Detection of sex-specific genetic markers in Silene exscapa	ddRAD, sex-specific genetic markers, dioecy	Silene exscapa
696	ToXAdapt	gene expression, aquatic biofilms, algae, ecotoxicology	Aquatic biofilms, Diatoms, Green algae, Cyanobacteria
695	Metagenomics in milk from cows with mastitis	Milk, mastitis	Bacteria
694	Sloppy ocean bottom hypothesis (SLOB)	hydrodynamics, anoxia, nepheloid layers, microbial community structure	Microbiome
693	Influence of Pesticides on Soil Fertility	soil microbiological activity, soil ecosystem functions, pesticides, soil fertility	environmental samples
692	Genomics and Quantitative Genetics of Plant Pathogens	Plant pathology, genetics, evolution, genomics	Zymoseptoria tritici, Cercospora beticola
691	RNAseq Analysis of Caulobacter crescentus	gene expression	Caulobacter crescentus
690	Mechanism of Color Leaf Variation During Different Seasons of Liquidambar formosana and Genetic Relationships of Liquidambar	gene expression; chloroplast genome assembly; phylogeny	Liquidambar spp.
689	Molecular identification of two groups of Malagasy Dalbergia	Dalbergia, DNA sequencing, molecular species identification	Dalbergia spp.
688	Genetic connectivity between coastal dolphin populations	Conservation biology, Next generation sequencing, SNP, ddRAD, Evolution	Bottlenose dolphin, Tursiops sp.; Australian humpback dolphin, Sousa sahalensis; Australian snubfin dolphin, Orcaella heinsohni)

ID	title	keywords	organism
687	Characterization of Avr genes of <i>Zymoseptoria tritici</i>	pathogen, gene expression, evolution	<i>Zymoseptoria tritici</i>
686	Fungal communities in soils of truffle grounds and on mycorrhizal roots of Scots pine grown in an irrigation experiment	fungal communities, Amplicon Barcoding, ectomycorrhiza	fungi
685	Metabarcoding BT group	16S metabarcoding, amplicon	human & food microbiota
684	Probing carbon limitation in marine phytoplankton	carbon limitation, coccolithophores, rubisco kinetics, rubisco fractionation, photorespiration	<i>Emiliana huxleyi</i> , <i>calcidiscus leptoporus</i> , <i>coccolithus braarudii</i>
683	Fish Welfare Assessment	stress, behaviour, gene expression regulation	<i>Cyprinus carpio</i> , <i>Oncorhynchus mykiss</i> , <i>Danio rerio</i> , <i>Perca fluviatilis</i>
682	GeneScale	landscape genomic, local adaptation, <i>Arabis alpina</i>	<i>Arabis alpina</i>
681	Cultivation of soil microbiome members with the nanoFleming	microbiome cultivation, 16S RNA sequencing	Soil samples
680	PiCadapt - Adaptive genetic variation of Swiss stone pine in response to environmental gradients across the Alpine timberline ecotone	climate change, local adaptation, Swiss stone pine, <i>Pinus cembra</i> , timberline, transcriptome, exome capture, SNP genotyping, environmental association analyses	<i>Pinus cembra</i>
679	Membrane Probiotics	Probiotics, community composition, 16S, Membrane filtration, opportunistic pathogens	Natural Bacterial Communities
678	Thrombin-induced exRNA supports thrombosis	exRNA quantification by qubit	human
677	Using environmental DNA (eDNA) for monitoring effects of wastewater pollutants on biodiversity	eDNA, wastewater pollution, eukaryotes, eubacteria	eukaryotes, eubacteria
676	MiCoDy-Lipids	Environmental bacterial community analysis	Environmental samples
675	Raman Sulfur SNF	organic sulfur	bacteria, archaea
674	Adaptive role of transposable elements in natural populations of <i>Brachypodium distachyon</i>	TEs, GWSS, <i>Brachypodium distachyon</i> , adaptation	<i>Brachypodium distachyon</i>

ID	title	keywords	organism
673	Leaf metabolomics on an altitudinal gradient	metabolomics, alpine plants, altitude, climate warming	Different species of alpine plants
672	Innovative $\mu$ Bead technology for controlled production of trophic microbial teams applicable as live biotherapeutics or synthetic microbial ecology tool	bacteria, spatial separation, trophic interaction, microbial ecology, production technology, live biotherapeutics	DNA from gut bacteria
671	Capturing fungal diversity using fruiting body surveys and modern molecular approaches	fungal diversity, conservation biology, metabarcoding	several
670	Influence of transposable elements on gene expression in <i>Brachypodium</i>	gene expression, transposable elements, <i>Brachypodium distachyon</i>	<i>Brachypodium distachyon</i>
669	Global phylogeography of <i>Lobaria pulmonaria</i> and its adaptive traits probed by single-nucleotide polymorphism towards developing a global conservation strategy	<i>Lobaria pulmonaria</i> SNP, conservation biology, global phylogeography,	<i>Lobaria pulmonaria</i>
668	Population structure and the breeding system of the wild and rewilded Aldabra giant tortoises	population genomics, conservation genomics, ddRAD-seq, SNP	<i>Aldabrachelys gigantea</i>
667	Population heterogeneity in the surface sediments of Lake Cadagno	evolution, SNP, diversity, 16S	metagenome
666	Main environmental drivers behind the community structure, diversity, activity, and abundance of methane-producing Archaea in deep seafloor sediments	qPCR, NGS	bacteria, archaea
665	Microbiome Forensics	microbiome forensics, body fluid identification, 16S rRNA gene, predictive power, individual identification	Human Microbiome
664	Impacts of micropollutants on stream periphyton	Ecotoxicology, stream periphyton, microbial community, genomic diversity	stream periphyton
663	Paleo-ecotoxicology	sedaDNA, amplicon sequencing, paleolimnology, chironomids, ecology	Bacteria, Chironomids, Eukaryota
662	Characterization of microbial communities of Lake Cadagno over Holocene	Cadagno, Bacteria, Archea, Sulfur, Anoxic, Sequencing	Bacteria and Archea

ID	title	keywords	organism
661	Influence of bioturbation on microbial communities in lake sediments	Bioturbation, lake sediments, microbial communities	Bacteria and archaea
660	Tracking antibiotic resistance from environmental reservoirs to the food chain	antibiotic resistance, plant foods, environment, contamination sources	n.a.
659	Re-sequencing the Alpine whitefish radiation	whitefish, whole genome re-sequencing, adaptive radiation	Coregonus spp
658	Silver Fir Genome Project-Assembly improvement	genome assembly, long-read sequencing	Abies alba
657	Calibrate: Transcriptomic profiling of zebrafish exposed to ENMs	ecotoxicology, nano materials	zebrafish (Dario serio)
656	ABA-dependent starch degradation under osmotic stress	starch, physiology, gene expression, gene promoter analysis	Arabidopsis thaliana
655	The role of the gut microbiota an impact of early life stress in pediatric functional abdominal pain disorders	functional abdominal pain disorders, gut microbiota, early life stress, early life trauma	Gut microbiota
654	NRP72-AMRChick	antimicrobial resistance, horizontal gene transfer, one health, gut microbiota	Gut microbiota, Enterococcus faecium, Enterococcus faecalis, Escherichia coli
653	Population genetics of quagga mussels	population genetics, SNP, quagga mussels,	Dreissena polymorpha, Dreissena bugensis
652	Manipulation From Within vç,ç",Äú How Does Functional Niche Occupancy Impact A Next Generation Probiotic?	Gut microbiota, acrolein, next generation probiotic	Gut Microbiota, Eubacterium hallii
651	Urease Assays	Urease	-
650	Mapping of UV-induced oxidative damage in the genome of human fibroblasts	DNA Damage, damage sequencing, UV, UV signature, mutation signature, 8oxoG	Homo Sapiens
649	Illuminating the secret life of Burgundy truffles	Burgundy truffle, population genetics, SSR, ectomycorrhiza, life history, mating type	Tuber aestivum
648	Nitrification of human urine for space application	waste water, nitrification, ammonia-oxidizing bacteria, nitrite oxidizing bacteria	ammonia-oxidizing bacteria, nitrite oxidizing bacteria
647	Grassland restoration using topsoil removal	conservation/restoration biology, amplicon sequencing, metabarcoding, soil samples	procaryotic communities

ID	title	keywords	organism
646	Illuminating the secret life of Burgundy truffles	Burgundy truffle, population genetics, SSR, ectomycorrhiza, life history, mating type	Tuber aestivum
645	GenTree	forest trees, exome capture, SNP genotyping, local adaptation, population genetics	12 forest tree species
644	Wildkatzenhybridisierung	conservation biology, applied biology, SNP, hybridization	Felis silvestris, Felis catus
643	Characterization of <i>C. vulgaris</i> associated microbiota PBRatLSR space flight experiment	Chlorella vulgaris, microbiome, NGS (MiSeq), 16S rDNA, 18S rDNA	Chlorella vulgaris
642	Establishing the moderlieschen ( <i>Leucaspius delineatus</i> ) genome	genome sequencing	Moderlieschen ( <i>Leucaspius delineatus</i> )
641	Lake Constance whitefish	whole genome re-sequencing, scale samples, extinct species	<i>Corgonus</i> spp
640	Human Milk Project	human milk proteins	human
639	Intracellular trace metal speciation analysis in phytoplankton cells	projectID: 476 (submitted by Ms Pauline BÉziat)	<i>Scenedesmus obliquus</i> and different types of pennate diatoms
638	Parasitoid adaptation to symbiont-conferred resistance	host-parasite coevolution, defensive symbiosis, insect parasitoids	<i>Lysiphlebus fabarum</i>
637	de-novo genome assembly of <i>Lolium multiflorum</i>	genome assembly	<i>Lolium multiflorum</i>
636	Deciphering the role of vitamins B9 and B12 as modulators of the human gut microbiota	gut microbiota, B vitamins, in vitro model, 16S rRNA	bacteria
635	Estimation of Postzygotic Isolation between two <i>Arabidopsis</i> species based on Pollen counts	Evolution, speciation, range limits, pollen counts	<i>Arabidopsis lyrata</i> subsp <i>lyrata</i> , <i>Arabidopsis arenicola</i>
634	Genetic variation in <i>Phragmites</i>	<i>Phragmites</i> , plastomes, sequence capture	<i>Phragmites australis</i>
633	Relation of DNA oxidation damage with neurodegenerative disease	DNA damage sequencing	Human brain tissue
632	High-density genetic map of <i>Arabidopsis arenosa</i> using ddRAD sequencing	<i>Arabidopsis arenosa</i> , genetic map, ddRAD-seq, meiosis	<i>Arabidopsis arenosa</i>
631	High throughput genotyping in Alpine ibex	population genomics, amplicon seq	Alpine ibex
630	Bioinformatics of microbiome data	bioinformatics, Euler	Microbiome



ID	title	keywords	organism
629	Ecology and evolution in practice	crop plants, evolutionary ecology, soil microbes, intercropping	Triticum aestivum, Avena sativa, Lens culinaris, Lupinus angustifolius, Camelina sativa
628	Evolutionary Engineering of Food-Associated Microorganisms	Adaptive evolutionary engineering, evolution, gut microbiota composition, single strain in complex ecosystem	DNA from Lactobacillus plantarum NZ3400Cm, human and chicken gut microbiota
627	Redox characterisation of peat organic matter - sample preparation	organic matter, carbon cycle	Not applicable
626	Malcom Barcoding	barcoding, CO1, butterfly	Graphium sp.
625	Characterization of microbial community shifts in plants hydroponically grown in a human urine derived nutrient solution inoculated a with commercial microbial consortium	hydroponics, microbial consortium, NGS, urine derived fertilizer, soybean	Soil and aquatic microorganisms (bacteria and fungi), rhizosphere microbial communities, plant assoc
624	Regulation of guard cell starch degradation	plant molecular physiology, cloning	Arabidopsis thaliana
623	Development and verification of a real-time PCR assay to detect geosmin-producing bacteria in recirculating aquaculture systems	none	Actinobacteria (mainly Streptomyces), Cyanobacteria, Myxococcus
622	Carex phylogeny and EAA	Phylogeny, SNP, Environmental association analyses, conservation genomics	Carex sect. Scirpinae
621	Starch biosynthesis in guard cells	Plant physiology, gene expression, Arabidopsis, guard cells, enzyme assay	Arabidopsis thaliana, E.coli, A. tumefaciens
620	Continuation of Using environmental DNA (eDNA) for monitoring effects of wastewater pollutants on biodiversity	eDNA, COI, Eukaryote, Switzerland	eukaryotes
619	Rhizobacteria-mediated effects on defense gene expression	RNA quality, Gene expression	Arabidopsis thaliana, Solanum lycopersicum
618	whitefish genomics	conservation genomics, adaptation genomics, speciation genomics	whitefish various species
617	Role of somatic testis cells in transgenerational epigenetic inheritance of early life trauma	epigenetic inheritance, sertoli, leading, postnatal trauma	mouse

ID	title	keywords	organism
616	Investigation of metabolic capacity of microbial consortia involved in micropollutant biotransformations	metagenomics, metatranscriptomics, micropollutants, biotransformations	Activated sludge communities
615	Activation of macrophages	gene expression	Mus Musculus
614	Lumbriculus population genetics	microsatellite, population genetics, ploidy, asexual	Lumbriculus variegatus
613	Time-course RNA-Seq of <i>A. thaliana</i> infected with <i>F. oxysporum</i>	Transcriptomics	<i>Arabidopsis thaliana</i> , <i>Fusarium oxysporum</i>
612	Protein content in tissues of insect-pollinated plants	protein quantitation, leaves, pollen	40 species of angiosperms native to Europe; checklist can be provided upon request.
611	Genetic monitoring in <i>Murbeckiella</i>	adaptation, conservation biology, herbarium genomics, phylogenetics, population genomics, systematics, taxonomy	genus <i>Murbeckiella</i> (especially <i>M. pinnatifida</i> - Brassicaceae)
610	Praktikum Mikrobiologie	Molekularbiologische Methoden	<i>Escherichia coli</i>
609	The functional basis of edaphic adaptation to high metal concentrations	adaptation, evolution, genomics, SNP, gene expression	<i>Arabidopsis arenosa</i> , <i>Arabidopsis halleri</i>
608	De novo assembly of plant genomes	Genome assembly, Oxford Nanopore Sequencing, PromethION	<i>Lolium perenne</i> , <i>Lolium multiflorum</i> , <i>Festuca pratensis</i>
607	PHB metabolism in marine microbial communities	Microbial ecology	Marine bacteria
606	Ecological genomics of altitudinal adaptation in wild carnations	Altitudinal adaptation, ecological genetics, demographic history	<i>Dianthus sylvestris</i> , <i>Dianthus carthusianorum</i>
605	Flowering time mechanisms	Flowering time	<i>Arabidopsis thaliana</i> , <i>Cuscuta campestris</i>
604	Phylogenomics and species delimitation within the genus <i>Hyphaene</i>	population genetics, phylogenetics, hybridization, species delimitation, admixture, conservation	<i>Hyphaene</i>
603	Identifying the ecological and genetic factors driving flower color diversification in a tropical plant lineage	anthocyanin pathway, diversification, Gesneriaceae, floral colour, macroevolution, pollination, sequence capture	Gesneriaceae
602	Species delimitation, phylogenomic diversity and niche modelling: implications for the	Sapotaceae, <i>Capurodendron</i> , conservation, phylogeny, speciation, phylogenomic,	Sapotaceae

ID	title	keywords	organism
	conservation of Madagascar endemic group of valuable trees in the family Sapotaceae	taxonomy, species delimitation, SNP, microsatellites, new species, niche modelling, red list, UICN category	
601	Plant root microbiomics	root microbiome, 16S and ITS amplicon, metagenomics	Arabidopsis thaliana and Zea mays
600	Evolutionary Conflicts in Arthropods	sexual conflict, Wolbachia	Wolbachia
599	Defensive symbiosis in the wild ñ the role of symbiont-conferred resistance in natural host-parasitoid communities	host-parasite coevolution, defensive symbiosis, insect parasitoids	Aphis fabae, Lysiphlebus fabarum, Hamiltonella defensa
598	Ecological genetics of speciation and dioecy in Nepenthes pitcher plants - II	Genotyping by sequencing (GBS), RAD sequencing, SNP discovery, RNAseq, population genetics, evolution, ecology	Nepenthes ssp.
597	Diversity of endophytic fungi in needles of the none-native Douglas fir (Pseudotsuga menziesii)	endophytic fungi, fungal communities, exotic forest tree species	Pseudotsuga menziesii, Picea abies
596	Plant-Soil Feedback	soil feedback, soil microbial communities, 16S and fungal ITS sequences	general soil bacteria, soil fungi incl. AMF
595	Effects of microplastics on freshwater biofilms - Amplebig	Periphyton, Microplastic, Grazers, Triclosan	Periphyton
594	Differential Gene Expression in insects exposed to pesticides	ecotoxicology, Non-Target Organisms, pesticides, beneficial insects	Chrysoperla carnea, Adalia bipunctata
593	Sequencing of Carboxymethyl DNA with Nanopore Sequencer	toxicology, DNA damage, nanopore sequencing	in vitro
592	Microbiome of Asellus aquaticus	evolutionary ecology, symbionts, microbiome	Asellus aquaticus
591	Assessing phylodynamic methods in silico and in vitro	phylodynamics, bacteriophage, E.coli	bacteriophage phiX174
590	Effects of environmental variation in resource availability on the ecological diversity of stickleback	SNP, evolution, ecology, environmental variation, speciation	Gasterosteus aculeatus
589	Impact of land-use intensity on soil microbiota and ecosystem multifunctionality	land use intensity, microbial diversity, ecosystem multifunctionality	environmental samples

ID	title	keywords	organism
588	Characterization of the microbial community in raw milk cheese by high-throughput qPCR	Swiss raw milk cheese, lactic acid bacteria, quantification, fermented foods, food microbial systems, cheese quality	Lactic acid bacteria
587	Evolutionary processes in <i>Usnea subfloridana</i> and <i>U. florida</i>	microsatellites, lichens, mating types, evolution, ecology	<i>Usnea florida</i> , <i>U. subfloridana</i>
586	Molecular Mechanisms of Fast-Evolving Mating System in <i>Brassica rapa</i>	molecular evolution	<i>Brassica rapa</i>
585	methylation profiling and diversity in Turkish accessions of <i>B.distachyon</i>	genetic diversity, methylation, RNAseq	<i>Brachypodium distachyon</i>
584	Impact of glycoside hydrolases on intestinal microbiota composition and susceptibility to colitis	Gut microbiota, carbohydrate hydrolases	Gut commensals
583	Implementing Oxford Nanopore MinION Sequencing Technology &#8232; for Forest Health Diagnostics and Research - II	Oxford Nanopore; RNA sequencing; virus; forest health; diagnostics	viruses; fungi
582	Implementing Oxford Nanopore MinION Sequencing Technology &#8232; for Forest Health Diagnostics and Research - I	Oxford Nanopore; DNA amplicon sequencing; forest health; diagnostics	fungi; insects; bacteria
581	LakeMP	Micropollutant, biotransformation, phytoplankton, cyanobacteria, planktonic bacteria	mixture of phytoplankton and bacteria from Greifensee
580	Plant immunity controlling microbial community composition	plant microbiota, plant immunity, synthetic community	<i>Arabidopsis thaliana</i> , commensal bacteria
579	MAT-locus evolution in <i>Lobaria</i>	conservation biology, phylogeny, evolution	<i>Lobaria pindarensis</i> , <i>Lobaria yunnanensis</i> ,
578	Characterization of vascular repair mechanisms after stroke	stroke, angiogenesis, vascular repair	mouse
577	Soil nematodes	nematodes, soil DNA, biodiversity, amplicon sequencing	soil nematodes
576	Protocolestablishment for sufficient chromatin fragmentation in mouse liver and skeletal muscle	histone modifications, transcription factors, ChIP	<i>Mus musculus</i>

ID	title	keywords	organism
575	Protocol establishment of chromatin fragmentation in mouse liver and skeletal muscle	Chromatin fragmentation, ChIP, Histone modification	Mus musculus
574	DNA extraction for PoolSeq	DNA extraction, Pool-Sequencing, Ecological genomic, Brassica incana	Brassica incana
573	Isomol PE	Anammox, Process Engineering, Wastewater treatment, AOB, NOB, AOA, Community Shifts	Mainly gram negative, activated sludge (Candidatus Brocadia anammoxidans, Nitrosomonas europaea, Nit
572	Soil microbiome	microbiome, NGS	Multiple
571	RiverDNA: uncovering fundamental biodiversity in riverine systems using environmental DNA	biodiversity, environmental DNA, river networks	Various
570	N2O emission & microbial community variation in full-scale wastewater treatment	Activated sludge, Bacterial assembly, temporal dynamics	Bacteria in activated sludge
569	Role of bioturbation in controlling microbial community structure and biogeochemical cycles in marine sediment	bioturbation, marine sediment, microbial communities, biogeochemistry, organic matter	Abarenicola pacifica, Amphiuira filiformis, Deltaproteobacteria
568	BLW McDonald (PGREG-NN-0034)	plant-pathogen interaction	Zymoseptoria tritici, Triticum aestivum
567	Gene expression in sheep after dietary polyphenol and tannin supplementation	gene expression	Ovis aries
566	Electrospun Nanofibrous Scaffolds for Acetabular Labrum Restoration	qPCR, RNA extraction, tissue disruption	cow
565	Molekulare Altersschätzung	Forensic epigenetics, Chronological age prediction, DNA methylation	Homo sapiens
564	Reconstructing the demographic history of Australian bottlenose dolphin (Tursiops spp.) populations	SNP, ddRAD, demography, phylogeny, genetic clusters	Tursiops spp.
563	Bacterial and archaeal community composition influenced by bioturbating macrofauna in lake sediments	Bioturbation, worms, larvae, DNA extraction, qPCR	oligochaete worms and chironomid larvae

ID	title	keywords	organism
562	Characterization of nitrogen dynamics in an aquaponic system	aquaponic, lettuce, tilapia, nitrogen, community analysis, metagenome	Oreochromis niloticus, Lacuca sativa, ammonium-oxidizing bacteria, nitrite-oxidizing bacteria, ANAMM
561	Lake Nitrogen	Metagenome, Metatranscriptome, nitrogen gene expression, microbial community composition	all microbes
560	Off-Flavour control in land-based salmon production	microbial off-flavour producers	Actinobacteria, Streptomyces, Cyanobacteria, Myxococcus
559	Digging Deeper	Fungi, biogeography, network structure	Fungi
558	Permafrost microbes	soil, warming, global change, microbiome	soil microbiome
557	NEXTERA low coverage library for Glossina	ecotone, local adaptation, landscape genetic	Glossina morsitans and Glossina fuscipes and Glossina fusca
556	Yeast lysis optimization	Lysis, protein extraction	Saccharomices Cerevisiae
555	Effect of prebiotics on iron absorption in women with low iron stores	Human Gut microbiota composition, prebiotics, iron absorption	Bifidobacterium, Lactobacillus
554	Quantitative genetics of natural populations of Lymnaea	quantitative genetics, genetic diversity, parental analysis	Lymnaea stagnalis
553	Systematics and floral evolution of Dracula orchids	phylogenetics, Illumina sequencing, genome skimming, chloroplast DNA	Dracula (Orchidaceae)
552	A comprehensive assessment of hydrological and gaseous nitrogen losses from the tropical forests in the Congo Basin	soil microbial community, N cycle	microbes
551	Infant gut bacteria and sleep	gut bacteria, infants, diversity, 16S, human	homo sapiens sapiens
550	Monitoring and diagnostics of forest quarantine pathogens in Switzerland	Monitoring, diagnostics, barcoding, amplicon sequencing	Microbes and insects
549	GWAS Yeast	GWAS, Coevolution	Saccharomyces cerevisiae, Drosophila simulans
548	In planta activity of transposable element	transposable elements, stress, genome sequencing, comparative genomics	Brachypodium distachyon
547	Function of rodent hepacivirus	IRES, RNA folding	RNA extracted from murine hepatocytes

ID	title	keywords	organism
546	Evolutionary responses to climate change in alpine plant species	alpine plant, climate change, elevation gradient, selection	Anthyllis vulneraria, Trifolium badium, Ranunculus alpestris, Plantago alpina
545	extracellular RNAs (exRNAs)	exRNA, Homo Sapiens	Homo Sapiens and Mus Musculus
544	Effects of microbial endosymbionts on aphid interactions with host plants and virus transmission	Aphid-borne viruses, symbiosis, persistent-transmitted virus, aphid symbionts	Acyrtosiphon pisum, Myzus persicae, Buchnera aphidicola, Serratia symbiotica, Hamiltonella defensa,
543	Lake Microbial Diversity	microbial diversity, biogeochemistry, evolution	Prokaryotes
542	Cas9 editing readout	Cas9, genome editing, HDR, mammalian	homo sapiens, mus musculus
541	Metagenomics and Metatranscriptomics in lake Rotsee	methanotroph diversity, methane-oxidizing bacteria, lake, MMO, pmoA, metatranscriptomics, metagenomics	Environmental lake bacterial community
540	Benzo(a)pyrene (Bap) induced DNA damage maps of BEAS-2B cells	BaP, DNA damage, HS-Damage-seq	Human bronchial epithelium, BEAS-2B cells
539	CAMPYCHICK: Application of Lactobacillus reuteri for naturally prevent Campylobacter colonization of chicken	Comparative genomics	Lactobacillus reuteri
538	Resistance evolution in a model gut system	Re-sequencing, Evolution, SNP, Antibiotic resistance	E.coli
537	Guaymas Bay Sediment Sequencing	Sequencing	
536	Bachelor thesis: Investigation of bacteria and archaea in sediments	bacteria, sediments	bacteria
535	Zonation of methane-cycling archaea in the Western Mediterranean	gene expression, methanogenesis, qPCR	environmental community
534	Genetic differentiation in physiology and responses to herbivory across different elevations	metabolomics, genetic structure, phylogeography, herbivory, adaptation, elevation gradients	Arabis alpina
533	Soil biodiversity and functioning in agricultural systems	microbiome, metabarcoding, metagenomics	soil microbial communities
532	Resistance and resilience of the forest soil microbiome to mechanical disturbance	microbiome, soil compaction, metabarcoding, metagenomics	soil microbial communities

ID	title	keywords	organism
531	RADseq. of <i>Amrasca biguttula</i>	SNP, evolution	<i>Amrasca biguttula</i>
530	OakID ñ Hybridization and introgression in white oak species	quercus, hybridization, introgression, SNP	<i>Quercus</i> spp.
529	BSF microbiome	NGS, microbiome, insect	Black soldier fly
528	Origin and population structure of <i>Pulmonaria helvetica</i>	conservation biology, ddRAD	<i>Pulmonaria</i> sp
527	NRP72: Swiss River Resistome	antibiotic resistance gene, ARG, antibiotic resistant bacteria, ARB, metagenomics	microbial community
526	IsoMol	microbial ecology, waste water treatment, biofilm	Mixed microbial communities
525	The effect of woodland expansion on Lyme disease risk in the Scottish Highlands	disease ecology, bacteriology	<i>Ixodes ricinus</i> , <i>B. burgdorferi</i> s.l.
524	Molecular Plant Breeding ñ core activities	Molecular Plant Breeding, Genotyping, Sequencing, Crop Genetics, Crop Genomics	Crop species
523	Cell-type specific RNAseq to understand lateral root formation in <i>Arabidopsis thaliana</i>	TRAPseq	<i>Arabidopsis thaliana</i>
522	<i>Gyrodactylus turnbulli</i> genome project	genome sequencing, parasites, adaptation to host environment, evolution	<i>Gyrodactylus turnbulli</i>
521	Frequency dependent evolutionary response in <i>Pseudomonas stutzeri</i> - genome resequencing	bacteria, resequencing	<i>Pseudomonas stutzeri</i>
520	Identification and characterization of a novel <i>Cryphonectria hypovirus</i> CHV	natural biocontrol; chestnut blight; genome characterization	double-stranded RNA mycovirus
519	Snail immune transcriptomics	transcriptomics, mollusc, immune defence, parasite resistance	<i>Lymnaea stagnalis</i>
518	Kurs 751-0206-00L: Agrarwissenschaftliches Labor- und Methodenpraktikum	Teaching	Plants (various species)
517	<i>Asellus aquaticus</i> genome	genome sequencing, evolutionary biology, non-model species, isopod	<i>Asellus aquaticus</i>
516	Edaphic adaptation in <i>Arabidopsis lyrata</i> and <i>Arabidopsis arenosa</i>	<i>Arabidopsis</i> , CNV variation, local adaptation, transplant experiment, whole-genome re-sequencing	<i>Arabidopsis lyrata</i> , <i>A. arenosa</i>



ID	title	keywords	organism
515	cold-adapted microbes	soil, warming, global change, microbiome	soil microbiome
514	Urban wildflower biodiversity	SNP, RAD, gene flow, urban ecology, landscape genetics	Centaurea Jacea, Cirsium Arvense, Lactuca Serriola, Hypochaeris Radicata
513	Characterization of microbial contaminations within <i>Chlorella vulgaris</i> cultivations and the impact of cultivation conditions thereon	<i>Chlorella vulgaris</i> , evolution, microbial contamination	<i>Chlorella vulgaris</i>
512	Phylogenomics with social bacteria	phylogeny; molecular ecology; population genetics; social evolution	<i>Myxococcus xanthus</i>
511	Evolutionary physiology and adaptation to multidimensional selection in moor frogs ( <i>Rana arvalis</i> )	evolutionary physiology, RNA, transcriptomics, genomics, gene expression	<i>Rana arvalis</i>
510	Duckweed genomics	herbicide resistance, <i>Spirodela polyrhiza</i> , duckweed, whole-genome sequencing, adaptive evolution, GWAS	<i>Spirodela polyrhiza</i>
509	<i>Pseudodidymella fagi</i>	neomycet, plant pathogen,	<i>Pseudodidymella fagi</i>
508	How social environments shape the evolution of a microbial developmental system at phenotypic and molecular levels	eco-evo-devo, transcriptomics, genomics, myxococcus	<i>Myxococcus xanthus</i>
507	Testings, consumables	genetics	Fungi, <i>Silene</i> ,
506	Landscape Genetics in Snow Ptarmigan	landscape genetics, conservation genetics, molecular marker comparison, genetic structure, SNP	<i>Lagopus muta</i>
505	From biogeochemistry to the ecological genomics of pelagic fish stocks	conservation genetics, local adaptation, sustainable fishery, Lake Tanganyika, freshwater Sardines, <i>Lates spp</i>	<i>Stolothrissa tanganyicae</i> , <i>Limnothrissa miodon</i> , <i>Lates stappersii</i> , <i>Lates mariae</i> , <i>Lates microlepis</i> , <i>Late</i>
504	round goby - nanopore	evolution - mitochondrial genome - nanopore sequencing	<i>Neogobius melanostomus</i>
503	Testing the limits and constrain of species radiation using population genomics	ppulation genomics, speciation, tropical ecology, NGS, WGS, target sequencing	University of fribourg
502	Amplicon Sequencing Libraries of <i>Fragaria vesca</i> microbiome	NGS, microbiome	<i>Fragaria vesca</i>

ID	title	keywords	organism
501	Fish ancient DNA	ancient DNA, metagenomics, environmental DNA, evolution, time-series	Actinopterygii
500	Cichlids RAD	Cichlids, RAD sequencing, Adaptive Radiation, Selection, QTL, Population genomics	Cichlid fish
499	Swiss fish genomics	evolution, speciation, adaptive radiation, stickleback, charr	Gasterosteus aculeatus, Salvelinus alpinus, Coregonus sp, Cottus sp
498	Experimental Evolution Acinetobacter/Pseudomonas consortia	Experimental evolution, adaptive mutations, bacterial communities	Acinetobacter johnsonii C6 and Pseudomonas putida KT2440
497	Linking effects: the Chlamydomonas transcriptome under stress	Chlamydomonas, transcriptome, diuron, Daphnia	Chlamydomonas reinhardtii
496	Genomic tools to assess within- and between-species diversity in grassland plants	Biodiversity, grasslands, forages	Alopecurus pratensis, Arrhenatherum elatius, Cynosurus cristatus, Dactylis glomerata, Festuca pratensis
495	Host-parasite interactions in hybridizing Daphnia	parasites gene expression genomics	Daphnia galeata, Caulleryia mesnili
494	Flagship: Low-coverage for the Holy Grail	Host-parasite, Low-coverage, GWAS, Bombus, Bees, Crithidia, Trypanosomatidae	Bombus terrestris
493	Molecular epidemiology of clonal lineages of an invasive fungal plant pathogen	Chestnut blight, invasion history, genetic differentiation, SNP, fitness	Cryphonectria parasitica
492	Distribution of methane-cycling Archaea across Namibian continental shelf sediment	methanogenic Archaea, anaerobic methanotrophic Archaea, marine sediment	mcrA genes of methanogenic Archaea and anaerobic methanotrophic Archaea
491	Permafrost soil microbiome	permafrost, microbiome, fungi, bacteria	soil microbiome
490	Comprehensive characterization by whole-genome sequencing of the genetic diversity of Escherichia coli from environmental and fecal sources within the context of households in low-income countries	E. coli	Escherichia coli
489	Rivermanagement	Conservation biology, floodplain, rivermanagement, SNP, msats, riparia	Myricaria germanica, Lobaria pulmonaria, Arthonia cinnabarina, Caloplaca alnetorum
488	Vertical distribution of methane-cycling Archaea in Black Sea sediment	Archae	Archae

ID	title	keywords	organism
487	Abundance Patterns and Community Zonation of Bacteria and Methane cycling Archea in Sediments of Guaymas Basin	bacteria	Bacteria, Archaea
486	Effects of novel soil biota on plant community response to climate change	climate change, soil biota, novel interactions, sequencing	Soil biota
485	Successional patterns of root associated fungal communities of planted Norway spruce trees in a protection forest completely destroyed by a forest fire	root-associated fungi, mycorrhiza, succession, natural hazards, soil stabilization	Picea abies, Phialocephala fortinii s.l., ectomycorrhizae
484	Resistance and resilience of the forest soil microbiome to mechanical disturbance	soil microbiome, bacteria, fungi, amplicon sequencing, metagenomics, metatranscriptomics	soil microbiome
483	3D bioprinting of complex cell-laden hydrogel scaffolds for bone regeneration	3D bioprinting, cell-laden scaffold, gene expression, bone regeneration	Institute for biomechanical
482	Footprinting of RNA G-quadruplexes	quadruplex, footprinting, secondary structure	Homo sapiens
481	Cas9 Cassava	Cassava, cas9	Cassava (Manihot esculenta)
480	Phenotypic heterogeneity in growth resumption after starvation in bacteria	experimental evolution, lag times	Escherichia coli
479	Genomics of edaphic adaption, ecological speciation and sex system evolution in the <i>Silene acaulis/exscapa</i> complex	adaptation, selection, speciation, sex chromosome evolution	<i>Silene acaulis</i> , <i>Silene exscapa</i>
478	Pilot study of bird's diet through metagenomics of fecal samples	bird, fecal samples, metagenomics	<i>Dendrocopos leucotos</i> , <i>Scolopax rusticola</i>
477	<i>Pulmonaria helvetica</i> : origin, population structure and introgression	microsatellites, parental lineages, hybridization, population structure	<i>Pulmonaria helvetica</i> , <i>P. collina</i> , <i>P. obscura</i> , <i>P. officinalis</i> , <i>P. montana</i>
476	Impact of combined water and nutrient stress on the below-ground diversity	combined stress, agriculture, microbiome, qPCR, NGS,	bread wheat, durum wheat and potato
475	<i>RCastanea</i>	forest tree, eco-physiology, modelling, java	silver fir
474	Phylogeny of Rust on Solanaceae	Taxonomy, rust, parasites, coevolution	<i>Puccinia</i> sps.
473	The role of <i>Propionibacterium acnes</i> infection in intervertebral disc inflammation	<i>Propionibacterium acnes</i>	hIVD

ID	title	keywords	organism
472	Improving the genome draft of <i>P. veris</i>	primrose, heterostyly, genome, bioinformatics, evolution	<i>Primula</i> sp.
471	O6-methylguanine mapping	O6MeG-IP-seq	homo sapiens
470	Towards nutritional security through organic management of soil fertility in orange-fleshed sweet potato systems	enzyme activity, soil	We will work with soil enzymes from various organisms
469	Hematopoietic Stem Cell Aging	gene expression	<i>Mus Musculus</i>
468	methanogenic archaea in marine sediments	methane-cycling archaea, marine sediments, mcrA	methane-cycling archaea
467	Starch modification for <i>Eragrostis tef</i> ( <i>tef</i> )	Gene expression and SNP calling	<i>Eragrostis tef</i>
466	Stability of <i>Arabidopsis thaliana</i> microbiota	phyllosphere microbiota engineering	<i>Arabidopsis thaliana</i> (bacteria)
465	Pollen Meta-barcoding of urban and rural bumblebees	mixed pollen samples, bumblebees, plant-pollinator networks, urban ecosystems	<i>Bombus pascuorum</i> , <i>Bombus lapidarius</i>
464	Community composition analysis of <i>A. thaliana</i> leaf colonizing bacterial strains	community dynamics, microbe-microbe interactions, phyllosphere	<i>A. thaliana</i> leaf commensal bacteria
463	REEFISH	Reef fish; evolution; sequencing, UCE	Reef fishes several species
462	Gene expression analysis of human pluripotent stem cells in stirred tank perfusion cultures	human pluripotent stem cells, bioreactor	homo sapiens
461	Inference of demography and selection in <i>Dianthus sylvestris</i>	population genetics, demography, adaptation, selection	<i>Dianthus sylvestris</i>
460	Metabarcoding of honey	urban ecology, metabarcoding, plant-pollinator interaction	Plant ITS2 Metabarcoding
459	Detection and monitoring of aquatic diseases with eDNA	environmental DNA, aquatic parasites, quantitative real-time PCR	<i>Aphanomyces astaci</i> , <i>Batrachochytrium dendrobatidis</i> , <i>Saprolegnia parasitica</i> , <i>Tetracapsuloides bryosal</i>
458	Sequencing of experimentally evolved populations of <i>E.coli</i>	Evolution, whole genome sequencing	<i>E.coli</i>
457	Theoretical modelling of adaptive radiation	adaptive radiation, genomes, hybridisation, individual based model, speciation	theory
456	Deciphering Coevolutionary Diversification in the Tangled Webs of Life	Coevolution, Inference, Food webs, Diversification, Sexual selection	fish

ID	title	keywords	organism
455	eukaryotic DNA records in Black Sea sediment	acteria, archaea, eukaryotes, rRNA genes, fossil DNA, Black Sea, sediment	bacteria, archaea, eukaryotes
454	Connectivity of <i>M. alcon</i> populations in Switzerland	connectivity, conservation, endangered populations	<i>Maculinea alcon</i>
453	Natural selection on immune defence: a genome-wide gene expression analysis	transcriptomics, quantitative genetics, evolutionary ecology, host-parasite interactions, ecological immunology	<i>Lymnaea stagnalis</i>
452	Dynamics and structure of the phyllosphere microbiome	Community ecology, Bacterial communities, 16S rRNA, phyllosphere, flowers, leaves	Bacteria
451	Linking symbiotic microbial community structure and soil conditions to plant nutrition for sustainable agriculture: the rooibos model case	symbiotic functioning, plant nutrition, legume, rhizobia, organic farming	Rooibos ( <i>Aspalathus linearis</i> ), Rhizobia ( <i>Mradyrhizobium</i> , <i>Sinorhizobium</i> , <i>Mesorhizobium</i> , <i>Burkholderia</i> ,
450	Mediterranean wrasses	RAD sequencing, evolution, wrasses	Labridae
449	Analyzing nitrifying bacterial dynamics in a salmon recirculation aquaculture system during start-up of a moving bed biofilm reactor	microorganisms quantification	bacteria, archaea
448	Population genomics analyses of pathogen populations	population genomics, pathogens, whole genome sequencing, GWAS	<i>Zymoseptoria tritici</i>
447	Mechanisms of Transgenerational Epigenetic Inheritance of Acquired Traits	Transgenerational epiegentic inheritance, DNA methylation. germ cells	<i>Mus Musculus</i>
446	Invasion history of the beetle <i>Ophraella communa</i>	introduced species, whole genome low coverage	<i>Ophraella communa</i>
445	Gross phosphorus fluxes in soil under drying and rewetting cycles	qPCR, soil microbial communities, P cycle	Soil microorganisms (Bacteria, Fungi)
444	Understanding the genetic basis of variability in melanin biosynthesis in <i>Z. tritici</i>	gene expression	<i>Zymoseptoria tritici</i>
443	Target capture and sequencing of microsatellites	microsatellites, population genomics, NGS, target capture and sequencing, illumina	humpback dolphin ( <i>Sousa chinensis</i> )
442	The forest soil microbiome in the face of climate change	microbiome, metabarcoding, metagenomics	soil microbial communities

ID	title	keywords	organism
441	Direct detection of DNA adducts by single molecule, real-time sequencing	DNA damage, SMRT sequencing	No
440	Eco Consumables	eco consumables	various
439	Maternal effects in cooperatively breeding fish	maternal effects, life history theory, ecology	Neolamprologous pulcher
438	Genetic diversity of grassland plants: the role of spatiotemporal landscape changes	landscape genomics, habitat fragmentation, adaptation, ddRAD, SNP	Primula veris
437	Kattegat	Bacteria, Archaea, Eukaryotes, rRNA genes, bioturbation, marine sediment, Kattegat, Skagerrak	Bacteria, Archaea, Eukaryotes
436	High-throughput quantification of electron donating capacity in dissolved organic matter	Environmental Science, Biogeochemistry	NA
435	Endospore diversity and abundance	endospores, Firmicutes	Endospore-forming Firmicutes
434	Re-evaluation of temperature correction in microbial biodegradation kinetics (ReArrhenius)	microbial community structure and activity	
433	The pea rhizosphere microbiome and disease resistance	Microbiome-mediated disease resistance, resistance breeding	Pea, microbial community
432	URBANGENE Bufo bufo	Adaptation, GBS, Gene Flow, Genetic Diversity, Landscape Genetics, RADSeq, SNP, Urbanisation	buffo
431	The utility of eDNA in the context of ecosystem functioning in freshwater systems	environmental DNA, diversity, metabarcoding, mitogenome sequencing	macroinvertebrates, bacteria
430	Hierarchical coevolution of Daphnia magna and Ordospora colligata	Coevolution, Genotype Frequencies	Daphnia magna and Ordospora colligata
429	MOB response to autumnal lake mixing	methanotroph diversity, methane-oxidizing bacteria, lake, MMO, pmoA, oxycline, 16S rRNA, transcriptomics	environmental bacteria
428	Diversity of Epichloa grass endophytes	Biodiversity, speciation, mutualism	Epichloa spp., Botanophila spp.
427	Molecular host adaptation of Epichloa endophytes	evolutionary genetics, host adaptation, gene expression	Epichloa spp.

ID	title	keywords	organism
426	Linking genetic diversity with ecosystem services in Brazil nut populations in Madre de Dios, Peru.	genetic diversity, genotype, gene flow, genetic erosion, conservation genetics, reforestation, human impact, Amazon, Peru, rain forest, fungal pathogens, ecosystem services	Bertholletia excelsa (and fungal communities associated with it)
425	Botrychium Transcriptome	plant evolution, RNA, gene expression	Botrychium lunaria
424	Soil DNA Analysis	soil, SNP, 16S, ITS	soil microbes (bacteria and fungi)
423	transposable elements and epigenetic regulation	transposable element, brachypodium, epigenetic	Brachypodium distachyon
422	Intelligent scaffolds for advanced tissue regeneration	Tissue engineering, nanoparticles, RNA, gene expression	human mesenchymal stem cells
421	The molecular basis of variation in priming and anti-herbivore defence induction along elevation gradients	chemical defences, herbivores, gene expression, priming, elevation gradients	Arabidopsis halleri, Arabis alpina
420	Inter- and intrapopulation diversity of a bacterial freshwater isolate evolved under different predator regimes and the genomic basis of phenotypic plasticity	Phenotypic plasticity, population heterogeneity, phenotypic plasticity	Sphingobium sp. Z007
419	Plant insect interaction network: structure and community shaping over spatial and temporal scales	interaction networks, plant-insects, elevation gradient, metabarcoding	Orthoptera, Plants
418	Population dynamics of Zymoseptoria tritici	Plant pathology, wheat, septoria tritici blotch, fungal pathogen	Zymoseptoria tritici
417	Detecting adaptive mutations of E coli to diverse in vitro conditions.	Evolution, adaptation, E coli, Resistance	Escherichia coli
416	The evolution of floral traits in a heterogeneous environment	Adaptation, heterogeneous environment, altitude	Dianthus Carthusianorum
415	Population-genomics of streamlined freshwater microbes	genome streamlining, population-genomics	Bacteria (Methylopusillus spp.)
414	Resequencing the Daphnia longispina complex	Daphnia evolution, hybridisation	Daphnia galeata, Daphnia longispina, Daphnia cucullata
413	WheatFT	Homeolog analysis	wheat

ID	title	keywords	organism
412	Triplex qPCR assay for PKD	eDNA; Myxozoan; qPCR; Bryozoan; PKD	Tetracapsuloides bryosalmonae; Fredericella sultana
411	Quantification of differentially expressed genes in the periconceptual environment during early embryo development	Embryo-maternal interaction, early pregnancy losses, mRNA and small RNA expression analysis, and DNA methylation	Bos taurus, Sus scrofa, Capreolus capreolus, Equus caballus, Homo sapiens, Mus musculus, Rabbit
410	Role of bioturbation in controlling microbial communities in lake sediments	PCR, qPCR, Illumina MiSeq	
409	Effects of pH manipulation on microbial community structure	ph, lake sediment, bacteria, archaea, 16S rRNA genes, qPCR, MiSeq	sediment bacteria and archaea
408	ALB mitochondria	mtDNA, Asian long-horned beetle, SNP	Anoplophora glabripennis
407	Assessing epigenetic variation in Arabis alpina along elevation gradients	Plant functional biology, ecological gradients, biotic and abiotic stress	Arabis alpina
406	Massive Sample Pooling to Estimate Prevalence of Target Genes	antimicrobial resistance, MiSeq, ligation dependent amplification	none, or enterobacteriaceae
405	Candidate genes for Maternal effects in Rana arvalis	adaptation, amphibians, egg coats, environmental stress, maternal effect genes, SNP	Moor frog Rana arvalis
404	METALink: Linking environmental, genomic, and phenotypic information to study the adaptation of Arabidopsis halleri to metal-polluted soils		Arabidopsis halleri
403	Misexpression in closely related Silene species	Silene latifolia, gene expression, hybrids, Haldane's rule	Silene latifolia
402	genomics of parasite adaptation	coevolution, adaptation, trematode, SNP, PacBio, resequencing	microphallus sp (trematoda)
401	Assessing diversity patterns of potential adaptive value during the development of Silene ciliata (Caryophyllaceae).	SNP, evolutionary ecology, gene expression	Silene ciliata
400	Characterization of the phyllosphere microbiome of potato	phyllosphere microbiome, potato, late blight, biocontrol, phytopathology	Solanum tuberosum, Phytophthora infestans, Pseudomonas
399	Predicting and Managing Microbial Biofilms in Building Plumbing Systems	Potable water, Biofilm, Polymeric material	Natural potable water bacteria



ID	title	keywords	organism
398	Population genetic analysis of white-clawed crayfish populations in Aargau	conservation biology, microsatellites, 3730xl DNA Analyzer, Austropotamobius pallipes	Austropotamobius pallipes
397	Environmental fate of double stranded RNA (dsRNA) from RNA interference crop protection technology in agricultural systems	dsRNA, environmental chemistry	Synthetic molecules (RNA, DNA)
396	Genes for plant defence in Solanaceae	Evolutionary Biology, Plant Defense	Solanaceae
395	Evaluating the potential of the subfossil 'Binz' pines for ancient DNA analyses (Binz-aDNA)	aDNA, barcoding, subfossil wood	Pinus
394	Marssonina-Popgen	genetic diversity Marssonina coronaria	Marssonina coronaria
393	dsr genes in Shimokita coalbeds	microbial sulfate reduction, deep biosphere, ancient coalbeds	microbial sulfate reducers
392	Population genetics and genomics of Arabidopsis lyrata populations	Population genetics, Arabidopsis lyrata	Arabidopsis lyrata
391	Single cell SEED	Single cell genomics	Diverse lake organisms.
390	Development and testing of a new iron-containing micronutrient powder containing a prebiotic with an improved safety profile for fortification of infant foods in Africa	Human gut microbiome, enteric pathogens, qPCR, Fluidigm BioMark	Human faecal DNA
389	Impact of warming on soil microbial communities in arctic and alpine environments	warming, microbial community, soil, sequencing	soil microbes
388	Conservation biology of the flora of siliceous erratic boulders	conservation biology, SNP, ploidy, population genetics	Asplenium septentrionale
387	Mesocosm selection on CSL3F2 sticklebacks 2015	experimental selection, ecotype, fish	Gasterosteus aculeatus
386	Reconstruction of A. dorsata foraging distances through genetic approach	A. dorsata, microsatellite, foraging, sibship reconstruction, pollination	Apis dorsata
385	Oral exposure of low-dose estrogens	Conjugated estrogens, membrane transporters, porcine tissue	Sus scrofa

ID	title	keywords	organism
384	Department Umweltwissenschaften / Integriertes Praktikum IV	molekularbiologische Methoden	Escherichia coli
383	COWBIA: Multi-purpose cowpea inoculation for improved yields in small holder farms in Kenya	Genetic diversity, symbiotic Nitrogen fixation, gene sequencing	Bradyrhizobia
382	The response of phytoplankton to turbulence	gene expression, stress, phytoplankton	Heterosigma akashiwo
381	Understanding forces driving development of postzygotic reproductive isolation in outcrossing Arabidopsis species	speciation, evolution	Arabidopsis lyrata, Arabidopsis halleri, Arabidopsis arenosa
380	fdhA and mcrA qPCR standard preparation	qPCR, functional gene, mcrA, fdhA	various
379	EcolImpact	periphyton, 16S ribosomal RNA, 18S ribosomal RNA, microbial ecology, aquatic ecology	Aquatic microbes
378	Molecular fingerprinting to assess forest microbial P cycling	T-RFLP, soil microbial communities, functional genes	Soil microorganisms (Bacteria, Fungi)
377	Life history of a potato pathogen: Quantification in raw peat	plant pathogen, potato, evolution	Spongospora subterranea f.sp. subterranea
376	DNA-sequencer assisted oligosaccharide analysis	starch structure, carbohydrate quantification	glucans isolated from Arabidopsis thaliana or Saccharomyces cerevisiae
375	Nitrogen dynamics in Swiss Agricultural Systems	functional genes, nitrification, mineralization, community composition	DNA from Swiss agricultural soil
374	High Energy Red Clover	TILLING, Red Clover, Starch, Sugar, Forage, Sustainable Agriculture	Red clover (Trifolium pratense)
373	A QST/FST Analysis of Quantitative Traits in the Parastagonospora nodorum - wheat pathosystem	Stagonospora, Evolution, Microsatellites, Population genetic	Parastagonospora nodorum
372	Functional analysis of candidate QTL genes involved in fungal virulence and other traits	molecular plant pathology, functional gene characterization, gene expression	Zymoseptoria tritici
371	Senecio diversity and hybridisation	SNP, ddRAD-seq, invasive species, hybridisation	Senecio spp.

ID	title	keywords	organism
370	Ac1 Actinobacteria in Lake Zurich	Actinobacteria, ac1, whole genome amplification, genome sequencing, aquatic microbial ecology	ac1 Actinobacteria
369	1-SRT	biotransformation, solids retention time, biodiversity	bacteria/archaea
368	RapidEvolution	rapid adaptation, coevolution, SNPs	Chlorella algae and their virus
367	Towards a mechanistic understanding of discrete active aerobic methane-oxidizing bacteria within lake oxyclines	methanotroph diversity, methane-oxidizing bacteria, lake, MMO, pmoA, oxycline, 16S rRNA, transcriptomics	Environmental microbial communities
366	The study of the avirulence gene in <i>Zymoseptoria tritici</i>	plant pathology	<i>Zymoseptoria tritici</i>
365	Cadagno-2014	phenotypic diversity versus genotypic diversity	Lagi di Cadagno
364	Functional characterization of pathogenesis-related genes in the pathogen of wheat <i>Zymoseptoria tritici</i>	Gene expression, host specialization, pathogenicity gene	<i>Zymoseptoria tritici</i>
363	Freq-Seq for coevolved <i>E. coli</i> and <i>M. xanthus</i> strains	SNP, Freq-Seq, MiSeq	<i>Escherichia coli</i> , <i>Myxococcus xanthus</i>
362	Elevational gene flow of the endemic African mountain forest herb <i>Impatiens kilimanjari</i>	elevational gradient, gene flow, pollinator behavior	<i>Impatiens kilimanjari</i>
361	Role of AMF in promoting plant tolerance under drought	mycorrhiza, <i>Brachypodium</i> , drought, gene expression	<i>Brachypodium distachyon</i>
360	Adaptive genomics of host-pathogen coevolution	Adaptation, introgression, fungi, demography, coevolution	<i>Dianthus carthusianorum</i> , <i>Microbotryum</i>
359	Understanding resistance gene flow during passage of wastewater treatment (ResistFlow)	antimicrobial resistance, wastewater, resistome, gene expression, selection	
358	Soil Mercury microcosms	microbial ecology	microorganisms
357	Molecular analysis to study microbial communities in deep sea sediments	deep sediments, qPCR, Next-generation sequencing	
356	DH induction in <i>Lolium perenne</i>	DNA extraction	<i>Lolium perenne</i>

ID	title	keywords	organism
355	Neomycetes of Switzerland	fungi, neomycetes, DNA-barcoding	Fungi
354	TE Adaptation Genomics	Adaptation genomics, transposable elements, arabidopsis	Arabidopsis species
353	3D co-culture of renal epithelial cells and fibroblast as an in vitro fibrosis mimicry	3D culture, fibrosis,epithelial,myofibroblast	human (cell lines)
352	ACE Microbiota of the rhizosphere of Arabidopsis lyrata	rhizosphere, microbial communities, Miseq	bacteria, fungi, protists
351	Antimony retention in waterlogged rhizosphere soil and its influence on plant uptake	antimony, waterlogged, shooting rang soil	L. perenne, F. pratensis, S. cereale, T. aestivum
350	Study of the bacterial gene expression on insects	bacteria, Pseudomonas, insects, RNA	Pseudomonas protegenes CHA0, Galleria mellonella, Plutella.
349	Influence of Cu on CH4 oxidation in lakes	Methane oxidation, copper, lakes, MOB, MMO, microbial community	Environmental microbial communities
348	WWTPs and impacted rivers Bacteria sequencing analysis	wastewater, river, communities, Ecolmpact	bacterial communities
347	Identification, functional characterization and evolutionary genetics of seminal fluid proteins in Macrostomum lignano	Seminal fluid protein, gene expression, post-copulatory sexual selection, sperm competition, simultaneous hermaphrodites	Macrostomum lignano
346	Genetic identification of endangered timber species	conservation genetics, SNP, targeted sequencing, microsatellites, genetic identification	Dalbergia spp., Diospyros spp.
345	Effect of drought and irrigation on root traits and root decomposition of Scots pine	root turnover, decomposition, microbiome, Scots pine	Pinus Sylvestris
344	Potamopyrgus SNP markers	SNP, host-parasite coevolution, parthenogenesis, Red Queen hypothesis.	Potamopyrgus antipodarum
343	Comparative LTR-RT dynamics and niche study in Brassicaceae.	evolution, gene expression, transposable elements, genome annotation	Arabis alpina, Biscutella laevigata
342	Bisulfite PCR	PCR, DNA methylation	Sus scrofa
341	Assessing hidden diversity of Borrelia pathogens along elevational gradients in the Swiss Alps	Vector-borne disease, genetic diversity, amplicon sequencing	Ixodes ricinus, Borrelia

ID	title	keywords	organism
340	ChlamEE - ACE	experimental evolution, competition, algal biodiversity, coexistence, metagenomics, whole genome sequencing	Chlamydomonas reinhardtii
339	Cryptic species diversity in Australian butterflies	taxonomy, Lepidoptera, cryptic species	Yoma spp., Pseudalmenus spp.
338	ZOMM (Zinc Biofortification of Wheat through Organic Matter Management in sustainable agriculture)	Microbiology, soil zinc solubilization processes	85 bacterial strains
337	Understanding consequences of introgression of insecticidal transgenes from Bt-maize into open pollinating maize varieties in South Africa and its impact on pest resistance evolution	transgenic plant, Bt maize, gene flow, pest resistance, gene expression, open pollinated varieties (OPV)	Zea mays
336	Quantification of methylation in the promoter of NR3C1	Methylation, HRM. NR3C1	DNA extracted from human saliva
335	Frequency and life-history consequences of mixed mating in the freshwater snail Radix balthica	mixed mating, mating system evolution, microsatellites, self-fertilization, natural population	Radix balthica
334	Dolphin genomics	RAD-seq, SNP, evolutionary biology, population genomics	Tursiops spp., several other Delphinid species
333	linking effects	ecotoxicology, evolution, pollution	Chlamydomonas reinhardtii, Daphnia pulicaria
332	RNA Isolation from bovine endometrium	RNA isolation, endometrium	Bos taurus
331	Progetto Fiumi ñ Assessing biodiversity from genes to communities in Swiss river fish: Main phase	Fish, biodiversity, pyrosequencing, lineages, trout	Multiple freshwater fish species, but primarily Salmo trutta
330	PKD genomics	parasites, PKD, bryozoa, environmental DNA, genome sequencing	Tetracapsuloides bryosalmonae, Fredericella sultana
329	Effects of soil biodiversity on ecosystem functionality	soil biodiversity, soil microorganisms, ecosystem functionality, amplicon sequencing	soil microbes
328	MERMAID ITN - microbial ecology of drinking water biofilms	environmental samples; biofilms; drinking water	environmental samples [i.e. community analysis]

ID	title	keywords	organism
327	Structure and function of the plant root-associated microbiota	plant root microbiota, bacteria, fungi, community sequencing	Bacteria and fungi on roots of maize, wheat and clover and soil
326	Influence of macromolecular organic matter composition in marine sediments on microbial communities structure	microbial ecology, marine sediments, organic matter	Microbial communities (Archaea, Bacteria)
325	Duckweed evolutionary community ecology	Evolutionary Ecology,	Leman minor, <i>L. minuta</i> , <i>Spirodela polyrrhyza</i> , & <i>Azolla</i>
324	<i>Pasteuria ramosa</i> genome sequencing	<i>Pasteuria ramosa</i> , genome sequencing	<i>Pasteuria ramosa</i>
323	Does biodiversity control the functional performance of WWTPs: environmental samples	ecology, biodiversity, functional performance, bacterial communities	Bacterial wastewater communities
322	Temporal profiling of transcriptome and physiological responses of perennial ryegrass to water stress	RNA-seq, time-series, drought	<i>lolium perenne</i>
321	Biodegradation of polyesters in soils	biodegradation, soil, fungi, bacteria, community structure analysis	soil organisms
320	WWTPs and impacted rivers Bacteria sequencing	Wastewater, surface water, microbial community, antibiotic resistance,	Environmental microbial communities
319	Atmospheric-methane oxidation in glacier-forefield soils	<i>pmoA</i> gene; MOB; glacier-forefield soils	Bacteria
318	Fate of methylated compounds in sulfate-reducing and methanogenic marine sediment investigated by nucleic acid-based stable-isotope-probing	marine sediments, C-cycle, SIP, methanogenesis, sulfate reduction, acetogenesis	Bacteria and Archaea from environmental samples
317	Epigenetics in Brown Adipose Tissue Activation	long non-coding RNA	Samples are from wild type mice, C57B6
316	PiCadapt - Adaptive genetic variation of Swiss stone pine in response to environmental gradients across the Alpine timberline ecotone	climate change, local adaptation, Swiss stone pine, <i>Pinus cembra</i> , timberline, transcriptome, exome capture, SNP genotyping, environmental association analyses	<i>Pinus cembra</i>

ID	title	keywords	organism
315	Genetic Diversity of Bactrospora dryina	Bactrospora dryina, Auen, Quercus, genetische Diversität	Bactrospora dryina
314	URPP conservation genomics of Alpine Ibex	ibex, conservation genomics, transcriptomics, genetic bottleneck, inbreeding, reintroduction, adaptive potential	Capra ibex
313	Lagopus landscape genetics	conservation genetics, landscape genetics, spatial structure, connectivity	Lagopus mutus
312	MauckPVBint	Virus-host interactions, vector behavior, rhizosphere bacteria, metabolomics, gene expression	Medicago truncatula, Acyrthosiphon pisum, Delftia acidovorans, Sinorhizobium meliloti, Cucurbita
311	Comparative phylogeography of wild wheats and their inhabiting transposable elements	Aegilops, transposable elements, genome size, phylogeography, phylogenomics, NGS, SSAP.	Aegilops species
310	Epigenetic regulation of GABAergic and glutamatergic gene expression in early life adversity	epigenetics, gene expression, early environment	Mus musculus
309	Evolution in spreading populations of Arabidopsis thaliana in patchy landscapes.	Landscape heterogeneity, plant invasions, spread dynamics, species range shifts, DNA fingerprinting	Arabidopsis thaliana
308	Ecological and Evolutionary insights from an invasive plant species, Solanum elaeagnifolium (silverleaf nightshade), in Greece.	Invasion biology, population genetics, chemical ecology, reproductive biology	Solanum elaeagnifolium
307	Daphnia QTL Microbiome study	Illumina MiSeq, 16S rRNA, Daphnia magna, QTL	Daphnia magna
306	Sinergia IBD Project: Project 1	IBD, intestinal fermentation, fecal microbiota transplant	gut microbiota
305	rgia IBD Project: Project 2	gut microbiota, intestinal fermentation modeling, fecal microbiota transplant	ETH
304	GeneScale	landscape genomic, local adaptation, Arabis alpina	Arabis alpina
303	Microbiota of Daphnia during and after diapause	daphnia, microbiota, 16S, community ecology	daphnia, bacteria

ID	title	keywords	organism
302	Interactions between cyanobacteria and zooplankton in algal blooms	Zooplankton, cyanobacteria, Microcystis aeruginosa, qPCR	Daphnia galeata, Microcystis aeruginosa
301	Genomics of a host-parasite interaction	specificity, host-parasite interaction, genomics,	Bombus terrestris, Crithidia bombi
300	Population genomics and local adaptation: genome wide analysis of transposable elements and natural population evolutionary trajectories.	genomics, transposable elements, Brachypodium distachyon, evolution	brachypodium distachyon
299	Towards conservation genomics - studying the migration of adaptation in a threatened non-model plant species	Conservation genomics, SNPs, arctic biodiversity	Carex scirpoidea
298	Fish Genomics	SNPs, whole genomes, recombination rates, genome architecture	Gasterosteus aculeatus, NA
297	Genetic diversity patterns of amphipods in Switzerland	Amphipoda, genetic diversity, distribution, barcodes, COI	Orchestia cavimana, Crangonyx pseudogracilis, Synurella ambulans, Niphargus sp., Gammarus sp., Echin
296	Spatially resolved osteocyte gene expression	osteocyte gene expression	Mouse
295	Transcriptional regulation during plant infection in the model plant pathogenic fungus Zymoseptoria tritici	RNAseq, gene expression	Zymoseptoria tritici, Triticum aestivum
294	Using environmental DNA (eDNA) for monitoring effects of wastewater pollutants on biodiversity	eDNA, wastewater pollution, eukayotes, eubacteria	eukayotes, eubacteria
293	Molecular characterization of pathogenicity in the wheat pathogen Zymoseptoria tritici (syn Mycosphaerella graminicola)	gene expression, pathogen, fungi	Zymoseptoria tritici
292	Regulation of small RNA production in Arabidopsis	epigenetics, library preparation, Arabidopsis, gene silencing	Arabidopsis thaliana



ID	title	keywords	organism
291	Application of qPCR with species-specific primers to quantify hydration-induced dynamics of model soil microbial community	Microbiology, bacteria, community, 16S rRNA, RNA, DNA, qPCR	Arthrobacter, Bacillus, Micrococcus, Pseudomonas, Rhizobium, Streptomyces, Xanthobacter
290	Homogenization test	Isolation of RNA	Capreolus capreolus
289	Sahara	16S rRNA, Sahara dust, Jungfrauoch	bacteria
288	Coevolution during successive range expansion	Coevolution, bacteria	Pseudomonas stutzeri
287	Trade-offs in siring success between first and second clutches in <i>F. auricularia</i> ?	microsatellites, paternity, conflict, trad-off	Forficula auricularia
286	Genetic map for <i>A. ostoyae</i>	<i>A. ostoyae</i> , linkage map, SNP	Armillaria ostoyae
285	Experimental evolution of HIV	experimental evolution, HIV, next generation sequencing	HIV-1
284	Early colonization of functional groups of microbes in healthy infants' gut: A cohort study	infant gut microbiota, microbial ecology, microbial succession, anaerobic culture, lactate utilizing bacteria	Human faecal microbes
283	Chestnut diseases	chestnut blight, biological control, hypovirus	Cryphonectria parasitica hypovirus (CHV-1)
282	Climate change soil RISA	RISA, Soil Ecology, fungi, bacteria	Bacteria, Fungi
281	Dynamics of the microbiota prior to and beyond death of the host	microbiota, death, decomposition, carcass, starvation	Daphnia magna + Bacteria
280	Daphnia associated microbiota composition	Daphnia, microbiota composition, reciprocal transplant experiment	Daphniidae ( <i>Daphnia magna</i> ; <i>Daphnia pulex</i> ; <i>Daphnia longispina</i> ; <i>Scapholeberis</i> sp.)
279	Low nucleic Acid Bacteria" und "Baikal sediment" sequencing	Microbial diversity, microbial functions, freshwater, sediment, drinking water	Environmental Bacteria
278	Genomic imprinting in wild tomatoes: transcriptomics of hybrid seed failure and evolution under contrasting mating systems		Solanum section Lycopersicon (wild tomato species)
277	Biodiversity-ecosystem functioning relationships in methanotrophic communities	biodiversity, ecosystem function, methane, methanotrophic bacteria	several strains of methanotrophic bacteria

ID	title	keywords	organism
276	Genetic adaptation to local environmental conditions across climatic gradients in <i>Rana temporaria</i>	SNP, adaptation, population structure, landscape genetics, <i>Rana temporaria</i>	<i>Rana temporaria</i>
275	Dispersal of members of the <i>Phialocephala fortinii</i> s.l - <i>Acephala applanata</i> species complex (PAC)	<i>Phialocephala fortinii</i> s.l., <i>Acephala applanata</i> , Dark Septate Endophytes	<i>Phialocephala fortinii</i> s.l , <i>Acephala applanata</i>
274	Barcoding the lichen symbiosis	conservation biology, barcoding, symbiosis, ITS, rbcL	Hundreds of lichen species
273	Cryptic extinctions in native fungal communities caused by an alien invasive pathogen	<i>Fraxinus excelsior</i> , fungal endophytes, <i>Hymenoscyphus pseudoalbidus</i> , amplicon sequencing	<i>Fraxinus excelsior</i>
272	16Sseq	sequencing, microbial populations	
271	Gene expression responses of <i>Arabidopsis thaliana</i> to the presence of commensal and pathogenic bacteria	gene expression	<i>Arabidopsis thaliana</i>
270	Next-generation sequencing of cyanobacterial DNA retrieved from lake sediments	community ecology, paleoecology, cyanobacteria, next-generation sequencing, lake sediments	Cyanobacteria
269	Sampling schemes and inferences on demographic history in <i>Drosophila melanogaster</i>	Demographic inference, <i>Drosophila</i> , sampling scheme, DNA sequence data, coalescent	<i>Drosophila melanogaster</i>
268	Gene expression analysis of leukemia patients using the fluidigm system	Leukemia, gene expression, fluidigm PCR	Human
267	Molecular systematics of Fungi	molecular systematics, fungi, evolution	fungi
266	GENETICS OF HOST-PARASITE INTERACTIONS	gene expression, coevolution, parasitoids	<i>Lysiphebus fabarum</i>
265	Experimental evolution in <i>E. coli</i>	microbial evolution, mutators, plasmids	<i>Escherichia coli</i>
264	Quantification of Arbuscular Mycorrhizal fungi in soil and plant samples	SNP, Symbiosis, Mycorrhiza,	<i>Rhizophagus irregularare</i>

ID	title	keywords	organism
263	Experimental Evolution in the trypanosome <i>Crithidia bombi</i> ñ Selection for growth rate fast vs slow	Host-parasite interactions, experimental evolution, growth rate, gene expression, host immunity	<i>Crithidia bombi</i> , <i>Bombus terrestris</i>
262	PIE: Pollution Induced Evolution	micropollutants, phytoplankton, cyanobacteria, evolution, resistance	<i>Microcystis aeruginosa</i>
261	Monitoring and diagnostics of forest quarantine pathogens in Switzerland	diagnostics, forest, pathogens, Switzerland	The sudden oak death pathogen, <i>Phytophthora ramorum</i> ; pine wood nematode, <i>Bursaphelenchus xylophilus</i> ;
260	Systems microbiology in process engineering	Water and wastewater treatment, biological processes, activated sludge, biofilms, molecular microbial ecology, gene expression, omics	Complex microbial communities (bacteria and eukarya)
259	Quantification and quality control of mRNA obtained from <i>Daphnia magna</i> clones for gene expression analysis	gene expression	<i>Daphnia magna</i>
258	RNA extraction	frog, RNA extraction	frog
257	The role of the gut microbiota in host-parasite interactions	host-parasite interactions, bacterial communities, symbionts, immunity, resistance, gene expression	<i>Bombus terrestris</i> , <i>Crithidia bombi</i>
256	Holzqualität Weisstanne	Keywords: Microsatellites, <i>Abies alba</i> , Postglacial colonization, timber quality	<i>Abies alba</i>
255	Biogeochemical controls of arsenic mobility in contaminated riverine soils (Ogosta, Bulgaria)	contaminated soil, arsenic, geochemical gradient, microbial metabolism, qPCR, gene abundance	Prokaryotic communities in contaminated soils
254	Adaptive gene expression and plasticity in <i>Arabidopsis halleri</i> under temperature stress	Adaption, altitude, plasticity, <i>A.halleri</i> , Temperature stress	<i>Arabidopsis halleri</i>
253	The effect of herbivory on AMF community structure: Does a shift in the AMF community increase plant resistance against herbivores.	AMF isolate quantification, Spodoptera littoralis, plant herbivory, plant stress, SNP, Pyrosequencing	<i>Rizophagus irregularis</i>

ID	title	keywords	organism
252	Development of double-resistance in sequential vs hybrid therapy	evolution, antibiotic, resistance, mutation	E.coli K12 MG1655
251	Paternity and cannibalism in broods of female <i>Forficula auricularia</i> with two different life history strategies.	paternity test, microsatellites, siblicide, parental antagonism, <i>Forficula auricularia</i> , life history strategies	<i>Forficula auricularia</i>
250	A theory for next-generation food web data	Individual-trait based approach, stochastic modeling, food webs	No
249	Biogeography study of <i>Ophrys</i> species by Genotyping-by-sequencing (GBS)	biogeography, genome wide SNP	<i>Ophrys aymoninii</i> , <i>Ophrys insectifera</i>
248	Phylogeny of the genus <i>Lobaria</i>	Phylogeny, hybridization, incomplete lineage sorting, species definition	Species of the genus <i>Lobaria</i>
247	Pesticides, parasites and gene expression in bumblebees	conservation biology, parasites, gene expression	<i>Bombus terrestris</i>
246	Genomic changes in the brain during helping	gene expression, brain, social behaviour	<i>Neolamprologus pulcher</i>
245	Development of new endpoints for characterization of periphyton on the molecular and functional level	freshwater periphyton, community composition, ARISA, sequencing	different periphyton species (i.e. Diatoms, Cyanobacteria, Green algae)
244	Utilising RNA-Seq to generate new insights in age-specific patterns of gene expression in <i>Daphnia</i>	gene expression, evolution, ageing	<i>Daphnia magna</i>
243	Genome sequencing of flow sorted bacterial populations		<i>Limnohabitans</i> sp.
242	Engineering apomixis in <i>Zea mays</i> L.	no keywords	<i>Zea mays</i> L.
241	Characterization of Swiss agricultural soils for disease and pest reducing <i>Pseudomonas</i> spp.	qPCR, <i>Pseudomonas</i> spp., biocontrol, soil borne pathogens	<i>Pseudomonas</i> spp.
240	controldieback	<i>Chalara fraxinea</i> , <i>Hymenoscyphus pseudoalbidus</i> , microsatellites, virulence, population genetics	<i>Hymenoscyphus pseudoalbidus</i>

ID	title	keywords	organism
239	CCES-ETH / GeneMig ñ Connectivity of populations of amphibian species across motorways by different types of passages	Connectivity, Landscape genetics, Conservation genetics, microsatellite analysis, amphibians, gene flow, passages	Pelophylax lessonae, Pelophylax ridibundus, Pelophylax esculentus, Ichthyosaura alpestris
238	Linking changes in N2O emissions to microbial nitrogen cycling gene abundances in biochar-amended soils	Nitrogen cycling bacteria; gene copy number; soil DNA	Soil Bacteria
237	Ecological Genomics of two Cyprinidae fish in Oligotrophic Lake Brienz	SNP	Rutilus rutilus
236	The effects of climate change in mountain regions	conservation biology, microsatellites, Taxus, Lobaria, population genetics	Taxus wallichiana, Lobaria pindarensis
235	Evolutionary consequences of interpopulation gene flow in alpine Arabidopsis thaliana populations.	evolutionary biology, conservation biology, population structure, gene flow,	Arabidopsis thaliana
234	lepidopteran midgut microflora screening	Biocontrol, pest management	gypsy moth (Lymantria dispar), bacteria
233	QuercAdapt	quercus, local adaptation, climate change, oaks	Quercus robur/petraea/pubescens
232	Reconstructing past cyanobacterial communities from lakes sediments	paleolimnology, cyanobacteria communities, sediments, lakes, diversity	Cyanobacteria
231	bee phylogeny	bee-flower relationships, phylogeny	Insecta, Hymenoptera, Apoidea
230	Adaptive Gene Expression Differences as a Consequence to the Adaptation to high Altitude in A. halleri	Gene Expression	Arabidopsis halleri
229	Whole genome sequencing of evolved E. coli strains	evolution, E.coli, sequencing	E. coli
228	Genetic diversity in Alpine trout	trout, adaptation, speciation, RAD-seq	Salmo trutta spp.
227	Demographic and genetic processes underlying regeneration in Lodoicea maldivica the largest seeded plant in the World	Lodoicea maldivica, Coco de mer, conservation biology, nSSR's	Lodoicea maldivica

ID	title	keywords	organism
226	Incidence of mycoviruses in epidemic and post-epidemic populations of the ash dieback pathogen <i>Chalara fraxinea</i> and evaluation of their potential for biological control of the disease	Ash dieback, <i>Chalara fraxinea</i> ( <i>Hymenoscyphus pseudoalbidus</i> ), mycoviruses, biocontrol, hypovirulence	<i>Chalara fraxinea</i>
225	Linkage mapping in <i>Silene latifolia</i> using microsatellite markers	SSr, linkage mapping, <i>Silene latifolia</i>	<i>Silene latifolia</i>
224	quantification of N cycling genes	quantitative PCR	soil bacteria and archaea
223	Transcriptomics of Grain Filling in Rice	Laser-Assisted Microdissection, RNA quality, RNA quantity, Transcriptome profiling	<i>Orzya sativa</i> (Rice)
222	Identification of genes associated with hematopoietic stem cell dysfunction during aging and inflammation	gene expression	mouse or human cells
221	Distribution and sustainable use of the Burgundy truffle in Switzerland	Burgundy truffle, population genetics, SSR, ectomycorrhiza, forest resource, sustainable use	<i>Tuber aestivum</i>
220	MicrobialDiversity	microbial diversity, Illumina, NGS	Microbes
219	<i>Dianthus</i>	adaptation, genome sequencing, genetic map	<i>Dianthus sylvestris</i> , <i>Dianthus carthusianorum</i> , <i>Dianthus caryophyllus</i>
218	Geographic distribution of cryptic bee species	Conservation biology, biogeography	<i>Bombus</i> , <i>Panurginus</i>
217	Phylogeny of bees of the genus <i>Osmia</i>	evolution, plant-animal interactions, bee biology	<i>Osmia</i>
216	Role of intestinal microbiota in fructose-induced obesity	obesity, mouse, intestinal microbiota	mouse, bacteria
215	Ecological genetics of speciation and dioecy in <i>Nepenthes</i> pitcher plants	Genotyping by sequencing (GBS), RAD sequencing, SNP discovery, RNAseq, population genetics, evolution, ecology	<i>Nepenthes</i> spp.
214	Gene expression analysis of <i>Malus × robusta</i> 5 after fire blight infection.	Gene expression analysis, Fluidigm, <i>Malus × robusta</i> 5, <i>Erwinia amylovora</i>	<i>Malus</i>

ID	title	keywords	organism
213	The evolution and stabilization of mutualistic interactions	coevolution, mutualism, spatial structure	E. coli K12
212	Aggregate stability effects of PAC: Is stability a result of glomalin?	PAC, aggregate stability, GRSP, Hsp60, glomalin, RT-PCR	PAC - fungi
211	Retinoblastoma related protein (RBR) influences dynamic chromatin landscapes during arabidopsis photomorphogenesis	retinoblastoma related protein (RBR), photomorphogenesis, dynamic chromatin landscapes	Arabidopsis thaliana
210	Eco Consumables	Consumables	none
209	Development of new strategies to maintain the high quality of foil-packaged cheese by controlling the smear-microflora	RNA Integrity, metabolic activity	red-smear cheese surface microorganisms
208	FUNCTIONAL GENOMICS OF GRASS REPRODUCTIVE TRAITS	Self-incompatibility (SI)	Lolium perenne
207	Genome sequencing and genotyping of the PGPRs R81 and R62	PGPR, Rhizosphere, Plant-Microbe Interaction	fluorescent Pseudomonas
206	The bumblebee genome project	genomics, bumblebee, evolution	Bombus
205	Neutral variation in Beech across Switzerland	nSSR, population genetics	Fagus sylvatica
204	Adaptive variation in Beech	SNP, candidate genes, evolution, climate change	Fagus sylvatica
203	Phylogenetic origin of Beech in Switzerland	cpSSR, population genetics	Fagus sylvatica
202	Transposon dynamics in A. lyrata	transposons, molecular markers, fragment analysis, transposon display, A. thaliana	Arabidopsis lyrata
201	Fungicide resistance in Rhynchosporium commune	Rhynchosporium commune, DMI fungicides, evolutionary potential, CYP51, association analysis	Rhynchosporium commune
200	Crithidia bombi Genome	genome, parasites, co-evolution, host-parasite interaction, SNP	Crithidia bombi, Trypanosomatidae, Kinetoplastida

ID	title	keywords	organism
199	Scaling Biodiversity to Ecosystem Services: Spatial Genetic Structure and Carbon Sequestration Potential in Tropical Forest Trees	Fine-scale genetic structure, microsatellites, forest degradation, Dipterocarpaceae, carbon sequestration	Dipterocarpaceae, mainly the genera Shorea and Parashorea
198	Extinction debt at the gene level	Conservation genetics, extinction debt, connectivity, nuclear microsatellites, wetland	Succisa pratensis
197	spatial genetic structure of an alpine mayfly (Baetis alpinus) and influence of mating system	Population genetics, microsatellites, evolution, gene flow, mating system, partenogenesis	Baetis alpinus
196	Adaptation to heterogeneous environments in Tribolium castaneum	quantitative genetics, evolution, gene expression, expression plasticity	Tribolium castaneum
195	Monitoring of QoI resistant strains of Venturia inaequalis in Swiss orchards	QoI fungicides, G143A mutation, Venturia inaequalis, Cyt b, Pyrosequencing, SNP, mtDNA, EC50	Venturia inaequalis
194	SNP-genotyping by melting curve and KASP analysis for E.coli F4ab/ac resistance in pigs	melting curve, SNP-genotyping, E.coli F4 ab/ac, KASP, HRM, TmShift	sus scrofa
193	Diversification and Biogeography of Leguminosae-Mimosoideae	systematic biology, diversification, biogeography, phylogenetics, hybrid sequence capture, massively parallel sequencing	Leguminosae-Mimosoideae
192	De novo transcriptome of the European earwig (Forficula auricularia)	RNAseq, de novo transcriptome, hybrid assembly, 454 reads, Illumina, social behaviour	European earwig (Forficula auricularia)
191	Sociogenomics of cooperation and conflict in animal families	evolution, gene expression, transcriptome, sociogenomics, coadaptation, insects	Eruopean earwig
190	Modulation of expression of the apple scab resistance gene HcrVf2 in classically bred and genetically engineered scab-resistant apple cultivars	HcrVf2 gene, Venturia inaequalis, modulation, gene expression, qPCR, apple	Malus domestica, Venturia inaequalis
189	Testing the utility of environmental DNA for describing biodiversity in aquatic systems	eDNA, biomonitoring, next generation sequencing, conservation, waste water treatment	taxa spanning two domains of life and including protists, bacteria, zooplankton, invertebrates and v



ID	title	keywords	organism
188	Next generation sequencing to assess forest soil microbial diversity	Soil microbial communities, biodiversity, indicator species, soil disturbances, soil quality, soil monitoring, genetic profiling, next generation sequencing	Soil microbial communities
187	Genes involved in the sRNA Pxr regulatory pathway in the bacterium <i>Myxococcus xanthus</i>	Non-coding small RNAs, gene regulation, bacterial development.	<i>Myxococcus xanthus</i>
186	The consequences of migration for the performance and adaptive potential within populations of an invasive species	invasive species, <i>Solidago</i> , microsatellite, genetic diversity, population genetics	<i>Solidago canadensis</i>
185	Sexual Reproduction in an facultatively sexual freshwater invertebrate; <i>Cristatella mucedo</i>	Microsatellite genotyping, Parentage Analysis, Sexual Reproduction, Population Structure, Red Queen	<i>Cristatella mucedo</i>
184	SNP development for the <i>Daphnia longispina</i> complex	Hybridization, SNP, population genetics, parasites, ancient DANN	<i>Daphnia galeata</i> , <i>Caulleria</i> Sp.
183	Molecular Characterization of Microbial P Cycling	soil microbial communities, primer designing, functional genes, sequencing	Soil Microorganisms (Archaea, Fungi, Bacteria)
182	Allele mining for novel rice blast resistance genes	Rice blast, Allele mining, germplasm, blast resistance genes, genetic diversity	<i>Oryza sativa</i>
181	Establishing of new methods	Gene expression, SNP, NGS	<i>Silene latifolia</i> , <i>Dianthus</i>
180	Sex-specific field performance in <i>Silene</i>	sexual dimorphism, Haldane's rule	<i>Silene dioica</i> and <i>Silene latifolia</i>
179	Genome Annotation of the PGPRs R81 and R62	PGPR, Rhizosphere, Plant-Microbe Interaction	fluorescent <i>Pseudomonas</i>
178	The Genetics and Epigenetics of floral scent evolution	evolution, floral signalling, selection, speciation, population genomics	<i>Brassicae rapa</i> , <i>Ophrys</i> spp.
177	Inactivation of Viruses at solid water interfaces	quantitative PCR, phage, virus, inactivation	RNA from bacteriophages (MS2, Qbeta, Phi)
176	DNA methylation analysis of Rheumatoid Arthritis Synovial Fibroblasts	Epigenetics, DNA methylation, rheumatoid arthritis, synovial fibroblasts, bisulfite sequencing.	<i>Homo Sapiens</i>

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175	Development of multifunctional bakery bioingredients by fermentation of co-cultures of lactic and propionic acid bacteria	protein profiling	<i>W. confusa</i> , <i>P. freudenreichii</i>
174	Competitive interactions between induced prophages under different levels of stress	Temperate bacteriophages, competition, genotype x environment interactions, microbial ecology, real-time PCR	<i>Escherichia coli</i> , lambdaoid bacteriophages
173	ELUCIDATING THE ROLE OF INTROGRESSIVE HYBRIDIZATION IN ALPINE IBEX USING POPULATION GENOMICS	Evolutionary Biology, Conservation Biology, Population genomics, RAD, Introgression	<i>Capra ibex ibex</i>
172	Microbiota community shift in disease	Microbiota, <i>Daphnia</i> , 16S rRNA	<i>Daphnia magna</i>
171	<i>Arabidopsis lyrata</i> RADSeq Project	population genetics, phylogenetics, next-generation sequencing, RAD-Tag, RADSeq, evolution, methylation	<i>Arabidopsis lyrata</i> ssp. <i>lyrata</i>
170	Gene expression profiles of putative sex differentiation genes during development of the cichlid fish <i>Astatotilapia burtoni</i>	sex determination, sex differentiation, cichlids, developmental series, <i>Astatotilapia burtoni</i>	<i>Astatotilapia burtoni</i>
169	Unraveling the causes and functions of five Hivp paralogs that evolved under strong positive selection in cichlid fishes	evolution, Hivp, cichlid fishes, positive selection, <i>Astatotilapia burtoni</i> , gene expression, Immune system	<i>Astatotilapia burtoni</i>
168	Margot-LabCourse-701-1416-00 P	tomato, sequencing, post-zygotic isolation	wild tomatoes
167	Global phylogeography and phylogenomics in social <i>Myxococcus</i> bacteria	Phylogeography; Population genomics; Molecular Ecology; Genomic Evolution; Kin selection	<i>Myxococcus xanthus</i>
166	Development of multifunctional bakery bioingredients by fermentation of co-cultures of lactic and propionic acid bacteria	protein profiling	<i>W. confusa</i> , <i>P. freudenreichii</i>
165	Development of different molecular markers for the study of <i>Pinctada radiata</i> , <i>P. maxima</i> and <i>P. margaritifera</i> populations	<i>Pinctada</i> spp., pearl oyster, DNA extraction, sequencing, molecular markers, microsatellites	<i>Pinctada radiata</i> , <i>P. maxima</i> and <i>P. margaritifera</i>

ID	title	keywords	organism
164	Kin discrimination in <i>Myxococcus xanthus</i>	Kin discrimination, <i>Myxococcus xanthus</i> , social antagonism, genetic variation, microbial intra-species interactions.	<i>Myxococcus xanthus</i>
163	Population genomics of fire blight.	plant pathology, bacteriology, population genomics, epidemiology, SNPs, CRISPRs, VNTRs	<i>Erwinia amylovora</i>
162	DNA methylation in melanoma	melanoma, methylation	homo sapiens
161	Functional Metagenomics, Microbiology part of the Practical Biogeochemistry for environmental scientists	environmental microbiology, antibiotic resistance genes, functional metagenomics, unculturable bacteria, DNA shearing	unknown, environmental samples
160	Mutation accumulation in <i>Arabidopsis thaliana</i> under heat and salt stress	Mutation rate, Bioinformatics, <i>Arabidopsis thaliana</i> , Stress, Mutation spectrum	<i>Arabidopsis thaliana</i>
159	Insecticidal activity in root-colonizing plant-beneficial pseudomonads: Molecular mechanisms and exploitation for pest control	<i>Pseudomonas</i> , plant-beneficial, toxin, insecticidal, biological pest control, rhizosphere, molecular host-microbe interactions, insects, autofluorescent reporters	<i>Pseudomonas fluorescens</i>
158	Population genetic structure of <i>Microphallus</i> parasites	microsatellites, parasite, population genetics, local adaptation, ecological genetics	<i>Microphallus</i> sp.
157	Population-genetic and population-ecological differences between small and large populations of <i>Silene flos-cuculi</i>	<i>Silene flos-cuculi</i> , Microsatellite, genetic variation, populations	<i>Silene flos-cuculi</i>
156	Himalayan <i>Daphnia dentifera</i>	biogeography, phylogenetics, COI, 12S, ND2, <i>Daphnia</i> ,	<i>Daphnia dentifera</i> (8)
155	RNA-Seq of an hemibiotrophic plant pathogen during the complete life cycle	Evolutionary Biology, Hemibiotroph Pathogen, Transcriptome, RNA-seq	<i>Mycosphaerella graminicola</i>
154	Building a draft reference genome sequence for <i>Primula veris</i>	primrose, heterostyly, genome, bioinformatics, evolution	<i>Primula veris</i>

ID	title	keywords	organism
153	Habitat adaptation and the acquisition of adaptive traits via introgression in an <i>Arabidopsis lyrata</i> - <i>arenosa</i> introgression zone	adaptation, <i>Arabidopsis lyrata</i> , <i>Arabidopsis arenosa</i> , calcicole, calcifuge, introgression, population genomics, substrate type	<i>Arabidopsis lyrata</i> , <i>Arabidopsis arenosa</i> , <i>Arabidopsis lyrata</i> x <i>A. arenosa</i> hybrids
152	Ecological and Evolutionary Plant Epigenetics- Individual project 2	epigenetic variation, evolution, MSAP, methylomes,	<i>Arabidopsis thaliana</i> , <i>Fallopia japonica</i>
151	Increasing the efficiency of marker assisted breeding	SNP, fruit breedomics, molecular marker, disease resistance	<i>Malus x domestica</i>
150	Plant genome evolution and reproductive isolation under the influence of transposable elements	ecological diversification; fragment analyses; genome evolution; landscape genetics; local adaptation; polyploidy; reproductive isolation; Transposable Elements; SNP	<i>Biscutella laevigata</i> cplx + <i>Aegilops</i> spp ( <i>Ae. comosa</i> , <i>Ae. tauschii</i> , <i>Ae. caudata</i> , <i>Ae. umbellulata</i> , <i>Ae.</i>
149	Mechanisms of pre- and postzygotic isolation in cryptic <i>Epichloë</i> species	Fungi, evolution, population biology	<i>Epichloë</i> spp.
148	Evolution of Mutualistic Interactions within Microbial Communities	Experimental evolution, Microbial interactions, SNP, indel, whole-genome resequencing	<i>Pseudomonas stutzeri</i>
147	Viral biodiversity during a species invasion: invasive bumblebees in South America	evolution, virus, pollinators, invasion, biodiversity	<i>Bombus terrestris</i>
146	454_chiA	bacteria, functional gene, chiA, lakes	environmental bacteria (Swiss lakes)
145	Assessing the hybridization rate between the European Wildcat and the domestic cat in Switzerland	conservation biology, introgression, SNP genotyping, non-invasive hair sampling, ancient DNA	<i>Felis silvestris</i>
144	Understanding species range limits: a comparative approach along a latitudinal and elevational gradient	range, limit, elevational, latitudinal	ruderal plant species ( <i>Senecio vulgaris</i> , <i>Senecio viscosus</i> , <i>Plantago major</i> , <i>Plantago lanceolata</i> )
143	Fungal community assembly and specific mycorrhizal association: Relating fungal and plant invasion in a field experiment (original title) Importance of relative phylogenetic relatedness and genetic di	community phylogenetics, above-belowground interactions, biological invasion, community assembly, dispersal, environmental filtering, functional niche	Glomeromycota (arbuscular mycorrhizal fungi); <i>Plantago lanceolata</i> , <i>Anthyllis</i> , <i>Salvia</i> , <i>Hypericum</i> (bio

ID	title	keywords	organism
		complementarity, anthropogenic disturbance, phylo	
142	Microsatellite markers in earwigs	Microsatellite, Family life, Evolution, Social conflicts, Paternity	Forficula auricularia
141	Analyzing vegetative growth rates of the endospore forming bacterium <i>Pasteuria ramosa</i> in its natural host <i>Daphnia magna</i>	host-parasite interactions, qPCR, bacterial growth rate, <i>Pasteuria ramosa</i> , <i>Daphnia magna</i>	<i>Pasteuria ramosa</i> / <i>Daphnia magna</i>
140	Genetic exploration of quantitative fungal resistance in wheat. Broad spectrum versus specific approaches	Fungal pathogens, <i>Triticum aestivum</i> , expression profiles, defense pathways, pleiotropic effects	<i>Triticum aestivum</i>
139	Costs and stability of plasmid-borne antibiotic resistance	antibiotic resistance, gene expression, regulation, cost of resistance, resistance plasmids, plasmid costs	<i>Escherichia coli</i>
138	Role of the alternative sigma factor RpoS in <i>E.coli</i>	Chromatin immunoprecipitation, bacterial networks, sigma factor, bacterial stress, gene expression	<i>E.coli</i>
137	Genetic analyses of four closely-related plant-pathogenic <i>Phytophthora</i> species to infer their population structure, pathways of spread, and demographic history.	<i>Phytophthora citricola</i> Complex, Microsatellites, Plant Pathogen, Population Genetics, Biodiversity	<i>Phytophthora citricola</i>
136	Co-evolutionary arms race between public good cooperators and cheats in a pathogenic bacterium	antagonistic co-evolution, evolution of cooperation, microbes, virulence factor, experimental evolution, genetics of adaptation	<i>Pseudomonas aeruginosa</i>
135	Evolution of Antibiotic Resistance	Evolution, antibiotic resistance, <i>Escherichia coli</i>	<i>Escherichia coli</i>
134	Characterization of polymorphic microsatellite markers for <i>Armeria caespitosa</i>	Microsatellite, <i>Armeria caespitosa</i> , Genetic diversity, Polymorphic marker, PCR.	ETH Zurich and Universidad Rey Juan Carlos
133	Understanding the origin and maintenance of biodiversity in dendritic freshwater metacommunities	metapopulation, river systems, dispersal, invasion	<i>Gammarus pulex</i> , <i>Gammarus fossarum</i>

ID	title	keywords	organism
132	Comparative transcriptomics to identify genes involved in Xap resistance	Bacterial spot, gene expression, prunus armeniaca, microarray, transcriptome	Prunus armeniaca
131	TIME AND CONCENTRATION DEPENDENT REGULATION OF THE TRANSCRIPTOME AND THE PHENOTYPE OF A MOUSE LIVER CELL LINE EXPOSED TO BAP	Hepa1c1c7 ; BaP; transcriptome; System Biology; phenotype	Hepa1c1c7
130	Barcoding in Scutellaria	barcoding, biodiversity, cpDNA	Scutellaria (plant family Lamiaceae)
129	Population Genomics of Adaptive Radiation	Speciation, adaptive radiation, SNP, RAD tag sequencing, evolution, genome scan	Cichlid fishes (various species), three-spined stickleback ( <i>Gasterosteus aculeatus</i> )
128	Usnea	Usnea, population genetics, barcoding, forest management, mycobiont	Lichen
127	Genetic structure of populations of the brachiaria-infecting pathogen <i>Rhizoctonia solani</i> AG-1 IA from Colombia	foliar blight disease, brachiaria, pathogen emergence, host specialisation, speciation	<i>R. solani</i> AG1-IA
126	Experimental evolution of transformation rates	evolution, transformation, sex, bacteria, recombination	<i>Pseudomonas stutzeri</i>
125	Identificaiton of mutations in evolved <i>Escherichia coli</i>	SNP, evolution	<i>Escherichia coli</i>
124	Predicting the micropollutant biotransformation capacity of microbial communities	Metatranscriptomics, metagenomics, pollutant biotransformation, metabolic potential, functional predictions	Undefined microbial communities
123	Ophrys Nuclear Genes	nuclear genes, allelic diversity, phylogeny, evolution, orchids	<i>Ophrys</i> spp.
122	Heavy metal tolerance in <i>S.dioica</i>	cDNA AFLP, gene expresion, heavy metal gene, metal homeostasis	<i>S. dioica</i> , <i>S. latifolia</i>
121	Ecology of <i>Phialocephala fortinii</i> s.l.	<i>Phialocephala</i> , community ecology, microsatellites, root endophytes, conifers	<i>Phialocephala fortinii</i> - <i>Acephala applanata</i> species complex
120	Impact of ironon infant gut microbiota in Kenya	Gut microbiota, iron fortification, enteropathogens, bacterial colonization, parasites	DNA of the following organisms: ,Ä Bacteroides spp. ,Ä Firmicutes ,Ä Roseburia spp./ <i>E.rectale</i> ,

ID	title	keywords	organism
119	Evolutionary costs and benefits of trans-generational immune priming in a sex-role reversed fish	Evolutionary ecological immunology, sex-role reversal, host-parasite interaction, evolution, gene expression	Syngnathus typhle
118	Genetic exchange in Crithidia	Crithidia bombi, Bombus terrestris, Genetic exchange, Microsatellites, Genetic diversity	Crithidia bombi, Trypanosomatidae
117	13C-labeled D-fructose in vitro fermentation	RNA-SIP, gut microbiota, fructose metabolism, T-RFLP, obesity	mixed gut microbiota (e.g. Bacteroides, Roseburia, Lactobacillus, Bifidobacteria, Enterobacteriaceae
116	The effects of iron deficiency and subsequent iron supplementation on the gut microbiota and prevalence of pathogens	Gut microbiota, iron deficiency, iron supplementation, in vitro fermentation, rat studies	Salmonella, gut microbiota (Bacteroides spp., Lactobacilli, Enterobacteriaceae, Roseburia spp, Rumin
115	Gynogenesis as a dispersal strategy in parasite communities vs. genetic structure of clonal stocks of invasive prussian carp (Carassius gibelio) in Finland and Germany	sperm-dependent parthenogenesis, parasites, Red Queen, evolution of sexual reproduction, fishes, invasive species	Carassius gibelio
114	Can epigenetic variation lead to adaptation to different soil conditions in Arabidopsis thaliana?	epiRIL, epigenetics, adaptation, gene expression, flowering pathway	Arabidopsis thaliana
113	Influence of parental treatment on fitness of Arabidopsis thaliana	epigenetics, maternal effects, Arabidopsis thaliana, stress, hybrids	Arabidopsis thaliana
112	Development and validation of a new in vitro colonic fermentation model for C. difficile infection in the elder gut	Clostridium difficile, CDI (C. difficile infection), elder gut, colonic fermentation model, quantitative real-time PCR, probiotics,	Clostridium difficile, Lactobacillus casei, gut microbiota (Bacteroides spp., Lactobacilli, Enterobac
111	Worldwide patterns of genetic differentiation in the invasive moth pest Grapholita (=Cydia) molesta	bioinvasions, crop pest, dispersal, genetic differentiation, microsatellites, populations	Grapholita (=Cydia) molesta
110	Microsatellite isolation and Development in Lodoicea maldivica	Lodoicea maldivica, Coco de mer, conservation biology, nSSR's, gene flow	Lodoicea maldivica
109	The immunological consequences of mating	evolution, parasites, gene expression, host-pathogen, specificity, immunity, costs of sex	Bombus, Crithidia
108	Edwards Teaching	Invasive plant, microsatellite, population structure, teaching, plant ecology	Impatiens glandulifera

ID	title	keywords	organism
107	Polycomb-mediated repression in early mouse embryogenesis	BioMark (Fluidigm), Dynamic Array 48x48 and 96x96 for gene expression, Mouse, single cell	Mus musculus
106	Investigating the effects of probiotics and prebiotics in an in vitro intestinal fermentation model and in vivo on Salmonella infection in swine	Gut microbiota, Salmonella, probiotic, prebiotic, swine	Bifidobacteria, Pediococci, Salmonella, gut microbiota(Bacteroides spp., Lactobacilli, Enterobacteri
105	Permanent sampling scheme in the Evoltree ISS Valais: genetic structure and gene flow in a landscape context (Quercus spp., Pinus sylvestris)	Landscape genetics, gene flow, hybridization, microsatellites, oak, Quercus, Valais	Quercus spp. (Pinus sylvestris samples will be analyzed later)
104	Development and validation of a novel barcoding strategy to support identification, tracing and trade regulation of precious timber trees in one of the world's most threatened biodiversity hotspots	barcoding, SNP, genotyping, sequencing, microsatellites	Dalbergia sp., Diospyros sp.
103	Selective depletion of Foxp3+ regulatory T cells promotes hypercholesterolemia and exacerbates experimental atherosclerosis	Gene expression, Affymetrix array technology, pathway analysis, Heat Map graphs, data analysis only	Mus musculus, liver tissue
102	Phylogenetic analysis of BZR-BAM proteins	beta-amylase, brassinosteroids, BZR-BAMs, carbohydrate metabolism, transcription factors	Arabidopsis thaliana
101	Meiotic Recombination in the Met-1 Genome (MRMG)	cytosine methylation, meiotic recombination, high-throughput SNP genotyping, Arabidopsis thaliana, met1 mutant	Arabidopsis thaliana
100	Evolution of prophage integration sites	Microbial ecology, Bacteriophages, Prophage attachment site	Escherichia coli, temperate lambdaoid bacteriophages
99	Genetic diversity plants in organic and conventional agri-culture	Dactylis glomerata, SSR, molecular marker, grassland management, organic and conventional agriculture	Dactylis glomerata
98	Evolutionary and ecological functional genomics of Arabidopsis relatives	evolution, polymorphism, SNP, gene expression, plants	Arabidopsis spp., Cardamine spp., Dipterocarpaceae



ID	title	keywords	organism
97	AVE_ETH- Adaptive genetic variation and plant adaptation to environmental heterogeneity	population resequencing, adaptation, candidate genes, SNPs, gene expression	Arabidopsis, Cardamine, Arabis
96	AVE_WSL - Adaptive genetic variation and plant adaptation to environmental heterogeneity	population resequencing, adaptation, candidate genes, SNPs, gene expression	Arabidopsis, Cardamine, Arabis
95	Genetic processes underlying species coexistence in the tropical rainforests of Borneo	Ecological genetics, seed and pollen dispersal, gene flow, species coexistence, population distribution, competition, nuclear and chloroplastic microsatellites, conservation biology	Shorea accutissima, Shorea argentifolia, Shorea beccariana, Shorea gibbosa, Shorea mecistopteryx, Sh
94	Comparison of defense gene expression between Arabidopsis Col-0 wild type plants and pepr1Xpepr2 mutant plants	Innate Immune Responses, Gene Expression, Bacterial Elicitors, Defense Receptors, Endogenous Danger Signals	Arabidopsis thaliana
93	Quantification of bacteriophages with real-time PCR	Microbial ecology, Parasite quantification, Bacteriophages	Escherichia coli, temperate lambdoid bacteriophages
92	Evolution of host-plant choice in a clade of osmiine bees	Bayesian analysis , evolution, host-plant preferences, maximum likelihood, oligolecty, parsimony, phylogeny	Osmia spp. (Apoidea, Megachilidae)
91	Assess genetic variation within and among natural populations of Asterionella formosa	population genetics, lake connectivity gradient versus gene flow, microsatellites	Asterionella formosa
90	Paleo ecology of hybridizing Daphnia: abiotic factors	Hybridization, climate change, evolution, population genetics, lakes, zooplankton, toxic compounds, biodiversity	Daphnia sp.
89	The influence of anthropogenic stressors on host-parasite interactions	coevolution, Daphnia, Diazinon, GxGxE, host, parasite	Daphnia sp.
88	Vernalization response of Arabidopsis thaliana	ecological genetics, Arabidopsis thaliana, Swiss Alps, altitude, vernalization, gene expression	Arabidopsis thaliana
87	Does transgenic wheat have an impact on the frequency and diversity of natural plant-beneficial Pseudomonads under field conditions?	DAPG-Pseudomonads, T-RFLP, GM wheat, rhizosphere, diversity	Different strains of Pseudomonas fluorescens

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86	Population Genetics and Phylogeny of the Plant Pathogenic Protozoan <i>Spongopora subterranea</i> f.sp. <i>subterranea</i>	Population Genetics, Phylogeny, Taxonomy, Fragment Analysis, Microsatellites/STRs/SSRs, Evolution, Biotrophic, Parasite, Genetic Variation	<i>Spongopora subterranea</i> f.sp. <i>subterranea</i> , <i>Spongopora subterranea</i> f.sp. <i>nasturtii</i>
85	Host specialization in aphid parasitoids	Cryptic species, Host specialization, Microsatellites, Morphometrics, Parasitoids,	<i>Lysiphlebus fabarum</i> , <i>Lysiphlebus testaceipes</i> , <i>Praon dorsale</i> , <i>Praon yomenae</i>
84	Population structure of the chub ( <i>Leuciscus cephalus</i> ), colonization history, habitat fragmentation, genetic diversity, and phenotypic variability	Conservation genetics, Dams, Gene flow, Habitat fragmentation, Phylogeography, River restoration,	<i>Leuciscus cephalus</i>
83	Der Kleine Rohrkolben - Genetische Grundlagen f,r eine erfolgreiche Wiederansiedlung in revitalisierten Flussauen	conservation biology, SSRs, riparian flood plains, <i>Typha minima</i> , conservation genetics	<i>Typha minima</i>
82	Phylogeny of the bee genus <i>Hoplitis</i> (Osmiini, Megachilidae)	evolution, nesting biology, biogeography, diversification, systematics	Ca. 60 species of the bee genus <i>Hoplitis</i>
81	Pollination and population biology of <i>Dianthus gratianopolitanus</i>	selfing rate, pollination, microsatellites, rare species, caryophyllaceae	<i>Dianthus gratianopolitanus</i>
80	Population genetics of <i>Fredericella sultana</i>	microsatellites, PKD, bryozoans, asexual animals, population genetics	<i>Fredericella sultana</i>
79	Primeval forest structure and biodiversity: population genetic investigation of <i>Lobaria pulmonaria</i> in beech primeval forest of Uholka-Schyrokyj Luh massive (Carpathan Biosphere Reserve, Ukraine)	conservation biology, primeval forest, demes, metapopulation, symbiosis	<i>Lobaria pulmonaria</i>
78	Genetic differentiation among selection lines of <i>Tribolium castaneum</i>	Sexual selection, sexual conflict, experimental evolution, biodiversity, speciation, extinction, genetic differentiation, microsatellites	<i>Tribolium castaneum</i>
77	Multiple infections and parasite genetic diversity	evolution, parasites, gene expression, qPCR, SNP	<i>Crithidia bombi</i> + <i>Bombus terrestris</i>

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76	Development of a SNP library for the trypanosomatid <i>Crithidia bombi</i>	<i>Crithidia bombi</i> , <i>Bombus terrestris</i> , host-parasite interactions, population genetics, multiple infections, SNP	<i>Crithidia bombi</i>
75	The transcriptional basis of host-pathogen specificity in bumblebees	evolution, parasites, gene expression, host-pathogen, specificity, immunity	<i>Bombus</i> , <i>Crithidia</i>
74	EvoTree: <i>Pinus cembra</i> SNP diversity	SNP diversity, <i>Pinus cembra</i> , environmental association, landscape genetics, population fragmentation	<i>Pinus cembra</i>
73	Spatial and temporal responses to natural selection of the threespine stickleback ( <i>Gasterosteus aculeatus</i> ) in Lake Myvatn, Iceland.	evolution, phenotypic variation, genetic variation, temporal response, threespine stickleback <i>Gasterosteus aculeatus</i>	Threespine stickleback - <i>Gasterosteus aculeatus</i>
72	Calcium-Dependent Alternative Splicing of the <i>igf1</i> Gene	C2C12, IGF, MGF, gene expression, alternative splicing	Mouse skeletal muscle
71	EVOLTREE-Influence of genetic variation within <i>Pinus sylvestris</i> and site water regime on the neutral and functional diversities of its ectomycorrhizal fungal associate <i>Cenococcum geophilum</i>	ectomycorrhizal diversity, community genetics, co-evolution, population genetics, SSR, gene expression	<i>Pinus sylvestris</i> / <i>Cenococcum geophilum</i>
70	AVE Uni- Adaptive genetic variation and plant adaptation to environmental heterogeneity	population resequencing, adaptation, candidate genes, SNPs, gene expression	<i>Arabidopsis</i> , Cardamine, <i>Arabis</i>
69	Phylogenetic diversity of <i>Epichloë</i> grass endophytes	Fungi, evolution, population biology	<i>Epichloë</i> , Botanophila
68	Genome-wide patterns of nucleotide diversity and divergence in wild tomatoes ( <i>Solanum</i> section <i>Lycopersicon</i> ): inferences on demographic history, speciation, and natural selection	plant evolutionary genetics, evolution, speciation, DNA sequences, coalescent, historical demography, genetic drift, natural selection, recombination rates, wild tomatoes, <i>Solanum</i>	several species of wild tomatoes ( <i>Solanum</i> section <i>Lycopersicon</i> ): <i>Solanum peruvianum</i> , <i>S. chilense</i> , <i>S.</i>
67	Genetic population structure after glacial expansion of <i>Radix balthica</i>	<i>Radix balthica</i> , genetic diversity, post-glacial expansion, phenotypic plasticity, morphotypes, rapid ecological divergence	<i>Radix balthica</i>

ID	title	keywords	organism
66	Genetic diversity in the invasive mollusc <i>Dreissena polymorpha</i>	invasive species, spread and distribution pathways, genetic diversity, population genetics, mollusca, microsatellites	<i>Dreissena polymorpha</i> and <i>Dreissena bugensis</i>
65	Plant factors influencing bacterial colonization of the <i>Arabidopsis thaliana</i> phyllosphere	microbial ecology, phyllosphere, community composition, ARISA, community size	<i>Arabidopsis thaliana</i> , <i>Sphingomonas</i> , <i>Methylobacterium</i> , <i>Pseudomonas</i> , other microbes
64	Intraspecific intron presence-absence polymorphism in a <i>Mycosphaerella graminicola</i> endoxylanase gene	Gene expression, Housekeeping genes, fungi, evolution, intron	<i>Mycosphaerella graminicola</i>
63	Rapid and automated sample handling and processing	sample processing, biomolecule, micro-/nanofluidics, analysis, automated handling	-
62	Genetic diversity in the freshwater isopod <i>Asellus aquaticus</i>	genetic diversity, population genetics, cryptic species, isopoda, microsatellites	<i>Asellus aquaticus</i>
61	Analysis of adaptive and neutral gene flow in an alpine plant, <i>Arabis alpina</i>	Climate warming, adaptation, <i>Arabis alpina</i> , landscape genomics, selection	<i>Arabis alpina</i>
60	Host-parasite interactions in variable environments	host-parasite interactions, evolution, <i>Diplostomum pseudospathaceum</i> , <i>Lymnaea stagnalis</i> , microsatellite	<i>Diplostomum pseudospathaceum</i> , <i>Lymnaea stagnalis</i>
59	Ectomycorrhizal fungi on forest fire sites	disturbance ecology, ectomycorrhizal fungi, diversity, forest fire sites,	ectomycorrhizal fungi
58	How important is phylogeny in the assembly of natural assemblages of arbuscular mycorrhizal fungi?	community phylogenetics, above-belowground interactions, biological invasion, community assembly, dispersal, environmental filtering, functional niche complementarity, anthropogenic disturbance, phylo	Glomeromycota (arbuscular mycorrhizal fungi); <i>Plantago lanceolata</i> (bioassay hostplant)
57	Relationships between dispersal modes and population genetic structure of aquatic/riparian organisms in a managed floodplain river	stream ecology, microsatellites, invertebrates, dispersal, population genetics	<i>Gammarus fossarum</i> , <i>Baetis rhodani</i>
56	Population Diversity of <i>Phaeosphaeria nodorum</i>	Sequencing, Diversity, Species Complex, Effectors, Host Specific Toxins, Center of Origin, Evolution of Pathogens	<i>Phaeosphaeria nodorum</i>

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55	Gene flow, virulence and evolutionary potential of the ash dieback pathogen <i>Chalara fraxinea</i>	population genetics, gene flow, evolution, disease control, ash dieback, phylogeography	<i>Fraxinus excelsior</i> , <i>Hymenoscyphus albidus</i> , <i>H. pseudoalbidus</i>
54	QTL mapping of virulence and other quantitative characters in the model plant pathogenic fungus <i>Mycosphaerella graminicola</i>	Host-pathogen interaction / QTL mapping / SSRs / SNPs / Genotyping / Phenotyping	<i>Phaeosphaeria nodorum</i> (anamorph: <i>Stagonospora nodorum</i> )
53	Evolutionary genetics of effector loci in plant pathogenic fungi	evolutionary genetics, population genomics, SNP, plant pathogens, <i>Rhynchosporium secalis</i>	<i>Rhynchosporium secalis</i>
52	Measuring the metabolic cost of bacterial stress responses	bacteria, experimental evolution, gene expression, individuality, phenotype	<i>E.coli</i> , <i>C. crescentus</i> , <i>P. stutzeri</i>
51	Probing the robustness of essential genes	experimental evolution, genome evolution, essential genes, gene expression	<i>Escherichia Coli</i>
50	Pollinators - selective agents for plant speciation? Pre- and postpollination processes in closely related, lepidoptera-pollinated wild carnations	conservation biology, evolution, plant-pollinator interactions,	<i>Dianthus silvestris</i> , <i>Dianthus carthusianorum</i>
49	Compensation, stress, and the maintenance of antibiotic resistance	antibiotics, stress, fitness, compensatory mutations, disease evolution	<i>E. coli</i> , <i>S. typhimurium</i>
48	Impact of maternal breast milk on the establishment of infant gut microbiota during early life	Gut microbiota, breast milk, infant gut colonization, probiotics, bacterial translocation	Unknown ( <i>Bifidobacterium</i> , <i>Lactobacillus</i> , <i>Streptococcus</i> , <i>Staphylococcus</i> spp.)
47	Insecticidal activity in plantbeneficial pseudomonads	Fluorescent pseudomonads, molecular diversity, biocontrol, biological activity, insecticidal toxins	<i>Pseudomonas</i> spp.
46	Acid and Predator stress in <i>Rana arvalis</i>	acid stress, predation, multiple stressors, amphibians	<i>Rana arvalis</i>
45	Application of wool hydrolysate as a biochelator for the biofortification of mineral micronutrients for human nutrition	biofortification, shifts in soil community, hydrolysed wool, trace element deficiency, TRFLP	soil bacteria and fungi
44	Ecological and genetic processes underlying Allee effects among plant populations in the context of divergent population histories	Conservation genetics, Microsatellites, Islands, Seychelles, Endemism, <i>Medusagynaceae</i> , <i>Dipterocarpaceae</i> , <i>Rubiaceae</i>	<i>Medusagyne oppositifolia</i> , <i>Vateriopsis seychellarum</i> , <i>Glionnetia sericea</i>

ID	title	keywords	organism
43	Selection on immune genes during the evolution of bumblebees	immune genes, selection, bumblebees, antimicrobial peptides, parasite recognition	Various bumblebee species <i>Bombus</i> spp
42	Genetic characterization of a <i>Cryphonectria hypovirus</i> population in western Switzerland	Phytopathology, virus, population genetics, snp, parasites, biological control	<i>Cryphonectria parasitica</i> Hypovirus
41	Patterns of adaptation during experimental host-parasite coevolution	parasites, coevolution, host-parasite system, Red Queen hypothesis, local adaptation	<i>tribolium castaneum</i> and <i>Nosema whitei</i>
40	Cross-infection of a trypanosome parasite between two bumble bee species	Co-evolution, <i>Crithidia bombi</i> , specificity, multiple host species, <i>Bombus terrestris</i> , <i>Bombus lapidarius</i>	<i>Crithidia bombi</i>
39	Gene Expression Analyses in <i>Silene latifolia</i>	gene expression, sex-chromosomes, next-generation sequencing, allele specific expression,	<i>Silene latifolia</i>
38	Pyrosequencing of naturally pooled parasite samples	SNP, parasites	<i>Diplostomum</i> sp., a trematode parasite
37	microRNA expression profiles of maize	microRNA	<i>Zea mays</i>
36	Natural disease control by root endophytes in a changing climate	parasites, root symbionts,	<i>Phialocephala</i> , <i>Acephala</i> and related species, <i>Picea abies</i>
35	ENHANCE grasshopper	Landscape genetics, grasshopper ecology, habitat fragmentation, ecological compensation areas, conservation genetics, AFLP, microsatellites	<i>Chorthippus albomarginatus</i> , <i>Chorthippus biguttulus</i> , <i>Gomphocerippus rufus</i> , <i>Stethophyma grossum</i>
34	Synergies between fragmentation and habitat patch degradation: Implications for species and population viability	conservation biology, fragmentation, patch quality, gene flow, inbreeding, fitness	<i>Vateria indica</i> , <i>Dysoxylum malabaricum</i>
33	Evolution of the mitochondrial genome in the <i>Phialocephala fortinii</i> s.l. - <i>Acephala applanata</i> species complex (PAC)	mtDNA, evolution, concordance, root endophyte, DSE	<i>Phialocephala fortinii</i> s.l. - <i>Acephala applanata</i> species complex
32	Paleo ecology of hybridizing <i>Daphnia</i> : abiotic factors	Hybridization, climate change, evolution, population genetics, lakes, zooplankton, toxic	<i>Daphnia</i> sp.

ID	title	keywords	organism
31	The Role of Genetic Diversity and Interaction of Fungal Symbionts in PAC-Woody-Plant Systems	parasites, root symbionts, ecology, DNA quantification, interactions	Phialocephala, Acephala and related species
30	Inbreeding in <i>Parashorea tomentella</i> as a function of density and nearest neighbour distance.	Conservation biology, Species coexistence, gene flow, pollination, inbreeding	Dipterocarpaceae
29	Bacterial Communities in the bumble bee gut: Diversity, Structure and Function	bumble bees, bacteria, microbial communities, biodiversity, biogeography, immunity, colonisation resistance, T-RFLP	<i>Bombus</i> spp., Bacteria
28	Comparative and molecular approach to the identification of receptors for <i>E.coli</i> with fimbriae F4ab/ac	<i>Sus Scrofa</i> , <i>E. coli</i> , F4ab/ac, receptors, SNP	<i>Sus Scrofa</i>
27	Belgaskogur threespine sticklebacks ( <i>Gasterosteus aculeatus</i> )	evolutionary biology, small geographic scale, adaptive radiation, divergence, microevolution	threespine sticklebacks ( <i>Gasterosteus aculeatus</i> )
26	Evaluation of Beech genetic resources for sustainable forestry	AFLP genom scan, evolution, climate change	<i>Fagus sylvatica</i>
25	Gene flow and lateral and longitudinal connectivity in riparian species	River management; endangered species; Switzerland; river restoration; genetic structure; landscape genetics	<i>Chorthippus pullus</i> ; <i>Myricaria germanica</i>
24	Genetic and demographic structure of a small population of the rare alpine plant <i>Eryngium alpinum</i> in Central Switzerland and their implications for conservation management	conservation biology, microsatellites, inbreeding depression, reinforcement, demography, germination, pollen dispersal, gene flow	<i>Eryngium alpinum</i>
23	Fire Blight resistance in <i>Malus robusta</i> 5	fire blight resistance, <i>Malus robusta</i> , bacterial disease,	<i>Malus robusta</i> 5
22	Genetic mechanisms of altitudinal adaptation in <i>Arabidopsis thaliana</i>	Altitudinal adaptation, candidate genes, molecular evolution, QTL mapping, natural variation, SNP	<i>Arabidopsis thaliana</i>
21	Assessing the effectiveness of connectivity measures on gene flow and genetic diversity of wildflowers in agricultural landscapes - a	agricultural landscapes, connectivity, landscape genetics, local adaptation, insect-pollinated plants, seed provenance	<i>Lychnis flos-cuculi</i> ( <i>Silene flos-cuculi</i> )

ID	title	keywords	organism
	landscape genetic approach (part of a larger CCES project ENHANC		
20	Neutral genetic diversity, differentiation and gene flow in low central vs. upper peripheral plant populations in the Swiss Alps	Local adaptation, Climate Change, Swiss Alps, Gene flow, Landscape genetics, BioChange	Briza media, Ranunculus bulbosus, Trifolium montanum
19	Disruption of local adaptation in peripheral alpine plant populations via central populations pollen immigration	Outbreeding, Microsatellites, Local adaptation, Swiss Alps, Gene flow	Ranunculus bulbosus, Trifolium montanum
18	Porous genomes and the nature of plant species differences	Silene, gene expression, hybridization, introgression	Silene latifolia, Silene dioica
17	Outcrossing rates and population structure of Arabidopsis thaliana	Arabidopsis thaliana, outcrossing rates, population structure, SSR	Arabidopsis thaliana
16	Microbial communities structures and functions in primary succession environments	microbial communities, soil, Nitrogen cycle, P, community structure	Bacteria, fungi
15	Diversity and abundance of methanotrophic communities in various different environments	greenhouse gases, methanotrophs, methane monooxygenase, stress response, atmospheric methane oxidation	unknown methanotrophic microorganisms
14	Divergence in gene expression between two closely related Silene species and their hybrids	Silene, gene expression, hybridization	Silene latifolia, Silene dioica
13	Importance of hybridization in asexual endophytes for grasses	evolution, Epichloe, hybridization, fungi	Hordelymus europaeus, Neotyphodium sp.
12	Phylogeography and conservation genetics of the calcareous fen specialist Scorpidium cossonii (Bryophyta)	Scorpidium cossonii, habitat fragmentation, conservation genetics, phylogeography, bryophyte, calcareous fen	Scorpidium cossonii
11	Geographic mosaics of coevolution of Lobaria pulmonaria and its photobiont Dictyochloropsis reticulata : reciprocal provenance-clone test and pattern of symbiont selectivity on Macaronesian Islands	Conservation Biology, symbiosis, lichen, algae, microsatellite	Lobaria pulmonaria, Dictyochloropsis reticulata
10	Genetics of host-parasite interactions in field samples	host-parasite interaction, haplotype frequencies, fitness, coevolution, red queen	Bombus terrestris, Crithidia bombi



ID	title	keywords	organism
9	Parasite diversity in bumble bee populations	host-parasite coevolution, parasite diversity, invasion biology, cytochrome b, small subunit RNA, barcode, biogeography	Bombus spp. (Apidae), Crithidia spp. (Trypanosomatidae), Nosema spp. (Microsporidia)
8	Arthrogryposis multiplex congenita in Swiss Large White	recessive disease, genotype, marker	Sus scrofa
7	Impact of genetically modified wheat on the frequency and genetic diversity of root-colonizing pseudomonads associated with soil fertility	Plant-growth promoting pseudomonads, bacterial diversity, DGGE, MPN, FACS	Pseudomonas
6	Genetically induced niche stability in alpine plants	Outliers, Niche Stability, Brassicaceae, Alpine Plants, AFLPs, Adaptation	Arabis alpina, Arabis jacquini, Cardamine resedifolia, Draba aizoides, Thlaspi rotundifolia
5	Biogeography of introduced Lactuca serriola populations	Invasion biology, microsatellites, biogeography, microevolution, introduction history	Lactuca serriola
4	Genetic diversity, contemporary evolution and the maintenance of biodiversity in changing alpine environment (Gammarus fossarum)	Evolution, molecular species identification, pyrosequencing, cryptic species, genetic diversity	Gammarus fossarum species complex (Amphipoda)
3	Genetic diversity, contemporary evolution and the maintenance of biodiversity in changing alpine environment (Salmo trutta)	Evolution, molecular species identification, pyrosequencing, cryptic species, genetic diversity	Salmo trutta species complex
2	Rust fungi on Annonaceae	Rust fungi, Uredinales, phylogenie, Dasyspora, Shaerophragmium, Annonaceae	Rust fungi, Uredinales, Dasyspora, Shaerophragmium, Aecidium