

Here you can find the list of poster presenters for the SMBE 2023 Conference

Each poster is identified by the venue (EC= Estense Castle; SP= San Paolo Cloisters), the day (24= 24th of July; 25= 25th of July) and a unique number (UnqN).

The SubID refers to the abstract management system and is provided just as an additional check.

Poster presenters are requested to attend their posters at the specified time (18:00 - 20:00) and venue in person, or via Gathertown for poster numbers marked with R.

Posters assigned to the July 24 session can be exhibited from the July 23 (afternoon) and should be removed before lunch time, July 25.

Posters assigned to the July 25 session can be exhibited from July 25 (afternoon) and should be removed before the end of the meeting.

First Name	Surname/Family Name	Symposium	Venue	Day	UnqN	SubID	Title
Julia	Barth	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	1	577	The role of genome mutation rates and life history traits on speciation in a cichlid fish adaptive radiation
William	Booker	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	2	1578	The evolution of cytoplasmic diploidization and the consequences of expansion load in polyploid species
Arun	Durvasula	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	3	837	Modeling pairwise site pattern co-occurrence to understand Great Apes speciation
James	Fleming	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	4	392	Specifying a species: whole genome inferred phylogenetic robustness metrics
Alice	Genestier	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	5	586	A model of the PIPER dynamics and its role in hybrid sterility and speciation
Ata	Kalirad	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	6	1186	Genetic drift promotes and recombination hinders speciation
Maël	Lefevre	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	7	432	A standardized comparative analysis of ancient DNA library estimation methods, using "MAGGER": a high-fidelity ancient DNA pipeline
Luísa	Marins	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	8	1342	Exploiting the evolutionary history of the two-toed sloth (<i>Choloepus</i>) with genomic data: in search of Amazonian cryptic biodiversity
Dashnell	Massey	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	9	755	Simulating assortative mating by global ancestry in admixed populations
Ferdinand	Paët	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	10	706	Topological comparison of coalescent tree inference tools
Yakov	Pichkar	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	11	1551	Five-scale cultural variation mediates genetic population structure in England
Iker	Rivas-González	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	12	828	TRAILS: tree reconstruction of ancestry using incomplete lineage sorting
Marjolaine	Roussette	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	13	1110	Evolution and determinants of reproductive isolation in the pea aphid speciation continuum
Luciana	Santoferrara	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	14	1057	The fuzzy line between species and populations in the marine microbial world: a study case based on shell-ed cladocera
Lodovico	Sterzi	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	15	997	Comparative genomics reveals clinical and environmental <i>Salmonella</i> successions lineages with specific gene content and gene flow patterns
Diego	Veliz-Otani	18 - Modeling the genomic, social, and ecological drivers of speciation	EC	24	16	1327	From Buffalo to Cattle: The Unidirectional Migration of <i>Theileria Parva</i> and the Emergence of East Coast Fever
Nadia	Aubin-Horth	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC	24	17	25	Genetic diversity and evolution in <i>Arabidopsis thaliana</i> in an urban setting: implications for the development of professional identity in undergraduate biology students
Joséfa	Gonzalez	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC	24	18	1657	Manoagostar: Catch The Fly! A Citizen Science Network in Adaptation Genomics
Florin Mircea	Ilescu	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC	24	19	1822	Science belongs to everyone in the genomic era
John	Lees	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC	24	20	261	Interactive population genetics for everybody
Michele	Leone	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC	24	21	862	meuting.org: Citizen Science for arthropod meuting
Sarah	Mueller	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC	24	22	629	Bridging the gap: How can genetic analysis translate to conservation action in the Eurasian lynx
Maddie	Olvey	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC	24	23	1457	Can standing genetic variation be detrimental for survival and adaptation to new environments?
Fernando	Racimo	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC	24	24	59	The bioprospecting emergency calls for scientists to change tactics
Daniel	Taub	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC	24	25	1900	Peer-reviewed Journal Articles Intended for a General Audience are Well-read and Well-Cited
Elena	Zerkin	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC	24	26	1134	Activation of heat shock gene in <i>Drosophila</i> species: a course-based undergraduate research project contributing to study of the evolution and function of the insulin signaling pathway through the Genomics Education Partnership (GEP)
Eva	Biggs	22 - Experimental evolution of non-model species and systems	EC	24	27	121	Beyond the theory: From habitat to control in microbial evolution
Marlin	Ceelen	22 - Experimental evolution of non-model species and systems	EC	24	28	1258	Not just nutrients: The effect of Horizontal Gene Transfer on the evolution of bacterial predator <i>Myxococcus xanthus</i> .
Luis Miguel	Cheyin	22 - Experimental evolution of non-model species and systems	EC	24	29	1528	Environmental evolution of eukaryotes, transposons, and higher-level plasticity in response to environmental predictability in a halobacterial microalgae
Amy	Gooch	22 - Experimental evolution of non-model species and systems	EC	24	30	950	Expanding the taxonomic scope of <i>Thraupis</i> Darwinian Evolution Experiments via Directed Evolution
Cecile	Lorrain	22 - Experimental evolution of non-model species and systems	EC	24	31	560	Evolutionary potential and constraints for a major wheat pathogen under fungicide stress
Jason	Pienaar	22 - Experimental evolution of non-model species and systems	EC	24	32	292	Coevolution between tardigrades and mosses and a signaling role for host secondary metabolites in tardigrad desiccation tolerance
Karissa	Plum	22 - Experimental evolution of non-model species and systems	EC	24	33	1070	Adaptation to Elevated Temperature and its Consequences
Gisela	Rodriguez Sanchez	22 - Experimental evolution of non-model species and systems	EC	24	34	1462	Unravelling the hidden genetics of Windy Spreaders
Shreya	Routh	22 - Experimental evolution of non-model species and systems	EC	24	35	283	Can standing genetic variation be detrimental for survival and adaptation to new environments?
Mario	Santoro	22 - Experimental evolution of non-model species and systems	EC	24	36	1581	The more, the merrier? The evolution of antibiotic resistance on multiple plasmids
Sarah	Schaack	22 - Experimental evolution of non-model species and systems	EC	24	37	1341	Causes and Consequences of Mutation Rate Variation: Testing Key Predictions With Experimental Data from <i>Daphnia magna</i>
Niklas	Steube	22 - Experimental evolution of non-model species and systems	EC	24	38	1073	Ferocious origin of allelic control in cyanobacterial photoprotection
Cecilia	Trivellin	22 - Experimental evolution of non-model species and systems	EC	24	39	1233	Evolution of microbial robustness in fluctuating environments
Pranav	Uthirakrishnan	22 - Experimental evolution of non-model species and systems	EC	24	40	1532	Evidence of ePgrh polymorphism in the wild and its associated tradeoffs in the history traits
Luis Ever	Vega Cabrera	22 - Experimental evolution of non-model species and systems	EC	24	41	1159	An increase in chromosome copy number drives rapid adaptation in a cold-adapted bacterium
Sarah	Wacker	22 - Experimental evolution of non-model species and systems	EC	24	42	84	Genetic diversity and evolution in <i>Arabidopsis thaliana</i> in an urban setting: implications for the development of professional identity in undergraduate biology students
Pu	Wang	22 - Experimental evolution of non-model species and systems	EC	24	43	864	Distinguishing selection, contingency, and chance during the convergent evolution of multicellular yeasts
Nico	Appold	23 - Evolutionary approaches to understand cancer across scales	EC	24	44	1067	Metabolic confinement and release of resistant mutants is governed by collective cell dynamics in dense populations
Charles	Baer	23 - Evolutionary approaches to understand cancer across scales	EC	24	45	636	CORMIC signature and transcriptional asymmetry of spontaneous mutations in <i>Caenorhabditis elegans</i>
Mary	Boyd	23 - Evolutionary approaches to understand cancer across scales	EC	24	46	905	The Diversity of Placenta Invasiveness in Mammals and the Relationship Between Placenta Invasiveness and Cancer Risk
Mertell	Brunet Guasch	23 - Evolutionary approaches to understand cancer across scales	EC	24	47	1424	Mutation-driven extinction of hyper-mutated tumours: a multi-type critical birth-death process
Ramon	Diaz-Urarte	23 - Evolutionary approaches to understand cancer across scales	EC	24	48	340	Cancer progression and evolutionary emergent phenotypes: implicit evolutionary assumptions, interpretational hurdles, and why computational/inefficient procedures might allow faster scientific exploration and critical assessment
Maximilian	Eiche	23 - Evolutionary approaches to understand cancer across scales	EC	24	49	685	Towards optimizing evolution-based therapy strategies: a tailored 3D tumour model for the real-time tracking of therapy failure dynamics
Alison	Feder	23 - Evolutionary approaches to understand cancer across scales	EC	24	50	1396	State-dependent evolutionary models reveal modes of allele growth
James	Ferrare	23 - Evolutionary approaches to understand cancer across scales	EC	24	51	1458	Evolution of Evolvability in Rapidly Adapting Populations
J Nicholas	Fisk	23 - Evolutionary approaches to understand cancer across scales	EC	24	52	676	Extreme selection induced by erlotinib therapy constrains mutational diversification of EGFR-driven lung adenocarcinoma
Theódora	Grohens	23 - Evolutionary approaches to understand cancer across scales	EC	24	53	1382	Quantification of selection against neofunction formation in human cancer tumors
Jaime	Irazo	23 - Evolutionary approaches to understand cancer across scales	EC	24	54	390	Permissive conditional selection of driver mutations and modular epistatic networks in cancer
Umesh	Kalathiya	23 - Evolutionary approaches to understand cancer across scales	EC	24	55	451	Investigating the quality control checkpoint components from the nonsense mediated mRNA decay pathway
Jona	Kayser	23 - Evolutionary approaches to understand cancer across scales	EC	24	56	955	Evolutionary rescue of resistant mutants is governed by a balance between radial expansion and selection in compact populations
Fransziska	Kellers	23 - Evolutionary approaches to understand cancer across scales	EC	24	57	710	Whole-exome sequencing of five mixed neuroendocrine-non-neuroendocrine neoplasms of the gastrointestinal tract
Elle	Loughran	23 - Evolutionary approaches to understand cancer across scales	EC	24	58	608	Karyotype Evolution of Near-Haploid and Low-Hypodiploid Tumours
Jeffrey	Mandell	23 - Evolutionary approaches to understand cancer across scales	EC	24	59	1603	Software supporting customizable models of oncogenesis makes somatic evolutionary hypotheses testable
Veselin	Mancovic	23 - Evolutionary approaches to understand cancer across scales	EC	24	60	637	Fluctuating methylation clocks for inferring the evolutionary history of human cancers
Conrado	Martinez-Cadenas	23 - Evolutionary approaches to understand cancer across scales	EC	24	61	1488	Evolution of small mutations in healthy cutaneous tissue: selection and expansion of cancer driver mutations in the skin
Nathaniel	Mon Pere	23 - Evolutionary approaches to understand cancer across scales	EC	24	62	349	Clonal interference in haematopoietic stem cells
Mariana	Natalino	23 - Evolutionary approaches to understand cancer across scales	EC	24	63	1242	From Yeast to Cancer: Understanding the Impact of Nutrient Sensing in the Evolutionary Adaptation to Genomic Instability
Madeleine	Oman	23 - Evolutionary approaches to understand cancer across scales	EC	24	64	48	Modeling the predictors of mutability variation in healthy tissues
Carmen	Ortega Sabater	23 - Evolutionary approaches to understand cancer across scales	EC	24	65	1547	Understanding the relationship between karyotype heterogeneity, chromosomal instability and prognosis in childhood B-Cell Lymphoblastic Leukemia through a mathematical and ecological lens
Cristiano	Parmeggiani	23 - Evolutionary approaches to understand cancer across scales	EC	24	66	903	Does maternal-fetal conflict explain the variation in cancer rates across mammals?
Yosuke	Saito	23 - Evolutionary approaches to understand cancer across scales	EC	24	67	863	Evolutionary rescue of resistant mutants is governed by a balance between radial expansion and selection in compact populations
Anastasia	Stolyarova	23 - Evolutionary approaches to understand cancer across scales	EC	24	68	805	Mutation bias in driver genes reveals distribution of effects of oncogenic mutations
Francesco	Terenzi	23 - Evolutionary approaches to understand cancer across scales	EC	24	69	511	A Bayesian framework to infer selection strengths of extrachromosomal DNAs in human cancers
Qianci	Yang	23 - Evolutionary approaches to understand cancer across scales	EC	24	70	936	Mathematical modeling of effector T cell stimulation, elimination and binding with target cancer cells
Anastasia	Yankovskiy	23 - Evolutionary approaches to understand cancer across scales	EC	24	71	410	Evolutionary prediction of the location of primary tumors using mutational signature
Noah	Bourne	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	72	810	The genomic basis of an obligate and parasitic symbiosis
Shuyi	Ding	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	73	314	A deep neural network for estimating branch lengths in phylogenetic trees
Janna	Fierst	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	74	1383	Structural mutations and Mitator transposons in <i>Phyllum</i> genomes
Michael	Goldberg	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	75	1452	Selective dynamics of intergenations at short tandem repeats
Einat	Hazkani-Covo	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	76	288	Compensatory frameworks are common in <i>Saccharomyces cerevisiae</i> genes
Gholamhossein	Jowkar	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	77	983	Patterns of Indel Evolution in Six Mammalian Orthologous Proteomes using Poisson Indel Process
Alma	Laurino	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	78	123	Inversions and deletions mediate cofactor specificity and functional transition
Alice	Ledda	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	79	1517	Is there such a thing as neutral phylogenetics?
Dorota	MacKiewicz	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	80	1275	The resurrection of harmful effects of point and frameshift mutations by the standard genetic code
Fabrizio	Maffessoni	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	81	843	A probabilistic method to infer the role of INDEL-generating DNA repair mechanisms on genome diversity across species
Rui	Pinto	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	82	1572	From Pseudochicklet 0 to Pseudoviz: a story of gene loss
Edmundo	Torres-Gonzalez	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	84	883	Age-Related Accumulation of De Novo Indels in Mitochondrial DNA of Mice, Macaques, and Humans
Fengyu	Tu	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	85	76	Impact of traits variation of random mutations on species diversity by predator-prey coevolution
Flavia	Viliani	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC	24	86	1404	Building a Panglossian Graph for the HBB/BBH Recombination Inbred Rat Strain Family: Enhanced Discovery of Complex Variants and Validation with Sanger Sequencing
Adrian	Arellano	25 - The puzzle of eukaryotic cellular origins	EC	24	87	920	Testing bacterial evolution using the Great Oxidation Event
Philip	Bell	25 - The puzzle of eukaryotic cellular origins	EC	24	88	19	Are viruses the key to unlocking the eukaryogenesis puzzle?
Hugo	Bonnefous	25 - The puzzle of eukaryotic cellular origins	EC	24	89	999	Phylogenetics: how to infer ancestral molecular interaction networks, and why it is exciting
Auden	Cote-Heureux	25 - The puzzle of eukaryotic cellular origins	EC	24	90	1480	Fossiliferous maintain consistent amino acid usage despite extreme codon usage bias in multiple non-monophyletic clades

Ore	Francis	25 - The puzzle of eukaryotic cellular origins	EC_24	91	1130	Expanding Protein Complex Prediction Across the Eukaryotic Tree of Life
Rebecca	Gawron	25 - The puzzle of eukaryotic cellular origins	EC_24	92	1363	Using single-cell omics data to identify species and symbionts in uncultivable microbes
Saïoa	Manzano	25 - The puzzle of eukaryotic cellular origins	EC_24	93	556	Horizontal Gene Transfer in Aquatic Archaea
Giacomio	Mullà	25 - The puzzle of eukaryotic cellular origins	EC_24	94	538	Using phylogenies to investigate non-vertical inheritance across subclades
Anna	Nenarokova	25 - The puzzle of eukaryotic cellular origins	EC_24	95	1089	Resolving the prokaryote-to-eukaryote transition using phylogenomics models of endosymbiosis
Paul	Taylor	25 - The puzzle of eukaryotic cellular origins	EC_24	96	804	The Evolution of Neurotransmission and the Origin of the Animals
Guffré	Torruella Cortés	25 - The puzzle of eukaryotic cellular origins	EC_24	97	381	Euk-2-Like: Linking the origin of eukaryotes to the diversification of animals and fungi with genomics of flagellates
Marica	Baldoni	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	98	1315	Insights on zoonotic disease in cat domestication through ancient pathogen genomics
Tim	Brändler	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	99	1336	Evaluating the Performance of Cophylogenetic Methods
Laura	Carriño Olivas	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	100	1384	Paleogenomics study of human pathogens in the colonial period of Mexico City
Margherita	Colucci	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	101	1175	Dominant and human co-evolution: modeling measles spread in the late Pleistocene
Flavio	De Angelis	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	102	413	Phylogenetic adaptation to pathogens was modulated by major infectious disease outbreaks in Western Eurasia
Daniel	Falush	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	103	485	Meat without vegetables: An ancient ecology of <i>Helicobacter pylori</i> found in indigenous populations and animal adopted lineages
Alan	Godínez-Plascencia	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	104	452	Evaluating in silico HLA typing of low-coverage, shotgun sequencing cDNA data
Tabila	Hünemeier	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	105	225	Unveiling the pathogen-driven evolution in Native American populations
Adigall	Jarosz	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	106	407	Functional determinants of an ERV-F(1a) ancestor and its derived variants
Enrah	Kirch	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	107	1520	Linking an accurate and narrow ancient pathogen phylogenetic profile to a specific host
George	Long	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	108	81	A 14th century <i>EC</i> Brucella melitensis genome and the recent expansion of the Western Mediterranean clade
Miguel Alejandro	Navarro	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	109	784	A new scope: Paleogenomics for paleopathogen identification
Xuebing	Ni	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	110	1006	Metagenome of 31 tick species provides a compendium of 1,861 RNA virus genomes
Jonas	Niemann	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	111	1098	Parasites lost: Parasite detection in ancient and modern metagenomic datasets
Zoe	Pochon	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	112	1515	Infectious diseases in the Late Mining Age town of Sigüenza
Nicola	Rambaldi Migliore	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	113	393	Genomic evidence for adaptation to lactulobiose in the Andes before European contact
Algerim	Rymbekova	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	114	540	A historical metagenome genome of a zoonotic outbreak
Patricia	Santos	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	115	1261	The Neolithic transition from a bacterial perspective: a population genetic approach
Frederik	Seersholm	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	116	1395	An Outbreak of the Stone Age Plague in a Large Extended Family
Cintia	Povill	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24	117R	1429	Evolutionary history of howler monkeys (<i>Alouatta</i> , Aotidae)
Carlos	Sarabia	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24	118R	1438	Proving the hidden hypotheses: how to detect signatures of selective sweeps under different demographic models in admixed populations using BSWP(v)
Xiaojun	Wang	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24	119R	521	A novel Bacterial Speciation Process Observed in a Symbiotic Marine Population
Anne	Genisiel	22 - Experimental evolution of non-model species and systems	EC_24	120R	1486	Adaptive transcription rewiring in a fungal pathogen in response to fluctuating environment
David	Castellano	23 - Evolutionary approaches to understand cancer across scales	EC_24	121R	486	The distributions of fitness effects of tumor mutational signatures
Kimberly	Stead	23 - Evolutionary approaches to understand cancer across scales	EC_24	122R	423	Selection acting on mosaic chromosomal alterations in blood impacts molecular function and cancer risk among humans
Michael	Tassia	23 - Evolutionary approaches to understand cancer across scales	EC_24	123R	908	Telomere shortening limits the evolution of somatic mutations in clonal hematopoiesis
Stephanie	Yan	23 - Evolutionary approaches to understand cancer across scales	EC_24	124R	383	Evolutionary simulations inform the origins of clonal hematopoiesis
Aaron	Kollasch	24 - In silico computational methods, evolutionary dynamics, and biological applications	EC_24	125R	1615	Predicting the functional impact of human HGT variants using deep generative models of evolutionary data
Charley	McCarthy	25 - The puzzle of eukaryotic cellular origins	EC_24	126R	1439	Host-like branch-specific amino acid compositional heterogeneity in phylogenetic datasets
Ruth	Hershberg	02 - Editor Symposium	SP_24	127	1649	Metabolic adaptation to consume karyate under prolonged resource exhaustion
Yuseob	Kim	02 - Editor Symposium	SP_24	128	939	Positive feedback between demographic and fitness fluctuation greatly amplifies population size oscillation and causes long-term, multi-focus oscillation of allele frequencies
Koichiro	Tamura	02 - Editor Symposium	SP_24	129	947	Reinforcing adaptive migration from tropical zone to temperate zone by <i>Drosophila albomicans</i> using evolution and resequencing
Anique	Ahmad	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	130	492	Falcon gut microbiome is shaped by diet and enriched in Salmonella
Tania	Alonso Vázquez	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	131	576	SPIT: Assessing the impact of HGT on metabolic fitness through the simulation of 11 million transfer events
Azadeh	Rajevy	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	132	309	Revealing recent horizontal gene transfer events in microbial phylogenies
Paul	Bansie	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	133	1034	Mixing the interplay between structural variations and substitutions generates sublineal evolutionary dynamics
Stephanie	Bedhomme	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	134	940	Deciphering the horizontal traffic rules of antisepticide resistance genes
João	Botelho	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	135	18	Defense systems are pervasive across chromosomally integrated mobile genetic elements and are inversely correlated to virulence and antimicrobial resistance
Patricia	Brito	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	136	1060	Comparative transcriptomic analysis of native and HGT genes in a tubolytic yeast lineage
Erin	Caffery	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	137	1587	Evolution of viral mimicry following host gene acquisition
Hsiao-Han	Chen	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	138	813	Evolution of a bacterial pathogen: the evolution of dengue viruses based on polymorphism data across geographic scales
Billie	Cullison	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	139	1393	Evaluating the specificity of metagenomic datasets
Tsedenia	Denekew	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	140	549	Cleavability is associated with distinct microbial composition and diversity in the oral microbiome of Eritreans
Johannes	Effe	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	141	1058	Stabilizing the unstable: How stability systems affect plasmid fitness
Daria	Evsheva	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	142	747	Diversification of two-partner secretion systems in the bacterial plant pathogen <i>Ralstonia solanaceorum</i>
Michael	Finnegan	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	143	300	Goldilocks and the synonymy variant that was just right: Antibiotic resistance levels determined by compatibility between host genome and the incoming horizontally transferred gene
Marco	Fandi	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	144	611	Evolution of quorum sensing regulatory circuits through the acquisition of additional feedback loops
Stefano	Galarza	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	145	1293	How to measure bacterial genomic plasticity? New insights and implications for human pathogens
Carla	Gonçalves	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	146	765	Interplay between gene loss and horizontal gene transfer shape evolutionary rates in a eukaryotic lineage
Padraic	Heneghan	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	147	699	To Catch a Killer: Killer Peptides and Anticodon Nucleoside Discovery, Characterization, and Phylogenetics
Samuel	Horsfield	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	148	137	Comparing evolutionary characteristics of diverse bacterial pathogens using PopPUNK
Philip	Johnson	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	149	1619	Acquisition losses in CRISPR-Cas adaptive immune systems
Catherine	Kösgemann	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	150	869	Evolution of <i>Drosophila melanogaster</i> female gene expression associated with the rescue of the bag of marbles (<i>bag</i>) hypomorph lethality defect by <i>Wobachia pipiens</i>
Justin	Liu	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	151	876	Dynamics of bacterial evolution in the human gut microbiome
Nell	Macalasdair	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	152	603	Probing Improved Pan-genome Phylogenies
Rebecca	Man	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	153	786	The influence of lateral transduction on bacterial genome content and structure
Gemma	Murray	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	154	1118	The emergence and diversification of a zoonotic pathogen from within the microbiota of intensively farmed pigs
Samuel	O'Donnell	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	155	60	Starships as a driving force during the domestication of <i>Pseudomonas fluorescens</i>
Kiran	Paranjape	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	156	771	Host-adaptation of <i>Legionella pneumophila</i> to macrophages and amoebae through experimental evolution
Elena	Romero	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	157	1407	Expanded HIV virality is associated with higher recombination rate events
Marcus Ho Hin	Shum	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	158	1052	Recombination associated with the emergence of <i>rsr-3</i> and <i>rsr-7</i>
Alix	Thivolle	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	159	1146	Genome of a highly specific obligate parasite reveals a high turnover rate of collagen-like genes
Yiqing	Wang	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	160	843	Transposable elements drive the evolution of multiple drug resistance plasmids
Aaron	Weimann	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	161	1229	Evolution and host-specific adaptation of <i>Pseudomonas aeruginosa</i>
Fiona	Whelan	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	162	1027	Gene-gene associations in microbes from human-associated microbial communities
Justin	Gupta	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	162	1335	Analysis as a Mechanism for Coping with <i>Pseudomonas aeruginosa</i>
Ogün	Ardabili	07 - Computational evolutionary genomics in the era of machine learning	SP_24	163	1595	PhACT: Phylogeny-Aware Computing of Homology for Missense Mutations
Carlos	Albors	07 - Computational evolutionary genomics in the era of machine learning	SP_24	164	1406	A Benchmark Task for Language Models of Human DNA
Jordan	Anderson	07 - Computational evolutionary genomics in the era of machine learning	SP_24	165	907	Machine Learning Inference Of Effective Population Size Over Time Using Single Diploid Samples
Lucia	Barzili	07 - Computational evolutionary genomics in the era of machine learning	SP_24	166	120	Signatures of natural selection on tree shape metrics from serially sampled intrahost viral phylogenies
Gherard	Balissi Biffignandi	07 - Computational evolutionary genomics in the era of machine learning	SP_24	167	1313	Classification or regression? Accuracy and interpretability of machine-learning based prediction accuracy of semi-quantitative genetic traits
Alan	Bavaro	07 - Computational evolutionary genomics in the era of machine learning	SP_24	168	364	Contingency, Reproducibility and Predictability in the Evolution of a <i>Palaemonetes</i> Pan-genome
Madeleine	Caduff	07 - Computational evolutionary genomics in the era of machine learning	SP_24	169	1312	Accurate identification of anciently sequenced and non-sequenced human haplotypes from low-depth and ancient samples
Alejandro	Caron-Noriega	07 - Computational evolutionary genomics in the era of machine learning	SP_24	170	491	Machine learning assisted gene annotation of a nematode phylogeny by proteobacteriomics
Moisés	Coli Maciá	07 - Computational evolutionary genomics in the era of machine learning	SP_24	171	1586	A genomic method for dating and geographically locating ancient samples
Trevor	Cousins	07 - Computational evolutionary genomics in the era of machine learning	SP_24	172	178	The effect of background selection on demographic inference
Keith	Crandall	07 - Computational evolutionary genomics in the era of machine learning	SP_24	173	115	SeqBreaks: a machine learning tool for identifying and prioritizing genotype-phenotype associations
Elizabeth	Cummins	07 - Computational evolutionary genomics in the era of machine learning	SP_24	174	399	Identifying genetic events that generate multi-drug resistance in <i>Escherichia coli</i> with machine learning
Maria	Fariello Rico	07 - Computational evolutionary genomics in the era of machine learning	SP_24	176	1588	Deep learning for genomic prediction and tasks beyond in bacterial DNA in the wild
M. A. Thanuja	Fernando	07 - Computational evolutionary genomics in the era of machine learning	SP_24	177	141	Testing the accuracy of phylogenetic trees built by placing DNA barcode sequences: implications of taxonomic tree completeness and species misassignment pattern
Valentina	Galeone	07 - Computational evolutionary genomics in the era of machine learning	SP_24	178	506	Risks of co-occurring mutations in Influenza Virus A
Marie-Claire	Harrison	07 - Computational evolutionary genomics in the era of machine learning	SP_24	179	191	Machine Learning Illuminates How Diet Influences the Evolution of Galactose Metabolism in <i>Saccharomyces cerevisiae</i> Yeasts
Mark	Harrison	07 - Computational evolutionary genomics in the era of machine learning	SP_24	180	958	Discovering Genetic Footprints of Eusocial Evolution with Machine Learning
Xin	Huang	07 - Computational evolutionary genomics in the era of machine learning	SP_24	181	27	A comprehensive benchmarking for <i>gtr</i> integration tract analysis with supervised learning
Meris	Johnston-Hagler	07 - Computational evolutionary genomics in the era of machine learning	SP_24	182	1395	How Many Features Are Needed to Train a Good Predictive Machine Learning Model?
Daniel	Jordan	07 - Computational evolutionary genomics in the era of machine learning	SP_24	183	1093	Prediction of recessive inheritance for missense variants in human disease
Kevin	Korfmann	07 - Computational evolutionary genomics in the era of machine learning	SP_24	184	174	Simultaneous Inference of Past Demography and Selection from the Ancestral Recombination Graph under the Beta Coalescent
Lukas	Kuderna	07 - Computational evolutionary genomics in the era of machine learning	SP_24	185	102	Identification of conserved sequence elements across 242 primate genomes with deep learning
Alexandre	Laverré	07 - Computational evolutionary genomics in the era of machine learning	SP_24	186	1204	Changes in transcription factor binding affinity reveal regulatory regions under positive selection and illustrate gene expression evolution in vertebrates
Tianhua	Liao	07 - Computational evolutionary genomics in the era of machine learning	SP_24	187	209	Machine learning and molecular dating techniques allow mapping the origin and expansion of aerobic bacteria to the redox history of the Earth
Oliver	Lynch	07 - Computational evolutionary genomics in the era of machine learning	SP_24	188	1540	Comparability of Taxonomic Time Scales: Implications for Ecological Population Size
Carlos	Marti Gómez-Aldaraví	07 - Computational evolutionary genomics in the era of machine learning	SP_24	189	1470	Towards inference and understanding complex experimental genotype-phenotype maps

Jazeps	Medina Treimanis	07 - Computational evolutionary genomics in the era of machine learning	SP_24	190	753	Joint Calling of Local Ancestry and Archaic Introgression Using Deep Learning
Fatima	Mostefaï	07 - Computational evolutionary genomics in the era of machine learning	SP_24	191	1523	Characterization of Emerging SARS-CoV-2 Mutations from Intra-host Sequences Using Unsupervised Learning
Diptarup	Nandi	07 - Computational evolutionary genomics in the era of machine learning	SP_24	192	1076	Distinguishing between the genomic signatures of selective sweeps and genetic drift in populations with a history of dramatic bottleneck
Adeleke	Owoyemi	07 - Computational evolutionary genomics in the era of machine learning	SP_24	193	910	Linking Ancient Mitochondrial Haplogroups to Modern Learning De Novo Gene Prediction Algorithm in Ancestral
Mark	Penjeli	07 - Computational evolutionary genomics in the era of machine learning	SP_24	194	1096	Genomic Insights into Demographic History of Neotropical Populations
Graziano	Pesole	07 - Computational evolutionary genomics in the era of machine learning	SP_24	195	605	Rapid detection of novel emerging variants of SARS-CoV-2 by unsupervised classification
Arnaud	Quelin	07 - Computational evolutionary genomics in the era of machine learning	SP_24	196	476	Inferring demographic history of diverging populations from human genomic data
Clara	Rehmann	07 - Computational evolutionary genomics in the era of machine learning	SP_24	197	431	Location, location, location: Dissecting errors in machine learning prediction of geography
Diego	Scazzari-Tortosa	07 - Computational evolutionary genomics in the era of machine learning	SP_24	198	1601	Modeling the genomic determinants of disease selective sweeps in the human genome
Mathews	Salinas	07 - Computational evolutionary genomics in the era of machine learning	SP_24	199	580	Reinforcement Learning informs optimal treatment strategies to limit antibiotic resistance
Lahru	Scorziabandara	07 - Computational evolutionary genomics in the era of machine learning	SP_24	200	133	Comparative Pan-genomics Reveals the Existence of Distinct Communities and Conserved Regions with Microbial Pan-genomes
Lucile	Vigue	07 - Computational evolutionary genomics in the era of machine learning	SP_24	201	522	Exploiting the variability and evolutionary dynamics of <i>Escherichia coli</i> through the analysis of 60,000 genomes
Fernando	Villanea	07 - Computational evolutionary genomics in the era of machine learning	SP_24	202	682	Implementing a better random seed generator for genomic simulation
Maria Teresa	Vizzari	07 - Computational evolutionary genomics in the era of machine learning	SP_24	203	1260	Robust demographic inference from low-coverage whole-genome data through Approximate Bayesian Computation
Davis	Weaver	07 - Computational evolutionary genomics in the era of machine learning	SP_24	204	40	Reinforcement Learning informs optimal treatment strategies to limit antibiotic resistance
Charlotte	West	07 - Computational evolutionary genomics in the era of machine learning	SP_24	205	839	Detecting Positive Selection Using Machine Learning
Lucia	Zifcakova	07 - Computational evolutionary genomics in the era of machine learning	SP_24	206	913	Perfectly conserved sequences (PCS) between human and mouse are significantly enriched for small proteins
Diana	Agular Gomez	15 - Animal genomics goes wild	SP_24	207	1610	Color and pattern genomics in the strawberry poison frog
Pascal	Angst	15 - Animal genomics goes wild	SP_24	208	1231	Genomic analysis of a highly dynamic metapopulation reveals the role of spatiotemporal dynamics on the evolutionary process
Ellie	Armstrong	15 - Animal genomics goes wild	SP_24	209	1360	Taking our bear-sig: A comprehensive reference genome database for North American brown bears (<i>Ursus arctos</i>)
Mateusz	Baca	15 - Animal genomics goes wild	SP_24	210	1378	Ancient DNA clarifies the evolution of the field vole species complex
Nicola Jane	Barson	15 - Animal genomics goes wild	SP_24	211	639	The emergence of sugarcane from invasions in Atlantic latitudes
Beno	Basse	15 - Animal genomics goes wild	SP_24	212	279	Independent haplogroup evolution contributes to novelty and persistence without sex in a mite
Melodie	Bastian	15 - Animal genomics goes wild	SP_24	213	217	Bridging the gap between population genetic and phylogenetic approaches by the study of mammals effective population size
Andrea	Benazzo	15 - Animal genomics goes wild	SP_24	214	1039	Assembly of polyploid genomes: identification and phasing of allelic variants using Hi-C
Florian	Benitère	15 - Animal genomics goes wild	SP_24	215	363	Random genetic drift sets an upper limit on mRNA splicing accuracy in metazoans
Juraj	Bergman	15 - Animal genomics goes wild	SP_24	216	829	A macrogenomic perspective of mammalian biodiversity, ecology and evolutionary history
Rajiv	Boscio Agostini	15 - Animal genomics goes wild	SP_24	217	1259	Disentangling the worldwide invasion process of <i>Helomyces</i> hails through AIC
Mirte	Bosse	15 - Animal genomics goes wild	SP_24	218	1381	New opportunities offered by genomics for the conservation of the Asian elephant: from captivity to the wild
Martina	Brasó	15 - Animal genomics goes wild	SP_24	219	563	Causative and consequences of extremely genetic high diversity of European amphibian wild populations
Theo	Busschau	15 - Animal genomics goes wild	SP_24	220	343	Evolution of cephalic horns in vipers
Matteo	Caldon	15 - Animal genomics goes wild	SP_24	221	165	A genomic perspective on the evolutionary history of <i>Therapsites</i> gelada
Gabriele	Coffing	15 - Animal genomics goes wild	SP_24	222	926	Leveraging a de-novo long read assembly for comparative and functional genomics of the <i>Odocoileus</i> timemobiles
Tristan	Cumer	15 - Animal genomics goes wild	SP_24	223	679	The genomic architecture of a continuous color polymorphism in the European barn owl (<i>Tyto alba</i>)
Martina	Da La Cámara	15 - Animal genomics goes wild	SP_24	224	649	Transmitting placology: From introgression to genomic islands of differentiation
Thomas	Decroly	15 - Animal genomics goes wild	SP_24	225	1470	Host-Wild degradation locally revealed by gene recombination events in the Spanish meadow white butterfly
Xiling	Deng	15 - Animal genomics goes wild	SP_24	226	375	Comparative phylogeography of <i>Hemaphysylla</i> (Trioletinae, Rhipycetidae) in the Tibeto-Himalayan Region: An assessment of the mountain-geobiodiversity hypothesis
Qiading	Deng	15 - Animal genomics goes wild	SP_24	227	982	Genetic parallelism and adaptation to brackish water bodies in sprat (<i>Sprattus sprattus</i>) and Atlantic herring (<i>Clupea harengus</i>)
Laurence	Despres	15 - Animal genomics goes wild	SP_24	228	359	Demographic and adaptive responses to climate change in cold-adapted European butterflies
Klara	Eleftheriadi	15 - Animal genomics goes wild	SP_24	229	1266	Isle first genome of the phylum Nematostomatia, a key resource to unravel Ecdysozoa evolution
Yu	Endo	15 - Animal genomics goes wild	SP_24	230	931	Local populations demographic history of brown bears <i>Ursus arctos</i> in Eurasia based on whole-genome resequencing
Emily	Engelvdosen	15 - Animal genomics goes wild	SP_24	231	365	Comparative and population genomics reveal highly repetitive landscape of honey bee genomes
Mario	Ernst	15 - Animal genomics goes wild	SP_24	232	1319	Influence of past climate on the evolutionary history of forest-dwelling frogs: <i>Rana</i> , <i>Craugastor</i> in Upper Guinea, West Africa
Sabine	Felkel	15 - Animal genomics goes wild	SP_24	233	1504	Conservation score analysis to validate selection signals and improve functional annotation of the Atlantic herring
Thais	Ferreira Pinto De Araújo	15 - Animal genomics goes wild	SP_24	234	1228	Resolving the mystery of freshwater breeding founders?
Joan	Ferrer Obiol	15 - Animal genomics goes wild	SP_24	235	555	To migrate or not to migrate: characterizing the interplay between genetic and environmental drivers of bird migration
Claudia	Fontserè	15 - Animal genomics goes wild	SP_24	236	247	Assessing the Genetic Composition of Cotton-Top Tamarins Before Bypassing Anthropogenic Impact
Natalie	Ford	15 - Animal genomics goes wild	SP_24	237	331	Genomic architecture of human <i>HLA</i> genes: Haplotype and gene structure
Fabrizio	Furni	15 - Animal genomics goes wild	SP_24	238	58	Five whale (<i>Balaenoptera physalus</i>) genomes reveal genomic erosion in baleen whales
Shan	Gao	15 - Animal genomics goes wild	SP_24	239	860	Horizontal gene transfer and differential allelic expression of the orbifold rite <i>Platyrrhinus</i> pelifer provide new insight of sexal genome evolution
Jake	Goodall	15 - Animal genomics goes wild	SP_24	241	584	Atlantic herring - an adaptive radiation with limited reproductive isolation
Genavieve	Gray-Sandoval	15 - Animal genomics goes wild	SP_24	242	1533	Quantifying virus-driven adaptation in <i>Myotis</i> genomes using the McDonald-Kreitman test
Carlos Eduardo	Guerra Amorim	15 - Animal genomics goes wild	SP_24	243	1494	Domestication as a Model for Extreme Environmental Change: Insights from <i>Caenorhabditis</i>
Nadège	Guglielmoni	15 - Animal genomics goes wild	SP_24	244	844	Comparative genomics of underrepresented avian neotropicals
Mario	Gurke	15 - Animal genomics goes wild	SP_24	245	1090	Uncovering hidden evolutionary processes: Range expansion and gene flow patterns in two cryptic bat species
Ewan	Harney	15 - Animal genomics goes wild	SP_24	246	735	Do interactions between chromatin and transposable elements contribute towards transgenerational plasticity in wild <i>Drosophila melanogaster</i> ?
Sofia	Hayden Boffill	15 - Animal genomics goes wild	SP_24	247	360	Idiosyncratic responses to climate change in an adaptive radiation of Australian <i>Cryptobryas</i> katers
Núria	Hermosilla-Albala	15 - Animal genomics goes wild	SP_24	248	251	Whole genome approach to the structure and dynamics of Casajús wild populations
Laura	Iacolina	15 - Animal genomics goes wild	SP_24	249	984	Ancient or modern? The role of natural and anthropogenic factors in shaping the European wild boar population structure
Julia	Jones	15 - Animal genomics goes wild	SP_24	250	1472	Investigating the genomic implications of importing non-native and commercially bred burrhead subspecies
Alicja	Kozmierkiewicz	15 - Animal genomics goes wild	SP_24	251	1362	Evolutionary history of <i>Myrica</i> clones: recorded using modern and ancient mtDNA
Tyler	Kent	15 - Animal genomics goes wild	SP_24	252	932	The demographic history and genetic consequences of the recent introduction of <i>Aedes aegypti</i> to the Americas
Keren	Klass	15 - Animal genomics goes wild	SP_24	253	70	Five-Scale Population Genetic Structure in a Fragmented Black Holar Monkey Population: Implications for Dispersal Patterns and Population Persistence
Romuald	Laso-Jadart	15 - Animal genomics goes wild	SP_24	254	290	Urban population genomics: structure, dispersal and adaptation of the brown rat (<i>Rattus norvegicus</i>) in Paris
Ana Victoria	Leon Apodaca	15 - Animal genomics goes wild	SP_24	255	93	Genomic consequences of isolation and inbreeding in an island dring population
Edgana	Lord	15 - Animal genomics goes wild	SP_24	256	389	Population genomics of the minkia resistance in the near absence of genetic variation
Mariana	Lucio Lyra	15 - Animal genomics goes wild	SP_24	257	1138	Exploiting genetic and phenotypic associations in the grass <i>Andropogon</i> populations
Katherine	McVay	15 - Animal genomics goes wild	SP_24	258	746	Causes and Consequences of Marine Adaptation in Brazilian Holar Minkia
Fahime	Mohamadnejad Sangdghi	15 - Animal genomics goes wild	SP_24	259	594	Characterization of genetic diversity and evolution of MHC class II genes in Atlantic herring using long-read sequencing
Paolo	Momigliano	15 - Animal genomics goes wild	SP_24	260	974	Rapid speciation, parallel and divergent selection: the evolution of <i>Psittaculopsittacus</i> since the last glaciation
Stefano	Mona	15 - Animal genomics goes wild	SP_24	261	763	Swimming in Troubled Seas: fall and fragmentation of World's White Shark Populations
Ariadna	Morales	15 - Animal genomics goes wild	SP_24	262	389	Mammalian genomes illuminate fast adaptations to viral tolerance and disease resistance
Benoit	Nathholz	15 - Animal genomics goes wild	SP_24	263	389	Incomplete lineage sorting entails the low performance of DNA barcoding in a Western European grasshopper radiation (<i>Orthoptera: Acrididae</i>)
Will	Nash	15 - Animal genomics goes wild	SP_24	264	1134	Genome wide signatures of range expansion in a key UK pollinator
Darren	Obbard	15 - Animal genomics goes wild	SP_24	265	80	Mutation, recombination, and transposition rates in wild <i>Drosophila melanogaster</i> and <i>D. simulans</i>
Mustafa	Ozkan	15 - Animal genomics goes wild	SP_24	266	1107	The first complete genome of the European wild ass (<i>Equus hydruntinus</i>) reveals its reticulate phylogenetic history, dramatic population decline, and its latest survivors
Hüsna	Oztoprak	15 - Animal genomics goes wild	SP_24	267	211	Ancient asexual speciation in the orbifold rite <i>Platyrrhinus</i> pelifer
Jeppe Bayer	Pedersen	15 - Animal genomics goes wild	SP_24	268	619	The Effect of Demographic Parameters on the Genetic Load in Danish Anthropoid Populations
Katja	Pfeifferburg	15 - Animal genomics goes wild	SP_24	269	1211	Translating identifying the drivers of divergence in an oceanic population
Joshua	Pinhaba	15 - Animal genomics goes wild	SP_24	270	1144	Rapid transition during speciation revealed from comparative study across an avian sister zone
Marie	Raynaud	15 - Animal genomics goes wild	SP_24	271	334	Population genomics support PRDM-dependent recombination landscapes in salmonids
Giulia	Riccioni	15 - Animal genomics goes wild	SP_24	272	1361	Improving the conservation status of <i>Austroptarmachus</i> palpeus species complex in the Italian North-western Apennines through population genomics and habitat modelling
Eleanor	Sheppard	15 - Animal genomics goes wild	SP_24	273	611	Genomic associations with pathogen gradients across divergent island populations of an endemic bird
Conor	Rossi	15 - Animal genomics goes wild	SP_24	274	591	Reconstructing the history of the extinct sauroch: structure, demography and genetic legacy
Nathanaëlle	Saint	15 - Animal genomics goes wild	SP_24	275	512	A new type of non-Mendelian transmission sustains unusual reproduction in the nematode <i>M. helmi</i>
Judith	Salces	15 - Animal genomics goes wild	SP_24	276	585	Genetic diversity and phenotypic plasticity in high diversity of RNA patterns across <i>Escherichia coli</i> strains on a new island
Sara	Sampaio	15 - Animal genomics goes wild	SP_24	277	799	Shedding light on the phylogenetic relationships of the Tapidae: insights using mtGenomes
André	Santos	15 - Animal genomics goes wild	SP_24	278	1061	A <i>Puettia</i> H-F1 genome assembly of the partner's meadow <i>Urosalpinx</i> (Linnaeus, 1758)
Ben	Schultz	15 - Animal genomics goes wild	SP_24	279	1456	Detangling the hybridization histories of two <i>Chrosomus</i> dice species
Nurislam	Shaikhutdinov	15 - Animal genomics goes wild	SP_24	280	1553	Absence of spliceosomal introns in the mitrochroite <i>Medusina</i> huronum - how did they disappear?
Rebecca	Shaw	15 - Animal genomics goes wild	SP_24	281	1290	Uncovering deleterious mutations in the genome of the Black-footed ferret, a severely endangered species
Stéphane	Shen	15 - Animal genomics goes wild	SP_24	282	519	Genomic signals of population history and ecological adaptation in an experimental introduction of <i>Escherichia coli</i> to a new island
Henry	Sliesser	15 - Animal genomics goes wild	SP_24	284	97	Genetic diversity of Humpback Whales (<i>Megaptera novaeangliae</i>) breeding in South Georgia and the Falkland Islands - Initial findings and next steps
Yassine	Soulimi	15 - Animal genomics goes wild	SP_24	285	543	Insights into Dingoas Evolutionary History Using Ancient Genomes
Daniela	Souza Costa	15 - Animal genomics goes wild	SP_24	286	1314	Diving into the historic origins of genetic diversity in cichlid fishes of African Lake Tanganyika
Marcella	Sozzoni	15 - Animal genomics goes wild	SP_24	287	573	Integration of environmental Niche Modeling and genomic data to investigate the demographic history of <i>Elymus obtusifolius</i> in relation to habitat availability
Bastiaan	Star	15 - Animal genomics goes wild	SP_24	288	1021	Hybridization of Atlantic puffins in the Arctic coincides with 20th-century climate change
Marcos	Suárez Menéndez	15 - Animal genomics goes wild	SP_24	289	1161	Direct estimation of genome mutation rates from pedigrees in free-ranging brown whales
Joanna	Sudjka	15 - Animal genomics goes wild	SP_24	290	57	De novo DNA methylation of avian sex-chromosomes

Marion	Talbi	15 - Animal genomics goes wild	SP_24	291	1206	Fine-scale recombination maps: From simulation to empirical data
Marianthi	Tangili	15 - Animal genomics goes wild	SP_24	292	241	Longitudinal changes in autosomal DNA methylation in two species of passerine birds
Livia	Tolve	15 - Animal genomics goes wild	SP_24	293	567	Whole mitochondrial genome sequencing provides new insights into the phylogeography of togetherhead sea turtles (<i>Caretta caretta</i>) in the Mediterranean Sea
Alexandros	Toupaoudis	15 - Animal genomics goes wild	SP_24	294	893	Evolution of the <i>hsp70</i> gene in the white shrimp <i>Litopenaeus setiferus</i> : evolutionary response to climate change in the Sargasso Sea (Type label)
Takeru	Tsunoi	15 - Animal genomics goes wild	SP_24	295	1038	Quantitative genetics and population genomics in the wild: Shikoku's evolutionary response to climate change in the Sargasso Sea (Type label)
Jozsefien	Van de Velde	15 - Animal genomics goes wild	SP_24	296	1277	Population genomics of Australian <i>Neobatrachus</i> frogs: Neobatrachus reveal adaptation to polyploidy
Romain	Villoutreix	15 - Animal genomics goes wild	SP_24	297	444	Ecological discontinuity packages genes into discrete units of diversity
Claudia	Weber	15 - Animal genomics goes wild	SP_24	298	1499	Accelerated protein evolution in parasitic ciliates
Alicja	Witwicka	15 - Animal genomics goes wild	SP_24	299	1633	Poster on pollinators submitted by Yannick Wurm (who already has another poster)
Yiny	Zhang	15 - Animal genomics goes wild	SP_24	300	935	Evolution of the <i>hsp70</i> gene in the white shrimp <i>Litopenaeus setiferus</i> : evolutionary response to climate change in the Sargasso Sea (Type label)
Valeria	Arnoche Garibay	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	301	871	The contribution of Neanderthal and Denisovan archaic introgression to the genetic architecture of complex traits in Mexican populations
John	Barton	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	302	1273	Using temporal genetic data to infer time-varying selection in viral evolution
Alison	Barton	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	303	1592	Time series data reveal selection on blood group phenotypes over the past 10,000 years in West Eurasia
Ronja Jessica	Billenstein	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	304	1001	Evaluation of Bayesian sequencing-based coalescent models for demographic inference
Simon	Botard	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	305	207	Whole-genome sequencing of cypriniform fishes from French Large White pike at two distinct sampling times reveals strong signatures of convergent and divergent selection between the dam and sire lines
Audrey	Bras	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	306	1374	Unravelling the link between population trends and changes in genetic diversity in Finnish butterflies
Emily	Breslin	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	307	699	Link Up! Paleolithic humans from the South of France
Marco Rosario	Capodiferno	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	308	1371	Achaeic introgression in ancient human genomes through time
Marta	Ciccarella	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	309	548	Comparing the adaptive landscapes of Cabo Verde and São Tomé & Príncipe: two early African outposts of the Transatlantic Slave Trade
Aina	Colomer i Vilaplana	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	310	1377	Evaluating Allele Frequency Trajectory and Selection Coefficient Estimates from Genetiages with Ancient DNA
Adèle	Crane	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	311	1128	Spatial distribution and intra-host dynamics of Mycobacterium leprae isolated from FFPE tissue samples in the Pacific
Mafias	Curral	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	312	299	Past human expansions shaped the spatial pattern of Neanderthal ancestry
Eugenia	D'Alessio	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	313	216	Genomes from the Red Queen: a great population of <i>Caenorhabditis</i> revealed from joint whole modern genome analysis of <i>Solenostoma</i> and ancient <i>Caenorhabditis</i>
Elizabeth	Finney	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	314	1400	Quantifying Sample Collection Time Uncertainty Improves Epidemiological Modelling of SARS-CoV-2 Evolution
Daria	Frolva	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	315	1132	Using historical samples, recombination distances and Approximate Bayesian Computation to analyse plasmid evolution
Vincent	Geyer	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	316	574	Exploiting the temporal limits of RNA preservation in historical and ancient biological material
Mogge	Hajjesmael	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	317	132	A comprehensive picture of the genetic history of Iran
Matthew	Hartfield	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	318	414	Inferring the distributions of these effects and proportions of strongly deleterious mutations
Anahit	Hovhannisyan	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	319	269	Genomic history of Armenian populations
Ali	Hudson	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	320	996	Genomes On the Move: Tracking genomic evolution over 20 generations of phenotypic convergence
Anastasia	Ignatieva	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	321	1481	Tracing new data into reconstructed genealogies
Hie Lim	Kim	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	322	918	Prehistoric human migration between Southeast and South Asia was driven by sea-level rise
Dilek	Koptekin	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	323	1153	A tale of three issues: New measures against natural and technical biases in paleogenomics data
Carolin	Kosiol	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	324	122	A Bayesian method to detect targets of selection in time-series data of EcoEvo-and-Resequencing experiments
Julia	Kreiner	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	325	56	Rapid evolution of a native weed to agriculture over the last 200 years
Patricia	Lang	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	326	441	200 years of herbicide genomes predict plant domestication response to climate change
Brian	Lee	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	327	1558	Using time-series genomic data for early detection of novel SARS-CoV-2 variants with increased transmissibility
Francisco Javier	Maravall Lopez	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	328	835	Paleogenomic insights into the deep population history of present-day Argentina
Markus	Möst	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	329	1498	Biological archives entering the genomic era
Uchenna	Nwaegbe	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	330	785	Inferring mutation rates from evolutionary histories with path integral methods
Vicharia	Obberleirer	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	331	869	A new method of extract-pooling for sediment ancient DNA analysis
Linda	Orlando	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	332	1401	Identifying nuclear DNA in ancient plant and animal remains using Next-Gen Sequencing
Silvia	Parretti	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	333	1268	Inference of phenotypic traits from low coverage ancient genomes: an operating manual
Alyssa	Pivrotto	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	334	1483	balancing selection is common for beneficial alleles in a human population
John	Pool	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	335	1423	Genomes From Museum Diaploids: metagenomic Specimens Illuminate More Than 200 Years of Evolution
Divya Ratan	Popli	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	336	1018	A joint framework for estimating F-statistics and PCA
Francesco	Ravasiini	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	337	298	Anthropogenics of Central Italy: A diachronic analysis of the Adriatic coast traced by ancient genomes
Ressia	Ravasiini	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	338	256	De novo assembly of a human genome from ancient DNA
Stefania	Sasso	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	339	1478	Ancient DNA perspectives on the origins and structure of a Mesolithic population in Belgium
Susanna	Sawyer	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	340	175	Improved methylation detection in ancient DNA
Doniké	Sejdu	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	341	661	Herbarium DNA confirms 20th-century presence in Europe of <i>Phytolacca</i> lineage that caused Irish Potato Famine
Patrizia	Serventi	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	342	1117	Inside the communities of Central Italian Peninsula in the Middle Ages: exploring human mobility and social organization through ancient DNA
Mafias	Sherman	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	343	858	Patterns of cytosine deamination in different aDNA library preparations
Divya	Smith	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	344	683	The evolution of the human mitochondrial genome
Bárbara	Sousa Da Mota	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	345	1375	Investigating the ecological niche of <i>Ursus arctos</i> in the Iberian Peninsula using ancient DNA data
Megha	Srigan	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	346	1427	Metagenomic analysis of a late Pleistocene jaguar from North America
Yaniv	Svivel	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	347	1074	Mapping biases lead to shorter branch lengths in Y chromosomes highly diverged from the human reference
Johanna	Von Seth	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	348	1230	Genomic effects of the creation of two Scandinavian dog breeds
Aleksandra	Zeromska	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	349	1205	The use of ancient DNA (aDNA) analysis to reconstruct the phylogeny and evolution of the northern vole population (Alexandromys oeconomus)
Zhuya	Zhang	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	350	104	Chromosomes and inversions in the Malakoff soldier, <i>Androsace</i> and long head
Illa	Arluışı	19 - Evolution of structural genomic variation in populations & species	SP_24	351	1355	Chromosomes and inversions in the Malakoff soldier, <i>Androsace</i> and long head
Cristina	Barragan	19 - Evolution of structural genomic variation in populations & species	SP_24	352	943	Adaptive Evolution and Horizontal Mini-Chromosome Exchange in the Bait Fungus <i>Magnaporthe oryzae</i>
Chloé	Beaulieu	19 - Evolution of structural genomic variation in populations & species	SP_24	353	342	The first pan-genome of a non-vascular plant broadens the understanding of land plant adaptation to their environment
Tiago	Belinfanti	19 - Evolution of structural genomic variation in populations & species	SP_24	354	1364	Improving Phylogenetic Signal with UCE Alike Sequences: A Comparative Analysis of Tricolored
Greta	Bellinzona	19 - Evolution of structural genomic variation in populations & species	SP_24	355	367	Genomic evolution of <i>Cryptosporidium parvum</i>
Cassy	Bergman	19 - Evolution of structural genomic variation in populations & species	SP_24	356	192	Reproducible evaluation of transposable element detectors with McClintock 2 guides accurate reference of Ty insertion patterns in yeast
Melanie	Brien	19 - Evolution of structural genomic variation in populations & species	SP_24	358	1085	A complex color polymorphism is associated with a gene duplication in wood frog mussels
Mario	Caceres	19 - Evolution of structural genomic variation in populations & species	SP_24	359	1238	Towards a complete characterization of human polymorphic inversions and their functional effects
Laetitia	Chauve	19 - Evolution of structural genomic variation in populations & species	SP_24	360	870	Is there an advantage to polyploidy in animals? Consequences of whole genome duplication in a synthetic, elegant tetraploid
Le Qin	Choo	19 - Evolution of structural genomic variation in populations & species	SP_24	361	1193	Role of chromosomal inversions in adaptation and speciation in the fat periwinkle, <i>Strombus</i> sp.
Catherine	Collins	19 - Evolution of structural genomic variation in populations & species	SP_24	362	1276	The spatial and temporal distribution of an adaptive lateral gene transfer in a grass
Lilla	Colston-Nepali	19 - Evolution of structural genomic variation in populations & species	SP_24	363	527	Parallel patterns of differentiation of chromosomal inversions and other genomic regions in the European flat flycatcher
Christophe	Condrea	19 - Evolution of structural genomic variation in populations & species	SP_24	364	1180	Genomic and behavioural variation in different ecotypes of the neogastropod <i>Neogastropoda</i>
Johann	Confais	19 - Evolution of structural genomic variation in populations & species	SP_24	365	1284	REPET: evolution, faster and easier
Emma	Curran	19 - Evolution of structural genomic variation in populations & species	SP_24	366	95	The impact of whole genome duplication on the landscape of structural variation and polyploid adaptation
Gabriel	David	19 - Evolution of structural genomic variation in populations & species	SP_24	367	1092	Calling Structural Variants with Confidence in Wild Bird Populations: Read-mapping & Pangenomic Approaches
Luis	Delayo	19 - Evolution of structural genomic variation in populations & species	SP_24	368	885	Highly branched patrilines in cyanobacterial genomes: an abominable mystery
Natalia	Diaz	19 - Evolution of structural genomic variation in populations & species	SP_24	369	267	Insights in the Atlantic <i>Staphylinus</i> lineage connectivity revealed by allopatric origin introgression preserved within a structural variant
Tristram	Dodge	19 - Evolution of structural genomic variation in populations & species	SP_24	370	469	The genetic architecture of adaptive pigmentation traits in <i>Arabidopsis thaliana</i>
Luke	Dunning	19 - Evolution of structural genomic variation in populations & species	SP_24	371	509	Large gene transfers accurately in ancient genomes in grass pangenomes
Tori	Eggers	19 - Evolution of structural genomic variation in populations & species	SP_24	372	927	Comparative genomics of outcrossing and selfing <i>Oenothera lamarckiana</i>
Katle	Emelianova	19 - Evolution of structural genomic variation in populations & species	SP_24	373	1565	Rapid adaptive radiation in the <i>Pinus</i> genus: investigating the diversifying role of transposable elements
Christopher	Fiscus	19 - Evolution of structural genomic variation in populations & species	SP_24	374	231	The genetic control of rapid genome content divergence in <i>Arabidopsis thaliana</i>
Hayley	Free	19 - Evolution of structural genomic variation in populations & species	SP_24	375	604	Endogenous Retroviruses in Avian Genomes
Sergio	Gonzalez Mollinedo	19 - Evolution of structural genomic variation in populations & species	SP_24	376	1408	Inferring the deictic effects of rewording on transposable element insertion rate in a small bird population
Landon	Gozshiti	19 - Evolution of structural genomic variation in populations & species	SP_24	377	1430	Genetic architecture of novel construction in eukaryotic genomes
Clara	Groot Crego	19 - Evolution of structural genomic variation in populations & species	SP_24	378	353	Short structural variation fueled CAM evolution within an explosive bromeliad radiation
Dustin	Hanke	19 - Evolution of structural genomic variation in populations & species	SP_24	379	1441	Frequent gene non-functionalization in plant genomes
Anne	Hatmaker	19 - Evolution of structural genomic variation in populations & species	SP_24	380	369	Evolution of human pathogenesis in <i>Aspergillus</i> flavus
Siv	Hoff	19 - Evolution of structural genomic variation in populations & species	SP_24	381	1190	Identification of multiple chromosomal inversions and fusions in a keyhole <i>Aspergillus</i> species with high gene flow
Stella	Huylth	19 - Evolution of structural genomic variation in populations & species	SP_24	382	1329	Large genomic structural variation in plants and their role in the domestication process across 14 plant models
Kim	Kang	19 - Evolution of structural genomic variation in populations & species	SP_24	383	1104	Genetic architecture of novel construction in eukaryotic genomes
Robert	Koffer	19 - Evolution of structural genomic variation in populations & species	SP_24	384	635	A β -element invasion in experimental populations sheds light on the silencing of a newly invading transposon
Marc	Krasovec	19 - Evolution of structural genomic variation in populations & species	SP_24	385	129	High rates of spontaneous chromosomal duplications reveal dosage compensation by transcriptional regulation
Amina	Kurbidaeva	19 - Evolution of structural genomic variation in populations & species	SP_24	386	1142	Micro-C reveals structural and functional differentiation of rice genomes
Wen-Juan	Lan	19 - Evolution of structural genomic variation in populations & species	SP_24	387	1040	Insights into the impact of life history and mating system on structural variation in <i>Incarvillea sinensis</i> genomes
Chiara	Leo	19 - Evolution of structural genomic variation in populations & species	SP_24	388	1179	Adaptation of the <i>Arabidopsis thaliana</i> ecotype to soil environment: a genomic perspective
Luigi	Liguoro	19 - Evolution of structural genomic variation in populations & species	SP_24	389	724	Evolution of structural genomic variation in populations & species
Adi	Livnat	19 - Evolution of structural genomic variation in populations & species	SP_24	390	1437	Genes that are used together are more likely to be fused together in evolution by retromer-mediated, the used-based effect and its consequences

Eugenio	López Cortegano	19 - Evolution of structural genomic variation in populations & species	SP_24	391	412	The complete spectrum of de novo mutations in mice from a MA experiment
Juliette	Luiselli	19 - Evolution of structural genomic variation in populations & species	SP_24	392	954	Robustness to structural variants lead to different types of genome streamlining in species with larger populations or higher mutation rates.
Simone	Marcotini	19 - Evolution of structural genomic variation in populations & species	SP_24	393	655	A comparative analysis of molecular markers and mitogenome structure to dissect intraspecific diversity within two model species of arboreal mycorrhizal fungi
Jacopo	Marielalosa	19 - Evolution of structural genomic variation in populations & species	SP_24	394	589	The contribution of transposable elements in the emergence of within and between individual structural variants in invasive mollusks
Flavia	Mascagni	19 - Evolution of structural genomic variation in populations & species	SP_24	395	128	Exploring models for novel genes evolution: demarcation of transposable elements into functional sequences in a large plant genome.
James	McQuillan	19 - Evolution of structural genomic variation in populations & species	SP_24	396	53	Estimating Transposome Complexities Across Eukaryotes
Laura	Meyer	19 - Evolution of structural genomic variation in populations & species	SP_24	397	541	Divergence and gene flow at two inversions involved in esophageal atresia formation
Giorgia	Modenini	19 - Evolution of structural genomic variation in populations & species	SP_24	398	495	Polymorphic transposable element insertions provide new insights into North Italian isolates genetic variability
Julia	Morales-García	19 - Evolution of structural genomic variation in populations & species	SP_24	399	130	Selection inference in invasion rich genomes
Anastasiia	Mykhailenko	19 - Evolution of structural genomic variation in populations & species	SP_24	400	108	Complex inversion polymorphism landscape in European spruce bark beetle
Anthony	Nguyen	19 - Evolution of structural genomic variation in populations & species	SP_24	401	653	Deletions and insertions on the Y-chromosome and subgenus in modern canine genomic assemblies
Ekaterina	Noskova	19 - Evolution of structural genomic variation in populations & species	SP_24	402	1514	Demographic inference using GADMA2
Jordan	Orosco	19 - Evolution of structural genomic variation in populations & species	SP_24	403	654	Genome expansions in the Trichomonas genus are mediated by relaxed selection and differential rRNA expression
Moritz	Otto	19 - Evolution of structural genomic variation in populations & species	SP_24	404	87	The structured coalescent in the context of gene copy number evolution
Giacomo	Potente	19 - Evolution of structural genomic variation in populations & species	SP_24	405	537	Origins and evolution of the B-tocopherol supergenes in primates
Stephen	Proulx	19 - Evolution of structural genomic variation in populations & species	SP_24	406	416	Migration selection balance and the evolution of gene interactions
Marta	Ruig	19 - Evolution of structural genomic variation in populations & species	SP_24	407	1589	Using long read data to build a complete curated catalog of human polymorphic inversions mediated by inserted repeats
Hadi	Quisenberry	19 - Evolution of structural genomic variation in populations & species	SP_24	408	724	Exploring genomic dark matter
Janina	Rinke	19 - Evolution of structural genomic variation in populations & species	SP_24	409	1333	The evolutionary role of transposable elements in genome compartmentalization of ants
Bianca	Sacchi	19 - Evolution of structural genomic variation in populations & species	SP_24	410	714	Y chromosome degeneration at different timescales: exploring newly assembled old and new sex chromosomes in <i>Rumex hastulatus</i>
Somia	Sadi	19 - Evolution of structural genomic variation in populations & species	SP_24	411	968	Characterization of Transposable Elements in Pangonies
Martine	Salfson	19 - Evolution of structural genomic variation in populations & species	SP_24	412	610	Super-dominance likely maintained 80 Mbases inversion polymorphism in pearl millet
Schäfer	Schäfer	19 - Evolution of structural genomic variation in populations & species	SP_24	413	833	Revealing the emergence of gene clusters under selective gene conversion to elucidate the evolutionary history of a heavy metal adaptation in <i>Akadabrya lutea</i>
Divya	Selvaraju	19 - Evolution of structural genomic variation in populations & species	SP_24	414	986	Evolutionary dynamics of P-element invasions in <i>Drosophila</i> species
Daniel	Siqueira De Oliveira	19 - Evolution of structural genomic variation in populations & species	SP_24	415	716	Genomics and transcriptomics of cactophilic <i>Drosophila</i> species: The divergence sources explained by transposable elements and gene expression variation
Rumiko	Suzuki	19 - Evolution of structural genomic variation in populations & species	SP_24	416	508	Paleolithic human migration inferred by Helicobacter pylori and its genome structure changes in the course of evolution
Brandon	Turner	19 - Evolution of structural genomic variation in populations & species	SP_24	417	3	Chromosomal rearrangements as a source of local adaptation in island <i>Drosophila</i>
Carlos	Vargas Chávez	19 - Evolution of structural genomic variation in populations & species	SP_24	418	727	Rearrangements genomic rearrangements at the origin of <i>Chilodactylus</i> as potential key drivers of anemal lateralization
Yunqiang	Wei	19 - Evolution of structural genomic variation in populations & species	SP_24	419	1078	Low history traits related with extreme losses driving population genetic dynamics of small mammals in the CDP
Daniel	Wood	19 - Evolution of structural genomic variation in populations & species	SP_24	420	520	A pan-genome for European ash uncovers the role of structural variants in resistance to ash dieback disease
Charlotte	Wright	19 - Evolution of structural genomic variation in populations & species	SP_24	421	873	Winging it: Understanding genome instability in <i>Polyommatus</i> and beyond
Kohta	Yoshida	19 - Evolution of structural genomic variation in populations & species	SP_24	422	281	Chromosome fusions facilitating speciation of nematodes
Panagiotis-Ioannis	Zervakis	19 - Evolution of structural genomic variation in populations & species	SP_24	423	1417	Genetic analyses of the breakdown of disily in <i>Linum catharticum</i>
Gaolian	Zhang	19 - Evolution of structural genomic variation in populations & species	SP_24	424	250	Polymorphic short tandem repeats and their impacts on gene expression variation in <i>Caenorhabditis elegans</i>
Yichen	Zheng	19 - Evolution of structural genomic variation in populations & species	SP_24	425	680	Diverging signatures of adaptation and demography in gene copy number changes in human populations
Martine	Poullart	19 - Evolution of structural genomic variation in populations & species	SP_24	426	1487	High-quality genome assembly to identify structural variants in a rice germline plant-parasitic nematode <i>Meloidogyne enterocoli</i>
Abraham	Aharonoff	20 - Evolutionary biology through a functional genomics lens	SP_24	428	878	An origin for condensation-mediated dosage compensation in nematodes
Luke	Arnce	20 - Evolutionary biology through a functional genomics lens	SP_24	427	395	Functional and Evolutionary Analysis of Germine Stem Cell Regulating Genes across Select <i>Drosophila</i> and Outgroup Species
Courtney	Babbitt	20 - Evolutionary biology through a functional genomics lens	SP_24	428	188	Ascolecites drive divergent metabolic gene expression in humans and chitarraceae
Samuel	Bogan	20 - Evolutionary biology through a functional genomics lens	SP_24	429	795	Integrating functional genomics and quantitative genetics to detect epigenetic interactions shaping gene expression
Caterina	Branco	20 - Evolutionary biology through a functional genomics lens	SP_24	430	739	Identifying the sex-determining genes on the giant Y chromosome of the dioecious plant <i>Salpiglossis helvola</i>
Christabel Flci	Bucuro	20 - Evolutionary biology through a functional genomics lens	SP_24	431	212	Gene expression variability drives range of evolutionary constraints across mammals
Steven	Chen	20 - Evolutionary biology through a functional genomics lens	SP_24	432	418	Defining the sampling criteria for rearing genotype space to fitness
Alexander	Cope	20 - Evolutionary biology through a functional genomics lens	SP_24	433	726	Coevolution between mRNA and protein abundances: resolving the direction of causality in gene expression evolution using phylogenetic comparative methods
Francieli	Das Chagas	20 - Evolutionary biology through a functional genomics lens	SP_24	434	1156	Comparative genomics and phenotypic loss in stingless bees
Quentin	Foucault	20 - Evolutionary biology through a functional genomics lens	SP_24	435	703	Methylation levels and embryogenesis: from the lab to the wild
Stephen	Gaughran	20 - Evolutionary biology through a functional genomics lens	SP_24	436	787	Intraspecific adaptations to deep diving in marine mammals
Sonal	Gil	20 - Evolutionary biology through a functional genomics lens	SP_24	437	840	Genetic diversity of <i>Plasmodium falciparum</i> from
Sania	Hakala	20 - Evolutionary biology through a functional genomics lens	SP_24	438	524	Sexual transmission of social control in a polymorphic ant
Sara	Hanson	20 - Evolutionary biology through a functional genomics lens	SP_24	439	186	Chromatin Structure in the <i>Opalaea</i> polymorphic Species Complex
Yael	Hazan	20 - Evolutionary biology through a functional genomics lens	SP_24	440	798	Genetic manipulation provides novel insights into the enigmatic roles of RNA-dependent RNA polymerases in the oxidized <i>Nematostella vectensis</i>
Qing	Huan	20 - Evolutionary biology through a functional genomics lens	SP_24	441	1059	Evolutionary Mechanisms of Emerging Plant Traits Revealed by Single-Cell Transcriptomics
Aashish	Jha	20 - Evolutionary biology through a functional genomics lens	SP_24	442	1035	Community-engaged multi-omics studies with indigenous populations: lessons learned and challenges ahead
Anaya	Khatel	20 - Evolutionary biology through a functional genomics lens	SP_24	443	1638	RNA methyltransferases in brain signal genomes
Jun	Kilano	20 - Evolutionary biology through a functional genomics lens	SP_24	444	453	Chromosome engineering in fish: toward understanding chromosome evolution
Anna	Kukekova	20 - Evolutionary biology through a functional genomics lens	SP_24	445	1617	Cell type specific deoxygenation of prefrontal cortex of young and aging lame and aggressive fowes
Katharina	Lange	20 - Evolutionary biology through a functional genomics lens	SP_24	446	358	Uncovering the sequence variants that drive human evolution
Felix	Langschieid	20 - Evolutionary biology through a functional genomics lens	SP_24	447	1370	Evolutionary dynamics of rRNA-protein invasions in the gene regulatory network of vertebrates
Christopher	Large	20 - Evolutionary biology through a functional genomics lens	SP_24	448	459	Development across evolutionary time at a single-cell resolution in the <i>Caenorhabditis</i> nematode embryo
Liam	Lu	20 - Evolutionary biology through a functional genomics lens	SP_24	449	860	Evolutionary forces shaping the genome-wide distribution of uORFs in eukaryotes
Brian	Metzger	20 - Evolutionary biology through a functional genomics lens	SP_24	450	1133	Seeing through the Mendelian Blur: Genetic crosses among distantly related species
Tomoya	Noma	20 - Evolutionary biology through a functional genomics lens	SP_24	451	951	Divergent evolution of group I introns in mammalian cells
Eiise	Parey	20 - Evolutionary biology through a functional genomics lens	SP_24	452	6	Phylogenetic modeling of enhancer shifts in African molluscs reveals regulatory changes associated with tissue-specific traits
Rachel	Petersen	20 - Evolutionary biology through a functional genomics lens	SP_24	453	1609	Applying multiplexed mTAR-seq to understand genetic effects on regulatory element function
Bharat	Ravi	20 - Evolutionary biology through a functional genomics lens	SP_24	454	83	Neutral models of de novo gene emergence suggest that gene evolution has a preferred trajectory
Christopher	Riccardi	20 - Evolutionary biology through a functional genomics lens	SP_24	455	582	Multiple independent origins of secondary regions in <i>Gammaglobulins</i>
Katherine	Ricketton	20 - Evolutionary biology through a functional genomics lens	SP_24	456	29	The human Y-chromosome structural changes in brain gene expression across primate evolution
Caio	Rosa	20 - Evolutionary biology through a functional genomics lens	SP_24	457	1613	Impact of synonymous mutations on the response and adaptation to an extreme environment
Navya	Shukla	20 - Evolutionary biology through a functional genomics lens	SP_24	458	464	Molecular basis of convergent evolution of the Thyroxine and Ethanolamine cands.
Yolandi	Swart	20 - Evolutionary biology through a functional genomics lens	SP_24	459	1641	co-eQTL mapping of TB-T2D comorbidity elucidates the involvement of African ancestry in TB susceptibility
Maria	Toro Moreno	20 - Evolutionary biology through a functional genomics lens	SP_24	460	1325	A massively parallel platform for evolutionary genetics of mammalian essential proteins
Wilfred	Vermeris	20 - Evolutionary biology through a functional genomics lens	SP_24	461	303	A systems biology approach to determine the evolutionary origin of biological nitrogen fixation on the aerial roots of <i>Sesbania bicolor</i>
Davide	Vespasiani	20 - Evolutionary biology through a functional genomics lens	SP_24	462	74	Insights into the evolution of gene expression differences across vertebrates using single-cell transcriptomics
Zorimar	Vieira-Pacheco	20 - Evolutionary biology through a functional genomics lens	SP_24	463	742	Developmental mechanisms of plasticity and their response to adaptation to rapid environmental change
Taurus	Vilgaly	20 - Evolutionary biology through a functional genomics lens	SP_24	464	1113	Common genetic variation affecting the transcriptomic response to <i>Yersinia</i> pests
Yirong	Wang	20 - Evolutionary biology through a functional genomics lens	SP_24	465	1028	Divergent Evolution Drives Metabolic Network Differences in <i>Drosophila melanogaster</i> and <i>Drosophila pseudoobscura</i> Under High-Fat Diet Conditions
Taylor	Wang	20 - Evolutionary biology through a functional genomics lens	SP_24	466	1575	Leveraging the awesome power of Saccharomyces to probe the evolution of genetic networks
Paul	Waters	20 - Evolutionary biology through a functional genomics lens	SP_24	467	919	DNA methylation and imprinted X chromosome inactivation in marsupials
Milwa	Wieland	20 - Evolutionary biology through a functional genomics lens	SP_24	468	802	A model of functionally buffered deleterious mutations can lead to signatures of positive selection in evolutionary simulations
Yannick	Wurm	20 - Evolutionary biology through a functional genomics lens	SP_24	469	1632	Are cox2a and cox2b genes cryptic duplicates of homologous tissue transcriptomes
Danat	Yermakovich	20 - Evolutionary biology through a functional genomics lens	SP_24	470	660	Long-range regulatory effects of Neandertal DNA in modern humans
Vera	Yilmaz	20 - Evolutionary biology through a functional genomics lens	SP_24	471	960	Cold acclimation: The effect of extended cold exposure on tropical vinegar flies
Gokberk	Alagoz	27 - Regulatory evolution and the emergence of diversity	SP_24	472	1519	Spatial and single-nucleus transcriptomic profile of the chimpanzee frontal pole
Isabel	Alves	27 - Regulatory evolution and the emergence of diversity	SP_24	473	1236	Predicting the evolution of cis-regulatory regions in the presence of allele-specific expression
Simon	Andri	27 - Regulatory evolution and the emergence of diversity	SP_24	474	1425	Evolutionary trade-off and mutational bias could favor transcriptional loss-translational divergence within paralog pairs
Mary	Baumgaether	27 - Regulatory evolution and the emergence of diversity	SP_24	475	1172	Revealing gene regulatory mechanisms contributing to the evolution of the human cerebral cortex
Folmer	Bokma	27 - Regulatory evolution and the emergence of diversity	SP_24	476	1590	A phylogenetic approach to distinguish between co-evolutionary patterns in incipient and established species
Ignacio	Bravo	27 - Regulatory evolution and the emergence of diversity	SP_24	477	1150	Impact of codon usage bias and exon splicing on gene expression from biotrophic rRNAs: development of an experimental model in human cells and application to oncogenic protein expression in infectious cancers
Samuel	Carthy	27 - Regulatory evolution and the emergence of diversity	SP_24	478	1183	Annotation and assessment of long non-coding RNA in blood transcriptomes of a wild-caught fish species
Angel	Cisneros Caballero	27 - Regulatory evolution and the emergence of diversity	SP_24	479	73	Epistasis between promoter activity and coding mutations shapes gene evolvability
Marta	Coronado-Zamora	27 - Regulatory evolution and the emergence of diversity	SP_24	480	615	Epigenetic changes induced by transposable elements drive gene up- and down-regulation across <i>D. melanogaster</i> body parts
Cédric	Côté	27 - Regulatory evolution and the emergence of diversity	SP_24	481	92	Integrating gene regulatory mechanisms contributing to the evolution of the human cerebral cortex
Alessandro	Formaggio	27 - Regulatory evolution and the emergence of diversity	SP_24	482	662	Evolution of the small RNA pathways in animals and the loss of endo-siRNAs among Lophotrochozoa
Marco	Fracassetti	27 - Regulatory evolution and the emergence of diversity	SP_24	483	526	Conservation of dominance relationships and tRNA-based dominance modifiers at the Brassicaceae S-locus across 8 million years of divergence
Timothy	Fuqua	27 - Regulatory evolution and the emergence of diversity	SP_24	484	377	Evoking insertion sequences into promoters
Michelle	Harwood	27 - Regulatory evolution and the emergence of diversity	SP_24	485	263	Increased allele-specific expression in blood can be beneficial for immune response in healthy ages
Charlotte	Huyghe	27 - Regulatory evolution and the emergence of diversity	SP_24	486	210	The molecular basis underlying digestive adaptations in the Lake Tanganyika cichlid fish radiation
Indier	Inel	27 - Regulatory evolution and the emergence of diversity	SP_24	487	92	Gene expression and adaptive divergence contribute to adaptive divergence of surfwrain acetylases
Hamit	Izci	27 - Regulatory evolution and the emergence of diversity	SP_24	488	1420	Landscape-specific gene expression patterns among primates

Adrian	Jaimes-Decerra	27 - Regulatory evolution and the emergence of diversity	SP_24	489	404	The evolution of toxin-producing cell types in <i>Cnidaria</i>
Kenneth	Kim	27 - Regulatory evolution and the emergence of diversity	SP_24	490	1372	Comparative gene expression analysis of resulting in Insect and Crustacean lineages
Audrey	Le Veve	27 - Regulatory evolution and the emergence of diversity	SP_24	491	67	The impact of genomic imprinting on genetic variation in <i>A. lyrata</i>
Mariana	Leir Cardin	27 - Regulatory evolution and the emergence of diversity	SP_24	492	1317	Differential Expression of Immune Genes in Two Recently Divergent <i>Drosophila</i> Species
Thomas	Lesaffre	27 - Regulatory evolution and the emergence of diversity	SP_24	493	547	On the origin of <i>X. laevis</i> chromosomes from sex allocation evolution
Clifton	Lewis	27 - Regulatory evolution and the emergence of diversity	SP_24	494	1291	Comparative evolution of neogenetic gene regulatory networks
Xueying	Li	27 - Regulatory evolution and the emergence of diversity	SP_24	495	151	Mutational scars reveal differential evolution of <i>Drosophila</i> promoters and enhancers
Wei-Han	Lin	27 - Regulatory evolution and the emergence of diversity	SP_24	496	948	Investigating The Regulatory Mechanism of Protein Expression Noise by Experimental Evolution in <i>Saccharomyces cerevisiae</i>
Yaow	Mathow	27 - Regulatory evolution and the emergence of diversity	SP_24	497	1346	Infring DNA methylation in nonvertebrate tissues of ancient specimens
Gemille	Mayerich	27 - Regulatory evolution and the emergence of diversity	SP_24	498	985	Consequences of viral infections on transposable element regulation in <i>Drosophila</i>
Adriaan	Melburg	27 - Regulatory evolution and the emergence of diversity	SP_24	499	949	The evolution of the avian-like dependent regulatory genome
Laura	Mulvey	27 - Regulatory evolution and the emergence of diversity	SP_24	500	1304	Estimating cell type trees using model-based phylogenetic inference
Nehemiah	Ongeso	27 - Regulatory evolution and the emergence of diversity	SP_24	501	1654	Co-expression network analysis of genes mediating <i>Meloidae</i> (<i>Incognita parasitum</i> in tomato) plant nematode interactions
Deniz	Ozbielik	27 - Regulatory evolution and the emergence of diversity	SP_24	502	1280	Understanding RNA polymerase structure-to-function relationship to predict evolution of rifampicin resistance
Juan	Pascual-Anaya	27 - Regulatory evolution and the emergence of diversity	SP_24	503	1581	Highly genome. <i>Burmannia verticillata</i> whole genome duplications and their evolutionary consequences
Valentine	Patterson	27 - Regulatory evolution and the emergence of diversity	SP_24	504	1139	Alba-Specific Expression in <i>Onchocerca volvulus</i> (Wolpin) Larvae
Blair	Perry	27 - Regulatory evolution and the emergence of diversity	SP_24	505	39	Regulatory sequence evolution and activity alteration in <i>hous</i>
Mitchell	Reynolds	27 - Regulatory evolution and the emergence of diversity	SP_24	506	840	Understanding the role of genetic background in determining the evolutionary outcome of gene regulatory network rewiring events
Carlos	Rivera Rivera	27 - Regulatory evolution and the emergence of diversity	SP_24	507	185	GenNet: a systems-level sequence evolution simulator
Carlos	Rodriguez-Ramirez	27 - Regulatory evolution and the emergence of diversity	SP_24	508	647	The contribution of alternative splicing to adaptation in threespine stickleback
Laasya	Samhita	27 - Regulatory evolution and the emergence of diversity	SP_24	509	1644	Mutation-selection alters the genetic basis of adaptation to antibiotics
Tharwi	Shikant	27 - Regulatory evolution and the emergence of diversity	SP_24	510	865	Chromatin-mediated gene-regulatory dynamics in adaptation to polybody
Caui	Townsend	27 - Regulatory evolution and the emergence of diversity	SP_24	511	1436	Gene duplication, chromosomal rearrangement, repeat-induced point mutation and fast divergence transform non-coding regions into a marriage regulator for tissue lineage-specific elements in <i>Neurospora crassa</i>
Marco	Trizzino	27 - Regulatory evolution and the emergence of diversity	SP_24	512	146	A <i>SMARCC4</i> genetic variant exclusive of the <i>Drosophila</i> lineage (<i>Citrobacter</i> , <i>Oribacter</i>) is responsible for major changes in enhancer activity and gene expression in hippocampal neurons
Shreya	Vichare	27 - Regulatory evolution and the emergence of diversity	SP_24	513	987	The LPP confers a habitat switch through chromosomal gene regulation in <i>Pantodon</i> agglomerates associated with wheat seeds
Yu	Wang	27 - Regulatory evolution and the emergence of diversity	SP_24	514	1062	Patterns and Evolutionary Mechanisms of Subgenomic Expression Differentiation in Common Wheat
Daniel	Weinreich	27 - Regulatory evolution and the emergence of diversity	SP_24	515	1474	The Evolution of Biological Noise
Yarden	Weiss	27 - Regulatory evolution and the emergence of diversity	SP_24	516	294	The effect of sequence changes in cis-regulatory elements on divergent gene expression between humans and chimpanzees
Caui	Westmann	27 - Regulatory evolution and the emergence of diversity	SP_24	517	1389	The evolution of bacterial transcription factor binding sites: Insights from high-resolution adaptive landscapes
Liduo	Yin	27 - Regulatory evolution and the emergence of diversity	SP_24	518	310	One nucleotide diversity in <i>Phlox</i> Zeller (<i>Empetrum</i> heath) and its association with <i>Phlox</i> adaptation
Xuefei	Yuan	27 - Regulatory evolution and the emergence of diversity	SP_24	519	1493	The molecular evolution of mammalian hears
Giulia	Zancoli	27 - Regulatory evolution and the emergence of diversity	SP_24	520	1239	Spatial functional specialization of a biochemical weapon factory
Xiaoyu	Zhou	27 - Regulatory evolution and the emergence of diversity	SP_24	521	1510	High-resolution RNA isoform variation analysis by combining the advantages of single-cell RNA and nanopore sequencing
Kabla	Baral	07 - Computational evolutionary genomics in the era of machine learning	SP_24	523R	1495	Power to detect episodic fitness shift at a small number of sites can be rescued with a covariate-informed branch-site type method
Bogdan	Elismenko	07 - Computational evolutionary genomics in the era of machine learning	SP_24	524R	1284	Genetic large-scale comparative genomics analyses of the Neutral Mutation Spectra - NMS pipeline
Tamás	Friedlander	07 - Computational evolutionary genomics in the era of machine learning	SP_24	525R	569	Inferring evolutionary dynamics on ecological networks: theory and application
Konstantin	Gurbin	07 - Computational evolutionary genomics in the era of machine learning	SP_24	526R	1285	Accurate reconstruction of the human mitochondrial genome mutations provide insight into the process of mutagenesis
Devashish	Tripathi	07 - Computational evolutionary genomics in the era of machine learning	SP_24	527R	1033	A Deep learning approach for modeling Development-Environment interaction to detect genomic regions under natural selection
Daniele	Battilani	15 - Animal genomics goes wild	SP_24	528R	561	Is the integration of the Dog Mosaic HB Allele at the <i>K1000</i> (<i>CD103</i>) gene Affecting the Evolutionary Trajectory of the Italian Wolf Population?
Meirav	Meiri	15 - Animal genomics goes wild	SP_24	529R	1348	The genetic history of the Jordan Desert leopard (<i>Panthera pardus</i>)
Hayley	Hassler	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	530R	361	Using temporal genomic information on the evolution of coronaviruses to identify the benefits of alternate frequencies of mRNA vaccine boosting for immune-logical and immunocompromised individuals
Gulnarg Merve	Kilinc	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	531R	1015	Evolutionary genomics better predicts traits in <i>Arabidopsis</i> over the past 10,000 years. What can ancient genomes tell?
Marlin	Patr	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	532R	1419	A simple and efficient R tool for Approximate Bayesian Computation
Kai	Shimigaki	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	533R	809	An efficient method for inferring epistasis from temporal genetic data, applied to HIV-1 evolution
Laura	Landweber	19 - Evolution of structural genomic variation in populations & species	SP_24	534R	304	Comparative genomics reveals insight into the origin of massively scrambled genomes
Domniki	Manousi	19 - Evolution of structural genomic variation in populations & species	SP_24	535R	769	Dynamic evolution and diversification of <i>ankyrin</i> <i>gyl1</i> and <i>gyl2</i> gene families in Atlantic salmon
Eri	Tabata	19 - Evolution of structural genomic variation in populations & species	SP_24	537R	454	The relationship of feeding behaviors and molecular evolution of acidic chitinase in <i>Dendroica</i>
Lina	Ullrich	19 - Evolution of structural genomic variation in populations & species	SP_24	538R	421	Demography of grasshopper with the root structure in the <i>Ernstia</i> population
Stepan	Denisov	20 - Evolutionary biology through a functional genomics lens	SP_24	539R	982	Evolution of antisense transcriptional terminators in their genomic context
Akshi	Gupta	20 - Evolutionary biology through a functional genomics lens	SP_24	540R	143	Ortholog replacement reveals a novel function of the transcription factor <i>TF10C</i> complex in mitotic chromosome segregation
Alba	Julia	20 - Evolutionary biology through a functional genomics lens	SP_24	541R	1178	High phenotypic plasticity of the azore damselfly (<i>Zygonyx punctata</i>) to reduced temperature stress
Alexey	Skidnov	20 - Evolutionary biology through a functional genomics lens	SP_24	542R	1176	The rocky road to aerobic and anaerobic prokaryotes: microbial speciation reconstruction and analysis
Alexandr	Voronika	20 - Evolutionary biology through a functional genomics lens	SP_24	543R	1306	Orion mutation pressure of SARS-CoV-2 helps to understand the past and predict the future evolution: C-to-U and G-to-U biased mutagenesis forces the majority of amino-acid substitutions to be from C-to-G to U-rich genes
Kimberly	Carlson	27 - Regulatory evolution and the emergence of diversity	SP_24	544R	1099	Testing the Role of <i>Dis-Active DNA Sequence</i> in Evolutionary Divergence of the <i>Brevortia</i> Chromatin State in Mammals
Julien	Gross-Sommer	27 - Regulatory evolution and the emergence of diversity	SP_24	545R	333	The influence of selection strength on variation in wildlife genetic variation
Sen	Hadife	27 - Regulatory evolution and the emergence of diversity	SP_24	546R	993	The role of DNA demethylation in embryogenesis and epigenome regulation
Manas	Joshi	27 - Regulatory evolution and the emergence of diversity	SP_24	547R	167	Comparative and population genomics analysis of TF-DNA interactions
Markéta	Vlková	27 - Regulatory evolution and the emergence of diversity	SP_24	548R	602	Natural selection forces acting on transcriptional control of the <i>luc2f</i> promoter
Lina	Abdelwahed	05 - New frontiers in conservation genomics	EC_25	549	63	How to evaluate the connectivity of plant communities in endangered habitats ? An ecological and genetic approach
Larissa	Adams	05 - New frontiers in conservation genomics	EC_25	550	1207	Are non-invasive samples a good DNA source for mtDNA-based genetic monitoring?
Gzde	Altag	05 - New frontiers in conservation genomics	EC_25	551	626	Genetic Insights into the Endangered Madroa Population of <i>Aspidochelone</i> and <i>Cyprina</i>
Roberto	Bielo	05 - New frontiers in conservation genomics	EC_25	552	1252	A comprehensive genetic approach for the critically endangered <i>Aspidochelone</i> brown bear: predicted best functional assays, simulations, and much more
Elena	Buzan	05 - New frontiers in conservation genomics	EC_25	553	496	Massbackcrossing the diet of grey wolf and Eurasian lynx in the Alps and the Dniepr Mountains
Jillian	Campbell	05 - New frontiers in conservation genomics	EC_25	554	1063	Insights on <i>Callosotus</i> sucker hybridization and spawning trends using genetic data
Louise	Camus	05 - New frontiers in conservation genomics	EC_25	555	513	Predicting species invasiveness with genomic data: is <i>Genotus</i> Offset related to establishment probability ?
Enrique	Olellamin Amaro	05 - New frontiers in conservation genomics	EC_25	556	35	Evolutionary history and seaquake genomics of Harbour porpoises (<i>Phocoena phocoena</i>) across environmental gradients in the North Atlantic and adjacent waters
Hedvig	Caspo	05 - New frontiers in conservation genomics	EC_25	557	1152	Emergent Arctic lineage of the northern arctic hare in Svalbard provides evidence against the hypothesis of recent identification
Marisol	Dominguez	05 - New frontiers in conservation genomics	EC_25	558	1531	Low polymorphism of <i>MHC</i> class I genes in a threatened passerine bird: insights from a genomic perspective
Rosie	Drinkwater	05 - New frontiers in conservation genomics	EC_25	559	1155	Conserving genomics and spatial models to improve long-term conservation management of island endemics
Erik	Embod	05 - New frontiers in conservation genomics	EC_25	560	1322	Comparative effective estimated migration surfaces
Huizhong	Fan	05 - New frontiers in conservation genomics	EC_25	561	503	Conservation priorities for global marine biodiversity across multiple dimensions
Eliska	Fajst	05 - New frontiers in conservation genomics	EC_25	562	1254	Establishing a framework for conservation genomics of freshwater biodiversity
Jonathan	Flowers	05 - New frontiers in conservation genomics	EC_25	563	1445	Hybridization, introgression and population decline in European last year (<i>Phlox</i> <i>heath</i>) forest
Maeva	Gabrielli	05 - New frontiers in conservation genomics	EC_25	564	731	Living on a rock with three heterogeneous sites per population: the genomics of the Aeolian wall lizard
Yuting	Gao	05 - New frontiers in conservation genomics	EC_25	565	1223	Dat. not analyse gene copy number. defines salivary amylase levels in closely related species
Daniel	Gygax	05 - New frontiers in conservation genomics	EC_25	566	777	Genomic and statistical tools for non-invasive monitoring of two endangered bats
Ulises	Hernandez	05 - New frontiers in conservation genomics	EC_25	567	898	Metastatal method revisited
Rus	Hoebel	05 - New frontiers in conservation genomics	EC_25	568	480	Genomics of post-drought recovery in the northern elephant seal
Sagana	Jain	05 - New frontiers in conservation genomics	EC_25	569	875	Allelic and reproductive <i>Saccharomyces</i> workflow for Pacific HPI long-term assembly and evolution
Thomas	Kaczmarek	05 - New frontiers in conservation genomics	EC_25	570	1396	Evolutionary genomics of <i>Form</i> (<i>Daphnia</i> spp.) lake of a large panmictic and diversity studies for conservation and sustainable use
Youngkyung	Ko	05 - New frontiers in conservation genomics	EC_25	571	22	Transposable elements derived from RNA expression patterns in TOGA: evolutionary analysis for 10 species
Mitchell	Lokoy	05 - New frontiers in conservation genomics	EC_25	572	1554	Recent population collapse shapes deleterious variation across subpopulations of the endangered Florida scrub-jay
Samantha	López Clinton	05 - New frontiers in conservation genomics	EC_25	573	518	Exploiting new computational methods for genome-wide eDNA biodiversity monitoring
Leandro	Lucero	05 - New frontiers in conservation genomics	EC_25	574	117	Non-functionalization of a LINK HETEROCHROMATIN PROTEIN 1 member of the plant Polycomb Repressive Complex 1 (PRC1) in <i>Brassica napus</i> (<i>Brassicaceae</i>)
Theresa	Markow	05 - New frontiers in conservation genomics	EC_25	575	233	Population and functional genomic diversity in the endangered Moorish butterfly, <i>Danaus plexippus</i>
Alicia	Mastretta-Yanes	05 - New frontiers in conservation genomics	EC_25	576	336	Taxonomic effective population size through time and space
Camila	Mazzoni	05 - New frontiers in conservation genomics	EC_25	577	780	Placing the way to support sea turtles conservation with high-quality genomic data
Olena	Meleshko	05 - New frontiers in conservation genomics	EC_25	578	1129	Genetic structure and reproduction in a clonal polyploid plant
Jess	Peers	05 - New frontiers in conservation genomics	EC_25	579	702	Introducing-associated gene pseudogenization in the cheetah, <i>Acinonyx jubatus</i>
Albert	Perlas Puente	05 - New frontiers in conservation genomics	EC_25	580	973	Towards non-invasive real-time monitoring of Asian influenza virus
Emily	Poycroft	05 - New frontiers in conservation genomics	EC_25	581	1051	The genetic impact of island isolation in Australian mammals
Román	Rodríguez	05 - New frontiers in conservation genomics	EC_25	582	651	Metagenomic diversity in the analysis of the metagenome of Iberian desert feces
Linnéa	Smeds	05 - New frontiers in conservation genomics	EC_25	583	203	Deleterious mutations and genetic load in island <i>Scaevola</i> wetlands
Jarro	Sopniewski	05 - New frontiers in conservation genomics	EC_25	584	197	Using novel population genomics methods to characterise the genomic consequences of a major environmental disturbance
Gabriella	Spatola	05 - New frontiers in conservation genomics	EC_25	585	193	Ancestry and origin of free-ranging dogs on the Galapagos Islands
Regine	Tiong	05 - New frontiers in conservation genomics	EC_25	586	468	Conservation genomics reveals inbred population of critically endangered hawksbill turtles in Singapore
Ana	Topasna	05 - New frontiers in conservation genomics	EC_25	587	196	Changes in gene expression in <i>Daphnia magna</i> in response to predation cues provide insight into the evolution of the stress response
Lidia	Torral Verba	05 - New frontiers in conservation genomics	EC_25	588	632	Genome-wide genetic divergence in a connected habitat: the case of the semi-arboreal <i>Artemisia</i> <i>fraxinifolia</i> <i>Artemisia fraxinifolia</i>
Felicita	Uzzi	05 - New frontiers in conservation genomics	EC_25	589	945	Hybridization and population genetic structure of European wildcats from <i>Dniester</i> , <i>Alps</i>

Maurine Vilcot	05 - New frontiers in conservation genomics	EC_25	590	321	Environmental DNA, a tool for systematic spatial conservation planning from inter- to intraspecific scales
John Bracht	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	591	1109	Evolutionary tuning of mitochondrial cytochrome c oxidase in the Devil Worm
Florencia Carmus	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	592	1367	Contribution of mitochondrial genomes to local adaptation
Diego Carr	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	593	1144	Evolutionary analysis of mitochondrial genomes to generate small RNA interference
Shu-Ming Chaw	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	594	461	Evolution of mitochondrial RNA editing in animal genomes
Yu-Chi Chen	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	595	242	Phylogenomics uncovers widespread abundance of ancient mitochondrial DNA buried in vertebrate genomes
Alizee Debelle	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	596	138	The male-specific copy of the paternally transmitted mtDNA in <i>Mylodon darwini</i> codes for a protein
Joseph Dubie	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	597	671	Using experimental evolution to elucidate the role of fusion, fission, and autophagy in the fate of selfish mitochondria in <i>Caenorhabditis elegans</i>
Yuyuan Fang	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	598	930	Estimating fine-scale mitochondrial DNA mutation rates using machine learning
Cecilia Fitzgerald-Cook	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	599	763	Evolutionary genomics in the Hawaiian volcanic shrimp (<i>Halocaridina rubra</i>): cryptic speciation and mitochondrial discordance
Finley Grovet-Thomas	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	600	819	Problems in the Ptolemaeus: do mitochondrial mismatches impact mitochondrial phylogeny
Justin Havird	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	601	229	Adaptive vs. relaxed selection on animal mitochondrial genes
AhRang Kang	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	602	494	Comparative mitochondrial genome analysis of two pear pests, <i>Carpomyia jakugui</i> and <i>Carpomyia burkhardtii</i> (Hemiptera: Psyllidae)
Ehsan Kayal	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	603	772	Gain, loss, and evolution of multi-homolog in mitochondrial genome of octocorals
Marina Khachatryan	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	604	289	Evolution of the plant organelles is characterized by similar substitution rates but different allele dynamics
Minjee Kim	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	605	1116	Comparative characteristics and phylogeny of complete mitochondrial genomes of four Caraganyina beetles (Coleoptera: Nitidulidae)
Pavel Kravchenko	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	606	1199	Evolution of mitochondrial genomes in deep-sea hydrothermal vent animals and other extremophiles
Chuan Ku	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	607	313	Lessons from oceans: rampant nuclear-mitochondrial-plastid phylogenomic discordance in macroalgae
Emelie Leroux	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	608	233	Mitochondrial DNA methylation and doubly uniparental inheritance
Stefano Lomello	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	609	565	Evolution of a fiber-forming enzyme in <i>Tetrahymena thermophila</i> : did protozoa evolve new cytoskeletal proteins?
Pawel Mackiewicz	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	610	1123	Evolution of duplicated regions in mitochondrial genomes of birds (Aves)
Alina Mihailova	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	611	1165	A billion-year trend of amino acid substitutions in the mitochondrial genome
Mirna Miral	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	612	331	COI-Seq Entrance Order from the CICEP2 MP: a candidate direct transcriptional coordinator of the mitochondrial and nuclear genomes
Serah Osborn	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	613	709	The role of mitochondrial remodeling in the phenotype of a selfish mitochondrial genome
Sylvie Parkus	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	614	672	Evolution and function of the stalk-eyed fly mitochondrial genome
Marco Passamonti	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	615	1066	Mitochondrially-mediated RNA interference, a fast-evolving retrograde signaling system to regulate nuclear gene expression
Federico Piazzi	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	616	376	Unravelling the phylogenetic signal by means of orthology clusters: the case of bilineae miRNAs
Andrea Pozzi	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	617	981	The mitochondrial interference hypothesis, a new hypothesis for an old story
Sofia Sabagh	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	618	781	Insights in hepatic cellular metabolism of naturally selected purpuriniferous siphon (<i>Liparis gibbosa</i>)
Ilze Skujina	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	619	1058	The keys to the greenhouse: novel insights of mitochondrial regulation using large-scale comparative genomics data of longjelly specialists 46° long lived microbial <i>Myxozoa</i> myxozoa
Jessica Warren	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	620	429	Transitions in translation: how some of the last remaining mitochondrial genes are finally lost
Dareen Almojil	26 - Genomics of Adaptations to Extreme Environments	EC_25	621	1012	Genomic signals of high-altitude in the allopolyploid African cleaved frog <i>Xenopus laevis</i>
Mahlide André	26 - Genomics of Adaptations to Extreme Environments	EC_25	622	224	Genomic Signatures of Local Adaptation to Extreme Environments in Papua New Guinean Highlanders and Lowlanders
Elisabeth Authier	26 - Genomics of Adaptations to Extreme Environments	EC_25	623	1391	Phenotypic responses of flowering plants to limited access to natural pollinator community
Bárbara Bastos	26 - Genomics of Adaptations to Extreme Environments	EC_25	624	15	Evolution of molecular mechanisms of thermoregulation in rodents
Ilana Bisla	26 - Genomics of Adaptations to Extreme Environments	EC_25	625	1294	Genomics of cold adaptations in the Arctic rockcod fish <i>Arcticochirocentrus</i>
Emmanuel Bost	26 - Genomics of Adaptations to Extreme Environments	EC_25	626	1131	Genomes of <i>Vibrio</i> spp. isolated from deep-sea hydrothermal vents highlight antibiotic resistance genes and ecological adaptation mechanisms
Yu Cao	26 - Genomics of Adaptations to Extreme Environments	EC_25	627	525	Genomic insights into <i>Quercus</i> to <i>Karst</i> limestone and incident speciation in East Asian <i>Platanus</i> spp. (<i>Juglandaceae</i>)
Rómulo Carlejal	26 - Genomics of Adaptations to Extreme Environments	EC_25	628	887	Genetic basis of <i>Quercus robur</i> resistance to acute oak decline in Britain
Edurdo Castro-Nallar	26 - Genomics of Adaptations to Extreme Environments	EC_25	629	436	Mobile genetic elements and the restructure of mitochondrial genomes in the <i>Corvus</i> <i>Flavus</i> <i>Patagonia</i> (<i>c2</i> <i>Y15</i>)
Chihak Chhak	26 - Genomics of Adaptations to Extreme Environments	EC_25	630	1161	Reconstructing adaptive history and its role in facilitating local adaptations among the <i>Balaia</i> and <i>Balika</i> in East-Central Africa
Chen Chao	26 - Genomics of Adaptations to Extreme Environments	EC_25	631	309	The hot of environmental adaptations of budding yeast
Chung Hyun Cho	26 - Genomics of Adaptations to Extreme Environments	EC_25	632	33	Genomic signatures of adaptation to hot springs in red algae
Gleb Ebert	26 - Genomics of Adaptations to Extreme Environments	EC_25	633	1049	No Need to Be Stressed: Regulatory Changes After High-Temperature Adaptation
Eisa Froufe	26 - Genomics of Adaptations to Extreme Environments	EC_25	634	1659	Genomic Adaptations Associated with Climate Change and Biological Changes in the univert mussel <i>Urosalpinx</i> (Sprenger, 1793)
Amit Ghosh	26 - Genomics of Adaptations to Extreme Environments	EC_25	635	1318	Population-specific adaptation to diverse environments in South America
Ruth Golomb	26 - Genomics of Adaptations to Extreme Environments	EC_25	636	1373	Exploring a novel context: cell-autonomous evolutionary adaptation
Ram Gram	26 - Genomics of Adaptations to Extreme Environments	EC_25	637	855	Genetic basis of adaptation to extreme environments across the Pacific: Signals of positive selection from the Drosophila Genome Variation Project
Allie Graham	26 - Genomics of Adaptations to Extreme Environments	EC_25	638	189	Convergent pseudogenization of olfactory receptors in mammalian living in high-altitude environments
Elena Gusareva	26 - Genomics of Adaptations to Extreme Environments	EC_25	639	312	Adaptation to the cold environment in indigenous Arctic populations
Yoelwyn Gutierrez Guerrero	26 - Genomics of Adaptations to Extreme Environments	EC_25	640	1338	Comparing continents: The genomic basis of environmental adaptation and parallel evolution in house mice (<i>Mus musculus domesticus</i>) from the Americas
George Hiron-Alecricm	26 - Genomics of Adaptations to Extreme Environments	EC_25	641	796	The genomic basis of obligate dependence in anti-plant mutations
Ozde Ighion	26 - Genomics of Adaptations to Extreme Environments	EC_25	642	1655	Ribosomal Species Enhanced Soybean Growth under Drought Stress Conditions
Iker Irizar	26 - Genomics of Adaptations to Extreme Environments	EC_25	643	307	Microevolutionary genomics of mitochondrial signals in land plants illuminate signaling network evolution
Deborah Leigh	26 - Genomics of Adaptations to Extreme Environments	EC_25	644	1148	Proteinase levels for the <i>Yersinia</i> <i>Y15</i> characteristic with acute adaptation
Melanie Lindner	26 - Genomics of Adaptations to Extreme Environments	EC_25	645	443	Genomic selection for early and late avian lay date led to differences at the phenotypic level, but not in fitness
Alexander Lucaci	26 - Genomics of Adaptations to Extreme Environments	EC_25	646	12	Evolutionary shortcuts via multi-nucleotide substitutions and their impact on natural selection analysis
Andrea Luchetti	26 - Genomics of Adaptations to Extreme Environments	EC_25	647	824	Branchpoint genomics: state of the art and future challenges
Hana Merchant	26 - Genomics of Adaptations to Extreme Environments	EC_25	648	339	Genetic adaptation in South African mole-rats along an aridity gradient
Mattin Miryeganeh	26 - Genomics of Adaptations to Extreme Environments	EC_25	649	307	Genomic, epigenetic, and transcriptomic study of mangrove tree species: <i>Begonia</i> (<i>Gymnorhiza</i>) (<i>Rhizophoraceae</i>)
Angel Ordoz	26 - Genomics of Adaptations to Extreme Environments	EC_25	650	1512	Unravelling the mechanisms of local genetic adaptation in <i>Heliconia</i> species: insights from gene expression analysis of Hsp90 and Hsp70
Giada Padovani	26 - Genomics of Adaptations to Extreme Environments	EC_25	651	425	Fruit-bait evolutionary adaptation: insights from non-coding accelerated regions
David Paeede	26 - Genomics of Adaptations to Extreme Environments	EC_25	652	875	The MUC19 gene in Denisovans, Neandertals, and Modern Humans: An Evolutionary History of Recurrent Introgression and Natural Selection
Claudia Pérez	26 - Genomics of Adaptations to Extreme Environments	EC_25	653	1163	Evolution of toxin resistance in the grasshopper mouse
Patricio Pazo	26 - Genomics of Adaptations to Extreme Environments	EC_25	654	1431	Genome-wide scans reveal selection signals to extreme conditions and pathogen-driven adaptation in advanced populations from Patagonia
Jasmin Rees	26 - Genomics of Adaptations to Extreme Environments	EC_25	655	546	Adaptation to Microsatellites in Modern Humans: A Case Study in Zinc
Verónica Reyes-Galindo	26 - Genomics of Adaptations to Extreme Environments	EC_25	656	1608	Population Migration: An experiment of genetic dispersal in trees into a polluted city
Gaston Rijo de Leon	26 - Genomics of Adaptations to Extreme Environments	EC_25	657	722	Expanding horizons: Unraveling the demographic and adaptive history of human populations from Palenque through genomics
Rebekah Rogers	26 - Genomics of Adaptations to Extreme Environments	EC_25	658	2	Strong, recent selective sweeps reshape genetic diversity in freshwater brackish <i>Megalops</i> <i>nerosa</i>
Kara Ryan	26 - Genomics of Adaptations to Extreme Environments	EC_25	659	792	Selection on standing genetic variation mediates convergent evolution in extremophile fish
Joana Santos	26 - Genomics of Adaptations to Extreme Environments	EC_25	660	1351	How sugar helps you to cope with stress
Maitida Scott	26 - Genomics of Adaptations to Extreme Environments	EC_25	661	387	The role of transposable elements in the evolution of deep-sea amphipods
Genlou Sun	26 - Genomics of Adaptations to Extreme Environments	EC_25	662	11	Molecular mechanisms governing autophagy-mediated <i>Heliconia</i> tuberosum adaptation
Bastiaan Tieng	26 - Genomics of Adaptations to Extreme Environments	EC_25	663	856	Genomics of flowering behavior provides evidence for adaptation to drought in Spanish <i>Arabidopsis thaliana</i>
Nhu Tran	26 - Genomics of Adaptations to Extreme Environments	EC_25	664	20	Unlocking the Secrets of Secondary Dormancy in <i>Anabasis</i> <i>italiana</i> : An Insight into Adaptive Strategies to Climate Change
Aleksia Vaattovaara	26 - Genomics of Adaptations to Extreme Environments	EC_25	665	1097	Allele-specific expression in Woodland Strawberry (<i>Fragaria vesca</i>)
Maya Weissman	26 - Genomics of Adaptations to Extreme Environments	EC_25	666	669	Look of the draw: how environmental variability shapes the evolution of conservative vs. diversified bet-hedging strategies
Xuhua Xia	26 - Genomics of Adaptations to Extreme Environments	EC_25	667	834	Roosting and Dating Large SARS-CoV-2 Trees
Takumi Yokoyama	26 - Genomics of Adaptations to Extreme Environments	EC_25	668	690	Environment-dependent endogenous <i>BtRNA</i> and transcriptomic differentiation in a freshwater fish
Alessia Cariani	05 - New frontiers in conservation genomics	EC_25	669	990	A multidisciplinary approach to describe population structure of <i>Sonchus oleraceus</i> in the Mediterranean Sea
Kunjulakshmi K	05 - New frontiers in conservation genomics	EC_25	670R	274	Assessing the conservation priority of freshwater shrimps (Family: <i>Atyidae</i> and <i>Palaeomonidae</i>) from the Central/Western Ghats, India
Luciana Moreira	05 - New frontiers in conservation genomics	EC_25	671R	1597	Diversification of <i>Bulbophyllum</i> <i>Microbatris</i> in campo rupestres: lineage delimitation and conservation implications
Surbhi Ranavat	05 - New frontiers in conservation genomics	EC_25	672R	732	Genomic signatures of inbreeding depression and mutation load in a threatened African timber tree, <i>Persea indica</i> (<i>Fabaceae</i>)
Yury Gusarov	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	673R	1287	Mitochondrial mutational signature of the increased base metabolic rate of birds: An -> Gb and -> Tg mutations
Ivan Kravchenko	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	674R	1631	Deep mitochondrial mutational spectrum of a thousand vertebrates: the rocky road to imaging threads of ecological divergence
Konstantin Popadin	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	675R	1541	Lineage-specific variation of oxidative damage in marine tissues: an excess of ATC-G on a heavy chain of mitochondrial genome in nematode tissues
Natalia Ree	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	676R	920	Analysis of 11,610 human embryonic WGS revealed maternal age-independent association between mitochondrial dysfunction and aneuploidy
Victor Shamansky	08 - Mitochondria across biodiversity, comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	677R	1376	Towards quantification of the mitochondrial component of aging: fragility score as a risk of mtDNA deletion formation
Andres Cortes	26 - Genomics of Adaptations to Extreme Environments	EC_25	678R	1550	Plant eco-evolutionary modeling for adaptation to extreme environments
Petr Dvorak	26 - Genomics of Adaptations to Extreme Environments	EC_25	679R	1096	The speciation continuum in cosmopolitan dryland quadrannual <i>Monolopia</i>
Joanna Mikulakiewicz	26 - Genomics of Adaptations to Extreme Environments	EC_25	680R	570	Surviving in Brazil's Extreme Semi-Arid Regions: Comparative and Population Genomics Reveal Adaptations in Fat and Glucose Metabolism with a Tradeoff for Small Size in the Black-Tufted Marmoset (<i>Callithrix jacchus</i>)
Cinta Pogue-Coles	26 - Genomics of Adaptations to Extreme Environments	EC_25	681R	365	Genetic diversity and adaptive evolution of the <i>Arabidopsis thaliana</i> (<i>Brassicaceae</i>) <i>Arabidopsis thaliana</i> (<i>Brassicaceae</i>) <i>Arabidopsis thaliana</i> (<i>Brassicaceae</i>)
Simone Andrea Biagini	01 - Open Symposium	SP_25	357	1221	Unlocking the Potential of NPT Data: Generating a Reference Resource With More Than 30,000 Individuals From The Farmland Region via SNP High-Throughput Sequencing for Population Genetics
Madison Altieri	01 - Open Symposium	SP_25	682	409	L1 mediated Retrotransposition of naturally occurring RNA-derived SINE Variants
Nefize Ezgi Altinisik	01 - Open Symposium	SP_25	683	1544	New Insights into the Population Structure of Pre-Pottery Neolithic Upper Mesopotamia
Isin Altinkaya	01 - Open Symposium	SP_25	684	1079	INGAMOVA: A Novel Probabilistic Framework for Analysis of Molecular Variance with Low-Depth Sequencing Data
Sônia Andrade	01 - Open Symposium	SP_25	685	802	Population connectivity in the intertidal environment: <i>Baccharis patula</i> (Proteaceae) in the Brazilian coastline with remarks on the phylogeny of the genus
Alcides de Brito	01 - Open Symposium	SP_25	686	45	The genetic history of non-melanistic <i>Ardea herodias</i> (<i>Ardeidae</i>) in the Amazon basin
Leonardo Arias Alvis	01 - Open Symposium	SP_25	687	1518	Genomic perspectives on the human population history of Northwestern Australia

Ayca	Aydogan	01 - Open Symposium	SP_25	688	811	Phylogenetic analysis of Neolithic populations in West Anatolia: preliminary observations
Emilyclare	Baker	01 - Open Symposium	SP_25	689	854	Rapid evolution of functional surfaces in response to microbial antagonism
Chiara	Barbereri	01 - Open Symposium	SP_25	690	808	A global analysis of matches and mismatches between human genetic and linguistic histories
Cökül	Bhaskaran	01 - Open Symposium	SP_25	691	845	The evolution of hunting behavior and its relation to cordoned cereals
Davide	Buzzi	01 - Open Symposium	SP_25	692	1120	Trends linking the geographical origin of ancient samples with mtDNA data
Seralina	Bracamonte	01 - Open Symposium	SP_25	693	855	Expression diversity of the Major Histocompatibility Complex in Neolithic salmon
Jaelle	Brealey	01 - Open Symposium	SP_25	694	625	Interplay between host genome and microbiota during parasite infection in farmed Atlantic salmon
Matteo	Brilli	01 - Open Symposium	SP_25	695	265	The selective force driving metabolic operon assembly
Jaclyn	Bubnoff	01 - Open Symposium	SP_25	696	1489	Testing the role of positive selection in shaping the function of a germline stem cell gene in <i>Drosophila</i>
Deathhalla	Casary	01 - Open Symposium	SP_25	697	525	Unraveling the mechanisms of neoplasia in the Paddleshell and Sturgeon by characterization of syntenic breakpoints in their genomes
Michele	Castelli	01 - Open Symposium	SP_25	698	1217	Comparative genomics indicates multiple independent evolutionary origins of host association and intracellularity within the <i>Rickettsia</i>
Luiz	Cauz Dos Santos	01 - Open Symposium	SP_25	699	1568	Phylogenomics and biogeography history of wild alkylglycerol tobacco (<i>Notolana section Sauerweites</i>)
Théo	Cavinato	01 - Open Symposium	SP_25	700	1121	A resampling-based approach to share reference panels
Jing-Lian	Chen	01 - Open Symposium	SP_25	701	472	Detecting late-onset disease causing variants in the genomes of Han Taiwanese people
Sophie-Carole	Chobert	01 - Open Symposium	SP_25	702	988	Unraveling the relative emergence of galactose biosynthetic pathways
Sehee	Choe	01 - Open Symposium	SP_25	703	306	Identification of key genes and pathways by co-expression analysis with blood transcriptome in NHP addition model
Rodrigo	Cojari	01 - Open Symposium	SP_25	704	277	Insulin-like growth factor 1 in a natural population of <i>Drosophila</i>
Omar	Cornejo	01 - Open Symposium	SP_25	705	1418	Distribution of diverse endophyte leaf communities across <i>Theobroma cacao</i> genetic groups
Claudio	Cucini	01 - Open Symposium	SP_25	706	318	raft de novo assembly and annotation of the nuclear genome of <i>Papilio japonica</i> from the invasive Italian population
Alice	De Sampaio Kalkuhl	01 - Open Symposium	SP_25	707	1192	Gene duplication in the coral genus <i>Acropora</i> : Was there a whole genome duplication?
Athena	di Proserpio	01 - Open Symposium	SP_25	708	273	The effect of methyl farnesolate on sex-determining genes in obligate parthenogenetic <i>Daphnia pulex</i>
Yoan	Diekmann	01 - Open Symposium	SP_25	709	213	hapBtoxic: efficient detection of positive selection in large population genomic datasets
Louise	Dupont	01 - Open Symposium	SP_25	710	769	Phylogenetic evidence of inter-platey introgression in the alder tree, <i>Alnus glutinosa</i>
Jacintha	Eilers	01 - Open Symposium	SP_25	711	1528	Neofungal functions promote preservation of the gene network when a phylogenetic trait is lost
Adam	Eyre-Walker	01 - Open Symposium	SP_25	712	1415	Mutation rate variation and genetic diversity across the human genome
Nicoletta	Favale	01 - Open Symposium	SP_25	713	1394	Dynamics of microbiome composition during anaerobic digestion of different renewable resources
Alice	Feurtey	01 - Open Symposium	SP_25	714	1143	A thousand-genes panel traces the global spread and adaptation of a major fungal crop pathogen
Simon	Fishilevich	01 - Open Symposium	SP_25	715	219	Compensatory mechanisms of human-specific disease mutations
Evan	Forythe	01 - Open Symposium	SP_25	716	406	Genome-wide co-occurrence networks point to conserved perturbations of plastid protein/taqI system
Silvia	Fustoli	01 - Open Symposium	SP_25	717	1303	Reanalysis of natural selection in the evolution of the past large fish genomes
Arya	Gautam	01 - Open Symposium	SP_25	718	928	Characterization of the bacterial and fungal communities found in traditional Nepali fermented foods
Jörn Frederik	Gerchen	01 - Open Symposium	SP_25	719	1137	Population genomic evidence of inter-platey introgression in the alder tree, <i>Alnus glutinosa</i>
Francesco	Giannelli	01 - Open Symposium	SP_25	720	1077	Investigating the relationship between sex-biased dispersal and mito-nuclear discordance, using a forward simulation method (SLIM)
Léa	Guyon	01 - Open Symposium	SP_25	721	112	Is evidence necessary to explain the post-Neolithic Y-chromosome bottleneck?
Yoonsoo	Hahn	01 - Open Symposium	SP_25	722	365	Quantifying the Efficiency of RNA Polymerase Slippage Leading to P2n-P1P0 Trans-Fusion Proteins in Polyvids
Yuchiro	Hara	01 - Open Symposium	SP_25	723	240	Gene loss spectrum as a reflection of local genomic properties
Tia	Harrison	01 - Open Symposium	SP_25	724	1507	Mutation with rhabdia accelerates rates of molecular evolution in legumes
Katie	Herron	01 - Open Symposium	SP_25	725	1008	Exploring the Evolutionary History of Heat Shock Proteins in the genus <i>Trifolium</i> using Comparative Genomics
Wei-Chin	Ho	01 - Open Symposium	SP_25	726	1604	Non-adaptive mechanisms of metabolic evolution in complex environments
Gavin	Huttley	01 - Open Symposium	SP_25	727	946	Mutation disequilibrium at prevalence, magnitude and implications
Risa	Inasaki	01 - Open Symposium	SP_25	728	483	Investigation of loci under positive selection in which <i>Mcaadivv3M</i> haplotype can differ spatially and temporally like PISCA in human populations
Hen-Ya	Ko	01 - Open Symposium	SP_25	729	469	Phylogenetic reconstruction of mitochondrial genomes of wild boar (<i>Sus scrofa</i>) in the Han Taiwanese archipelago
Anne	Kupczok	01 - Open Symposium	SP_25	730	405	Co-transfer of functionally interdependent genes contributes to genome mosaicism in lambdoid phages
Alessandra	Lamarca	01 - Open Symposium	SP_25	731	269	Why is it hard to root evolutionary radiations? Testing outgroup-free methods and how we can predict their accuracy
Cheng-Ruei	Lee	01 - Open Symposium	SP_25	732	275	Environment as a limiting factor of the historical global spread of mungbean
Weiyi	Li	01 - Open Symposium	SP_25	733	155	A Narrow Range of Transcript-error Rates Across the Tree of Life
Ke	Li	01 - Open Symposium	SP_25	734	995	Selectional Fibrosis: Scanning Constraints the Evolution of Protein-Coding Genes
Lading	Lorenzgan	01 - Open Symposium	SP_25	735	1046	Sex-related genomic dynamics in wheat, in a hybrid form
Halwei	Luo	01 - Open Symposium	SP_25	736	237	Genetic drift has an important role in Prochlorococcus genome reduction
Milan	Malinsky	01 - Open Symposium	SP_25	737	773	Disentangling the genomic interplay of selection and recombination
Galen	Martin	01 - Open Symposium	SP_25	738	1324	Diverse patterns of secondary structure across genes and transposable elements are associated with siRNA production and epigenetic fate
Hanon	McShea	01 - Open Symposium	SP_25	739	1630	The effectiveness of selection in a species affects the direction of amino acid frequency evolution
Molly	Miraglia	01 - Open Symposium	SP_25	740	NA	Relative model selection of evolutionary substitution models can be sensitive to multiple sequence alignment uncertainty
Ludovica	Molinaro	01 - Open Symposium	SP_25	741	1316	Genetic characterization of individuals with non-European ancestry in Flanders, Belgium from HPT data of 30,000 individuals
Emiliano	Mora-Carrera	01 - Open Symposium	SP_25	742	607	Linking the genome-wide consequences of a recent range expansion and multiple mating system transitions in <i>Prunella vulgaris</i>
Adriana	Morales-Guerrero	01 - Open Symposium	SP_25	743	295	Ecological and demographic drivers of immune-related genomic signatures across human populations
João	Moreno	01 - Open Symposium	SP_25	744	686	Proteome and phosphoproteome reveal differences in phenotypic plasticity in fish under different scenarios of climate change
Alice	Mouton	01 - Open Symposium	SP_25	745	692	The European Reference Genome Atlas
Kasper	Munch	01 - Open Symposium	SP_25	746	1173	Recombination hotspots are not universally stable across birds
Victor	Muñoz Mora	01 - Open Symposium	SP_25	747	651	The fitness consequences of genetic load in diploid vs tetraploid populations, a simulation study
Jonathan	Naccache	01 - Open Symposium	SP_25	748	614	Lite-High Throughput Evaluation of Genes Cloning Populations for Improved Enzyme Activity in Diagnostic Tests
Yannis	Nevers	01 - Open Symposium	SP_25	749	1326	Multifactorial quality assessment of gene repertoire annotation with OMAK
Lukasz	Niezablowski	01 - Open Symposium	SP_25	750	1274	Building a high-confidence ortholog dataset
Robert	Noble	01 - Open Symposium	SP_25	751	616	A new system of root-tree indices
Riccardo	Nodari	01 - Open Symposium	SP_25	752	641	SR modeling suggests an evolutionary trade-off in the transatlantic spread of human-to-human transmitted pathogens in the centuries following the Americas discovery
Masafumi	Nozawa	01 - Open Symposium	SP_25	753	357	Mimicking sex-chromosome turnover using hybrids reveals flexibility of dosage compensation on neo-sex chromosomes in <i>Drosophila miranda</i>
Wei-Chen	Pan	01 - Open Symposium	SP_25	754	657	Studying genetic adaptation and admixed ancestry of the Simpa people in Taiwan
Tin Yau	Pang	01 - Open Symposium	SP_25	755	822	Natural selection for the optimal cytosolic density of a bacterial cell
Tom	Parée	01 - Open Symposium	SP_25	756	571	Reduced selective interference increases experimental adaptive rates in <i>C. elegans</i>
Anieli	Pereira	01 - Open Symposium	SP_25	757	1106	Relationships between fossilability, liveness and selective pressures acting on mitochondrial genes in <i>Squamata</i>
Cassius Manuel	Pérez	01 - Open Symposium	SP_25	758	1191	How much phylogenetic information is in a branch? Subtle gives an answer
Aaron	Pfennig	01 - Open Symposium	SP_25	759	91	Challenges of accurately estimating sex-biased admixture from X-chromosomal and autosomal ancestry proportions
Sujal	Phadke	01 - Open Symposium	SP_25	760	922	Evolution of survival response in diabetes
Mac	Pierce	01 - Open Symposium	SP_25	761	1075	Phylogenomic insights into the evolutionary history of mesquite
Estella	Poloni	01 - Open Symposium	SP_25	762	1003	Joint analysis of phenotypic and genomic diversity sheds light on the evolution of aerobic metabolism in humans
Kay	Prüfer	01 - Open Symposium	SP_25	763	683	Down syndrome in ancient societies
Anthony	Redmond	01 - Open Symposium	SP_25	764	708	Independent reduplication masks shared whole genome duplication in the sturgeon-paddlefish ancestor
Simon	Reila	01 - Open Symposium	SP_25	765	465	Cloning Pathogen Evolution with a Mosaic of Vaccines
Alan	Ribe	01 - Open Symposium	SP_25	766	1226	Characterizing <i>Pseudomonas</i> TPA-dependent virulence-binding proteins
Marie	Riffes	01 - Open Symposium	SP_25	767	554	Analysis of comparative evolution following gBCD events using whole-exome phylogenetic analysis in <i>Mutinus</i>
Niccolò	Righetti	01 - Open Symposium	SP_25	768	338	A fossil-evidence, dated phylogenetic analysis of taraxacoid crustaceans
Emma	Rowley	01 - Open Symposium	SP_25	769	1608	Genome-wide signatures of host adaptation in <i>Theileria parva</i> , an apicomplexan parasite of bovine
Jan-Niklas	Runge	01 - Open Symposium	SP_25	770	532	A species-wide map of transmission distortion in yeast
Lehti	Saag	01 - Open Symposium	SP_25	771	135	Population history of Ukraine
Mvudula	Sane	01 - Open Symposium	SP_25	772	977	Mutation bias shifts alter the distribution of fitness effects of new mutations
Cecilia	Sensaları	01 - Open Symposium	SP_25	773	725	Using divergent balance-aneuploidy gene families as markers for plant whole-genome duplications
Ahmed	Shihl	01 - Open Symposium	SP_25	774	696	Metagenomically assembled genomes from the oral microbiome reveal distinct functional capacities in obesity in the Emirati population
Andrea	Silverj	01 - Open Symposium	SP_25	775	1449	Evolutionary analysis of viral metagenome-assembled genomes from Italian fish populations sampled on a latitudinal gradient
Elpidia	Skarlou	01 - Open Symposium	SP_25	776	NA	tBA
Thomas	Staedler	01 - Open Symposium	SP_25	777	656	Differences in effective ploidy drive parental expression proportions in wild tomato hybrid endemics
Jan	Stefka	01 - Open Symposium	SP_25	778	1524	Genomic differentiation in populations of a tapeworm parasite associated with specificity to different sympatric hosts, a case of ecological speciation?
Sfarc	Stift	01 - Open Symposium	SP_25	779	495	Evolution of host-competitiveness and genetic interaction between a specific <i>Salvella</i> and an unrelated modifier
Stefan	Strütt	01 - Open Symposium	SP_25	780	1270	Weak purifying selection in human mitochondrial DNA and Y-chromosomes
Aram	Stump	01 - Open Symposium	SP_25	781	900	Evolution of human menopause-associated genes
Peter	Szovenyi	01 - Open Symposium	SP_25	782	493	The masking hypothesis in complex multicellular organisms with biphasic life cycles
Aglaia	Szukala	01 - Open Symposium	SP_25	783	1208	Ash in Distress - results from a large experimental field trial on ash dieback in Austria
Nacko	Takezaki	01 - Open Symposium	SP_25	784	235	The effect of different types of sequence data on phylogenetic phylogeny
Alessia	Tal	01 - Open Symposium	SP_25	785	1527	Evolutionary background of a comprehensive <i>Perla</i> package for admixture barcode analysis
Eliasa	Toini	01 - Open Symposium	SP_25	786	1309	Exploring the genetic variability and evolution of <i>Bromelia</i> fish inhibitors in <i>Yorgia unguiculata</i> (L.) Web.

Marcy	Uyenoyama	01 - Open Symposium	SP_25	787	183	The Role of Mutation in Fix and LD
Gustavo	Valadares Barroso	01 - Open Symposium	SP_25	788	1222	Investigating the transferability of polygenic scores between populations using two-locus models
Hannah	Verdonk	01 - Open Symposium	SP_25	789	270	Redefining the neutral set in codon evolutionary models
Gwenaelle	Vigo	01 - Open Symposium	SP_25	790	507	Detecting orthologous genomic markers for evolutionary outcomes (Phylogenetic)
Viridiana	Villalobos	01 - Open Symposium	SP_25	791	924	Genetic diversity at Toba: A Neogene human genetic site (1300-1521 CE)
Shamam	Waldman	01 - Open Symposium	SP_25	792	1491	Genome-wide data from medieval German Jews show that the Ashkenazid event pre-dated the 14th century
Yusuke	Watanabe	01 - Open Symposium	SP_25	793	497	Detecting signals of positive natural selection in the Japonic people, prehistoric hunter-gatherers in the Japanese archipelago
Senja	Wulsch	01 - Open Symposium	SP_25	794	542	A ZW sex determination system in the coralbird mite <i>Hemertania gibba</i>
Hartuka	Yamashita	01 - Open Symposium	SP_25	795	934	Distinguishing among forces underlying fixation biases: Population genetic tests of selection on synonymous mutations in <i>Drosophila</i>
Shu-Ting	Yao	01 - Open Symposium	SP_25	796	285	Ongoing genotypes of microbial cooperation
Rafael	Zardoya	01 - Open Symposium	SP_25	797	1320	Comparative genomics of cone snails
Tianqi	Zhu	01 - Open Symposium	SP_25	798	118	Complexity of the simplest species tree problem
Lison	Zunino	01 - Open Symposium	SP_25	799	1209	Genetic structure and admixture of wild olive tree populations in western Mediterranean basin: a conservation issue?
Niloofar	Alaei Kakhki	03 - The dark side of introgression	SP_25	800	291	A bunting hybrid zone: natural laboratory to understand how color pattern maintains species boundaries in birds
Hisham	Ali	03 - The dark side of introgression	SP_25	801	447	The effect of Dobzhansky-Muller incompatibilities on the genetic landscape under parallel and divergent selection
Margot	Besseiche	03 - The dark side of introgression	SP_25	802	1145	Diversification of the date palm (<i>Phoenix dactylifera</i> L.) and introgression from a wild relative
Valentina	Burksta	03 - The dark side of introgression	SP_25	803	1195	Does hybridization facilitate adaptive speciation of <i>Lasius aphidivorus</i> ?
Elizabeth	Chevy	03 - The dark side of introgression	SP_25	804	560	Consequences of sex-bias and background selection for introgression on chromosome X
Adam	Ciezarok	03 - The dark side of introgression	SP_25	805	260	Ongoing and ancient genomic introgression in <i>Drosophila</i> flies
Russ	Corbett-Delig	03 - The dark side of introgression	SP_25	806	1482	Estimating the effect of interference among selected sites in admixed populations
Elli	Cryan	03 - The dark side of introgression	SP_25	807	442	Molecular evolution of a reproductive barrier across twelve million years
Tomás	Flouri	03 - The dark side of introgression	SP_25	808	1369	Efficient Bayesian inference under the Multispecies Coalescent with Migration
Niccolò	Foley	03 - The dark side of introgression	SP_25	809	1843	Phylogenetic basis and patterns influenced the evolution of viral tolerance in a species-rich bat radiation
Jorge	García	03 - The dark side of introgression	SP_25	810	126	Adaptive archaic introgression related to cellular zinc homeostasis in humans
Diego	Hartasánchez	03 - The dark side of introgression	SP_25	811	1269	Cisgenic adaptive radiation shaped by large-scale structural variation
Tania	Holtzern	03 - The dark side of introgression	SP_25	812	1476	Shielding light on mechanisms maintaining species boundaries despite extensive hybridization in cyclical pathogens
Axel	Jensen	03 - The dark side of introgression	SP_25	813	1271	Large-scale phylogenomics uncover complex evolutionary history with extensive ancestral gene flow in an African primate radiation
Teerama Saugata	Khasitjir	03 - The dark side of introgression	SP_25	814	1278	The drivers of the adaptive radiation of passeriforms on New Caledonia: a biodiversity hotspot
Matiasz	Konczal	03 - The dark side of introgression	SP_25	815	803	Genomic consequences of artificial translocation, admixture and population replacement in the Trinidad guppies
Martin	Kühwilm	03 - The dark side of introgression	SP_25	816	243	Introgression drives <i>BE-1</i> primate speciation
Guillaume	Lavanchy	03 - The dark side of introgression	SP_25	817	975	Large-scale genotyping reveals widespread hybridization among central European ants
Tomasz	Mamos	03 - The dark side of introgression	SP_25	818	749	Is isolation of <i>Gammarus</i> species flock in ancient Lake Ohrid an effect of hybridization?
Alice	Manuzzi	03 - The dark side of introgression	SP_25	819	1213	Genomic Signatures Of Hybridization For Two Anglerfish Species In The North-East Atlantic
Valentina	Mastrantonio	03 - The dark side of introgression	SP_25	820	385	A hidden road to diversity: mtDNA introgression promotes intra-specific paternal leakage and heteroplasmy in hybridized beetles
Sofia	Mendes	03 - The dark side of introgression	SP_25	821	758	Multiple outcomes of hybridization in Iberian chub inferred from whole genome data
Lukas	Metzger	03 - The dark side of introgression	SP_25	822	1331	Inference of demography and introgression in multiple populations using Approximate Bayesian Computation (ABC)
Amanda	Meuser	03 - The dark side of introgression	SP_25	823	757	Hybridization among <i>Leucisidaceae</i> minor species in anthropogenically disturbed environments
Leonie	Moyle	03 - The dark side of introgression	SP_25	824	440	Change in the new red: hybridization, introgression, and trait convergence among wild invasive and endemic tomatoes on the Galapagos
Sandra	Oliveira	03 - The dark side of introgression	SP_25	825	515	Assessing the limits of local ancestry inference through simulations
Jill	Olfesson	03 - The dark side of introgression	SP_25	826	489	Ecological sorting maintains species identity despite frequent gene exchange
Daniel	Powell	03 - The dark side of introgression	SP_25	827	227	Complex hybridization between deeply diverged fish species in a disturbed ecosystem
Neda	Rahmamae	03 - The dark side of introgression	SP_25	828	65	The genetic architecture of phenotypic differences between admixed <i>Escherichia coli</i> species
Fabrizia	Ronco	03 - The dark side of introgression	SP_25	829	723	Shielding light on a species-tree obscured by introgression: A case from sixed fishes of the Lake Tanganyika drainage
Erik Fogh	Sørensen	03 - The dark side of introgression	SP_25	830	807	Admixture, reproductive barriers and adaptive introgressions in baboons using 225 genomes from six species
Markus	Stetter	03 - The dark side of introgression	SP_25	831	1447	Evolutionary rescue through gene flow despite genetic incompatibilities shaped diversity of the pseudo-cereal grain amaranth
Jesper	Svedberg	03 - The dark side of introgression	SP_25	832	1443	Signals of Adaptive Introgression Across Diverse Species
João	Teixeira	03 - The dark side of introgression	SP_25	833	1048	Long-term balancing selection has maintained shared genetic variation across great ape species for millions of years
Tram	Vi	03 - The dark side of introgression	SP_25	834	473	Genome-wide admixture mapping using admixed human populations identifies auto-ancestry-of-origin segments in Vietnamese cultivated <i>Rubus</i> coffee
Lin	Yu-En	03 - The dark side of introgression	SP_25	835	921	The Triplet Mystery: How Come a Triplet Codon Encodes Proteins in <i>Caenorhabditis</i> ?
Xinjun	Zhang	03 - The dark side of introgression	SP_25	836	818	Decoding archaic introgressed ancestry identifies recessive deleterious mutations in the human genome
Carolina	Barata	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	837	569	Single-cell resolution of sex differences in <i>Drosophila</i> melanogaster
Debra	Brandt	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	838	1535	Genome-wide signatures of balancing selection in <i>Drosophila</i> melanogaster
Leo Tomás	Camino Cedeño	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	839	1426	Gene expression of <i>Hsp70</i> genes as a response of the thermal stress in the tropical butterfly <i>Heliconius erato</i>
Ching-Ho	Chang	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	840	391	Stochastic drive shapes rapid evolution of <i>Drosophila</i> antennae
Alberto	Civetta	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	841	1127	Evolution of female-limited colour polymorphism through sex-specific genetic architecture in <i>Lycaon</i>
Zachary	Dietz	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	842	851	Evolution of mitochondrial mismatched C. elegans: Effects of adaptation, mating system and mitochondrial mutations
Ewan	Flintham	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	843	1004	The scope for genetic polymorphism in sexually antagonistic traits
Simon	Jacobsen Ellerstrand	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	844	1171	PhageWY: A bioinformatic pipeline for phasing and retrieving Y and W sequences from population genomic data
Jihwon	Kim	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	845	499	Unexpected conservation of ZFP91 binding sequence, a marker of genomic imprinting, in gibbons
Li	Cheng	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	846	456	The genetic mechanism of sexual dimorphism in snail species of phlebotomus
Cristiana	Marques	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	847	1072	Evolution of female-limited colour polymorphism through sex-specific genetic architecture in <i>Lycaon</i>
Miriam	Merenciano	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	848	673	Contribution of transposable elements in the sex gap longevity of different <i>Drosophila</i> species
Marlo	Moller	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	849	355	Slave Trade and Colonial Expansion Resulted in Strong Sex-Biased Admixture in South Africa
Filippo	Nicolini	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	850	1147	Comparative genomics reveals that sex-determination related genes in bivalves are novel acquisitions of molluscs and have a high rate of amino acid evolution
Naoki	Osada	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	851	914	Genomic insights into the hybridization of house Mouse Subspecies in East Asia
John	Parsch	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	852	350	A regulatory polymorphism subject to sexually antagonistic and temporally fluctuating selection in <i>Drosophila</i> melanogaster
Bahar	Prica	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	853	1660	Integrating molecular signatures of adaptation in different tissues in several <i>Drosophila</i> melanogaster
Peter	Pruca	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	854	596	The genomic basis of <i>de-gust</i> gene TM in stalk-eyed flies
David	Rand	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	855	1618	Pervasive absence of Mother's Curse among divergent mtDNAs in heterozygous nuclear backgrounds of <i>Drosophila</i>
Leticia	Rodriguez-Montes	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	856	759	Sex-biased gene expression across mammalian organ development and evolution
Christian	Schloetterer	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	857	284	Mutation-order speciation is driven by the combined effects of sexual conflict and adaptation
Tatiana	Teixeira Torres	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	858	1477	Molecular Basis of Genital Plasticity in Males of a Neotropical Bug in Response to Intrasexual Competition
Camille	Thomas-Bulle	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	859	865	Uncovering the genetic basis of horn size reduction in island populations of <i>Phacusa</i> beetles
Monica	Vallender	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	860	877	Genotyping-by-Sequencing Reveals Male-Female Bateson's Influence on Cryptic Female Choice in <i>Chironomus</i> (Drosophilinae)
Tamsin	Woodman	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	861	1244	The role of DNA methylation in sex-biased gene expression in the chiral methylating <i>Phacusa</i> cili
Prem	Aguilar	09 - Evolution on repeat in the genomics era	SP_25	862	704	The evolution of centromere colouration through cis-regulatory variation at <i>BCO2</i> in a colour polymorphic bird
Luz Angela	Alonso-Morales	09 - Evolution on repeat in the genomics era	SP_25	863	1125	Synonymous mutations under selection on a Pseudomonas Phylogeny
Stephan	Baehr	09 - Evolution on repeat in the genomics era	SP_25	864	435	Liquid mutation accumulation in E coli MMR- compared with plate mutation accumulation
Denis	Baurain	09 - Evolution on repeat in the genomics era	SP_25	865	1102	High and Evolution of Pseudomonas Biocytogenic Gene Clusters
Viktoria	Bednarski	09 - Evolution on repeat in the genomics era	SP_25	866	1084	Consequences of reproductive trade-off on repeat dynamics in orchard mice
Romain	Boisseau	09 - Evolution on repeat in the genomics era	SP_25	867	970	On the importance of phenotypic evolutionary trajectories in predicting genetic parallelism
Bastien	Boussau	09 - Evolution on repeat in the genomics era	SP_25	868	1536	Genome scale genotype-phenotype associations using phylogenetics to understand the genetic basis of convergent evolution
Nathalie	Brenner	09 - Evolution on repeat in the genomics era	SP_25	869	1170	Evolutionary genetics of convergent mimicry color patterns in tumbweed
Alaksh	Choudhury	09 - Evolution on repeat in the genomics era	SP_25	870	1552	Staying change in the evolutionary dynamics during the Escherichia coli long term evolution experiment (LTEE) using molecular barcodes
Elvira	Cioni	09 - Evolution on repeat in the genomics era	SP_25	871	182	Convergence or deep homology? Comparative genomics elucidates the origins of the heterotely supagene
Carolin	Dahms	09 - Evolution on repeat in the genomics era	SP_25	872	586	Protein Evolution Despite Low Genetic Diversity in <i>Escherichia</i> and Ancient <i>Staphylococcus</i>
Giulia	Fabrizi	09 - Evolution on repeat in the genomics era	SP_25	873	760	On the repeatability of nuclear deaflum: comparing Corsican and Sardinian wild boar
Jeffrey	Fawcett	09 - Evolution on repeat in the genomics era	SP_25	874	1138	Genome sequencing reveals the genetic architecture of heterotely in common buckwheat
Rosa Maria	Fernández Garcia	09 - Evolution on repeat in the genomics era	SP_25	875	816	Exploiting the genetic basis of repeated evolution in sea-to-land transitions across animal lineages
Giobbe	Forni	09 - Evolution on repeat in the genomics era	SP_25	876	402	Shared signatures of the shifts to endosymbiosis across <i>Enterobacteriales</i> evolutionary history
Andrea	Guarracino	09 - Evolution on repeat in the genomics era	SP_25	878	1490	Recombination between heterologous human acrocentric chromosomes
Mariangela	Iannello	09 - Evolution on repeat in the genomics era	SP_25	879	535	Signatures of extreme longevity, a perspective from brain molecular evolution
Maddie	James	09 - Evolution on repeat in the genomics era	SP_25	880	890	Uncovering the genetic architecture of parallel evolution in <i>Sarcodes</i>
Min-Gyeong	Ko	09 - Evolution on repeat in the genomics era	SP_25	881	322	A whole <i>Thrips</i> cytomorphome resequence transcriptome reveals age-related immune patterns
Uliana	Kolesnikova	09 - Evolution on repeat in the genomics era	SP_25	882	1344	Strain selfing/autogamy lysate and its role in formation of <i>Arabidopsis hirsuta</i> : an example of repeated allopatric evolution in Brassicaceae
Emily	Kopania	09 - Evolution on repeat in the genomics era	SP_25	883	872	Recurrent shifts in sperm competition intensity shape the phenotypic and molecular evolution of male reproduction across diverse marine rodents
Adria	Labouff	09 - Evolution on repeat in the genomics era	SP_25	884	697	The evolution of anti-crop milk proteins over independent gains of a social transfer behavior
Junjung	Lee	09 - Evolution on repeat in the genomics era	SP_25	885	324	Fast and slow specific tandem of <i>ParM</i> domain in <i>EM17</i> gene during genome evolution
Cardi	Lee	09 - Evolution on repeat in the genomics era	SP_25	886	1464	Positive Epistasis and Selection from Standing Variation could Drive Parallel Polygenic Adaptation

Emmanuelle	Lerat	09 - Evolution on repeat in the genomics era	SP_25	887	1272	Function and conservation of <i>Drosophila</i> paralogs in the light of their redstone neighborhood
Veronika	Lipánová	09 - Evolution on repeat in the genomics era	SP_25	888	1271	Repeated adaptation in wild Arabidopsis and carnation: genomic convergence and the phenotypic manifestation of adaptation to challenging soils
Irma	Lozada Chavez	09 - Evolution on repeat in the genomics era	SP_25	889	1564	The genome intricateness of Complex Multicellular Organisms has been repeatedly decoupled from genome size evolution in Eukarya
Sarah	Lucas	09 - Evolution on repeat in the genomics era	SP_25	890	845	The Mammals Lose Their Vision: According to Genetics
Jilong	Ma	09 - Evolution on repeat in the genomics era	SP_25	891	1203	Three independent social transitions reveal the locality evolved after the speciation in spider genus <i>Stegodyphus</i>
Gemma	Martinez Redondo	09 - Evolution on repeat in the genomics era	SP_25	892	587	The march to land: unearthing how gene repertoire evolution triggered animal terrestrialization
Axel	Meyer	09 - Evolution on repeat in the genomics era	SP_25	893	1050	Genomes of adaptation and speciation in sympatry with a dose of nonreciprocal hybrid speciation
Anamaria	Neculescu	09 - Evolution on repeat in the genomics era	SP_25	894	1174	Why did the chicken lose its genes? Evolutionary processes and molecular mechanisms associated with the repeated losses of the intronless phallos in avian lineages
Hye-Ri	Park	09 - Evolution on repeat in the genomics era	SP_25	895	323	Three distinct integration and deletion events of SVA, D, Alu and AluY elements generate diverse NKX structures during primate evolution
Ohad	Pisnik	09 - Evolution on repeat in the genomics era	SP_25	896	273	The complex evolution of social complexity in bees
Giovanni	Piccinini	09 - Evolution on repeat in the genomics era	SP_25	897	717	Evolutionary consequences of the Yule birth appear associated to convergent genomic and phenotypic evolutions in <i>Melanota</i>
Ana	Pontes	09 - Evolution on repeat in the genomics era	SP_25	898	740	The molecular underpinnings of convergent evolution in bee-associated facultative bacteria
Anggun	Sausan Firdaus	09 - Evolution on repeat in the genomics era	SP_25	899	1227	Convergent changes on ebony gene regulation associated to the evolution of melanin body color in <i>Drosophila</i> <i>elegans</i>
Joshua	Schraiber	09 - Evolution on repeat in the genomics era	SP_25	900	424	A unified approach to trait mapping within and between species
Alison	Scott	09 - Evolution on repeat in the genomics era	SP_25	901	1166	Recurrent adaptation to whole genome duplication in wild Arabidopsis
Avery	Selberg	09 - Evolution on repeat in the genomics era	SP_25	902	847	BESTED-PM: A likelihood framework for detecting positive selection associated with convergent phenotypes
Rossini	Simson	09 - Evolution on repeat in the genomics era	SP_25	903	259	Genomic signatures of parallel evolution of predator <i>Blattella</i> in four miles
Kaston	Sinclair	09 - Evolution on repeat in the genomics era	SP_25	904	665	Parallel Evolution in Diverse Strains of <i>Pseudomonas aeruginosa</i>
Tanja	Slotte	09 - Evolution on repeat in the genomics era	SP_25	905	252	Genomic analyses of the <i>Linum</i> distally supergene reveal convergent evolution at the molecular level
Dylan	Sosa	09 - Evolution on repeat in the genomics era	SP_25	906	160	Origination and evolution of lineage-specific transfer RNA genes in <i>Drosophila</i>
Irène	Tanneur	09 - Evolution on repeat in the genomics era	SP_25	907	1279	Mismatch repair in <i>Bacillus subtilis</i> compensates for the correction bias of the PfuC endonuclease
Sophie	Touillet	09 - Evolution on repeat in the genomics era	SP_25	908	202	Convergent dietary adaptation in myrmecophilous mammals: insights from the study of the chitase gene family in the host and its associated gut microbiota
Arturo	Torres Ortiz	09 - Evolution on repeat in the genomics era	SP_25	909	913	Convergent evolution and genetic markers of pre-evolution in <i>M. adenitarsis</i>
Yen-Wen	Wang	09 - Evolution on repeat in the genomics era	SP_25	910	1087	Evolution of recombination: focusing on the gene expression regulation in <i>Trichomonas axosporoides</i> and <i>Trichomonas vaginalis</i> species permutation
Shira	Zion	09 - Evolution on repeat in the genomics era	SP_25	911	553	Adaptation under Protected Resource Exhaustion Is Characterized by High Levels of Convergence and Frequent Historical Contingency
Moisés	Bernabeu	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	912	664	Relative dating of evolutionary events from gene trees
Alessio	Capobianco	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	913	1009	A new relaxed probabilistic model of morphological evolution for robust phylogenetic inference
Zehui	Chen	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	914	734	The origin and dynamic demography of ancient southern Chinese panda lineages
Sofia Amanda	De Lellis Stroustrup	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	915	94	Archaeal megalomycetes - evolutionary modeling of ancient data
Harrist	Drage	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	916	152	Neural form of <i>AF104</i> in <i>Mytilus</i> in ancient oceans
Zhen	Li	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	917	79	Revisiting ancient polyphidy in leptocephale ferns
Yichen	Liu	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	918	478	Ancient DNA reveals key fermentative microbes in Bronze Age kefir dairy
Sinbad	Lynch	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	919	170	Development and routing behaviour in estrid and ectoparasitoids
Beatriz	Mello	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	921	179	Assessing the relative performance of fast molecular dating methods for phylogenetic data
Morena	Nave	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	922	558	Integrating Molecular Data And Novel Fossil Knowledge Reminds The Tricoum D Sea Spiders Evolution
Mark	Nikolic	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	923	1571	Comparing evolutionary radiations: divergence times and rates of evolution with Bayesian phylogenetic methods in a tritrophic group
Ioannis	Patramanis	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	924	504	Using simulations to assess the power and limits of evolutionary inference based on ancient protein sequences
Davide	Pisani	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	925	1265	The Cat is out of the bag: modelling across-site compositional heterogeneity is key to improve accuracy in datasets affected by long branch attraction
Cristina	Pokorny Montero	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	926	1570	Genomic Incongruence Underlies the Evolution of Flower Symmetry in Eudicots
Marc	Robinson-Rechavi	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	927	609	Integration of genomic, developmental and palaeontological information in <i>Moultis</i> to study arthropod evolution
Romain	Sabroux	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	928	529	Integrating fossil and extant sea spiders into a total evidence phylogeny (Phylogenetics)
Shan	Shen	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	929	297	The multiple roles of the egg protein <i>ovulin</i> and its evolutionary variability in hermaphroditic insect development
Jessica	Thorpe	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	930	181	Phylogenomics of isopods supports a single early-divergent origin of terrestriality in Onychophora
Tharsika	Vimala	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	931	1002	Genome from 60,000 year old Neanderthal reveals deeply diverged and isolated late Neanderthal population in western Europe
Shihuo	Wang	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	932	41	Dating the bacterial tree of life based on ancient symbiosis
Pao	Abondio	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	933	659	Exploring apolipoprotein E (APOE) haplotypes in healthy subjects: a population genetics perspective
Simon	Aeschbacher	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	934	1392	Historical specimens shed light on the origins and fates of early European foragers
Omar	Alam	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	935	730	The post-domestication history of Asian rice: insights from haplotype genomes and ancestral recombination graphs
Sara	Armas-Quintana	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	936	1031	The forgotten cemetery of Aboon (Mauretania): paleogenomics, ethnology and the demography of the Indian Ocean slave trade
Celine	Bon	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	937	348	Genome-wide analysis of a collective grave from Metchah Tepe, one of the early Stone/Upper Paleolithic sites in South Caucasus
Katia	Bougouri	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	938	502	Imputation of ancient dog genomes informs on their breeding history since the onset of domestication
Diego	Carmagnini	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	939	720	Paleogenomic evidence for the long-term reproductive isolation between wild and domestic cats
Alberto	Coutinho Lima	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	940	1160	Disentangling the complex genomic architecture and evolutionary history of livestock guarding dogs spread across Eurasia
Olivian	Crucian	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	941	689	Uncovering the genetic diversity and structure of <i>Phaenocarpa</i> populations from the Neolithic site territory in the Eastern Italian Alps
Roslyn	Curry	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	942	1642	Reconstructing Western and Human Migration: The Past through the PIPANAMA Project
Kevin	Daly	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	943	741	Paleogenomics insights into the origin and trajectory of domestic sheep
Marco	De Martino	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	944	1502	PALEOGENOMICS OF EUROPEAN WILD AND DOMESTIC CATS
Clara Isabel	Díaz Pérez	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	945	420	Paleogenomics analysis of goats present with the indigenous people of the Canary Islands
Eran	Ehlik	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	946	14	In search of Many origins: tracking the big WHEN and WHERE questions
Erolin	Enlhi	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	947	1453	Insulation is a reliable method to infer population dynamics in prehistoric Canis
Rosa	Fregel	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	948	1030	The impact of the European colonization on the indigenous people of the Canary Islands
Muriel	Gros-Balthazard	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	949	1115	Tracing the origins of oases agroecosystems: Insights from genomic and morphometric analyses of ancient date palms
Christian	Huber	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	950	783	A novel reaction-diffusion model of the European Neolithic farming expansion
Damia	Kaptan	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	951	366	Archaeogenetic analysis of Neolithic sheep from Anatolia
Yosuke	Kawai	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	952	1043	Genetic diversity and structure of Japanese populations revealed by whole genome sequencing
Masatoshi	Matsunami	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	953	315	The prehistoric peopling of the Ryukyu Archipelago
Francesco	Montinaro	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	954	246	Sexual selection through physical component analysis
Pedro	Morell Miranda	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	955	613	Genomic insights into the disconnected Demographic History between Sheep and Humans in Iberia
Fusun	Özer	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	956	1448	Prehistory archaeogenomics insights into Anatolia-Caucasus interactions since Neolithic
Shiyu	Qiao	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	957	1177	Esophageal population history of the Central Plains in China with ancient genomes
Valentina	Rovelli	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	958	971	Paleogenomics insights into cat domestication in ancient Egypt
Marcela	Sandoval Velasco	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	959	889	Paleogenomics of Agave domestication in Mesoamerica: preliminary results from whole cpDNA and nuclear genes
Juliette	Sauvage	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	960	667	When cultural traits of admixture deep and shallow the genome ancestry: the case of the Corny culture (Middle Neolithic, Northern France)
Javier	Serrano	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	961	1036	The genomic history of the Canary Islands
Mehmet	Somel	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	962	1432	Temporal changes in inter-regional human mobility patterns through the Holocene: paleogenomics insights
Contran	Sonet	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	963	597	Using ancient DNA to identify <i>Bos primigenius</i> in ancient cattle remains from Belgium
Arev Pein	Sumner	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	964	712	High coverage genomes of two of the earliest Homo sapiens in central Europe
Leonardo	Valini	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	965	1310	Phylogenetic Persian Plateau sea as Hubs for Homo sapiens population after the Out of Africa
Yoshiaki	Wakayama	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	966	933	Genomic analysis of human bones excavated from Jomon sites based on paleogenomics
Tianyi	Wang	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	967	566	The Genetic History of Southern East Asia
Alessandra	Aleotti	12 - Evolution of sensory systems	SP_25	968	1379	The molecular evolution of animal photoreduction and photoreceptor cells
Gwénaëlle	Bontoucu	12 - Evolution of sensory systems	SP_25	969	517	Origin of a novel olfactory sensory neuron population
Gianni	Castiglione	12 - Evolution of sensory systems	SP_25	970	738	Adaptation of Antarctic loachfish Vision to Extreme Environments
Fabio	Cortesi	12 - Evolution of sensory systems	SP_25	971	1543	What the latest advances in molecular approaches and technologies can teach us about the evolution and function of fish vision
Kathy	Ding	12 - Evolution of sensory systems	SP_25	972	15	The repeated evolution of terpene synthases in insects: convergence at multiple levels
Giacinto	De Vito	12 - Evolution of sensory systems	SP_25	973	1022	Darkvision and loss of cone opsins genes in tapetochthonous evolution
Melanie	Deblais-Thibaud	12 - Evolution of sensory systems	SP_25	974	662	The sensory shark: Evolution of vertebrate sensory organs through the eye of high-quality phenotypic, genomic and transcriptomic data in the lesser spotted catshark <i>Squalius laietanus</i>
Julien	Déviillers	12 - Evolution of sensory systems	SP_25	975	1334	Multiple emergences of hemitaphy in Diptera: which genetic background is needed for it?
Bruno	Fonseca Simoes	12 - Evolution of sensory systems	SP_25	976	1240	Molecular Evolution of Vision in Lozards and Snakes
Jake	Fowler	12 - Evolution of sensory systems	SP_25	977	776	Insights into the Structure and Function of Ionotropic Glutamate Receptors through a Study of their Evolution in Bacteria
Jibin	Johny	12 - Evolution of sensory systems	SP_25	978	1584	Functional evolution of olfactory receptors in bark beetles
Dawn	Jordana	12 - Evolution of sensory systems	SP_25	979	832	Evolution of <i>Emmersonia</i> Purkinje to Eye Development
Daemia	La Rodd	12 - Evolution of sensory systems	SP_25	980	1416	The evolution of cPRCs
Jean-Marc	Lassance	12 - Evolution of sensory systems	SP_25	981	1308	The genetic and functional basis of olfactory evolution in monogamous and promiscuous deer mice
Zibo	Li	12 - Evolution of sensory systems	SP_25	982	325	A tale of two copies: evolutionary trajectories of moth pheromone receptors
Alejandro	Lozada Chavez	12 - Evolution of sensory systems	SP_25	983	1567	Genomics of domestication in the arboviral vector <i>Aedes aegypti</i>
Valeria	Maselli	12 - Evolution of sensory systems	SP_25	984	842	Not only the nose knows: <i>IR</i> TRAR gene expression in the octopus sucker
Katsuhiko	Miyata	12 - Evolution of sensory systems	SP_25	985	373	Comparative genomics of <i>Emmersonia</i> Purkinje cells: convergent evolution of olfactory metabolism genes
Peter	Mulhair	12 - Evolution of sensory systems	SP_25	986	370	Diverse sampling reveals dynamic rates and mechanisms of origin gene duplication across <i>Leptothorax</i>

Sergio	Olivera Vazquez	12 - Evolution of sensory systems	SP_25	987	1140	Evolutionary dynamics of two prominent chemosensory gene families in crop pest- sucking pests: insight from the aphids
Lino	Ometto	12 - Evolution of sensory systems	SP_25	988	1064	Evolutionary dynamics of open genes in Brachyera bees
Juan	Opazo	12 - Evolution of sensory systems	SP_25	989	226	Evolution of ion channels in ciliates
Margot	Papezki	12 - Evolution of sensory systems	SP_25	990	140	Investigating the role of epigenetics in the fly <i>Drosophila melanogaster</i>
Isaac	Rossetto	12 - Evolution of sensory systems	SP_25	991	8	Visual Evolution of <i>Drosophila</i> Torus: Molecular, Taxonomic
Bastien	Saint-Leandre	12 - Evolution of sensory systems	SP_25	992	1149	Evolution of chemosensory tissues and cells across ecologically diverse <i>Drosophila</i>
Harini	Suresh	12 - Evolution of sensory systems	SP_25	993	1307	Seeing to believing: Spatial expression of photo pigments in malaria mosquito heads
Johanne	Adam	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	994	1637	Detection of positive selection traces in Central and South-East Asian populations using genome wide scans
Cathrine	Brekke	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	995	1029	Sex-differences in the genetic architecture of allelic shuffling in domestic pig
Victoria	Casali	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	996	430	Seeing Evolution: Consequences of Splice Dynamics on Coexisting Polygenic Traits
Vanessa	Cunha	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	997	427	The impact of selection in contrasting environments on behavioral gene expression and polymorphisms in a facultative parasitic fly
Leah	Darwin	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	998	1126	Using replicate experimental <i>Drosophila</i> populations to test for molecular co-adaptation
Archana	Devi	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	999	817	Adaptation of polygenic traits in fruit populations
Sara	Duari	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1000	618	Unraveling dynamics of long-term polygenic adaptation in <i>D. simulans</i>
Giulia	Ferrarelli	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1001	245	Investigating the evolution of polygenic traits through the reconstruction of adaptive gene-networks able to modulate related functional pathways
Francesco	Ganau Penella	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1003	1090	Can GWAS data be used to detect adaptation on human complex phenotypes?
Olivia	Ghosh	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1004	881	Islandity and pleiotropy in the origin of adaptation
Mateus	Gouveia	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1005	617	Subcontinental structure in Europeans and European Americans: implications for genome-wide association studies (GWAS)
Matthew	Hansen	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1006	899	Genetic analysis of adaptive anthropometric and cardio-metabolic traits in a multi-population African cohort
Keith	Harris	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1007	1485	The effect of selection on predicting the direction of phenotypic difference in polygenic traits
Petri	Kempainen	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1008	473	Epistatic shielding of low ancestral genetic variation for local adaptation can be preserved across multiple habitats
Ivan	Kuznetsov	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1009	1026	Contrasting patterns of present-day and historical natural selection for educational attainment in the Estonian population
Liam	Li	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1010	1635	The evolution of direct selection and pleiotropy during adaptation
Davide	Marnetto	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1011	991	Historical ancestries are consistently associated to the complex trait landscape in European Biobanks
Diogo	Melo	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1012	778	Longitudinal sequencing reveals polygenic and epistatic nature of genetic response to selection
Richard	Nichols	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1013	44	Rapid polygenic adaptation in a wild population of ash trees under a novel fungal epidemic
Sebastian	Ramos-Onsins	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1014	674	Detection of Divergence Signals through the Analysis of the Full Distribution of Fitness Effects using Forward Simulations and Polygenic Adaptation
Bao-Hua	Song	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1015	733	Genetic basis and selection of phytochemical variation in wild soybean
Ann	Tale	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1016	103	The evolution and maintenance of developmental pleiotropy in insect immune systems
Maud	Tenallon	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1017	531	Evolution of phenotypic space as evidence in recent divergent selection experiments
Henrique	Teotónio	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1018	28	Selection and the direction of phenotypic evolution
Benjamin	Wolff	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1019	1658	A theory of oligogenic adaptation of a quantitative trait
Changyi	Xiao	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1020	347	Subtle genetic differences could result in distinct genetic responses to temperature adaptation
Josué	Barrera Redondo	14 - Novel proteins and their emergence from LUCA until today	SP_25	1021	147	Uncovering gene-family founder events during major evolutionary transitions in animals, plants and fungi using GenEra
Juan David	Bayona Serrano	14 - Novel proteins and their emergence from LUCA until today	SP_25	1022	1611	Independent recruitments of different types of phospholipase A2 to the venom of <i>Cariacus</i> snakes
Frederic	Brunet	14 - Novel proteins and their emergence from LUCA until today	SP_25	1023	536	Translational readthrough of the <i>hmr</i> that gene in <i>Drosophila</i> reveals a universal Eukaryote domain
Claudio	Casola	14 - Novel proteins and their emergence from LUCA until today	SP_25	1024	446	Low stability may affect functionality of human microproteins
Carolin	Freye	14 - Novel proteins and their emergence from LUCA until today	SP_25	1025	373	Substrate Specificity and Conformational Heterogeneity in Ancestral and Extant Glucokinases
Dusan	Kordis	14 - Novel proteins and their emergence from LUCA until today	SP_25	1026	77	The origin and early diversification of eukaryotic retroelements
Victor	Luria	14 - Novel proteins and their emergence from LUCA until today	SP_25	1027	1593	Novel genes enable protein structural innovation and function in the brain
Josép	Mari-Solans	14 - Novel proteins and their emergence from LUCA until today	SP_25	1028	1353	Functional divergence in the DEGR/NaCABC protein family: the quest for protein-saving determinants
José Carlos	Montañés Domínguez	14 - Novel proteins and their emergence from LUCA until today	SP_25	1029	378	Translating evolutionary landscapes of study protein genes
Edmund	Moody	14 - Novel proteins and their emergence from LUCA until today	SP_25	1030	344	The return of LUCA and its impact on the early Earth system
Petar	Pajic	14 - Novel proteins and their emergence from LUCA until today	SP_25	1031	54	A mechanism of gene evolution generating multi-function
Christos	Papadopoulos	14 - Novel proteins and their emergence from LUCA until today	SP_25	1032	394	High novel gene diversity across <i>Saccharomyces cerevisiae</i> strains
Carolina	Rocha	14 - Novel proteins and their emergence from LUCA until today	SP_25	1033	836	Interactions of ancient coenzymes reflect a reduced repertoire of amino acids
Paul	Rogneski	14 - Novel proteins and their emergence from LUCA until today	SP_25	1034	345	Impact of GC content on de novo gene birth
Duncan	Sainsford	14 - Novel proteins and their emergence from LUCA until today	SP_25	1035	1056	Genetic marker repeat expansion in ancient highly divergent groups of environmental variants in ancient gene families
Emilio	Tassiou	14 - Novel proteins and their emergence from LUCA until today	SP_25	1036	1402	Tracing the birth and evolution of novel genes across the entire budding yeast subgenus
Nikolaos	Vakrilis	14 - Novel proteins and their emergence from LUCA until today	SP_25	1037	329	Evolutionary origins of orphan genes in prokaryotes of the human gut
William	Vilas Boas Nunes	14 - Novel proteins and their emergence from LUCA until today	SP_25	1038	400	A comprehensive evolutionary scenario for the origin and refunctionalization of the <i>Drosophila</i> speciation gene <i>Odsless</i> (<i>OdsH</i>)
Francesco	Licausi	17 - Roles and Evolution of Oxygen Sensing across kingdoms	SP_25	1039	268	Snapping scenarios: rewriting the evolution of O ₂ sensing to study functional convergence and molecular divergence in eukaryotes
Samuel	Madden	17 - Roles and Evolution of Oxygen Sensing across kingdoms	SP_25	1040	621	Plant Cysteine Oxidase (PCO) Oxygen-Sensing Function is Conserved in Unicellular Algae
Monica	Pal	17 - Roles and Evolution of Oxygen Sensing across kingdoms	SP_25	1041	263	Evolution of low oxygen sensing in trypanozoa
Heun	Seo	17 - Roles and Evolution of Oxygen Sensing across kingdoms	SP_25	1042	235	The role of H ₂ O ₂ in insect pathic cells
Alex	Auyang	29 - Leveraging evolution: controlling wild populations using gene drives and pathogens	SP_25	1043	1037	Private PMAs in the <i>A. gambiae</i> complex for homing gene drive localization
Anna	Clark	29 - Leveraging evolution: controlling wild populations using gene drives and pathogens	SP_25	1044	894	Predicting gene drive outcomes in multi-species models
Tin-Yu	Hui	29 - Leveraging evolution: controlling wild populations using gene drives and pathogens	SP_25	1045	1016	Estimating the proportion of assuaging mosquitoes from genetic data
Bhavin	Khatri	29 - Leveraging evolution: controlling wild populations using gene drives and pathogens	SP_25	1046	1005	A theory of resistance to multigene drive demonstrates the significant role of weakly deleterious natural genetic variation
Anna	Langmueller	29 - Leveraging evolution: controlling wild populations using gene drives and pathogens	SP_25	1047	90	Lessons effects of CRISPR-embryonics in <i>Drosophila</i> melanogaster populations
Liu	Yan	29 - Leveraging evolution: controlling wild populations using gene drives and pathogens	SP_25	1048	552	Development of a CRISPR-based Trans-Acting Gene Drive System in <i>Aedes albopictus</i>
Geoffrey	McFadden	29 - Leveraging evolution: controlling wild populations using gene drives and pathogens	SP_25	1049	1045	A gene drive that reduces the fertility of malaria parasites
Fabio	Barteri	31 - Causation in Protein Evolution	SP_25	1050	1189	Introducing CAAStools, a bioinformatics toolbox to identify and test Convergent Amino Acid Substitutions
Camille	Bédard	31 - Causation in Protein Evolution	SP_25	1051	354	Quantifying the evolutionary tradeoff between resistance and function using antifungal drugs
Alessandro	Bevilacqua	31 - Causation in Protein Evolution	SP_25	1052	624	Enzymatically self-generated chemical gradient induces motility of membraneless proteoceans
Philippe	Despres	31 - Causation in Protein Evolution	SP_25	1053	705	Trans epistasis potentiates non-adaptive complexification by gene duplication
Chenlu	Di	31 - Causation in Protein Evolution	SP_25	1054	869	Human protein adaptation in response to viruses happened through protein stability evolution
Jamie	Herzig	31 - Causation in Protein Evolution	SP_25	1055	1253	The performance of an amino acid substitution model across different viral proteins and evolutionary time
Lada	Isakova	31 - Causation in Protein Evolution	SP_25	1056	678	The geometric and topological properties of sequence space reflect the rate of evolution of protein families
Milind	Jagota	31 - Causation in Protein Evolution	SP_25	1057	906	Integrating predicted interaction structures with variant effect prediction and measurement
Margaux	Jullien	31 - Causation in Protein Evolution	SP_25	1058	206	COCCA-Tree: a tool to benchmark coevolution and sector analyses, with an application to Flaviviruses Monoclonal Antibodies
Hannah	Kim	31 - Causation in Protein Evolution	SP_25	1059	380	Phylogenetic Informed Models of Evolution (PIIME), the implementation (PIRE), and the visualization (PIREV)
Dan	Kozome	31 - Causation in Protein Evolution	SP_25	1060	124	Beyond the Active Site: The Addition/Removal of remote loops reveal the emergence of antifungal activity for chitinase enzyme and potential remote loop engineering
Nurdan	Kuru	31 - Causation in Protein Evolution	SP_25	1061	1492	Phylogeny-based co-evolution
Pascal	Lemieux	31 - Causation in Protein Evolution	SP_25	1062	88	Investigating the role of SH3 domains in parasitoid protein evolution
Kait	Malewicz	31 - Causation in Protein Evolution	SP_25	1063	434	Using Molecular Dynamics Simulations to Connect Genotype to Phenotype
Ricardo	Muniz Trejo	31 - Causation in Protein Evolution	SP_25	1064	845	Benchmarking ancestral sequence reconstruction with deep mutational scanning data: ASR is robust to among-site substitution model heterogeneity
Andrei	Papkou	31 - Causation in Protein Evolution	SP_25	1065	208	A rugged yet easily navigable fitness landscape of antibiotic resistance
Yeonwoo	Park	31 - Causation in Protein Evolution	SP_25	1066	574	The genetic architecture of protein is simple and facilitates functional evolution
Jaesha	Pattin	31 - Causation in Protein Evolution	SP_25	1067	1122	Intramolecular deep mutational scanning reveals biased accessibility of molecular phenotypes in an ancient genotype-phenotype landscape
Christina	Pleschka	31 - Causation in Protein Evolution	SP_25	1068	745	De-novo NAD biosynthesis in avian species
Francis	Rouleau	31 - Causation in Protein Evolution	SP_25	1069	396	Dissection of biophysical determinants and evolutionary tradeoffs of competitively-inhibiting drug resistance from deep mutational scanning and in silico data in <i>Pneumocystis jirovecii</i>
Lisa	Schmelkin	31 - Causation in Protein Evolution	SP_25	1070	762	Neutral evolution with epistasis: a mechanism for non-linear protein evolution
David	Schnettler Fernandez	31 - Causation in Protein Evolution	SP_25	1071	801	How does temperature adaptation influence the evolvability of proteins?
Olivier	Toussier	31 - Causation in Protein Evolution	SP_25	1072	1454	Structural scanning of the RNA polymerase reveals that multiple independent interactions control beta2-associated co-regulated global traits
Douglas	Theobald	31 - Causation in Protein Evolution	SP_25	1073	1249	Exact sequence reconstruction for evaluating and improving ancestral sequence reconstructions
Vjaceslav	Trejácenko	31 - Causation in Protein Evolution	SP_25	1074	719	To misadaptate or not survive
Dulce Irene	Valdivia Martínez	31 - Causation in Protein Evolution	SP_25	1075	1343	Exploiting gene evolution in the 3D genetic context in <i>Drosophila</i>
Patricia	Zito	31 - Causation in Protein Evolution	SP_25	1076	917	Molecular Evolution of the NHA gene family
Eduardo	Dupim	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	SP_25 A	770	Duplication and subfunctionalization of the male fertility gene <i>kl2</i> in <i>Drosophila</i> shows evolutionary convergence
Juan Phillip	Köster	01 - Open Symposium	SP_25	1077	1007	Using machine learning to distinguish genealogical trees generated by branching of lineages with and without gene duplication
Alma	Martínez Zurita	01 - Open Symposium	SP_25	1078	1623	Evolutionary dynamics of <i>Drosophila</i> populations after altering the distribution of fitness effects in non-synonymous mutations
Kevin	Murray	01 - Open Symposium	SP_25	1079	1446	The coevolutionary race between <i>Hyalestherosoma</i> arthropods and <i>Aedes albopictus</i> thalassa at a transcontinental scale
Alexander	Brandt	03 - The dark side of introgression	SP_25	1080	652	Hybridisation without introgression: diversification of F1 hybrid lineages with alternative reproductive strategies in <i>Bacillus</i> stock insects
Damodhan	Kaur	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	1081	1095	Effects of Male Limited X-chromosome evolution on sex-specific fitness?
Hao Cuhk	Zhang	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	1082	895	Prokaryotic Emergence around the Early Stage of Neoproterozoic Oxygenation Event
Meghana	Natesh	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	1083	880	Population genomics and domestication history of yaks from the Indian Himalayas: preliminary insights from ancient DNA
Guil	Can	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	1084	286	Using machine learning to distinguish genealogical trees generated by branching of lineages with and without gene duplication
Yanlieth-Fernanda	López	14 - Novel proteins and their emergence from LUCA until today	SP_25	1085	1397	Genomic profiles from the site selection of the Eukaryotic last common ancestor (LECA)