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 25 (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.

Elect Manua	Our Commence (Francisco Norma					
First Name	Surname/Family Name Barth		Venue_Day EC_24	VINU	SUD	D Title
Julia William	Barth Booker	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24 EC_24	1	157	7 The role of germine mutation rules and the history traits on speciation in a cichlid fish adaptive radiation
		18 - Modeling the genomic, social, and ecological drivers of speciation				The evolution of cylogenetic diploidization and the consequences of expansion load in polypioid species
Arun James	Durvasula	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24 EC 24	3	83	Modeling pairwise site pattern cc-occurrence to understand Great Ape speciation
Alice	Genestier	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24 EC 24	4	59	2 Socialité Anàie, while genome informed phylogenetic robusticity metric
Alice	Kalirad	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24 EC_24	5	58	6 Anotol of the PROM9 dynamics and its role in hybrid startility and speciation
	Lefeuvre	18 - Modeling the genomic, social, and ecological drivers of speciation		6	118	6 Genetic drift promotes and recombination hinders speciation
Maël		18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24	1	43.	A standardized comparative analysis of ancient DNA kinship estimation methods, using "BADGER": a high-fidelity ancient DNA pedgese simulations pipeline.
Luísa	Marins	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24 EC 24	8	134	2 Exploring the evolutionary Nistory of the two-toed sloths (Choloepus) with genomic data: in search of Amazonian crystic biodiversity
Dashiell	Massey	18 - Modeling the genomic, social, and ecological drivers of speciation		9	/5	5 Simulating assortative mating by global ancestry in admixed populations
Ferdinand	Petit	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24	10	70	6 Topological companiison of coalescent the interence tools
Yakov	Pichkar	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24	11	155	1 Fire-scale cultural variation reinforces genetic population structure in England
Iker	Rivas-González	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24	12		8 TRAILS: tree reconstruction of ancestry using incomplete lineage sorting
Marjolaine	Rousselle	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24	13	111	0 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	105	The fuzzy line between species and populations in the marine microbial work: a study case based on shelled cillated profilsts
Lodovico	Sterzi	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24	15		7 Comparative genomics reveals clinical and environmental Serratia mancescens lineages with specific gene content and gene flow patients
Diego	Veliz-Otani	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24	16	132	7 From Buffaib to Cattle: The Unidirectional Migration of Theleria Parva 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	2	5 Using authentic situations in evolutionary biology in an active-learning activity to support the development of professional identity in undergraduate biology students.
Josefa	Gonzalez	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC_24	18	165	7 Melanogaskir: Catch The Fyl: A Cilizen Science Network in Adaptation Genomics
Florin Mircea	lliescu	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC_24	19	128	2 Bicknee belongs to everyone in the genomic era
John	Lees	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC_24	20	26	1 Interactive population genetics for everybody
Michele	Leone	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC_24	21	86	2 mouting org: Citizen Science for arthropod mouting
Sarah	Mueller	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC_24	22	62	8 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	145	Annotation of the Roc1a gene in Drosophila species, a course-based undergraduate research project contributing to study of the evolution and function of the insulin signaling pathway through the Genomics Education Pathreship
Fernando	Racimo	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC_24	24	5	9 The biospheric emergency calls for scientists to change tactics
Daniel	Taub	21 - Science For Everybody: Education and Outreach in Molecular Biology and Evolution	EC_24	25	130	0 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	119	4 Annotation of thisrif gene in Drosophila 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	12	Beyond the theory: From holobiont concept to microbiome engineering
Marijn	Ceelen	22 - Experimental evolution of non-model species and systems	EC_24	28	125	8 Not just nutrients. The effect of Horizontal Gene Transfer on the evolution of bacterial predator/Mysococcus xanthus.
Luis Miguel	Chevin	22 - Experimental evolution of non-model species and systems	EC_24	29	152	9 Experimental evolution of epigenetic, transcriptomic, and higher-level plasticity in response to environmental predictability in a halotolerant microalga
Amy	Gooch	22 - Experimental evolution of non-model species and systems	EC_24	30	95	Expanding the Substrate Scope of Fluoreacetate Dehalogenase Enzymes via Directed Evolution
Cecile	Lorrain	22 - Experimental evolution of non-model species and systems	EC_24	31	56	Evolvability 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	293	2 Coevolution between tardgrades and mosses and a signaling role for host secondary metabolites in tardigrade desiccation tolerance
Karissa	Plum	22 - Experimental evolution of non-model species and systems	EC_24	33	107	0 Adaptation to Elevated Temperature and its Consequences
Gisela	Rodriguez Sanchez	22 - Experimental evolution of non-model species and systems	EC_24	34	146	2 Unavelling the hidden genetics of Winkly Spreaders 3 One standing genetic variations be detrimental for survival and adaptation to new environments?
Shreya	Routh	22 - Experimental evolution of non-model species and systems	EC_24	35	29	3 Can standing genetic variations be detrimental for survival and adaptation to new environments?
Mario	Santer	22 - Experimental evolution of non-model species and systems	EC_24	36	156	The more, the merrier? The evolution of antibiotic resistance on multicopy plasmids
Sarah	Schaack	22 - Experimental evolution of non-model species and systems	EC_24	37	134	Causes and Consequences of Mutation Rate Variation: Testing Key Predictions With Experimental Data from Daphnia magna
Niklas	Steube	22 - Experimental evolution of non-model species and systems	EC 24	38	107	3 Fortuitous origin of alkosteric control in cyanobacterial photoprotection
Cecilia	Trivellin	22 - Experimental evolution of non-model species and systems	EC_24	39	123	3 Evolution of microbial robustness in fluctuating environments
Pranav	Unnikrishnan	22 - Experimental evolution of non-model species and systems	EC_24	40	153	2 Evidence of EPgth polymorphism in the wild and its associated tradeoffs in IRe-history traits
Luis Ever	Vega Cabrera	22 - Experimental evolution of non-model species and systems	EC_24	41	115	9 An Increase in chromosome copy number drives rapid adaptation in a col8-adapted bacterium
Sarah	Wacker	22 - Experimental evolution of non-model species and systems	EC_24	42	74	Genotype -Phenotype Characterization of Biofilms Produced by Bacillus Wild Isolates
Pu	Wang	22 - Experimental evolution of non-model species and systems	EC_24	43	86	Disertanging selection, contingency, and chance during the convergent evolution of multicellular yearts
Nico	Appold	23 - Evolutionary approaches to understand cancer across scales	EC_24	44	106	7 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	63	6 COSMIC signature and transcriptional (a)symmetry of spontaneous mutations inCaenorhabdits elegans
Mary	Boyd	23 - Evolutionary approaches to understand cancer across scales	EC 24	46	90	5 The Diversity of Placenta Invasiveness in Marmals and the Relationship Between Placenta Invasiveness and Cancer Risk
Meritxell	Brunet Guasch	23 - Evolutionary approaches to understand cancer across scales	EC_24	47	142	Addator-adven extinction of hyper-mutated tumours: a multi-type critical tetrit-death process
Ramon	Diaz-Uriarte	23 - Evolutionary approaches to understand cancer across scales	EC 24	48	34	Cance progression and evolutionary event accumulation models: implicit evolutionary assumptions, interpretational hurdes, and why computationally inefficient procedures might allow faster scientific exploration and ortical assessment
Maximilian	Eiche	23 - Evolutionary approaches to understand cancer across scales	EC 24			Forwards optimizing evolution-based therapy strategies: A tailored 3D turnored model for the real-time tooking of therapy failure dynamics
Alison	Feder	23 - Evolutionary approaches to understand cancer across scales	EC 24	50	139	State-dependent evolutionary models reveal modes of solid tumor growth
James	Ferrare	23 - Evolutionary approaches to understand cancer across scales	EC 24	51	145	8 Evolution of Evolvability in Rapidly Adapting Populations
J Nicholas	Fisk	23 - Evolutionary approaches to understand cancer across scales	EC_24	52	67	6 Externe selection induced by antitrib therapy constrains mutational diversification of EGFR-driven lung adenocarcinoma
Théotime	Grohens	23 - Evolutionary approaches to understand cancer across scales	EC 24	53	138	2 Quantification of selection against neoantigen formation in human cancer humors
Jaime	Iranzo	23 - Evolutionary approaches to understand cancer across scales	EC 24	54	39	Pervasive conditional selection of driver mutations and modular epistasis networks in cancer
Umesh	Kalathiya	23 - Evolutionary approaches to understand cancer across scales	EC_24	55	45	I hinsingsing the quality-control characterization composition from the nonzerose mediated nRNA decay pathway
Jona	Kayser	23 - Evolutionary approaches to understand cancer across scales	EC 24	56	05	International on a device of the second s
Franziska	Kellers	23 - Evolutionary approaches to understand cancer across scales	EC 24	57	71	Evolutionary rescue of resistant mutants is governed by a balance between radial expansion and selection in compact populations 0 Whole-exome sequencing of five mixed neuroendocrine-con-neuroendocrine neoplasme of the pastrointestinal tract
Elle	Loughran	23 - Evolutionary approaches to understand cancer across scales	EC_24	59	60	Transmonte anoperating on the transmontendent-extendent-extendent on the galaction extendent extendent A sector of the transmontendent extendent on the galaction extendent extendent
Jeffrev	Mandell	23 - Evolutionary approaches to understand cancer across scales 23 - Evolutionary approaches to understand cancer across scales	EC_24	59	160	8 Karyotypic Evolution of Near-Huppioli and Low-Hypotipicit Tumours 3 Software supporting customizable models of oncogenesis makes somatic evolutionary hypotheses testable
Veselin	Manojlovic	23 - Evolutionary approaches to understand cancer across scales 23 - Evolutionary approaches to understand cancer across scales	EC 24			Software supporting customation motes of oncogenesis makes somatic evolutionary hypotheses testative Fluctuating methylation clocks for inferring the evolutionary history of human cancers
Conrado	Martinez-Cadenas	23 - Evolutionary approaches to understand cancer across scales 23 - Evolutionary approaches to understand cancer across scales	EC_24 EC_24	61	148	Fixculary mempiation access for intering the evolution in tracking in tracking of transmission of access Fixculary mempiation access for intering the evolution in the access Fixculary of security calculary sciences discuss acquisition, section and expansion of cancer driver multiplices in the skin
Nathaniel	Mon Pere	23 - Evolutionary approaches to understand cancer across scales 23 - Evolutionary approaches to understand cancer across scales	EC 24	62	3/1	Eviduan of some mations in meanly calendo assue, equisition, selection and expansion of cancer otiver impations in the swith Concert interference in hermatopoletic state of the calendo assue, explanation of cancer otiver impations in the swith
Mariana	Natalino		EC_24 EC_24			
Madeleine	Oman	23 - Evolutionary approaches to understand cancer across scales		64	124	Priori Yeast to Cancer: Understanding the Impact of Native Stensing in the Evolutionary Adaptation to Genomic Instability Note: The Stensing of the Adaptation in the Adaptation to Genomic Instability Section the memory adaptation of the Adaptation to Cancer: Understanding
Carmen		23 - Evolutionary approaches to understand cancer across scales	EC_24 EC_24			8 Modeling the predictors of mutability variation in healthy tissues
Carmen Cristiano	Ortega Sabater Parmeggiani	23 - Evolutionary approaches to understand cancer across scales 23 - Evolutionary approaches to understand cancer across scales	EC_24 EC_24	65	104	Z Understanding the relationships between karyotype heterogenesity, commissional instability and progressis in childhood B-Acute Lymphoblastic Leukenia through a mathematical and ecological lens
Yosuke	Seto		EC_24 EC 24			3 Does maternal-tetal conflict explain the variation in cancer rates across mammals?
Anastasia	Seto Stolyarova	23 - Evolutionary approaches to understand cancer across scales 23 - Evolutionary approaches to understand cancer across scales	EC_24 EC_24	0/	90	3 Elucidating molecular mechanisms of anti-cancer drug tolerance in lung cancer using single-cell technology 6
Anastasia Francesco	Stolyarova Terenzi			60	54	5 Mataron has in driver gene neveals distribution of effects of oncognic mutations
		23 - Evolutionary approaches to understand cancer across scales	EC_24 EC_24	69 70	51	1 A Bayesian framework to liter selection strongts of establishmental DNAs in human cancers
Qianci	Yang	23 - Evolutionary approaches to understand cancer across scales	EC_24 EC 24			6 Mathematical modeling of effector. T cell stimulation, elimination and binding with target cancer cells
Anastasia	Yankovskiy	23 - Evolutionary approaches to understand cancer across scales		/1	41	0 Evolutionary prediction of the location of primary tumors using mutational signature
Noah	Bourne	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC_24	/2	81	The generic basis of an objecte and r-jater symbolis
Shuyi	Deng	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC_24 EC_24	73	31	4 A deep learning method for estimating time-scale INDEL mutation rates
Janna	Fierst	24 - Indels: computational methods, evolutionary dynamics, and biological applications		74	138	Structural mutations and Mutator transposons in Phytum Nematoda
Michael	Goldberg	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC_24		145	Selective dynamics of interruptions at short tandem repeats
Einat	Hazkani-Covo	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC_24	76	28	Compansatory frameshifts are common in Saccharomyces cerevisiae genes
Gholamhossein	Jowkar	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC_24	77	98	Platems of Indel Evolution in Six Mammalian Othologous Proteomes using Poisson Indel Process
Paola	Laurino	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC_24	78	12	3 Insertions and deletions mediate cofactor specificity and functional transition
Alice	Ledda	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC_24	79	151	7 is there such a thing as plasmid phylogenetics?
Dorota	Mackiewicz	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC_24	80	127	5 The minimization of harmful effects of point and frameshift mutations by the standard genetic code
Fabrizio	Mafessoni	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC_24	81		3 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		157	2 From PseudoCheckar2.0 to PseudoViz a story of gene loss
Edmundo	Torres-Gonzalez	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC_24	84	88	3 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	7	6 Impact of trails variation of random mutations on species diversity in predator-prey coevolution
Flavia	Villani	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC_24	86	140	4 Building a Pangenome Graph for the HKB/BXH Recombinant 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	92	9 Timing bacterial evolution using the Great Oxidation Event
Philip	Bell	25 - The puzzle of eukaryotic cellular origins	EC_24	88	1	9 Are viruses the key to unlocking the eukaryogenesis puzzle?
Hugo	Bonnefous	25 - The puzzle of eukaryotic cellular origins	EC_24	89	99	9 Phylosystemics: how to infer ancestral molecular interaction networks, and why it is exciting.
Auden	Cote-l'Heureux	25 - The puzzle of eukaryotic cellular origins	EC_24	90	148	Foraminitera maintain consistent amino acid usage despite extreme codon usage bias in multiple non-monophyletic clades

Ore		25 - The puzzle of eukaryotic cellular origins	EC_24	9	01 113	30 E	Deparding Protein Complex Prediction Across the Eukaryotic Tree of Life
Rebecca	Gawron	25 - The puzzle of eukaryotic cellular origins	EC_24	6	32 136	63 u	Ising single-cell omics data to identify species and symbionts in uncultivable microbes
Saioa	Manzano	25 - The puzzle of eukaryotic cellular origins	EC_24 EC_24				Ionizontal Gene Transfer in Asgard Archaea
Giacomo Anna	Mutti Nenarokova	25 - The puzzle of eukaryotic cellular origins	EC_24 EC_24		34 53	38 U	king phytems to investigate non-vertical interitance across eukaryotes
Paul	Taylor	25 - The puzzle of eukaryotic cellular origins	EC_24 EC_24		100	04 T	Resolving the prokaryote-to-exilaryote transition using new phylogenomic models of endosymbiosis
Guifré	Torruella Cortés	25 - The puzzle of eukaryotic cellular origins 25 - The puzzle of eukaryotic cellular origins	EC 24		97 38	B1 F	The Evolution of Neurotransmission and the Origin of the Animals Euk-2-Us: Linking the origin of eukaryotes to the diversification of animals and fungi with genomics of flagelates
Marica	Baldoni	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC 24				sameder: cheng ne organe resources pour a une meanmanement and prime genomics neights on zoonolic disease in cat domestication through ancient pathogen genomics
Tim	Brandler	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC 24		9 133	36 E	steptier of induction, database in the contractance of another generations and another generations another generations and ano
Laura	Carrillo Olivas	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24				Paleogenomic 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				Iseases and human co-evolution: modeling malaria spread in the late Pleistocene
Flavio	De Angelis	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	10	02 41	13 р	Polygenic 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	10	3 48	85 N	Aeat without vegetables: An ancient ecotype of Helicobacter pylori found in indigenous populations and animal adapted lineages.
Alan	Godínez-Plascencia	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	10)4 45	52 е	Evaluating in silico HLA typing of low-coverage, shotgun sequencing aDNA data
Tábita	Hünemeier	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	10	05 22	25 u	Inveiling the pathogen-driven evolution in Native American populations
Abigail	Jarosz	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	10	36 40	J/ F	unctional determinants of an ERVF-c1(a) ancestor and its derived variants.
Emrah George	Kirdök	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics 28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24 EC_24	10	0/ 152	20 a	Meta: an accurate and memory-efficient ancient Metagenomic profiling workflow
Miguel Alejandro	Long Navarro	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics 28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24			BI A	Vith century CE Brucela meltersis genome and the recent expansion of the Western Mediterranean clade
Xuebing	Ni	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	11	10 100	06	x new scope. Paleoproteomics for paleopathogen identification ettavirone of 31 fick species provides a compendium of 1,801 RNA-virus genomes
Jonas	Niemann	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	11	11 109	98 P	Namenie of a receptorary provider a compensation of your receiver as genomes Arasites lost: Parasite detection in ancient and modern metagenomic datasets
Zoé	Pochon	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	11	12 151	15 Ir	rectious diseases in the Late Viking Age town of Sigtuna
Nicola	Rambaldi Migliore	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	11	13 39	93 g	Senomic evidence for adaptation to tuberculosis in the Andes before European contact
Aigerim	Rymbekova	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	11	14 54	40 A	Nistorical monkeypox genome of a zoo outbreak
Patrícia	Santos	28 - Host-pathogen co-evolutionary dynamics through the lens of Paleogenomics	EC_24	11	15 126	61 т	he 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	11	16 139	95 A	in 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	117	'R 142	29 E	Evolutionary history of howler monkeys (Atelidae, Alouattinae)
Carlos	Sarabia	18 - Modeling the genomic, social, and ecological drivers of speciation	EC_24 EC_24	118	R 143	38 F	Inding the history haplotypes: how to detect signatures of selective sweeps under different demographic models in admixed populations using SWIF()
Xiaojun Anne	Wang Genissel	18 - Modeling the genomic, social, and ecological drivers of speciation 22 - Experimental evolution of non-model species and systems	EC_24 EC 24	119	R 149	<1 A	Novel Bacterial Speciation Process Observed in a Symbiotic Marine Population devices and the second process of the second proces of the second process of the second process of the second pr
David		22 - Experimental evolution of non-model species and systems 23 - Evolutionary approaches to understand cancer across scales	EC_24 EC_24	120	R 44	B6 -	kdaptive transcriptione rewriting in a fungal pathogen in response to fluctuating environment. The distributions of fitness effects of turnor mutational signatures
Kimberly		23 - Evolutionary approaches to understand cancer across scales 23 - Evolutionary approaches to understand cancer across scales	EC 24	122	R 42	23	ne ostitutionis o minasi entectis or tumor mutatoriai signatures 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	123	R 90	08 T	lebrene shortering limits the evolution of somatic mutations in cloral hematopolesis
Stephanie		23 - Evolutionary approaches to understand cancer across scales	EC_24	124	R 38	83 E	volutionary simulations inform the origins of clonal hematopolesis
Aaron	Kollasch	24 - Indels: computational methods, evolutionary dynamics, and biological applications	EC_24	125	R 161	15 р	Yredicting the functional impact of human indel variants using deep generative models of evolutionary data
Charley	McCarthy	25 - The puzzle of eukaryotic cellular origins	EC_24	126	R 143	39 N	Addeling branch-specific amino acid compositional heterogeneity in phylogenetic datasets.
Ruth	Hershberg	02 - Editor Symposium	SP_24	12	27 164	49 N	Adabablic adaptation to consume butyrate under prolonged resource exhaustion
Yuseob	Kim	02 - Editor Symposium	SP_24	12	28 93	39 P	Sostive feedback between demographic and fitness fluctuation greatly amplifies population size oscillation and causes long-term, multi-locus oscillation of allele frequencies
Koichiro	Tamura	02 - Editor Symposium	SP_24 SP_24				Reenacting adaptive migration from tropical zone to temperate zone by Drosophila albomicans using evolve and resequence
Anique	Ahmad	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24 SP_24	12	50 45	92 F	aktorn gut microbiome is shaped by diet and enriched in Salmonella
Tania	Alonso Vásquez Azad	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24 SP_24	13	31 3/	70 H	GRTE-Assessing the impact of HGT on metabole times through the simulation of 11 million transfer events
Rajeev Paul	Banse	04 - Origins, evolution and ecology of microbial hopeful monsters 04 - Origins, evolution and ecology of microbial hopeful monsters	SP 24	12	33 103	34	Reconstructing thorizontal gene flow network to understand prolaryosic evolution dodeling the interplay between structural variations and substructions generates satisational evolutionary dynamics.
Stephanie	Bedhomme	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	13	34 94	40 n	Accessing one metabolise and second and substantion is generated second and control of generates. Deciphering the horizontal traffic rules of aminophycoside resistance genes
João	Botelho	04 - Origins, evolution and ecology of microbial hopeful monsters	SP 24	13	35 1	18 0	steines systems are pervasive across chomosomaly integrated mobile genetic elements and are inversely correlated to visitence and artimicrobial resistance
Patricia	Brito	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	13	36 106	60 c	Comparative transcriptomic analysis of native and HGT genes in a fluitophylic yeast lineage.
Erin	Cafferty	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	13	37 158	87 е	Evolution of viral minricry following host game acquisition
Hsiao-Han	Chang	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	13	38 91	12 Ir	rferring recert selection forces shaping 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	13	39 139	93 е	Evaluating the specificity of melosis-specific genes
Tsedenia	Denekew	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	14	10 54	49 o	Desity is associated with distinct microbial composition and diversity in the onal microbiane of Emiratis
Johannes	Effe	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	14	11 105	58 s	Rabilizing the unstable: How stability systems affect plasmid fitness
Daria	Evseeva	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	14	2 74	47 0	Aversification of two-partner secretion systems in the bacterial plant pathogen Raisbonia solanaceanum
Michael	Finnegan Fondi	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24 SP_24		13 30		licitlification and the synonymous variant that was just right. Antibiotic resistance levels determined by compatibility between host genome and the incoming horizontally transferred gene
Marco Stefano	Gaiarsa	D4 - Origins, evolution and ecology of microbial hopeful monsters D4 - Origins, evolution and ecology of microbial hopeful monsters	SP_24 SP_24	14	15 126	01 E	Volution of quorum sensing regulatory circuits through the acquisition of additional feedback loops.
Carla	Gonçalves	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	14	16 76	85	kew to measure bacterial genomic plasticity? New insights and implications for human pathogens determine backets on the second bacteriant and the second second second second second second second second second
Padraic	Heneghan	04 - Origins, evolution and ecology of microbial hopeful monsters	SP 24	14	17 65	99 T	tergisy between gene bios and horizontal gene transfer shage evolutionary rates in a exisaryotic lineage Di Catch a Killer Killer Plaunid and Antocoko Nuclease Discovery, Characterization, and Phylogenetics
Samuel	Horsfield	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	14	18 13	37 c	Comparing evolutionary characteristics of diverse bacterial pathogens using PopPUNK
Philip	Johnson	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	14	19 161	19 A	loguisition blases in CRISPR-Cas adaptive immune systems
Catherine	Kagemann	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	15	50 88	89 A	in evaluation of Drosophila melanogater female gene expression associated with the rescue of the bag of marbles (barn) hypomorph fertility delect by Wolbachia pipientis.
Zhiru	Liu	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	15	51 87	76 🛛	Dynamics of bacterial recombination in the human gut microbiome
Neil	Macalasdair	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	15	52 60	03 р	Yoducing Improved Pangenome Phylogenies
Rebecca	Man	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	15	53 78	86 т	The influence of lateral transduction on bacterial genome content and structure
Gemma	Murray	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	15	54 111	18 т	he emergence and diversification of a zoonolic pathogen from within the microbiola of Intensively farmed pigs
Samuel	O'Donnell Deseniene	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24 SP_24	15	05 6	50 s	Barahips is diving force during the domestication of Penicilium species
Kiran	Paranjape	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24 SP_24	15	7 4/	7 T H	ksc-adaptation of Legionelia pneurophila to macrophages and amoetae through experimental evolution
Elena Marcus Ho Hin	Romero Shum	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24 SP 24	15	58 104	52 n	Beveled HV viral bad is associated with higher recombination rate in vivo. Accombination associated with the emergence of mcr-3 and mcr-7
Alix		04 - Origins, evolution and ecology of microbial hopeful monsters 04 - Origins, evolution and ecology of microbial hopeful monsters	SP 24	15	59 114	46	tecontrination associated with the emergence of mcr-3 and mcr-7 anome 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 04 - Origins, evolution and ecology of microbial hopeful monsters	SP 24	16	30 64	43 1	Parente or a might specie colpus panale reveals a might canoer have on collegeness Transposable elements drive the evolution of multiple drug resistance plasmids
Aaron	Weimann	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	16	61 122	29 E	Volution and host-specific adaptation of Pseudomona services as enginesa
Fiona	Whelan	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	16	32 102	27 g	Bene-gene associations in microbes from human-associated microbial communities
Justin	Gupta	04 - Origins, evolution and ecology of microbial hopeful monsters	SP_24	52	22 133	35 A	utolysis as a Mechanism for Coexistence inPseudomonas aeruginosa
Ogün	Adebali	07 - Computational evolutionary genomics in the era of machine learning	SP_24	16	3 150	05 P	PHACT: Phylogeny-Aware Computing of Tolerance for Missense Mutations
Carlos	Albors	07 - Computational evolutionary genomics in the era of machine learning	SP_24	16	54 140	06 A	A Benchmark Task for Language Models of Haman DNA
Jordan	Anderson	07 - Computational evolutionary genomics in the era of machine learning	SP_24	16	35 90	07 N	Aschine Learning Inference Of Effective Population Size Over Time Using Single Diploid Samples.
Lucia	Barzilai Batisti Biffignandi	07 - Computational evolutionary genomics in the era of machine learning	SP_24 SP 24				Signatures of natural selection on tree shape metrics from serially sampled intrahost viral physigenies
Gherard Alan	Batisti Biffignandi Beavan	07 - Computational evolutionary genomics in the era of machine learning	SP_24 SP_24	10	1 13	13 C	Sassification or regression? Accuracy and interpretability of machine-learning based prediction accuracy of semi-quantitative genetic traits
Madleina	Caduff	07 - Computational evolutionary genomics in the era of machine learning 07 - Computational evolutionary genomics in the era of machine learning	SP 24	10	39 121	12	Zontrigency, Repeatability and Predictability in the Evolution of a Probanyotic Pargenome. Incurate identification of sex-linked scatificitis and sex karyotypes from low-depth and ancient samples
Aleiandro	Ceron-Noriega	07 - Computational evolutionary genomics in the era of machine learning 07 - Computational evolutionary genomics in the era of machine learning	SP 24				courare ionitrication of sex-initial scattors and sex karyotypes from low-agen and ancent samples fachine learning assisted gene annotation of a nematode phylogeny by protectranscriptomics
Moisès	Coll Macià	07 - Computational evolutionary genomics in the era of machine learning 07 - Computational evolutionary genomics in the era of machine learning	SP_24	17	1 158	B6 4	Accine learning assisted gine annotation of a nematode physigenty by protectranscriptomes. Spenomic method for dating and geographically locating ancient samples
Trevor	Cousins	07 - Computational evolutionary genomics in the era of machine learning 07 - Computational evolutionary genomics in the era of machine learning	SP_24	17	12 17	78 T	Parcellaric manage and saving a
Keith	Crandall	07 - Computational evolutionary genomics in the era of machine learning	SP_24	17	73 11	ہ 15	keepBreaks: 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	17	74 39	99 k	dentifying genetic events that potentiate multi-drug resistance in Escherichia coli with machine learning
Maria	Fariello Rico	07 - Computational evolutionary genomics in the era of machine learning	SP_24	17	76 158	88 🗅	Deep learning for genomic prediction and tasks learned on the way.
M. A. Thanuja	Fernando	07 - Computational evolutionary genomics in the era of machine learning	SP_24	17	77 14	41 т	esting the accuracy of phylogenetic trees built by placing DNA barcode sequences: implications of backbone tree completeness and species missingness pattern
Valentina	Galeone	07 - Computational evolutionary genomics in the era of machine learning	SP_24	17	78 50	06 R	Rules of co-occurring mutations in Influenza Virus A
Marie-Claire	Harrison	07 - Computational evolutionary genomics in the era of machine learning	SP_24	17	79 19	91 N	Aachine Learning Illuminates How Diet Influences the Evolution of Galactose Metabolism in Saccharomycotina Yeasts
Mark	Harrison	07 - Computational evolutionary genomics in the era of machine learning	SP_24	18	30 95		Isscovering Genomic Pootprints of Eucocial Evolution with Machine Learning
Ain	Huang	07 - Computational evolutionary genomics in the era of machine learning	SP_24	18	20 400	21 A	A comprehensive benchmarking for gloss introgression tract analysis with supervised learning
Meris	Johnson-Hagler	07 - Computational evolutionary genomics in the era of machine learning	SP_24 SP_24	18	32 139 33 109	99 H	kow Many Bacterial Samples Do We Need to Make a Good Predictive Machine Learning Model?
Daniel Kevin	Jordan Korfmann	07 - Computational evolutionary genomics in the era of machine learning 07 - Computational evolutionary genomics in the era of machine learning	SP_24 SP_24		33 105 34 17		Vediction of recessive inheritance for missense variants in human disease imutaneous inference of Part Demography and Selection from the Ancestral Recombination Graph under the Beta Coalescent
Lukas	Kuderna	07 - Computational evolutionary genomics in the era of machine learning 07 - Computational evolutionary genomics in the era of machine learning	SP 24		35 10		smittateous interence of r-siz Lenngraphy and selection from the Ancestral Reconstruction or large under the beta Lobalescent dentification of conserved sequence elements across 242 primate genomes with deep learning
Alexandre	Laverré	07 - Computational evolutionary genomics in the era of machine learning 07 - Computational evolutionary genomics in the era of machine learning	SP 24		36 120		semination or conserved sequence elements across 242 primate genomes with deep learning Zhanges 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		37 20		Aachine learning and molecular dating techniques allow mapping the origin and expansion of aerobic bacteria to the redox history of the Earth
Oliver	Lyon	07 - Computational evolutionary genomics in the era of machine learning	SP_24	18	38 154	40 🛛	Sistinguishability of Episodic Fitness Shifts from Changes in Effective Population Size
Carlos	Martí Gómez-Aldaraví	07 - Computational evolutionary genomics in the era of machine learning	SP_24	18	39 147	70 T	owards inference and understanding complex experimental genetype-phenotype maps

Physical							
NameNot were the stand of the stand	Jazeps	Medina Tretmanis	07 - Computational evolutionary genomics in the era of machine learning	SP_24	190	753	Joint Caling of Local Ancestry and Archaic Introgression Using Deep Learning.
NAMENo.<	Fatima	Mostefai	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
		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
Sector <t< td=""><td></td><td></td><td>07 - Computational evolutionary genomics in the era of machine learning</td><td>SP_24</td><td>193</td><td>910</td><td>Winning Against Urbalanced Datasets in a Machine Learning De-Nevo Genes Prediction Algorithm in Angiosperms</td></t<>			07 - Computational evolutionary genomics in the era of machine learning	SP_24	193	910	Winning Against Urbalanced Datasets in a Machine Learning De-Nevo Genes Prediction Algorithm in Angiosperms
			07 - Computational evolutionary genomics in the era of machine learning	SP_24			
PAN	Graziano		07 - Computational evolutionary genomics in the era of machine learning		195	605	Rapid detection of novel emerging variants of SARS-CoV-2 by unsupervised classification
Band <t< td=""><td>Arnaud</td><td>Quelin</td><td>07 - Computational evolutionary genomics in the era of machine learning</td><td></td><td></td><td></td><td></td></t<>	Arnaud	Quelin	07 - Computational evolutionary genomics in the era of machine learning				
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Interpart Proceedings	Diego				198	1601	Modeling the genomic determinants of diverse selective sweeps in the human genome
Bit Bit<			07 - Computational evolutionary genomics in the era of machine learning		199	580	Machine learning in species delimitation
			07 - Computational evolutionary genomics in the era of machine learning		200	133	Comparative Pangenomics Reveals the Existence of Distinct Communities and Conserved Regions within Microbial Pangenomes.
		Vigue	07 - Computational evolutionary genomics in the era of machine learning	SP_24	201	522	Exploring the variability and evolutionary dynamics of Escherichia coli through the analysis of 60,000 genomes
			07 - Computational evolutionary genomics in the era of machine learning		202	682	Implementing a better random seed generator for genomic simulation
				SP_24			
			07 - Computational evolutionary genomics in the era of machine learning	SP_24			Beinforcement Learning informs optimal treatment strategies to limit antibiotic resistance
				SP_24	205	839	Detecting Positive Selection Using Machine Learning
Name				SP_24	206	913	Perfectly conserved sequences (PCS) between human and mouse are significantly enriched for small proteins
BALBA	Jiana						
NAMENo. 10No. 10No	Pascal			SP_24			
	±llie	Armstrong			209	1360	Taking our bear-ings: A comprehensive reference genome database for North American brown bears (Usus arctos)
						039	The emergence of supergenes from inversions in Adartic salmon
Nome	Jens			SP_24	212	2/9	Independent haptotype evolution contributes to novelty and persistence without sex in a mite
BondBondBond and a stand and a	Vielodie			SP_24			Bridging the gap between population genomic and phylogenetic approaches by the study of mammals effective population size.
			15 - Animal genomics goes wild	SP_24	214	1039	Assembly of polyploid genomes: identification and phasing of alkilo variants using H-C
							Random genetic drift sets an upper limit on mRNA splicing accuracy in metazoans
NumN	Juraj	Bergman Rescele Agertic	15 - Animal genomics goes wild	SP_24	216	829	A macrogenerative perspective of mammalian biodiversity, ecology and evolutionary history
MADP	NajiV	Duscolo Agostini	10 - Animai genomics goes Wild	SP_24	217	1259	I Disentangling the worldwide invasion process of Halyomorpha halys through ABC
TheBodyA standy and any	Virte	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
MemM	Thee		15 - Animal genomics goes Wild	SP_24	219	040	Lucases and consequences of extremely genome right aversity of European amphioous wild populations
	Matteo		15 - Animal genomics goes wild		220	343	Levelon or cognate norms in vigers
BitsB	Cabrielle		15 - Animal genomics goes Wild		221	165	In Agromic perspective on the evolutionary instory or interoprificitia gelada
NameN	Jabrielle		15 - Animal genomics goes wild		222	926	Leveraging a de-novi outgread assembly for comparative and functional genomics of the Octopus timaculoides
NameN					223	6/9	Integenenie architecture of a communus dolle polymorphism in the European barn owl (Tylo abba)
Main<			to - Animal genomics goes wild		224	648	Iowards piscology: trom morgetesion to genomic islands of differentiation
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YNo.	Jiaoling	Deng	15 - Animal genomics goes wild		227	982	Genetic parallelism and adaptation to brackish water bodies in sprat (Sprattus sprattus) and Atlantic henting (Oupea harengus)
YNo.	aurence		15 - Animal genomics goes wild	SP_24			
SymbolSymmolSymmolSymbolSymbolSymbolSymbolSymmolSymmolSymmolSymbolSymbolSymmolSymmolSymmolSymmolSymmolSymmolSymmolSymmolSymmolSymmolSymmolS	Klara	Eleftheriadi	15 - Animal genomics goes wild	SP_24	229	1266	Interfacts genome of the phylum Nematomorpha, a key resource to unveil Ecdysozoa evolution
Math Math Math Math Math Math Math 				0F_24	230	931	Local populations demographic history of brown bears Ursus arctos in Eurasia based on whole-genome resequencing
SkineFieldSkine <th< td=""><td>=mily</td><td></td><td></td><td>SP_24</td><td>231</td><td>1365</td><td>Comparative and population genomics reveal highly repetitive landscape of snowy owl genomes</td></th<>	=mily			SP_24	231	1365	Comparative and population genomics reveal highly repetitive landscape of snowy owl genomes
BandProceedings							
SectorSect	Sabine			SP_24	233	1504	Conservation score analysis to validate selection signals and improve functional annotation of the Atlantic herring
BandsetBit Amount of the second					234	1228	Resolving the mystery of freshwater breeding flounders?
NameProblemProblemProblemProblemProblemProblem0And and any					235	555	To nigrate or not to nigrate: characterising the interplay between genetic and environmental drivers of bird migration
FactorFact						247	Assessing the Genetic Composition of Cotton-Top Tamarins Before Sweeping Anthropogenic Impact
Share <th< td=""><td></td><td></td><td></td><td>SP_24</td><td>237</td><td>301</td><td>Conservation genomics of kuaka Whenua Hou/Codfish Island diving petrel</td></th<>				SP_24	237	301	Conservation genomics of kuaka Whenua Hou/Codfish Island diving petrel
BéndéSolution<				SP_24			Ein whale (Baiaenoptera physalus) genomes reveal genomic erosion in baleen whales
Gamba Gamba Gamba Gamba GambaGamba Gamba		Gao	15 - Animal genomics goes wild	SP_24	239	860	Holzontal gene transfer and differential allele expression of the oribatid mites Platynothus petitier provide new insight of asexual genome evolution
Chef And Control			15 - Animal genomics goes wild	SP_24		584	Atlantic herring - an adaptive radiation with limited reproductive isolation
NameN	Genavieve	Gray-Sandoval	15 - Animal genomics goes wild	SP_24	242	1533	Quantifying virus-driven adaptation in Myotis genomes using the McDanald Kreitman test
Main Main			15 - Animal genomics goes wild	SP_24	243	1494	Domestication as a Model for Extreme Environmental Change: Insights from Canid Genomes
Bund Bund <th< td=""><td>Vadège</td><td>Guiglielmoni</td><td>15 - Animal genomics goes wild</td><td>SP_24</td><td>244</td><td>844</td><td>Comparative genomics of understudied asexual nematodes</td></th<>	Vadège	Guiglielmoni	15 - Animal genomics goes wild	SP_24	244	844	Comparative genomics of understudied asexual nematodes
ShafeHydre Media91-American generation of sector of	Marie		15 - Animal genomics goes wild	SP_24	245	1080	Uncovering hidden evolutionary processes: Range expansion and gene flow patterns in two cryptic bat species
NineHonding binHonding with and sequence of a seque	Ewan		15 - Animal genomics goes wild		246	735	Do interactions between chromatin and transposable elements contribute towards transgenerational plasticity in wild Drosophila melanogaster?
LardUeddmaUe Admin geomes pay with a symph geomes and any admin geomes and admin geo			15 - Animal genomics goes wild		247	360	Islosyncratic responses to climate change in an adaptive radiation of Australian Cryptoblepharus lizards
AhnSeries9. And groups gaves9. Al9. Al9	Núria	Hermosilla-Albala			248	251	Whole genome approach to the structure and dynamics of Cacajao wild populations
MightKommer beingB- Andragonic goard and constraintsB- 24A25B120Subony those stars are used and squares and constraints of the start and and squares and	aura				249	984	Ancient or modem? The role of natural and anthropogenic factors in shaping the European wild boar population structure
TypeFund61. A change poorts goars allow of goars allow of goars and	Julia		15 - Animal genomics goes wild		250	1472	Investigating the genomic implications of importing non-native and commercially bred bumblebee subspecies
MemMess61- And generation genes and62- Add72- Bd72- Bd72	Alicja		15 - Animal genomics goes wild		251	1362	Evolutionary history of Microtus obscurus reconstructed using modern and ancient mitogenomes
MemberMess95. And generic gest side95. Add95. Add	Tyler	Kent	15 - Animal genomics goes wild		252	932	The demographic history and genomic consequences of the recent introduction of Aedes aegypti to the Americas
Romal NumberLook JackUse Jack <t< td=""><td>Keren</td><td>Klass</td><td>15 - Animal genomics goes wild</td><td></td><td></td><td></td><td>Fire-Scale Population Genetic Structure in a Fragmented Black Howler Monkey Population: Implications for Dispensal Patterns and Population Pensistence</td></t<>	Keren	Klass	15 - Animal genomics goes wild				Fire-Scale Population Genetic Structure in a Fragmented Black Howler Monkey Population: Implications for Dispensal Patterns and Population Pensistence
EdnaIndexI	Romuald	Laso-Jadart	15 - Animal genomics goes wild	SP_24		290	Urban population genomics: structure, dispersal and adaptation of the brown rat (Ratus norvegicus) in Parts
EdnaUrdUrdUrdUrdName provide goalsSp2 4Sp2 4	Ana Victoria	Leon Apodaca		SP_24			Genomic consequences of isolation and intreeding in an island dingo population
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KatherineMcVig <td>Mariana</td> <td></td> <td></td> <td>SP_24</td> <td>257</td> <td>1136</td> <td>Exploring genetic and phenotypic associations in the green andle natural populations</td>	Mariana			SP_24	257	1136	Exploring genetic and phenotypic associations in the green andle natural populations
PableMonig15 - Annal genomes gene wildSP-24SP-24VP24Igenomes gene winds on the section of the sectio	Katherine				258	746	Causes and Consequences of Malaria Adaptation in Brazilian Howler Monkeys
PableMonig15 - Annal genomes gene wildSP-24SP-24VP24Igenomes gene winds on the section of the sectio	Fahime			SP_24	259	594	Onaracterization of genetic diversity and evolution of MHC class II genes in Atlantic herring using long-read sequencing
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AriadraMorale15 - Avinal genomics goes wildSP, 24262388Binvasie genome iterative the stateme entranceWillNatholz15 - Avinal genomics goes wildSP, 242681138Biomace iteratives are stateme entranceWillNatholz15 - Avinal genomics goes wildSP, 242681138Biomace iteratives are stateme entranceMustafiaObbard15 - Avinal genomics goes wildSP, 242681100Biotace iteratives are stateme entranceAustafiaObbard15 - Avinal genomics goes wildSP, 242681100Biotace iteratives are stateme entranceAuge BiotaceSP, 242681100The toropits genome iterative iterative are stateme entranceAuge BiotaceSP, 242681100The toropits genome iterative iterative are stateme entranceAuge BiotaceSP, 242681100The toropits genome iterative iterative are stateme entranceAuge BiotaceSP, 242681100The toropits genome iterative iterative are stateme entranceAuge BiotaceSP, 242681100The toropits genome iterative iterative are stateme entranceAuge BiotaceSP, 24268110011001100Auge BiotaceSP, 2426811001100Auge BiotaceSP, 2426811001100Auge BiotaceSP, 2426811001100Auge BiotaceSP, 2426811001100Auge BiotaceSP, 242781200 <t< td=""><td>Stefano</td><td>Mona</td><td></td><td>SP_24</td><td>261</td><td>763</td><td>Bivirming in Troubled Seas: fail and tragmentation of Work's White Shark Populations</td></t<>	Stefano	Mona		SP_24	261	763	Bivirming in Troubled Seas: fail and tragmentation of Work's White Shark Populations
Will Name 5 - Arima genomes genes will SP-24 254 154 Journee was genes wind rup genes wind	Ariadna	Morales			262	388	Mammalian genomes illuminate bat adaptations to viral tolerance and disease resistance
WillNach15 - Animal genomes goes weldSP - 24256113Goos welk angement or ange kongement				SP_24	263	389	Incomplete-lineage sorting explains the low performance of DNA barcoding in a Western European grasshoppers radiation (Orthoptera: Acrididae)
DarmetObta5				SP_24	264	1134	Genome wide signatures of range expansion in a key UK polinator
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HistaOzfork15 - Armal genonics goes wild92 - 4260171Note access tracket for the output of the fourth of the fourt	Mustafa	Ozkan	15 - Animal genomics goes wild	SP_24		1107	The first complete genome of the European wild ass (Equus hydruntinus) reveals its reticulate phylogenetic history, dramatic population decline, and its latest survivors
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Johnson Panala S - Animal genomes spoe wild SP- 24 270 Th 144 Reparation state state means that presents spoe wild means that presents state mediation state means that mea	Katja	Peijnenburg	15 - Animal genomics goes wild	SP_24	269	1211	Towards identifying the drivers of divergence in an oceanic zooplankton
Marie Rayad 5 - Arimal genomes goes wild SP- 24 271 333 Proparties properties and sequent transformation structures and sequent transformatin structures and sequent transfor	Joshua	Penalba	15 - Animal genomics goes wild	SP_24	270	1144	Rapid transition during speciation revealed from comparative study across an avian subure zone
Gluid Riccion 15 - Animal genomics goes wild SP24 SP24<	Marie	Raynaud	15 - Animal genomics goes wild		271	334	Population genomics support PRDM9-dependent recombination landscapes in salmonids
ElectricShep draft15 - Animal genomes goes wildSP-24273611Joint association with particular dynamic strategy taked products of an edwards. Under Schemale Sch		Riccioni	15 - Animal genomics goes wild		272	1361	Improving the conservation status of Austropotamobius pallipes species complex in the Italian North-western Apennines through population genomics and habitat modelling
Control Rossi 15 - Animal genomics goes wild SP_24 SP_24 ZPI Boil Routing the future of a words whords whords, whorque to gue to support t		Sheppard	15 - Animal genomics goes wild		273	611	Genomic associations with pathogen gradients across divergent island populations of an endemic bird
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JuditSales15 - Animal genomes goes wildSP_24SP_24276585Journames/mons/mode wind words in the fundy of the galanty maxima.March words in the fundy of the galanty maxima in the manufal the fundy of the galanty maxima.March words in the fundy of the fu	Nathanaelle				275	512	A new type of non-Mendelian transmission sustains asexual reproduction in the nematode M. belari.
Sampaio Sampaio <t< td=""><td></td><td></td><td>15 - Animal genomics goes wild</td><td></td><td>276</td><td>585</td><td>Animal transcriptomics goes wild: high diversity of RNA patterns across invertebrates defies the concept of a€ good quality RNA4€™</td></t<>			15 - Animal genomics goes wild		276	585	Animal transcriptomics goes wild: high diversity of RNA patterns across invertebrates defies the concept of a€ good quality RNA4€™
André Santos 15 - Animal geronicios goes wild SP24 276 1061 I Anifor Le Trabanca Ulto platoma (Transa Ultoplatoma (Transa Ultoplato (Sara	Sampaio	15 - Animal genomics goes wild		277	799	Shedding light on the phylogenetic relationships of the Talpidae: insights using mitogenomes
Ben Schult	André	Santos	15 - Animal genomics goes wild		278	1061	A PacBio H-Fi genome assembly of the painter's mussel Unio pictorum (Linnaeus, 1758)
Nurlsdam Shakku difforv 15 - Animal genomics goes wild SP_24 280 15533 [akunca or a glassionan nature. No ski they dasguar? Nurlsdam Shaky 15 - Animal genomics goes wild SP_24 281 1280 [uccoss grass in them in the interprise facilitation in an expensive facilitation in a new work Stephane Shaky 15 - Animal genomics goes wild SP_24 281 1290 [uccoss grass in genomics facilitation in a new work Stephane Stepsane 15 - Animal genomics goes wild SP_24 281 97 [doet cherry of thesis in the interprise facilitation in a new work Vasible South 15 - Animal genomics goes wild SP_24 281 97 [doet cherry of thesis into drongs and the at Abace facilitation in a new work Vasible South 15 - Animal genomics goes wild SP_24 284 97 [doet cherry of thesis into drongs and the at Abace facilitation in a new work Vasible South 15 - Animal genomics goes wild SP_24 286 1314 [dowg ne to facilitation in a new might the drong and the at Abace facilitation in a new model the drong and the at Abace facilitation in a new model Vasible South 15 - Animal genomics goes wild SP_24 286 531 [mounts the at Advance and the advance in attrangent the advanc	Ben	Schultz	15 - Animal genomics goes wild	SP_24	279	1456	Detanging the hybridization histories of two Chrosomus dace species
Reflection Sharpa 15 - Antimal genomics goes wild SP_24 281 1200 [provides genesition matchins in the genom of the Bioch does first in a second s	Nurislam	Shaikhutdinov	15 - Animal genomics goes wild	SP_24	280	1553	Absence of spliceosomal Introns in the mixotrophic olliate Mesodinium rubrum - how did they disappear?
Shefpa Shefpa 15 - Animal genomics goes wild SP_24 285 519 Journel speak of paguation have and exclosed affected in a na exercised featry Glesser 15 - Animal genomics goes wild SP_24 286 97 Gancies howay of threpack thread howay of thr	Rebecca		15 - Animal genomics goes wild	SP_24	281	1290	Uncovering deleterious mutations in the genome of the Black-footed ferret, a severely endangered spacies.
Henry Sless 15 - Animal genomics goes wild SP_24 284 07 [] Genetic density of thempice What (henry beneficial to density) and the grant one stage and the density of the densit density of the densit densit	Stéphanie			SP_24	283	519	Genomic signals of population history and ecological differentiation in an experimental introduction of lizards on a new island
Damble Souzzo Souzo Souzzo Souzzo Souzzo <td>Henry</td> <td></td> <td></td> <td></td> <td>284</td> <td>97</td> <td>Genetic diversity of Humpback Whales (Megaptera novaeangliae) feeding in South Georgia and the Falkland Islands - Initial findings and next steps.</td>	Henry				284	97	Genetic diversity of Humpback Whales (Megaptera novaeangliae) feeding in South Georgia and the Falkland Islands - Initial findings and next steps.
Source Oracle Sour			15 - Animal genomics goes wild	SP_24	285	543	Insights Into Dingoes Evolutionary History Using Ancient Genomics
Marcolla Sozoni 15 - Animal geromotics goes wild SP_24 287 573 (lengator of environment Note Modeling are grounds data binestigate the demographe testory of Emps calculars in nation to Induitat availability Bastiana Slar 15 - Animal geromotics goes wild SP_24 288 1021 windstant or Adata prime in the Action of are grounds and a binestigate the domographe testory of Emps calculars in nation to Induitat availability Marcolla Sularz Marcollang geos wild SP_24 288 1021 windstant or Adata prime in the Action of antime testory of testory actionation to Induitat availability	Daniela				286	1314	Diving into the historic origins of genetic diversity in cichild fishes of African Lake Tanganyika
Star 15 - Animal genomes goes wild SP_24 288 1021 Importance on Administration of Administration And Administration Administration and Administration Admininter Administration Administr	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 Emys orbicularis in relation to habitat availability
Marcos Suárez Menéndez 15 - Animal genomics goes wild SP_24 289 1187 Direct estimation of genome mutation raises from pedigees in tree-ranging baleen whates	Bastiaan	Star			288	1021	Hybridization of Atlantic puffins in the Arctic coincides with 20th-century climate change
lanna Suduka 15 Asimol approving approving approved SP 24 200 57	Marcos	Suárez Menéndez	15 - Animal genomics goes wild	SP_24	289	1187	Direct estimation of genome mutation rates from pedgrees in free-ranging baleen whales
Joanna Jouryka 10 - Animial genomics goes wird 01 _ 24 250 37 [Differential DNA methylation of avian sex-chromosomes			15 - Animal genomics goes wild	SP_24	290	57	Differential DNA methylation of avian sex-chromosomes

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Marion	Talbi	15 - Animal genomics goes wild	SP_24 SP_24	291	1206	Pre-scale recombination maps: From simulation to empirical data
Marianthi	Tangili Tolve	15 - Animal genomics goes wild	SP_24 SP_24	292	241	Longtudinal changes in autosomal DNA methylation in two species of passerine birds
Livia		15 - Animal genomics goes wild	SP_24 SP_24			Whole mitochondrial genome sequencing provides new insights into the phylogeography of loggerhead sea turities (Carretta carretta) in the Mediterranean Sea
Alexandros Takeru	Topaloudis Tsunoi	15 - Animal genomics goes wild 15 - Animal genomics goes wild	SP 24	294	1039	Quantitative genetics and population generics in the wild. Short term encludorary response to climate change in the barn out (Tho aba)
Jozefien	Van de Velde	15 - Animal genomics goes wild	SP_24	205	1277	Uncovering the role of environmental fluctuations in shaping the population structure of Japanese makes through genome sequencing Population genomics of Australian turowing flogs Neobatracturus reveal adaptation to polybioldy
Romain	Villoutreix	15 - Animal genomics goes wild	SP 24	200	444	Conception generation of gener
Claudia	Weber	15 - Animal genomics goes wild	SP_24	298	1499	Accelerated protein evolution in parasitic cridiarians
Alicja	Witwicka	15 - Animal genomics goes wild	SP_24	299	1633	Poster on pollinators submitted by Yannick Wurm (who already has another poster)
Ying	Zhen	15 - Animal genomics goes wild	SP_24			Evolution of firefly toxin lucibulingins
Valeria	Anorve 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 archeic 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 SP_24	302	1273	Using temporal genetic data to infer time-varying selection in viral evolution
Alison Ronja Jessica	Barton Billenstein	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24 SP_24	303	1592	Time selection on blood group phenotypes over the past 10,000 years in West Eurasia
Simon	Boitard	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24 SP_24	304	1001	Evaluation of Bayesian genesiong-based coalescent models for demographic inference
Audrey	Bras	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology 16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	305	1374	Whole-genome sequencing of cryopreserved resources from French Large White pigs at two distinct sampling times reveals strong signatures of convergent and divergent selection between the dam and site lines Unaveling the link between population trends with charges in genetic diversity in Finish butterflees
Emily	Breslin	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	307	698	Los Upper Palaeolitirs human genomes from the south of France.
Marco Rosario	Capodiferro	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	308	1371	Archaic trilogession in ancient turnan 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 admixture landscapes of Cabo Verde and SAEo TomAR e PrA-ncipe: 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 Genealogies with Ancient DNA
Adele	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 lookated from FFPE facue samples in the Pacific Part human expansions shaped the spatial partner of Neuroderthal ancestry
Mathias	Currat	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'Atanasio	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24 SP_24	313	216	Echoes from the last Green Sahara: a ghost population of cattle herders unveiled from joint whole modern genome analysis of Sahelian Futuri and ancient Attican individuals.
Elizabeth Daria	Finney Frolova	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24 SP 24	314	1400	Quantifying Sample Collection Time Uncertainty Improves Epidemiological Modeling of SARS-CoV-2 Evolution
Vincent	Geyer	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology 16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP 24	210	574	Using historical samples, restarangement distances and Approximate Bayesian Computation to analyse plasmid evolution
Mogge	Hajiesmaeil	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology 16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP 24	310	132	Exploring the temporal limits of RNA preservation in historical and ancient biological material 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 bloogy 16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP 24			A compensione picture of the genetic rationy of train Thering the distributions of these sefects and proportions of atrongly deleterious mutations
Anahit	Hovhannisyan	16 - From the under to the recent: using temporal generative decisions in evolutionary biology 16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	319	266	Internet processing on the second of the properties of the second processing of the second of the se
Ali	Hudson	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	320	996	Guppies On Repeat: Tracking genomic evolution over 20 generations of phenotypic convergence
Anastasia Hie Lim	Ignatieva	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	321	1481	Threading new data into reconstructed genealogies
	Kim	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	322	916	Prehistoric human migration between Sundaland 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 blasss in paleogenomic data
Carolin	Kosiol	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24 SP_24	324	122	A Bayesian method to detect targets of selection in time-series data of Evolve-and-Resequence experiments
Julia Patricia	Kreiner	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24 SP_24	325	56	Reple exclusion of a native week to agriculture over the last 200 years
Brian	Lang	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP 24	320	1559	200 years of heterative generoses predict plant stronger to climate change
Francisco Javier	Maravall Lopez	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology 16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP 24	328	835	Using time-series genomic data for early detection of novel SARS-CoV-2 valuets with increased transmissibility. 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	I and particular and particular in a day paparation into a presence of a particular and a p
Uchenna	Nwaege	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
Victoria	Oberreiter	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	331	969	A new method of extract-pooling for sediment anderet DNA analyses
Linda	Ongaro	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	332	1401	Investigating population structure and patterns of natural selection in NeoHhic Europeans
Silvia	Perretti	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	Pivirotto	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 Drosophila melanogaster 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			A joint framework for estimating F-statistics and PCA
Francesco	Ravasini Renton	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24 SP_24			Archaeogenetics of Central Italy: A dischortic analysis of the Adviatic coast traced by ancient genomes.
Jessie Stefania	Sasso	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology Erem the present to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	330	1479	Ber molecular clock in a cload agamian
Susanna	Sawyer	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology 16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	340	14/0	Ancient DNA perspective on the origins and structure of a Merovingian population in Beiglum Improved methylation detection in ancient DNA
Donikë	Sejdiu	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	340	661	Improve interpreter interpreter in accuse of the second se
Patrizia	Serventi	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24			Inside the communities of Central Italian Perinsula in the Middle Ages: exploring human mobility and social organization through ancient DNA
Mattias	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
Olivia	Smith	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	344	687	The evolution of the human methylome in ancient Europe
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 suicide (a@coecocidea@) theory in Rapa Nui with ancient DNA data
Megha	Srigyan	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	346	1427	Miogenenic analysis of a late Pleistocene jaguar from North America
Yaniv	Swiel	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 Scanshavian dog trends
Aleksandra	Zeromska Zhang	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24 SP_24	349	1205	The use of ancient DNA (aDNA) analyses to reconstruct the phylogeny and evolution of the northern vole population (Alexandromys oeconomus) Archaeogenomics of maize evolution in the South American Andes
Shuya Ilia	Artiushin	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology 19 - Evolution of structural genomic variation in populations & species	SP 24	351	1355	Verbacegeromiss of make evolution in the south American Andes Oricomosome-scale inversions in the Malawi cichild radiatore widespread and long-lived.
Cristina	Barragan	19 - Evolution of structural genomic variation in populations & species	SP_24	352	943	United by the second se
Chloé	Beaulieu	19 - Evolution of structural genomic variation in populations & species	SP 24	353	342	The first par-genere of a non-vascular plant trooders for and plants adaptation to the environment
Tiago	Belintani	19 - Evolution of structural genomic variation in populations & species	SP_24	354	1364	Improving Phylogenetic Signal with UCE Alele Sequences: A Comparative Analysis of Triatominae
Greta	Bellinzona	19 - Evolution of structural genomic variation in populations & species	SP_24	355	367	Genomic evolution of Cryptospontilum parvum
Casey	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 inference of Ty insertion patterns in yeast.
Melanie	Brien	19 - Evolution of structural genomic variation in populations & species	SP_24	358	1065	A complex colour polymorphism is associated with a gene duplication in wood Siger moths
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 SP_24	360	870	Is there an advantage to polyploidy in animals? Consequences of whole genome duplication in a syntheticC. elegans tetraploid
Le Qin Catherine	Choo Collins	19 - Evolution of structural genomic variation in populations & species	SP_24 SP_24	361	1193	Res of chromosomal investions in adaption and speciation in the flar previousled.titoring faatalis
Catherine Lila	Collins Colston-Nepali	19 - Evolution of structural genomic variation in populations & species	SP_24 SP_24	362	12/0	The spatial and temporal distribution of an adaptive lakeral gene transfer in a grass
Giuseppe	Colston-Nepali Condorelli	19 - Evolution of structural genomic variation in populations & species 19 - Evolution of structural genomic variation in populations & species	SP_24	363	1180	Parallel patents of differentiation at chromosomal inversions and other genomic negions in the European fait cyster Conomic and behavioural variation in different ecotypes of the mosquite Acopheles coluzal
Johann	Confais	19 - Evolution of structural genomic variation in populations & species	SP 24	365	1264	Centre and the elevendate and elevendate of the
Emma	Curran	19 - Evolution of structural genomic variation in populations & species	SP_24	366	95	The last of solutions includes a solution of the landscape of structural variation and polypiold adaptation
Gabriel	David	19 - Evolution of structural genomic variation in populations & species	SP_24			Calling Structural Variants with Confidence in Wild Brid Populations: Read-mapping & Pangenomic Approaches
Luis	Delaye	19 - Evolution of structural genomic variation in populations & species	SP_24	368	885	Hgbly Iterated patindromes in cyanobacterial genomes: an abominable mystery
Natalia	Diaz	19 - Evolution of structural genomic variation in populations & species	SP_24	369	1267	Insights in the Atlantic bluefin tuna population connectivity revealed by altacore origin introgression preserved within a structural variant
Tristram	Dodge	19 - Evolution of structural genomic variation in populations & species	SP_24	370	466	The genetic architecture of adaptive pigmentation traits in sworttal (Xiphophonus) fishes
Luke	Dunning	19 - Evolution of structural genomic variation in populations & species	SP_24	371	509	Lakral gane transfers accumulate as accessory ganes in grass pangenomes
Tori	Eggers	19 - Evolution of structural genomic variation in populations & species	SP_24	372	927	Comparative genomics of outcossing and selfing Oschelus nematodes
Katie Christopher	Emelianova Fiscus	19 - Evolution of structural genomic variation in populations & species 19 - Evolution of structural genomic variation in populations & species	SP_24 SP 24	3/3	1005	Repld adgree relation in the Persimon genux: investigating the diversitying role of transposable elements Description address in the Persimon genux: investigating the diversitying role of transposable elements
Christopher Hayley	Free	19 - Evolution of structural genomic variation in populations & species 19 - Evolution of structural genomic variation in populations & species	SP_24 SP 24	3/4	604	The genetic control of rapid genome context divergence in Analidopsis thaliana Endogenous Retrovinses in Aruran Genomes
Sergio	Gonzalez Mollinedo	19 - Evolution of structural genomic variation in populations & species 19 - Evolution of structural genomic variation in populations & species	SP 24	375	1409	Endogenous Netroinitudes in Anurain contines Stuffing the deck; effects of inbreeding on transposable element insertion rate in a small bird population
Landen	Gozashti	19 - Evolution of structural genomic variation in populations & species	SP_24	377	1430	Universal signatures of repeat compartmentalization in eukaryotic genomes
Clara	Groot Crego	19 - Evolution of structural genomic variation in populations & species	SP_24	378	353	Short structural variation fuelled 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 plasmid genomes
Anne	Hatmaker	19 - Evolution of structural genomic variation in populations & species	SP_24	380	369	Evolution of human pathogenesis in Aspergillus 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 keystone Arctic species with high gene flow
Stella	Huynh	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
Erna	King	19 - Evolution of structural genomic variation in populations & species	SP_24	383	I 1104	Nematode ancestral linkage groups beyond the great divide
Robert Marc	Kofler Krasovec	19 - Evolution of structural genomic variation in populations & species	SP_24 SP_24	384	635	A Pelement invation is experimental populations shock light on the silencing of a newly invating transpoon
Marc Amina	Kurbidaeva	19 - Evolution of structural genomic variation in populations & species 19 - Evolution of structural genomic variation in populations & species	SP_24 SP_24	365	1149	High nates of sportaneous chromosomal displications reveal dosage compensation by translational regulation Micro-C reveals structural and functional differentiation of rice genomes
Wen-Juan	Lan	19 - Evolution of structural genomic variation in populations & species 19 - Evolution of structural genomic variation in populations & species	SP 24	380	1040	Intersect reveals structural and turbohing dimensional dimensional and the second dimensional
Chiara	Leo	19 - Evolution of structural genomic variation in populations & species	SP 24			
Raquel	Linheiro	19 - Evolution of structural genomic variation in populations & species	SP_24	389	728	Adaptation of the Angheles coluzif inorgalitous to lab environment: a genomic perspective Investigating the contribution of transposable elements intraspectific polymorphism to grapevice resistance to high temperatures.
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 mutational mochanisms: the used-fused effect and its consequences

Eugenio	López Cortegano	19 - Evolution of structural genomic variation in populations & species	SP_24	391	1 4	12 The complete spectrum of do novo mutations in mice from a MA experiment
Eugenio Juliette	Luiselli	19 - Evolution of structural genomic variation in populations & species	SP_24	392	2 9	D4 Robustness to structural variants lead to different types of genome streamlining in species with larger populations or higher mutation rates.
Simone	Marcolini	19 - Evolution of structural genomic variation in populations & species	SP_24	393	3 6	55 A comparative analysis of molecular markers and mitogenome structure to dissect intraspecific diversity within two model species of arbuscular mycorrhizal fungi
Jacopo	Martelossi	19 - Evolution of structural genomic variation in populations & species	SP_24	394	1 5	89 The contribution of transposable elements in the emergence of within and between individual structural variants in bivalve molluscs
Flavia	Mascagni	19 - Evolution of structural genomic variation in populations & species	SP_24	395	5 13	28 Exploring models for novel genes evolution: domestication 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	6	53 Estimating Transcriptome Complexities Across Eukaryotes
Laura	Meyer	19 - Evolution of structural genomic variation in populations & species	SP_24	397	7 5	41 Divergence and gene flow at two inversions involved in seahorse ecotype formation
Giorgia	Modenini	19 - Evolution of structural genomic variation in populations & species	SP_24 SP_24	398	3 4	95 Roymorphic transposable element insertions provide new insights into North Italian isolates genetic variability
Julia Anastasiia	Morales-Garcia Mykhailenko	19 - Evolution of structural genomic variation in populations & species	SP_24 SP_24			
		19 - Evolution of structural genomic variation in populations & species	SP_24 SP 24	400		Deg Complex inversion polymorphism landscape in European spruce bark beets or
Anthony Ekaterina	Nguyen Noskova	19 - Evolution of structural genomic variation in populations & species	SP 24	401	1 0	53 Displations and retrogenes are numerous and widespread in modern carline genomic assemblies
Jordan		19 - Evolution of structural genomic variation in populations & species	SP 24	402	2 13	14 Demographic Inference using GADMA2 E
Moritz	Orosco Otto	19 - Evolution of structural genomic variation in populations & species	SP 24			Ad openne expansions in the Trichmonas genes are mediated by instead selection and differential piRNA expression. The trick openness are mediated by instead selection and differential piRNA expression.
Giacomo	Potente	19 - Evolution of structural genomic variation in populations & species 19 - Evolution of structural genomic variation in populations & species	SP 24	404	5 5	The structured coalescent in the context of gene copy number evolution Origins and evolution of the S-boox supergene in primoses
Stephen	Proulx	19 - Evolution of structural genomic variation in populations & species 19 - Evolution of structural genomic variation in populations & species	SP_24	400	3 4	Cryan and evolution of the s-excit supergrave in primotes [6] Migratin selection balance and the evolution of grave interactions
Marta	Puig	19 - Evolution of structural genomic variation in populations & species	SP 24	407	7 15	Dury long wead data is built a complete curated catalog of human polymorphic investions mediated by inverted repeals
Hadi	Quesneville	19 - Evolution of structural genomic variation in populations & species	SP_24	408	3 7	Exploring promote data interest and a construction of the state population of the state of the s
Janina	Rinke	19 - Evolution of structural genomic variation in populations & species	SP_24	409	9 13	33 The evolutionary role of transposable elements in genome compartmentalization of ants
Bianca	Sacchi	19 - Evolution of structural genomic variation in populations & species	SP_24			14 Y chromosome degeneration at different timescales: exploring neeky assembled old and new sex chromosomes in Rumax hastatulus
Somia	Saidi	19 - Evolution of structural genomic variation in populations & species	SP_24	411	1 9	88 Characterization of Transposable Elements in Pargenomes
Marine	Salson	19 - Evolution of structural genomic variation in populations & species	SP_24	412	2 6	10 Buper-dominance likely maintained 80 Mbases inversion polymorphism in pearl millet
Yannick	Schäfer	19 - Evolution of structural genomic variation in populations & species	SP_24	413	3 6	33 Modeling the emergence of gene clusters under ectopic gene conversion to elucidate the evolutionary history of a heavy metal adaptation in Arabidopsis halteri
Divya	Selvaraju	19 - Evolution of structural genomic variation in populations & species	SP_24	414	1 9	86 Evolutionary dynamics of P-element invasions in Drosophila species
Daniel	Siqueira De Oliveira	19 - Evolution of structural genomic variation in populations & species	SP_24	415	5 7	16 Genomics and transcriptomics of cactophilic Drosophila species: The divergence sources explained by transposable elements and gene expression variability
Rumiko	Suzuki	19 - Evolution of structural genomic variation in populations & species	SP_24	416	3 5	08 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 Drosophila
Carlos	Vargas Chávez	19 - Evolution of structural genomic variation in populations & species	SP_24	418		Transmark genomic rearrangements at the origin of Citelata as potential key drivers of annelid terrestrialization
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Adrian Kenneth	Jaimes-Becerra Kim	27 - Regulatory evolution and the emergence of diversity	SP_24 SP 24	489	404	4 The evolution of toxin-producing cell types in Critikaria
Kenneth	Kim Le Veve	27 - Regulatory evolution and the emergence of diversity 27 - Regulatory evolution and the emergence of diversity	SP_24 SP_24	490	13/2	Comparise gene spression analysis of mouting in insect and Chastacean Inseges The James de advectory functional sectors and advectory of the Advectory
Audrey Mariana	Le Veve Leal Cardin	27 - Regulatory evolution and the emergence of diversity 27 - Regulatory evolution and the emergence of diversity	SP_24 SP_24			The Impact of genomic imprinting on genetic variation in A lyrata. Differential Expression Cf Immune Genes In Two Recently Differentiated Cichid Species
Thomas	Lesaffre	27 - Regulatory evolution and the emergence of diversity 27 - Regulatory evolution and the emergence of diversity	SP 24	492	54	Dimenential Expression of Immune Genes In two Recently Linerentiated Cicrite Species 7 On the origins of Y and W chromosomes from sex allocation evolution
Clifton	Lewis	27 - Regulatory evolution and the emergence of diversity	SP 24	494	129	Comparative evolution of neurogenic gene regulatory networks
Xueying	Li	27 - Regulatory evolution and the emergence of diversity	SP 24	495	15	Comparise tensions interception interception, get in registrary interception Matalonal scars reveal officerial evoluatily official evoluation of other
Wei-Han	Lin	27 - Regulatory evolution and the emergence of diversity	SP_24			8 Investigating The Regulatory Mechanism of Protein Expression Noise by Experimental Evolution in Saccharomyces cerevisiae
Yoav	Mathov	27 - Regulatory evolution and the emergence of diversity	SP_24	497	1346	6 Inferring DNA methylation in non-skeletal tissues of ancient specimens
Camille	Mayeux	27 - Regulatory evolution and the emergence of diversity	SP_24	498	989	9 Consequences of viral infections on transposable element regulation in Drosophila
Adriaan	Meiborg	27 - Regulatory evolution and the emergence of diversity	SP_24	499	949	9 The evolution of the planarian size-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 Metoidogyne incognita parasitismin tomato&Cplant nematode interactions
Deniz	Ozbilek	27 - Regulatory evolution and the emergence of diversity	SP_24	502	1280	U Understanding RNA polymerase structure-to-function relationship to predict evolution of rifampioin resistance
Juan	Pascual-Anaya	27 - Regulatory evolution and the emergence of diversity	SP_24 SP 24	503	158	1 Hegital genome illuminates vertebrate whole genome deplications and their evolutionary consequences
Valentine	Patterson	27 - Regulatory evolution and the emergence of diversity	SP_24	504	113	Akek-Spectrc Expression in Clonal Hybrid Whiptial Lizards
Mitchell	Perry Reynolds	27 - Regulatory evolution and the emergence of diversity	SP 24	506	040	Regulary sequence evolution underlying hiterration in bears Original and a sequence and a se
Carlos	Rivera Rivera	27 - Regulatory evolution and the emergence of diversity 27 - Regulatory evolution and the emergence of diversity	SP_24			Understanding the role of genetic background in determining the evolutionary outcome of gene regulatory network rewring events. Cathlet a system-level sequence evolution simulator
Carlos	Rodriguez-Ramirez	27 - Regulatory evolution and the emergence of diversity 27 - Regulatory evolution and the emergence of diversity	SP 24	508	64	accurece a systema-even sequence evolution simulation The contribution of alternative splicing to adaptation in threespine stickleback
Laasya	Samhita	27 - Regulatory evolution and the emergence of diversity 27 - Regulatory evolution and the emergence of diversity	SP 24	500	164	In contraction or automative specify to additation in previous sectoreads. 4 Mistranslation abors the genetic basis of additation to antibiotics
Thanvi	Srikant	27 - Regulatory evolution and the emergence of diversity	SP 24	510	66	Chromatin-mediated gens-regulatory dynamics in adaptation to polypooly
Jeffrey	Townsend	27 - Regulatory evolution and the emergence of diversity	SP 24	511	1436	Beene duplication, chromosomal namrangement, repeat-induced point mutation and fast divergence transform non-coding regions into a nummage regionfor de novo lineage-specific elements in Neurospora crassa
Marco	Trizzino	27 - Regulatory evolution and the emergence of diversity	SP 24	512	148	A SMARCA4 genetic variant exclusive of the Dolphin lineage (Delaceans, Ostortocet) 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			The LPP conters a habitat switch through chromosomal gene regulation inPartose agglomerans associated with wheat seeds
Yu	Wang	27 - Regulatory evolution and the emergence of diversity	SP_24	514	1063	2 Patterns and Evolutionary Mechanisms of Subgenome Expression Differentiation in Common Wheat
Daniel	Weinreich	27 - Regulatory evolution and the emergence of diversity	SP_24	515	1474	4 The Evolution of Biological Noise
Yarden	Weiss	27 - Regulatory evolution and the emergence of diversity	SP_24	516	294	4 The effect of sequence changes in cis-regulatory elements on divergent gene expression between humans and chimpanzees
Cauã	Westmann	27 - Regulatory evolution and the emergence of diversity	SP_24	517	1388	B 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	D DNA methylation diversity in Plateau Zokor (Eospalax balleyi) and its association with plateau adaptation
Xuefei	Yuan	27 - Regulatory evolution and the emergence of diversity	SP_24	519	1493	3 The molecular evolution of mammalian livers
Giulia	Zancolli	27 - Regulatory evolution and the emergence of diversity	SP_24	520	1239	Spatial functional specialisation of a biochemical weapon factory
Xiaoyu	Zhou	27 - Regulatory evolution and the emergence of diversity	SP_24	521	1510	Hyp-resolution RNA isoform variation analysis by combining the advantages of single-cell RNA and nanopore sequencing
Rogdan	Efimenko	07 - Computational evolutionary genomics in the era of machine learning 07 - Computational evolutionary genomics in the era of machine learning	SP_24	523F	149	U prover to center appsoent mess sens dita a mar number of table can be rescued with a covariate-informed branch-safe type method A Transit former to center appsoent inserting and the table table to table can be rescued with a covariate-informed branch-safe type method A Transit former to center appsoent inserting and the table table table table table.
Bogdan	Elimenko		SP_24 SP_24		1284	Towards large-scale comparative species analyses of the Neutral Mutation Spectra - NetMu pipeline
Konstantin	Gunhin	07 - Computational evolutionary genomics in the era of machine learning 07 - Computational evolutionary genomics in the era of machine learning	SP 24	525F 526F	128	I forming evolutionary dynamics on empirical incomplete threes undicapee D Accurate reconstruction of the human mitochondial genemics multication provide insight into the process of mutagenesis D Accurate reconstruction of the human mitochondial genemics D Accurate reconstruc
Devashish	Tripathi	07 - Computational evolutionary genomics in the era of machine learning 07 - Computational evolutionary genomics in the era of machine learning	SP_24 SP_24	5275	103	Accurate reconstruction of the numan micromonal germine mutations provide indiger into the process of nuclagenesis A Deep learning approach for modeling Genotype-Environment interaction to detect genomic regions under natural selection
Daniele	Battilani	15 - Animal genomics goes wild	SP 24	528F	56	Long harming uppears on income consuper-invention in instances to execute constraints register activates instances instan
Meirav	Meiri	15 - Animal genomics goes wild	SP_24 SP_24			The genetic history of the Judean Desert leopard (Panthera pardus nim) The genetic history of the Judean Desert leopard (Panthera pardus nim)
Hayley	Hassler	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP 24	5305	36	Disc generation approximation on the evolution of consistences to learning the benefits of alternate frequencies of nRNA vaccine boosting for immune-typical and immunocompromised individuals
Gulsah Merve	Kilinc	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP 24	531E	101	Evolutionary gramics behind metabolic traits in Anatolia over the last 10,000 years: What can ancient genomes ket?
Martin	Petr	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP 24	532F	1419	A simple and efficient R tookit for Approximate Bayesian Computation
Kai	Shimagaki	16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	SP_24	533F	809	P An efficient method for inferring epistasis from temporal genetic data, applied to HV-1 evolution
Laura	Landweber	19 - Evolution of structural genomic variation in populations & species	SP_24	534F	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 SP_24	535F	769	9 Dynamic evolution and diversification of antivital gigt and gig2 gene families in Atlantic salmon
Eri	Tabata	19 - Evolution of structural genomic variation in populations & species	SP_24	537F	454	The relationship of feeding behaviors and molecular evolution of acido chitmase in Cetartiodactyta
Lina	Utenova	19 - Evolution of structural genomic variation in populations & species	SP_24	538F	42	Association of gingival bleeding with the onal inforcatione in the Emirati population
Stepan	Denisov	20 - Evolutionary biology through a functional genomics lens	SP_24	539F		2 Evolution of intrinsic transcriptional terminators in their genomic context
Akshi	Gupta	20 - Evolutionary biology through a functional genomics lens	SP_24	540F	143	3 Ortholog replacement reveals a novel function of the transcription factor TFIIIC complex in mitotic chromosome segregation
Alba	Julia	20 - Evolutionary biology through a functional genomics lens	SP_24	541F	1178	B High phenotypic plasticity of the azure damsetty (Coernagrion puella) to induced temperature shock
Alexey	Skudnov	20 - Evolutionary biology through a functional genomics lens	SP_24	542F	1176	The rocky road to aerobic and anaerobic prokaryotes mutational spectra reconstruction and analysis
Alexandr	Voronka	20 - Evolutionary biology through a functional genomics lens	SP_24	543F	1306	
Kimberly	Griffin	27 - Regulatory evolution and the emergence of diversity	SP_24	544F	1099	Defining the Role of Cis-Acting DNA Sequence in Evolutionary Divergence of the Bivakent Chromatin State in Mammals
Julie	Grosse-Sommer	27 - Regulatory evolution and the emergence of diversity	SP_24	545F	33	3 The influence of selection strength on variation in additive genetic variance
Sen	Hadife	27 - Regulatory evolution and the emergence of diversity	SP_24 SP_24	546F	99	5 The role of DNA demethylation in embryogenesis and epigenome regulation
Manas	Josni	27 - Regulatory evolution and the emergence of diversity 27 - Regulatory evolution and the emergence of diversity	SP_24	5405	10	
Lina	Abdelwahed	05 - New frontiers in conservation genomics	EC 25	540	61	Natural selection forces acting on transcriptional control of the Iac2 promoter How to evaluate the connectivity of plant communities in endargened habitats ? An ecological and genetic approach.
Larissa	Arantes	05 - New frontiers in conservation genomics	EC 25	550	129	Ver non-invester samples agood DM source for NAR see-based genetic monitoring?
Gözde	Atag	05 - New frontiers in conservation genomics	EC 25	551	626	6 Genomic Insights into the Endangened Moufon Populations of Anatolia and Oypna
Roberto	Biello	05 - New frontiers in conservation genomics	EC 25	552	125	A comprehensive genomic approach for the critically endangered Apermine brown bear: predicted load, functional essays, simulations, and much more
Elena	Buzan	05 - New frontiers in conservation genomics	EC 25	553	496	B Metabarcoding the diet of grey wolf and Eurasian lynx in the Alps and the Dinario Mourtains
Jillian	Campbell	05 - New frontiers in conservation genomics	EC 25	554	1063	3 Insights on Catostomus sucker hybridization and spawning trends using genomic data
Louise	Camus	05 - New frontiers in conservation genomics	EC_25 EC_25	555	513	Predicting species invasiveness with genomic data: is Genomic Offset related to establishment probability ?
Enrique	Celemin Amaro	05 - New frontiers in conservation genomics	EC_25	556	55	Evolutionary history and seascape genomics of Haitbour porpoises (Phocoena phocoena) across environmental gradients in the North Atlantic and adjacent waters
Hedvig	Csapo	05 - New frontiers in conservation genomics	EC_25	557	115	2 Divergent Arctic lineage of the northern acorn barracle in Svalbard provides evidence against the hypothesis of recent Atlantification.
Marisol	Dominguez	05 - New frontiers in conservation genomics	EC_25	558	153	Low polymorphism of MHC class I genes in a threatened passerine bird: insights from a genomic perspective
Rosie	Drinkwater	05 - New frontiers in conservation genomics	EC_25	559	115	5 Combining genomics and spatial models to improve long-term conservation management of Island endemics
Erik	Enbody	05 - New frontiers in conservation genomics	EC_25	560	1322	2 Comparative effective estimated migration surfaces
Huizhong	Fan	05 - New frontiers in conservation genomics	EC_25 EC_25	561	503	3 Conservation priorities for global marine biodiversity across multiple dimensions
Ellika Jonathan	Faust Flowers	05 - New frontiers in conservation genomics	EC_25 EC_25	502	1/254	4 Establishing a framework for conservation genomics of freshwater biodversity
Maeva	Gabrielli	05 - New frontiers in conservation genomics 05 - New frontiers in conservation genomics	EC_25 EC_25	500	72	S Hydridzation, intereding and population decline in Europede ^{rm} s lass pairn (Phoenix theophrasti) forests Living on a rock with three heteropyous sites per megabase: the genomics of the Acolan wall loard
Yuting	Gao	05 - New frontiers in conservation genomics 05 - New frontiers in conservation genomics	EC_25	56	122	2 Uving on a rook with three neterooppous seas per megatasize the genomics of the aeotan wait taard 3 Det, not amyliase gene copy number, defines salivary amylase levels in closely related species
Daniel	Gygax	05 - New frontiers in conservation genomics	EC_25	566	77	Dec. In call where gene copy names, summary any any and even in covery returned species Concrete and statistical tools for non-invasive monitoring of two endangered birds
Ulises	Hernandez	05 - New frontiers in conservation genomics	EC 25	567	898	Centrer callo statistical code no rest-levastre manufangi o neo ensangereo cross.
Rus	Hoelzel	05 - New frontiers in conservation genomics	EC_25 EC_25	568	480	D Genomics of post-bottleneck recovery in the northern elephant seal
Sagane	Joye	05 - New frontiers in conservation genomics		569	979	9 A fexible and reproducible Snakemake workflow for PacBio HFI long-read assembly and evaluation
Thomas	Kaczmarek	05 - New frontiers in conservation genomics	EC_25	570	1386	B Evolutionary genomics of fonio (Digitaria exilis): value of a large partnership and diversity studies for conservation and sustainable use.
Youngkyung	Ko	05 - New frontiers in conservation genomics	EC_25	571	22	2 Transposable elements derived microRNA expression patterns in TCGA: evolutionary analysis for 10 species
Mitchell	Lokey	05 - New frontiers in conservation genomics	EC_25	572	1554	4 Recent population collapse shapes deleterious variation across subpopulations of the endangered Florida sorub-jay.
Samantha	López Clinton	05 - New frontiers in conservation genomics	EC_25	573	518	B Exploring new computational methods for genome-wide eDNA biodiversity monitoring
Leandro	Lucero	05 - New frontiers in conservation genomics	EC_25	574	17	Nec-functionalization of a LIKE HETEROCHROMATIN PROTEIN 1 member of the plant Polycomb Repressive Complex 1 (PRC1) in Brassica rapa (Brassicaceae)
Therese	Markow	05 - New frontiers in conservation genomics	EC_25 EC_25	575	232	2 Population and functional genomic diversity in the endangered Monarch butterity, Danaus plexopus
Alicia	Mastretta-Yanes	05 - New frontiers in conservation genomics	EC_25	5/6	330	D Teosintes effective population size through time and space
Camila	Mazzoni	05 - New frontiers in conservation genomics	EC_25 EC_25	571	180	Paring the way to support sea burtles conservation with high-quality genomic data A A
Olena	Meleshko	05 - New frontiers in conservation genomics	EC_25 EC_25			Genetic structure and reproduction in a donal polyhoid plant
Jess Albert	Peers Perlas Puente	05 - New frontiers in conservation genomics	EC_25 EC_25	579	/02	2 Intreening-associated gene pseudogenization in the chetethy, kelonovy (batus
Albert Emily	Perlas Puente Roycroft	05 - New frontiers in conservation genomics	EC_25 EC_25	580	973	3 Towards non-invasive mailum antibiting of Anian influenza virus.
	Sapino	05 - New frontiers in conservation genomics 05 - New frontiers in conservation genomics	EC_25 EC_25	581	100	The genomic impact of island isolation in Australian mammals
	Sapino		EC_25 EC_25			Methodological advances in the analysis of the metagenome of liberian desman feces. Advances on which and analysis of the metagenome of liberian desman feces.
		05 - New frontiers in conservation genomics 05 - New frontiers in conservation genomics	EC_25	584	10	Deterious mutations and genetic load in internet Scandrawian welves Julier novel population genomics methods to characterise the genomic consequences of a major environmental disturbance
Linnéa	Sopniewski					
Linnéa Jarrod	Sopniewski Spatola	05 - New frontiers in conservation genomics	EC 25	584	191	3 Ancestry and origin of free-roaming dogs on the Galapagos Islands
Gabriella	Sopniewski Spatola Tiong	05 - New frontiers in conservation genomics	EC_25 EC_25	585	193	Ancestry and origin of free-roaming dogs on the Galapagos Islands
Linnéa Jarrod Gabriella Regine Ana	Spatola Tiong Topasna	05 - New frontiers in conservation genomics 05 - New frontiers in conservation genomics 05 - New frontiers in conservation genomics	EC_25 EC_25 EC_25	586	i 193 i 468	A Recentry and origin of free-roaming dogs on the Galapages Islands Conservation genomics reveals inbred population of critically endungered hawisbill turties in Singapore
Linnéa Jarrod	Spatola	05 - New frontiers in conservation genomics	EC_25 EC_25	586	i 193 i 468 i 196	Ancestry and origin of free-roaming dogs on the Galapagos Islands

Maurine	Vilcot	05 - New frontiers in conservation genomics	EC_25	59	321	Environmental DNV: a tool for systematic spatial conservation planning from inter- to intraspecific scales
	Bracht	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	59	1 1109	Evolutionary tuning of mitochondrial cytochrome c oxidase in the Devil Worm
	Camus	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	59	2 1367	Contribution of mitonuclear genomes to local adaptation
	Carli Chaw	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25 EC 25	59	3 1141	Esploratory analysis in mitochondrial ability to generate small RNA interference.
Yu-Chi	Chen	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25 EC_25	59	5 242	Evolution of mitochondus RHA edition in state granosperms
	Debelli	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution 08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC 25	59	3 138	Phylorunitonics uncovers widespread abundance of ancient mitochondrial DNA burried in vertebrate genomes The male-specific of of the patemaly-transmitted mDNA in Myllus edulis codes for a protein
	Dubie	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC 25			Using experimental evolution to elucidate the role of fusion, fission, and autophagy in the fate of selfish mitotypes in Caenonhabditis elegans
Yiyuan	Fang	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	59	3 930	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			Population genomics in the Hawaiian volcano shrimp (Halocaridina nubra): cryptic speciation and mitonuclear discordance
	Grover-Thomas	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	60	819	Problems in the Powerhouse do mild mitonuclear mismatches impact mitochondrial physiology
	Havird	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	60	1 229	Adaptive vs. relaxed selection on animal mitochondrial genes
	Kang	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	60	2 494	Comparative milochondrial genome analysis of two pear pests, Cacopsyla Jukyungi and Cacopsyla burchhandti (Hemiptera: Psylidae)
	Kayal	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25 EC_25	60		Gain, loss, and evolution of multi homolog in mitochondrial genome of octocorals
	Khachaturyan	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25 EC 25	60	1 289	Evolution of the plant organelies is characterized by similar substitution rate but different allele dynamics
	Kim Kravchenko	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25 EC_25	60	2 1100	Comparative characteristics and phylogeny of complete mitochondial genomes of four Carpophilus beetles (Coeloptera: Nitiolidae)
	Kiavonenko	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution 08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC 25	60	7 313	Survey of mEDNA recombination in Metazoa and other evaluayotes Lessons from oceans: rampart nuclear-intochondrial-plastid phylogenomic discondance in microalgae
	Leroux	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC 25	60		Extractor intervolutor manyour indexterminectantine plante by operating externation in metalogue Mitochnolfial DNA methylation and doubly uniparential interfrance
	Lometto	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC 25	60	9 565	Evolution of a fiber-forming enzyme in Tetrahymena Brennophilic did proteits evolve new cytoskeletal proteins?
Pawel	Mackiewicz	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	61	1123	Evolution of duplicated regions in mitochondrial genomes of birds (Aves)
	Mikhailova	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	61	1 1165	A billion-year trend of amino acid substitutions in the mitochondrial genome
	Minor	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	61		CICAAT Enhancer binding protein B (C/EBPB) 46" 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	61		The role of mitochondial remodeling in the phenotype of a selfsh mitochondial genome
	Parkus	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	61	4 672	Evalution and function of the stalk-eyed By mitochondrial genome
Marco	Passamonti	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	61	5 1066	Mitochondrally-mediated RNA interference, a fast-evolving retrograde signaling system to regulate nuclear gene expression.
	Plazzi Pozzi	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25	61	3 376 7 861	Unaveling the phylogenetic signal by means of ortholog dusters: the case of bivalve moliculas The mitichondelial Interfacence Interface
Sofia	Sabbagh	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution 08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25 EC_25			The mitochendrial interference hypothesis, a new hypothesis for an old story Variations in hepatic cellular metabolism of naturally intected pumpkinseed sunfah (Laponis gibbosus)
	Skujina	08 - Milochondria across biodiversity: comparative genomics as a tool to unraver milochondrial biology and evolution 08 - Milochondria across biodiversity: comparative genomics as a tool to unravel milochondrial biology and evolution	EC 25	61	9 1068	vaniatom in reparc celular metadolami of naturaly intected purportised sumsin (Lapono globosus) The lays to the powerhouse: novel insights of mitochondrial regulation using large-scale comparative genomics data of longevity specialists &? long lived microbat Myotis myotis.
	Warren	08 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	EC_25			Transitions in the production for some of the last remaining mitochooking and a set of the last remaining mitochooking and the set of the set of the last remaining mitochooking and the set of the last remaining mitochooking and the set of the
Dareen	Almojil	26 - Genomics of Adaptations to Extreme Environments	EC_25	62	1 1012	Genetic signals of high-atitude in the allopolypioid African clawed frog Xenopus laevis
	André	26 - Genomics of Adaptations to Extreme Environments	EC_25	62	2 224	Genomic Signatures of Local Adaptation to Extreme Environments in Papua New Guinean Highlanders and Lowlanders
	Authier	26 - Genomics of Adaptations to Extreme Environments	EC_25	62	3 1391	Phenotypic response of flowering plants to limited access to natural pollinator community
	Bastos	26 - Genomics of Adaptations to Extreme Environments	EC_25	62		Evolution of molecular mechanisms of thermoregulation in rodents
	Bista	26 - Genomics of Adaptations to Extreme Environments	EC_25	62	5 1294	Genomics of cold adaptations in the Antarctic nototherioid fish radiation.
	Bosi	26 - Genomics of Adaptations to Extreme Environments	EC_25 EC_25	62	1131	Genoms of White spp. isolated from key-sea hydrothermal verse hydrothe
	Cao Carleial	26 - Genomics of Adaptations to Extreme Environments		62	6 525	Genomic Insights into Adaptation to Karit Limestone and Insigerst Speciation in East Aeian Platycarya spp. (Juglandaceae)
Eduardo	Castro-Nallar	26 - Genomics of Adaptations to Extreme Environments 26 - Genomics of Adaptations to Extreme Environments	EC_25 EC_25	62	436	derwinis basis of Quercus (shour resistance to acute auX decline in Billiain derwinis (shour cus shour cus
Bridget	Castro-Inalian	26 - Genomics of Adaptations to Extreme Environments	EC 25	63	1161	Mobile genetic elements and the resistome of microbial communities in the Comeur Eprint, Patagonia (42 AVS) Reconstructing admituture history and its note in facilitating local adaptations among the Batwa and Bakiga in East-Central Africa
Piaopiao	Chen	26 - Genomics of Adaptations to Extreme Environments	EC 25	63	1 309	Reconstructing automate instantly with its room in accurating local adaptations among the Ballina and Balling in East-central versus The loci of environmental adaptations of budding yeast
	Cho	26 - Genomics of Adaptations to Extreme Environments	EC_25	63	2 33	Ins door sensetiments adaptation to code y france
Gleb	Ebert	26 - Genomics of Adaptations to Extreme Environments	EC_25	63	3 1049	No Need to Be Stressed: Regulatory Charges After High-Temperature Adaptation
Elsa	Froufe	26 - Genomics of Adaptations to Extreme Environments	EC_25	63	1659	Genomic Adaptations Associated with Climate Change and Biological Changes in the unionid mussel Unio delphinus (Spengler, 1793)
	Ghosh	26 - Genomics of Adaptations to Extreme Environments	EC_25	63	5 1318	Population-specific adaptation to diverse environments in South America
	Golomb	26 - Genomics of Adaptations to Extreme Environments	EC_25	63	3 1373	Exploring a novel concept: cell-autonomous evolutionary adaptation
	González Buenfil	26 - Genomics of Adaptations to Extreme Environments	EC_25	63	7 859	Adaptation to high abitude and other extreme environments across the Pacific: Signals of positive selection from the Oceanian Genome Variation Project
	Graham	26 - Genomics of Adaptations to Extreme Environments	EC_25	63	3 199	Convergent pseudogenization of effactory receptors in mammalian living in of Nigh-altitude environments
	Gusareva	26 - Genomics of Adaptations to Extreme Environments	EC_25 EC_25			Adaptation to the cold environment in indigenous Arctic populations.
	Gutierrez Guerrero	26 - Genomics of Adaptations to Extreme Environments		04	1338	Comparing continents: The genomic basis of environmental adaptation and parallel evolution in house mice (Mas musculus domesticus) from the Americas
George	Hirons-Alecrim	26 - Genomics of Adaptations to Extreme Environments	EC_25	64	1 796	The genomic basis of obligate dependence in ant-plant mutualisms
George Ozede	Hirons-Alecrim Igiehon	26 - Genomics of Adaptations to Extreme Environments 26 - Genomics of Adaptations to Extreme Environments	EC_25 EC_25	64	1 796 2 1655	The genomic basis of obligate dependence in ant-plant mutualisms Rhzobium Species Enhanced Soybean Growth under Drought Stress Conditions
George Ozede Iker	Hirons-Alecrim Igiehon Irisarri	26 - Genomics of Adaptations to Extreme Environments 26 - Genomics of Adaptations to Extreme Environments 26 - Genomics of Adaptations to Extreme Environments	EC_25 EC_25 EC_25	64 64 64	1 796 2 1655 3 1357	The genome basis of obligate dependence in an state of matulitarian Relation Tipocies Enhanced Soybean Caveth rude Discupt Stress Conditions Conconsent-well openders of multiclash and galaxies basis for particular dependence evolution
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Ayca Emilyclare Chiara	Aydogan	01 - Open Symposium	SP_25	688	811	Paleogenomic analyses of Neolithic populators 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	Barbieri	01 - Open Symposium	SP_25	690	808	A global analysis of matches and mismatches between human genetic and linguistic histories
Gokul Davide	Bhaskaran Bozzi	01 - Open Symposium	SP_25 SP 25	691	545	The evolution of hursting behavior and its relation to conflocaterone levels
		01 - Open Symposium	SP_25	692	1120	Towards pradicing the geographical origin of anisets samples with metagenomic data
Seraina Jaelle	Bracamonte Brealey	01 - Open Symposium 01 - Open Symposium	SP 25	694	625	Expression diversity of the Major Hatacompatibility Complex in Neotropical circleds therping between host genome and microbiota during parasite infection in farmed Atlantic salmon
Matteo	Brilli	01 - Open Symposium	SP 25	695	265	Interplay between ross genome and metodota doing paraotic mecodo in raimed valance samon The selective force driving metabolic operon assembly
Jaclyn	Bubnell	01 - Open Symposium	SP_25	696	1489	Testing the risk of positive selection in shaping the function of a germline stem cell gene in Drosophia
Dearbhaile	Casey	01 - Open Symposium	SP 25	697	52	Investigating the mechanisms of rediploidsation in the Paddefish and Sturgeon by characterisation of synteric breakpoints in their genomes.
Michele	Castelli	01 - Open Symposium	SP_25	698	1217	Comparative genomics indicate multiple independent evolutionary origins of host association and intracellularity within the Rickettsiales
Luiz Théo	Cauz Dos Santos	01 - Open Symposium	SP_25	699	1568	Phylogenomics and biogeography history of wild allopolyploid lobaccos (Necetiana section Suavedientes)
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 Talwanese people
Sophie-Carole	Chobert	01 - Open Symposium	SP_25			Unaveiling the reliative emergence of quinones biosynthetic pathways
Sehee Rodrigo	Choe	01 - Open Symposium	SP_25			Identification of key genes and pathways by co-expression analysis with blood transcriptome in NHP addiction mode!
Rodrigo	Cogni	01 - Open Symposium	SP_25 SP 25	704	277	Wolbachia reduces virus infection in a natural population of Drosophia
Omar Claudio	Cornejo Cucini	01 - Open Symposium 01 - Open Symposium	SP_25	705	319	Distribution of dwarse endophyse kall communities across Theoberna caceo genetic groups
Alice	De Sampaio Kalkuhl	01 - Open Symposium 01 - Open Symposium	SP_25	700	1102	Dail de novo assembly and amotation of the nuclear genome of Popilia japorica from the invasive Italian population. Gene diplication in the coral genus Acropons: Was there a whole genome duplication?
Alice Athena	di Properzio	01 - Open Symposium	SP_25	708	273	Dene digitazioni ni ne cona ginna Actigota, vita inter a vitute genane operative concentri. The effect of methyl famesate on sex-determining genes in obligate partherogenetic Daphnia pulex
Yoan	Diekmann	01 - Open Symposium	SP_25	709	213	HaploBlock: efficient detection of positive selection in large population genomic datasets
Louise	Dupont	01 - Open Symposium	SP 25	710	768	Phylogenry-aware sparse learning to build genetic models of HV drug resistance
	Ellers	01 - Open Symposium	SP_25	711	1528	Peliotropic functions promote preservation of the gene network when a phenotypic trait is lost
Jacintha 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.
Nicoletta Alice Simon	Feurtey	01 - Open Symposium	SP_25	/14	1143	A thousand-genome panel retraces the global spread and adaptation of a major fungal crop pathogen
Simon	Fishilevich	01 - Open Symposium	SP_25	/15	219	Compensatory mechanisms of human-specific disease mutations
Evan Silvia	Forsythe	01 - Open Symposium	SP_25	716	406	Genome-wide coevolution networks point to repeated perturbations of plastid proteostasis systems
Silvia	Fuselli	01 - Open Symposium	SP_25			
Arya Jörn Frederik	Gautam Gerchen	01 - Open Symposium	SP_25 SP_25	718	928	Characterization of the bacterial and lungal communities found in traditional Nepail formerted foods Description second audioses of later reliable intervencements for the defort trans.
Francesco	Giannelli	01 - Open Symposium 01 - Open Symposium	SP_25	719	1077	Population genomic evidence of Inter-pilody Introgression in the abler tree, Altura glutinosaagg Insurfaction the orbitionship behaves new Narod discount of mile and end discounts a forward similarities mathed (SI ND
Léa	Guyon	01 - Open Symposium 01 - Open Symposium	SP 25	721	112	Investigating the relationship between sex blased dispersal and mito-nuclear discordance, using a forward simulation method (SLIM) Is violence necessary to explain the post-Neclific Y chromosome bottleneck?
Yoonsoo	Hahn	01 - Open Symposium	SP_25	722	365	a violente intelessary or apparente posi-monitori i contractore apparente posi-monitori i contractore apparente posi- Cantifying the Efficiency of RNA Plantance Stepage Leading to PSA-Plant Drans-Frame Fusion Proteins in Potyvirids
Yuichiro	Hara	01 - Open Symposium	SP_25	723	240	Cene fale spectrum as a reflection of local genomic properties
Tia	Harrison	01 - Open Symposium	SP_25	724	1507	Mutualism with rhizobia 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 Trifolum 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 &C prevalence, magnitude and implications
Risa	Iwasaki	01 - Open Symposium	SP_25	728	483	Investigation of loci under positive selection in which &Ceadeptive&Enaplotype can differ spatially and temporally like PSCA in human populations
Wen-Ya	Ko	01 - Open Symposium	SP_25 SP_25	729	469	Phenome-wilde association studies of evolutionary deleterious variants in the Han Talwarese people
Anne Alessandra	Kupczok Lamarca	01 - Open Symposium	SP_25	730	405	Co-transfer of functionally interdependent genes contributes to genere mosaicies in lambdaid phages
Chong Duoi	Lee	01 - Open Symposium	SP 25	731	209	Why is hand to not evulnonary ratiations? Testing outprop-free methods and how we can predict their accuracy.
Cheng-Ruei Weiyi	Li	01 - Open Symposium 01 - Open Symposium	SP 25	733	155	Environment as a limiting factor of the historical global spread of mungbean A Narrow Range of Transcript-error Rates Across the Tree of Life
Ke	Li	01 - Open Symposium	SP_25			Animotorial per la material per la material de la celebra de
Ke Tadhg	Lonergan	01 - Open Symposium	SP_25			Age-related telomene dynamics in short- vs long-lived bats
Haiwei	Luo	01 - Open Symposium	SP 25			Genetic drift has an important role in Prochitorococcus genome reduction
Haiwei Milan	Malinsky	01 - Open Symposium	SP_25			Disertanging the genomic interplay of selection and recombination
Galen Hanon	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 SP_25	740	NA	Reliative model selection of evolutionary substitution models can be sensitive to multiple sequence alignment uncertainty
Ludovica Emiliano	Molinaro Mora-Carrera	01 - Open Symposium	SP_25 SP_25	741	1316	Centric characterization of individuals with non-european ancestries in Flanders, Belgium from NFT data of 30,000 individuals
Adriana	Morales-Guerrero	01 - Open Symposium 01 - Open Symposium	SP_25	742	205	Unveiling the genome-wide consequences of a recent range expansion and multiple mating system transitions in Primula vidgers.
João	Moreno	01 - Open Symposium	SP_25	743	686	Ecological and demographic drivers of Immune-Heland genomic signatures across human populations Protecme and phosphoprotecme reveal differences in phenotypic plasticity in fail under different scenarios of climate change
João Alice	Mouton	01 - Open Symposium	SP_25	745	692	The European Reference Genome Adas
Kasper	Munch	01 - Open Symposium	SP_25	746	1173	Recontinuition holipots 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	Utra-High Throughput Directed Evolution of Strand Displacing Polymerases for Improved Enzyme Activity in Diagnostic Tests
Yannis	Nevers	01 - Open Symposium	SP_25	749	1326	Multifacet quality assessment of gene repertoire annotation with OMArk
Lukasz	Niezabitowski	01 - Open Symposium	SP_25	750	1274	Building a high-confidence ohnolog dataset
Robert	Noble	01 - Open Symposium	SP_25	751	616	A new system of rooted-tree indices
Riccardo Masafumi	Nodari	01 - Open Symposium	SP_25 SP 25	752	641	SR modeling suggests an evolutionary trade-off in the translations pread of human-to-human transmitted pathogens in the centralise following the Americas discovery
Masafumi	Nozawa	01 - Open Symposium	SP_25	/53	357	Minicking sex-chromosome turnover using hybrids reveals feability of dosage companation on nec-sex chromosomes in Drosophila miranda
Wei-Chen Tin Yau	Pan Pang	01 - Open Symposium 01 - Open Symposium	SP_25	754	100/	Studying genetic adoptation and admised ancestry of the Siraya people in Talwan Natural selection for the optimal cytosolic density of a bacterial cell
Tom	Pang Parée	01 - Open Symposium 01 - Open Symposium	SP 25	756	571	Natural selection for the optimal cylosolic density of a bacterial cell Reduced selective interference increases experimental adaptive rates in C. elegans
Anieli		01 - Open Symposium	SP_25	757	1106	Relationships between fossoriality. Iintelesses and selective pressures acting on mitochondrial genes in Squamata
Anieli Cassius Manuel	Pérez	01 - Open Symposium	SP_25	758	1191	New much physippenetic information is na tranch? Battace gives an answer
Aaron	Pfennig	01 - Open Symposium	SP_25	759	91	Challenges of accurately estimating see-based admixture from X chromosomal and addisomal ancestry proportions
Aaron Sujal	Phadke	01 - Open Symposium	SP_25	760	922	Evolution of starvation response in cliates
Mac Estella	Pierce	01 - Open Symposium	SP_25	761	1075	Phylogenomic insights into the evolutionary history of mosquitoes
Estella	Poloni	01 - Open Symposium	SP_25	762	1003	Joint analysis of phenotypic and genomic diversity sheds light on the evolution of xenobiotic metabolism in humans
Kay	Prüfer	01 - Open Symposium	SP_25	763	683	Down syndrome in ancient societies
Anthony Simon Alan	Redmond	01 - Open Symposium	SP_25 SP_25	764	708	Independent rediploidzation masks shared whole genome duplication in the sturgeon-paddlefish ancestor
Omition Alion	Rella	01 - Open Symposium	SP_25 SP_25			Directing Pathogen Evolution with a Mossic of Vaccines
Alan Marie	Rice Riffis	01 - Open Symposium 01 - Open Symposium	SP_25	706	554	Characterising Pseudomona (154-dependent enhance-binding proteins Adultaria of Generation and King Materia ad Disc aware advisoration and advisoration and advisoration and advisoration ad
Niccolò	Righetti	01 - Open Symposium 01 - Open Symposium	SP 25			Analysis of compensatory evolution following gRGC events using whole-exome phylogenetic analysis in Murinae. A totak-evidence, dated phylogenomic analysis of branchiopod cruateceans
Emma	Rowley	01 - Open Symposium	SP 25	769	1608	A table whomeve, taken perpendicular analysis of same tappoor tables tappoor tables and tappoor tappoor tappoor tables and tappoor tappoor tables and tappoor tappoor tappoor tables and tappoor tappoor tables and tappoor tappoor tables and tappoor tappoor tappoor tappoor tappoor tappoor tables and tappoor t
	Runge	01 - Open Symposium	SP_25			Centerine water and an and a second s
Lehti	Saag	01 - Open Symposium	SP_25	771	135	Population history of Ukraine
Lehti Mrudula	Sane	01 - Open Symposium	SP_25		977	Adation bias shifts after the distribution of timess effects of new mutations
Cecilia Ahmed	Sensalari	01 - Open Symposium	SP_25	773	725	Using dosage balance-sensitive gene families as markers for plant whole-genome duplications.
Ahmed	Shibl	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 tick populations sampled on a latitudinal gradient
Elpida	Skarlou	01 - Open Symposium	SP_25	//6	NA	TBA
Thomas	Staedler	01 - Open Symposium	SP_25	777	656	Differences in effective pickly drive parental expression proportions in wild tomato hybrid endosperms
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?
	Stift Strütt	01 - Open Symposium	SP_25 SP_25	779	490	Breaktown of self-incompatibility due to genetic interaction between a specific S-aliele and an uninked modifier
Marc Stefan		01 - Open Symposium	SP_25 SP_25	780	900	Weak putyling saketon in human mitochondial DNA and Y chromosomes
Marc Stefan Aram	Stump					
Stefan Aram	Stump	01 - Open Symposium 01 - Open Symposium	SP 25	782	493	Evolution of human menopause-associated genes The masking hwothesis in connex multicelular organisms with behasis. He cycles.
Stefan Aram Peter Aglaia	Stump Szovenyi Szukala	01 - Open Symposium	SP_25	782	493	The masking hypothesis in complex multicellular organisms with biphasic life cycles.
Stefan Aram Peter Aglaia	Stump Szovenyi	01 - Open Symposium 01 - Open Symposium 01 - Open Symposium	SP_25 SP_25 SP_25 SP_25	782 783 784	493 1208 235	The marked hypothesis in compare multicular anguments with the parties. Ach in Distriss - results from a large experimental field trial on and detack in Austia Period of them they so of sequence data on adjuscipant physicaperus Period of them they are sequence data on adjuscipant physicaperus Period of them they are sequence data on adjuscipant physicaperus Period of them they are sequence data on adjuscipant physicaperus Period of them they are sequence data on adjuscipant physicaperus Period of the them they are sequence data on adjuscipant physicaperus Period of the them they are sequence data on adjuscipant physicaperus Period of the theory and theory and the theory and the theory and the theory and the theory and theory and the operation of the theory and the theory and theory and theory and the theory and the theory and theory and theory and theory and theory and the theory and theory a
Stefan Aram Peter Aglaia Naoko Alessia	Stump Szovenyi Szukala Takezaki Tatti	01 - Open Symposium 01 - Open Symposium 01 - Open Symposium 01 - Open Symposium	SP_25 SP_25 SP_25 SP_25 SP_25	782 783 784 785	493 1208 235 1527	The making hypothesis is complex nucleafaster argument with hypothesis The option. The hypothesis is complex nucleafaster argument with hypothesis The option. The officient of definent types of sequent data on pationspatial hypothyse. The officient of definent types of complex nucleafaster for the option of t
Stefan Aram Peter Aglaia	Stump Szovenyi Szukala Takezaki	01 - Open Symposium 01 - Open Symposium	SP_25 SP_25 SP_25	782 783 784 785	493 1208 235 1527	The masking hypothesis in complex mutificeblar organisms with biphasic life cycles. Anh in Distress - results from a large experimental field trial on ach deback in Austria

Marcy	Uyenoyama	01 - Open Symposium	SP_25	787	183	The Role of Mutation in Fst 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 SP_25	790	507	Detecting orthologous genomic markers for swallowfail butterfiles (Papilionidae)
Viridiana	Villa-Islas Waldman	01 - Open Symposium	SP_25 SP 25	791	924	Genetic diversity at Tateloloo, a Messamerican human sacrifice site (1300-1521 CE)
Shamam Yusuke	Watanabe	01 - Open Symposium 01 - Open Symposium	SP 25	792	149	Genome-wide data from metiserial demandees allower the Address allower and event pre-stated the 14th century
	Wulsch		SP_25			Detecting signals of positive natural selection in the Jonon people, prehinition harter-gatherers in the Japanese archipelage
Svenja Haruka	Yamashita	01 - Open Symposium 01 - Open Symposium	SP_25	795	934	A ZW sex determination system in the oritatid mite Hermannia gibba Distinguishing among broces underlying fination biases: Population genetic tests of selection on synonymous mutations in Drosophila
Shu-Ting	You	01 - Open Symposium	SP 25	796	285	Advances of the control of the contr
Rafael	Zardoya	01 - Open Symposium	SP_25	797	1320	Comparative genomics of cone snails
Tianqi	Zhu	01 - Open Symposium	SP 25			Complexity of the simplest species tree problem
Lison	Zunino	01 - Open Symposium	SP_25			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 buriting hybrid zone: natural laboratory to understand how color pattern maintains species boundaries in birds
Hisham	Ali	03 - The dark side of introgression	SP_25			The effect of Dobthansky-Muler Incompatibilities on the genomic landscape under parallel and divergent selection
Margot	Besseiche	03 - The dark side of introgression	SP_25			Diversification of the date paim (Phoenix dactylifera L.) and introgression from a wild relative
Valentina	Burskaia	03 - The dark side of introgression	SP_25 SP 25	803	1195	Does hybridization facilitate explosive speciation of Lake Baikal amphipods?
Elizabeth	Chevy	03 - The dark side of introgression	SP_25 SP_25	804	590	Consequences of sex-bias and background selection for introgression on chromosome X
Adam Russ	Ciezarek Corbett-Detig	03 - The dark side of introgression 03 - The dark side of introgression	SP_25 SP 25	805	200	Orgoing and anciert genomic introgression in Oreochromis Stapias
Elli	Cryan	03 - The dark side of introgression 03 - The dark side of introgression	SP_25	807	1402	Estimating the effect of interference among selected sites in adminud populations Molecular evolution of a reproductive barrier across tealer million years
Tomas	Flouri	03 - The dark side of introgression	SP 25	808	1360	Referent average information of a reproductive turners activates retrieved years Referent Bayesian Information Under Multispoles Conductor turners (Magdoon Referent Bayesian Information Under Humitispoles Conductor turner)
Nicole	Foley	03 - The dark side of introgression	SP_25	809	1643	Another backward and the exception of well became in a species-full tradition.
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	Cowritish adaptive radiation shaped by large-scale structural variation
Tania	Holtzem	03 - The dark side of introgression	SP_25	812	1476	Shedding light on mochanisms maintaining species boundaries despite entensive hybridization in cyclical parthenogens
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
Teerna Saugata	Khastgir	03 - The dark side of introgression	SP_25	814	1278	The drivers of the adaptive radiation of persimmons on New Caledonia, a biodiversity hotspot
Mateusz	Konczal	03 - The dark side of introgression	SP_25	815	803	Genomic consequences of artificial translocation, admixture and population replacement in the Trinidadian guppies
Martin	Kuhlwilm	03 - The dark side of introgression	SP_25	816	243	5 Introgression deserts AC° a primate perspective
Guillaume	Lavanchy	03 - The dark side of introgression	SP_25	817	975	Large-scale genotyping reveals widespreadhybridization among central European ants
Tomasz	Mamos	03 - The dark side of introgression	SP_25 SP_25	818	1249	Is in addition of Gammanu species flock in ancient Like Oridi an effect of hybridisation?
Alice Valentina	Manuzzi Mastrantonio	03 - The dark side of introgression 03 - The dark side of introgression	SP_25 SP_25	819	1213	Genomic Signatures Of Hybridization For Two Angentish Species In The Narth-East Atlantic A Motion and to durative of TMA Interconnection provide units and the Interconnection and the Interconnection provide units and the
Sofia	Mendes	03 - The dark side of introgression 03 - The dark side of introgression	SP_25	821	758	A hidden road to diversity: mIDNA introgression promotes intra-specific paternal leakage and heteroplasmy in hydraenid beetles Matigle outcomes of hydridzation in berian chube inferred from whole genome data
Lukas	Metzger	03 - The dark side of introgression	SP 25	822	1331	Makeper doctomes or nyratazatane misma crate miemer zom wroze genome taka Inference of menosysty and intergression in selling opportantiate Bayesian Computation (ABC) Defense of menosysty and intergression in selling opportantiate Bayesian Computation (ABC)
Amanda	Meuser	03 - The dark side of introgression	SP_25			Intereste a dambijanty za na majeteo m semi jepidanote uni jepidan
Leonie	Moyle	03 - The dark side of introgression	SP_25	824	440	Orange is the new red. Hybridzation, introgression, and tail convergence among wild invasive and endemic tomatoes on the Gal4pagos
Sandra	Oliveira	03 - The dark side of introgression	SP_25	825	515	Assessing the limits of local ancestry inference through simulations
Jill	Olofsson	03 - The dark side of introgression	SP_25	826	489	Ecological sorting maintains species identity despite frequent genetic exchange
Daniel	Powell	03 - The dark side of introgression	SP_25	827	227	Complex hybridization between deepty diverged fish species in a disturbed ecosystem
Neda	Rahnamae	03 - The dark side of introgression	SP_25	828	68	Genetic architecture of phenotypic differences between endangered floodplain Arabis species
Fabrizia	Ronco	03 - The dark side of introgression	SP_25	829	723	Shedding light on a species-tree obscured by introgression: A case from cichlid fishes of the Lake Tanganylka drainage
Erik Fogh	Sørensen	03 - The dark side of introgression	SP_25 SP_25	830	807	Administure, reproductive barriers and adaptive introgressions in baboons using 225 genomes from six species
Markus		03 - The dark side of introgression	SP_25 SP 25	831	1447	Evolutionary rescue through gene flow despite genetic incompatibilities shaped diversity of the pseudo-ceneal grain amaranth
Jesper João	Svedberg	03 - The dark side of introgression	SP_25	832	1040	Biglia of Adaptive Inforgression Across Diverse Species
Tram	Teixeira	03 - The dark side of introgression 03 - The dark side of introgression	SP 25	834	479	Long-term balancing selection has maintained shared genetic variation across great ape species for millons of years Genome-wide admixture mapping using admixed source populations identifies wild ancestry-of-origin segments in Vehramese cultivated Robusta colfee
Lin	Yu-En	03 - The dark side of introgression	SP 25			Denotes a canonical service in a service in a service in postantine we access - outrage in service in retrained connect to the service in the
Xinjun	Zhang	03 - The dark side of introgression	SP 25	836	818	Instructional and the second and the
Carolina	Barata	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP 25	837	569	Single-cel resolution of sex differences in Drosophila metanogaster
Debora	Brandt	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	838	1535	Genome-wide signatures of balancing selection in Drosophia melanogaster
Leo Tomás	Camino Cedeño	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	839	1426	Gene expression of Hsp70 genes as a response of the thermal stress in the tropical butterfly Heliconius enalo
Ching-Ho	Chang	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	840	391	Meiodic drive shapes rapid evolution of Drosophila protamines
Alberto	Civetta	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25 SP_25	841	1127	Selection upon expression of reproductive genes and post-mating reproductive isolation in Drosophila
Zachary	Dietz	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict		842	851	Evolution of mitoruclear mismatched C. elegans: Effects of adaptedness, mating system and mitochondrial mutations
Ewan	Flintham	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25 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 SP_25	844	1171	PhaseWY: A bioinformatic pipeline for phasing and retrieving Y and W sequences from population genomic data
Jiwon Zheng	Kim	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	845	495	Interpreted conservation of ZFPS7 binding sequence, a marker of genomic impliciting, in globons
Cristiana	Marques	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict 06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	847	400	The genetic mechanism of sexual distribution is state species of presents
Miriam	Merenciano	06 - Molecular Evolutionary Patterns under SexDependent Selection and Sexual Conflict	SP_25	848	673	Evolution of female-Initiad colour polymorphism through sex-specific genetic architecture in cuckoos Contribution of transposable elements in the sex gap longevity of different Dirocophila species
Marlo	Moller	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25			Considered to a subsport the strength of the s
Filippo	Nicolini	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25			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 Drosophila melanogaster
Bahar	Patlar	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	853	1660	Investigating molecular signatures of adaptation to different latitudes in seminal fluid proteins of Diosophila melanogaster
Peter	Price	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	854	596	The genomic basis of 8€ good genes8€™ in stalk-eyed files
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 mDNAs in heteropygous nuclear backgrounds of Drosophia
Leticia	Rodríguez-Montes	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	856	759	Bex-blased gane expression across mammalian organ development and evolution
Christian	Schloetterer	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25 SP_25	857	284	Multion-order speciation is driven by the contributed effects of sexual conflict and adaptation
Tatiana	Teixeira Torres Thomas-Bulle	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict 06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25 SP_25	858	14/7	Molecular Bases of Gendal Flasticity in Malks of a Notificial Base in Response to Intrasenal Competition
Camille Monica	Vallender	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict 06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25 SP_25	960	905	blocvening the genetic basis of hom size reduction in lateral populations of thirocenes besters Concentration Development and the Enroth Balance Underson I Amore Concentration II. Concentration Development and the Enroth Balance Underson II. Concentration II. Concentration Development and the III. Concentration Development and the IIII. Concentration Development and the III. Concentration Development and the III. Concentration Development and the III. Concentration Development and the IIII. Concentration Development and the IIIII. Concentration Development and the IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Tamsin	Woodman	06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict 06 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	SP_25	861	1244	Cencitysing By-Sequencing Reveals Main-Female Relatedness Influences Cryptic Female Choice in Chinock Salmon (Disconflynchus Tahawytscha) The role of DNA methylation is sex-Mased gene expression in the clinus mealytup Panococcus citri
Prem	Aguilar	09 - Evolution on repeat in the genomics era	SP_25	862	704	The role of over memparatin in sec-based prime expression in the clubs mempanyad mandoceces on The evolution of carolenoid colouration through cis-regulatory variation at BCO2 in a colour polymorphic loard
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	Origin and Evolution of Pseudomunin Biosynthetic Gene Clusters
Viktoria	Bednarski	09 - Evolution on repeat in the genomics era	SP_25	000	1084	Consequences of reproductive modes on repeat dynamics in oribatid mites
Romain	Boisseau	09 - Evolution on repeat in the genomics era	SP_25	867	970	On the importance of phenotypic evolutionary trajectories in predicting genomic parallelism.
Bastien	Boussau	09 - Evolution on repeat in the genomics era	SP_25	868	1530	5 Genome scale genotype-phenotype associations along phylogenies to understand the genomic 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 bumblebees
Alaksh	Choudhury	09 - Evolution on repeat in the genomics era	SP_25 SP_25	870	1552	Studying change in the evolutionary dynamics during the Escherichia coli long term evolution experiment (LTEE) using melecular barcodes
Elena Carolin	Conti Dahms	09 - Evolution on repeat in the genomics era				
Giulia	Fabbri	09 - Evolution on repeat in the genomics era	SP_25 SP_25	8/2	760	Parallel Evolution Despite Low Genetic Diversity in Europea® ** Ancient Sticklebacks
Giulia Jeffrey	Fawcett	09 - Evolution on repeat in the genomics era 09 - Evolution on repeat in the genomics era	SP_25 SP_25	873	1129	On the repeatability of insular dwarfam: comparing Consican and Sandinian wild boar. Sinome sequencing reveals the genetic architecture of heterosyty in common buckeheat
Rosa Maria	Fernández García	09 - Evolution on repeat in the genomics era 09 - Evolution on repeat in the genomics era	SP_25		816	
Giobbe	Fernandez Garcia	09 - Evolution on repeat in the genomics era 09 - Evolution on repeat in the genomics era	SP 25			Exploring the genomic basis of repeated evolution in sea-to-land transitions across animal lineages 2 sthand signatures of the shifts to endosymbiosis across Enterobacterales evolutionary history.
Andrea	Guarracino	09 - Evolution on repeat in the genomics era	SP 25	878	1490	Instee spanne of we train a rendomination and one of the spanne of the s
Mariangela	lannello	09 - Evolution on repeat in the genomics era	SP_25	879	535	Signatures of entreme longevby a perspective from binative molecular evolution.
Maddie	James	09 - Evolution on repeat in the genomics era	SP_25	880	890	Incovering the genetic architecture of parallel evolution in Senecio
Min-Gyeong	Ко	09 - Evolution on repeat in the genomics era	SP_25	881	322	A whole Hespin cynonolgus macague transcriptome reveals age-related immune patterns
Uliana	Kolesnikova	09 - Evolution on repeat in the genomics era	SP_25	882	1344	Siberian selfingArabidopsis lyrata and its role in formation of Arabidopsis kamchatica: an example of repeated allotetrapioid 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 murine rodents
Adria	Leboeuf	09 - Evolution on repeat in the genomics era	SP_25	884	697	The evolution of ant crop milk proteins over independent gains of a social transfer behavior
Yunjung	Lee	09 - Evolution on repeat in the genomics era	SP_25	885	324	Old world monkey specific insertion of AU/Pa1 element in BHMT gene during primate evolution
Carol	Lee	09 - Evolution on repeat in the genomics era	SP_25	886	1 1464	Positive Epistasis and Selection from Standing Variation could drive Parallel Polygenic Adaptation

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Emmanuelle	Lerat	09 - Evolution on repeat in the genomics era	SP_25		887	1272 Fund	rotion and conservation of Drosophila paralogs in the light of their mobiliome neighborhood
Veronika	Lipánová	09 - Evolution on repeat in the genomics era	SP_25		888	821 Repe	peated adaptation in wild Arabidopsis and carnations: genomic convergence and the phenotypic manifestation of adaptation to challenging soils
Irma	Lozada Chavez	09 - Evolution on repeat in the genomics era	SP_25 SP_25	-	889	1564 The (e genome intro-richness of Complex Muticelular Organisms has been repeatedly decoupled from genome size evolution in Eukarya.
Sarah	Lucas Ma	09 - Evolution on repeat in the genomics era	SP_25	-	890	649 How	w Mammala Lose Their Vision, According to Genetica
Jilong	Martínez Redondo	09 - Evolution on repeat in the genomics era	SP_25	+	802	597 m	ee indspendert social tarsetisiens reveal that sociality evolved after the speciation in spider genus Stegodyptus
Gemma Axel	Meyer	09 - Evolution on repeat in the genomics era 09 - Evolution on repeat in the genomics era	SP 25	+	893	1050 Geor	e murch to land; unearthing how gene repertoire evolution triggered animal terrestriatization nomics of adeptation and speciation in sympatry with a dose of homopioid hybrid speciation
Anamaria	Necsulea	09 - Evolution on repeat in the genomics era	SP_25	+	894	1174 why	of the chicken lose is period 7 Evolutionary processes and melocular mechanisms associated with the repeated losses of the informatient phallus in avian lineages.
Hye-Ri	Park	09 - Evolution on repeat in the genomics era	SP_25		895	323 Three	e distinct integration and deletion events of SVA, D., AuSig2 and AuSp elements generate diverse NEKS structures during primate evolution
Hye-Ri Ohad	Peled	09 - Evolution on repeat in the genomics era	SP_25		896	272 The	a complex evolution of social complexity in basis
Giovanni	Piccinini	09 - Evolution on repeat in the genomics era	SP_25		897	717 Expa	pansions/reductions of the Tudor family appear associated to convergent genomic and phenotypic evolutions in Metazoa
Ana	Pontes	09 - Evolution on repeat in the genomics era	SP_25		898	740 The r	e molecular underpinnings of convergent evolution in bee-associated fructophilic bacteria
Anggun	Sausan Firdaus	09 - Evolution on repeat in the genomics era	SP_25		899	1227 Conv	nvergent changes on ebony gene regulation associated to the evolution of melanic body color in Drosophila elegans
Joshua	Schraiber	09 - Evolution on repeat in the genomics era	SP_25	_	900	424 A uni	nified approach to trait mapping within and between species
Alison	Scott	09 - Evolution on repeat in the genomics era	SP_25 SP_25	_	901	1166 Rect	current adaptation to whole ganome duplication in wild Arabdopsis
Avery Rosalin	Selberg Simpson	09 - Evolution on repeat in the genomics era 09 - Evolution on repeat in the genomics era	SP_25	+	902	047 BUS	STED-PH: A likelihood framework for datecting post-like selection associated with convergent phenotypes
Keaton	Sinclair	09 - Evolution on repeat in the genomics era	SP_25	+	903	666 Bara	nomic signatures of parallel evolution of predatory litestyles in Acari mites raliel Evolution in Diverse Strains of Pseudomonas aeruginosa
Tanja	Slotte	09 - Evolution on repeat in the genomics era	SP_25	+	905	252 Gend	The canadian of the Linum disky suppreprine reveal convergent evolution at the molecular level
Dylan	Sosa	09 - Evolution on repeat in the genomics era	SP_25	+	906	160 Origi	gination and evolution of lineage-specific transfer RN4 genes inDrosophila
Irène	Tanneur	09 - Evolution on repeat in the genomics era	SP_25		907	1279 Mism	match repair in Bacillus subtilis compensates for the correction bias of the PoIC exenuclease
Sophie	Teullet	09 - Evolution on repeat in the genomics era	SP_25		9081	262 Conv	nvergent dietary adaptation in myrmecophagous mammals: insights from the study of the chilinase gene family in the host and its associated out microbiota
Arturo	Torres Ortiz	09 - Evolution on repeat in the genomics era	SP_25		909	911 Conv	wegnet evolution and genetic makem of pre-resistance in M. Meteodosis adder of mycesparatilism, Noundy on the gene expression regulation. This Trichodema agreentides and Toipoculadam ophiciplescedes spore genetination addered and meteodosis and addered and addered and M. Martin and M. Cananasana and Banard Martinia Conferences
Yen-Wen	Wang	09 - Evolution on repeat in the genomics era	SP_25		910	1087 Evol	olution of mycoparasitism, focusing on the gene expression regulation in Trichoderma asperelicides and Tolypocladium ophioglossoides spore germination
Shira	Zion	09 - Evolution on repeat in the genomics era	SP_25	-			
Moisès	Bernabeu	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	-	912	664 Rela	lathe dating of evolutionary events from gane trees
Alessio Zehui	Capobianco	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25 SP_25	+			ew relaxed probabilistic model of morphological evolution for robust phylogenetic inference
Sofia Amanda	De Lellis Stroustrup	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time 10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP 25	+	914	94 me	e origin and ghamic demographical Nations of ancient southem Chinese pands Integes
Sofia Amanda Harriet	Drage	10 - Integrating lossis and molecules to reconstruct the evolution of life in deep time 10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP 25		916	152 Noue	chasis morphometrics - woldforwry modelling of shape data wri form of & Dephasicals ^{ee} mouding in circlaind isopods
Zhen	Li	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25			79 Revi	ver krimitori ete oppraasizete mooanniti in toroanno soopoas visiting ancient polypiloidy in leptosporangialet ferns
Yichen	Liu	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25		918	478 Ancie	nang mang benar populari pengangkan penga
Sinéad	Lynch	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25		919	170 Deve	velopment and moulting behaviour in extinct and extant decapods
Beatriz	Mello	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25		921	179 Asse	sessing the relative performance of fast molecular dating methods for phylogenomic data
Morena	Nava	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25		922	558 Integ	agrating Molecular Data And Novel Fossil Knowledge Illuminate The Timescale Of Sea Spiders Evolution
Mark	Nikolic	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25		923	1571 Clari	inflying evolutionary relationships, divergence times and rates of evolution with Bayesian phylogenetic methods in a trilobite group
Ioannis	Patramanis	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25 SP 25	_	924	504 Using	ing 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		_	925	1265 The (e Cat is out of the bag modelling across-site compositional heterogeneity is key to improve accuracy in datasets affected by long branch attraction.
Cristina Marc	Pokorny Montero Robinson-Rechavi	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25 SP_25	+	920	600	norric Inconguence Underlies the Evolution of Flower Symmetry in Euclose
Romain	Sabroux	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time 10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	-	927	520 Integ	spation of genomic, developmental and pakentological information in Mouldo to study anthropod evolution spating fosail and extant sea spiders into a total evidence phylogeny (Pycnopanida)
Idan	Sheizaf	10 - Integrating lossis and molecules to reconstruct the evolution of life in deep time	SP 25	+	929	297 Trai	grammit room are extrain see spoors into a countervisione physician (*) encoderman) e multiple roles of the gap genes network and its evolutionary versatility in hemimetabolous insect development
Jessica	Thorpe	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25	+	930	181 Phyle	managements of the gap gap was standard and a standard a
Tharsika	Vimala	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP 25		931	1002 Gene	ones from 50,000 year old Neanderthai reveals deeply diverged and isolated late Neanderthai population in western Europe
Sishuo	Wang	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	SP_25		932	41 Datir	ting the bacterial tree of Ife based on ancient symbiosis
Paolo	Abondio	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25		933	659 Explo	skoling apolypoprotein E (APOE) haplotypes in healthy subjects: a population genetics perspective
Simon Ornob	Aeschbacher	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25		934	1392 Herb	tarium specimens shed light on the origins and flavour of early European tomatoes
Ornob	Alam	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25		935	730 The p	e post-domestication history of Asian rice: insights from herbarium genomes and ancestral recombination graphs
Sara Celine	Armas-Quintana	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25		936	1031 The f	e forgotten cemetery of Ablon (Mauritus): paleogenomic analysis of the demography of the Indian Ocean slave trade
	Bon	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	-			nome-wide analysis of a collective grave from Mentesh Tepe, one of the early Shortu-Shulaven sites in South Caucasus.
Katia Alberto	Bougiouri	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25 SP_25	-			utation of ancient dog genomes informs on their inbreeding history since the onset of domestication
Diogo	Carmagnini Coutinho Lima	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics 11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	+	939	1160 Pala	leopennic evidence for the long-term reproductive isolation between wild and domestic cats
Myriam	Croze	11 - Entangled instolles, insights into the evolution of humans and their domesticates through paleogenomics 11 - Entangled histories; insights into the evolution of humans and their domesticates through paleogenomics	SP_25	+	941	688 Use	entanging the complex genomic architecture and evolutionary history of livestock parading dogs spread across Eurapia covering the Genetic Diversity and Structure of Prehistoric Individuals from the Learnah&" is territory in the Eastern Italian App
Roslyn	Curry	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	-	942	1642 Reco	Constructing Western and Northern Mexicole ²⁷ Past through the PIPANDM Project
Kevin	Daly	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25		943	741 Pale	Reogenomic 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 PALE	LEOGENOMICS 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 Pale	leogenomic analysis of goats present with the indigenous people of the Canary Islands
Eran	Elhaik	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25		946	14 In se	search of Viking origins: tackling the big WHEN and WHERE questions
Jolijn	Erven	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25		947	1453 Impu	sutation is a reliable method to infer population dynamics in prehistoric Cattle
Rosa	Fregel	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	_	948	1030 The i	e impact of the European colonization on the indigenous people of the Canary Islands
Muriel Christian	Gros-Balthazard Huber	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25 SP_25	+	949	1115 Traci	cing the origins of oasis agrosystems: Insights from genomic and morphometric analyses of ancient date pairs
Damla	Kaptan	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics 11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	-	950	366 Aug	ovel reaction-diffusion model of the European Noolthic taming expansion haeogenetic analysis of Neolthic sheep from Acatalia
Yosuke	Kawai	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25	+	952	1043 Georg	nanogement unalysis or wootents streep non-wateria
Masatoshi	Matsunami	 Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics 	SP_25		953	315 The	hete diversity and structure of appliances populations revealed by whole genome sequencing a prehistoric peopling of the Ryulyu Archipelago
Francesco	Montinaro	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25		954	246 Asse	prevenue people provide a company of the company of
Pedro	Morell Miranda	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25		955	613 Gend	nomic insights into the interconnected Demographic History between Sheep and Humans in Iberia.
Füsun	Özer	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25		956	1448 Preli	Iminary archaeogenemics 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 Expl	slove 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 Pale	leogenomic 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	888 Pala	laeogenomics 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 SP_25		960	067 Whe	en cultural insight of admixing who does not match the genome ancestry: the case of the Cenry culture (Middle Neclifice, Northern France)
Javier Mehmet	Serrano Somel	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25 SP 25		961	1432 m	e genomic history of the Canary Islands
Gontran	Sonet	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics 11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25		902	597	reported changes in inter-regional human mobility patterns through the Holocene: paleogenomic insights
Arev Pelin	Sumer	 Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics 	SP 25		964	712 Hot	ing ancient DNA to identify Bos printigenius in ancient cattle remains from Belgium In coverage genomes of two of the earliest Homo sagions in central Europe
Leonardo	Vallini	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP 25		965	1310 Preh	n coverage generation can also car the carteria theorem and the carterian technic carterian c
Yoshiki	Wakiyama	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP_25 SP_25		966	933 A kin	Institute and the second s
Tianyi	Wang	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	SP 25		967	566 The	s Genetic history of southern East Asia
Alessandra	Aleotti	12 - Evolution of sensory systems	SP_25		968	1379 The I	e molecular evolution of animal phototransduction and photoreceptor cells
Gwénaëlle	Bontonou	12 - Evolution of sensory systems	SP_25		969	517 Origi	gin of a novel offactory sensory neuron population
Gianni	Castiglione	12 - Evolution of sensory systems	SP_25		970	738 Adap	aplation of Antarctic Icelish Vision to Extreme Environments
Fabio	Cortesi	12 - Evolution of sensory systems	SP_25		971	1543 Wha	at the latest advances in molecular approaches and technologies can teach us about the evolution and function of fish vision
Kathy	Darragh	12 - Evolution of sensory systems	SP_25 SP 25		972		repeated evolution of tarpene synthesis in insects: convergence at multiple levels
Giacinto Melanie	De Vivo Debiais-Thibaud	12 - Evolution of sensory systems	SP_25 SP_25				placion and bases of gain gains in lighthroughnass evolution
Julien		12 - Evolution of sensory systems	SP_25 SP 25		974	1334 V	s sensory shark: Evolution of ventebrate sensory organs through the eye of high-quality phenotype, genomic and transcriptomic data in the lesser spotted catchark Scyliothinus canicula
Julien Bruno	Devilliers Fonseca Simoes	12 - Evolution of sensory systems 12 - Evolution of sensory systems	SP_25 SP_25		975	1334 Milli	Itple emergences of hematophagy in Diptora: which genetic background is needed for It? lecular Evolution of Vision in Lizards and Snakes
Jake	Fonseca Simoes	12 - Evolution of sensory systems 12 - Evolution of sensory systems	SP_25				leoular Evolution of Vision in Lizards and Smales ights into the Structure and Function of Ionotropic Glutamate Receptors through a Study of their Evolution in Bacteria
Jibin	Johny	12 - Evolution of sensory systems 12 - Evolution of sensory systems	SP_25		978	1584 Euro	ights into the Structure and Function of Ionetropic Glutamate Receptors through a Study of their Evolution in Bacteria Inclonal evolution of odorant receptors in bark beetles
Dwon	Jordana	12 - Evolution of sensory systems	SP_25				Instant or evaluation to obcart in response in task tension Instantion of Enhances Partitions to Sign Development Officiation of Enhances Partitions to Sign Development
Daenia	La Rodé	12 - Evolution of sensory systems	SP_25		980	1416 The e	e evolution of GPCRs
Jean-Marc	Lassance	12 - Evolution of sensory systems	SP_25		981	1308 The	a genetic and functional basis of offactory evolution in monogamous and promiscuous deer mice
Zibo	Li	12 - Evolution of sensory systems	SP_25		982	325 A tai	ale of two copies: evolutionary trajectories of moth pheromone receptors
Alejandro	Lozada Chavez	12 - Evolution of sensory systems	SP_25		983	1007 Gend	nomics of domestication in the arboviral vector Aedes aegypti
Valeria	Maselli	12 - Evolution of sensory systems	SP_25		984	842 Not a	t only the nose knows &P" TAAR gene expression in the octopus sucker
Katsuhiko	Mineta	12 - Evolution of sensory systems	SP_25		985	879 Gluta	tamate-sensing genes are conserved among populations compared to glutamate metabolism genes
Peter	Mulhair	12 - Evolution of sensory systems	SP_25		986	370 Dens	nse sampling reveals dynamic rates and mechanisms of opein gene duplication across Lepidoptera

Sergio	Olvera Vazquez	12 - Evolution of sensory systems	SP_25		987 114	10 Evolutionary dynamics of two prominent chemosensory gene tamilies in crop plant-sucking pests: insight from the aphids
Lino	Ometto	12 - Evolution of sensory systems	SP_25		988 106	34 Evolutionary dynamics of opsin genes in Brachycera files
Juan	Opazo	12 - Evolution of sensory systems	SP_25		989 22	26 Evolution of Ion channels in celacoans
Margot	Popecki	12 - Evolution of sensory systems	SP_25		990 14	10 investigating the role of pigmentation in firefly bioluminescence color
Isaac	Rossetto	12 - Evolution of sensory systems	SP_25		991	8 Visual Evolution of Snakes During Terrestrial-Marine Transitions.
Bastien	Saint-Leandre	12 - Evolution of sensory systems	SP_25		992 114	Evolution of chemosensory tissues and cells across ecologically diverse Drosophila
Harini	Suresh	12 - Evolution of sensory systems	SP_25		993 130	17 Seeing is believing: Spatial expression of photo pigments in malaria mosquito heads
Johanne	Adam	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25		994 163	37 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		995 102	29 Sex-differences in the genetic architecture of allelic strutting in domestic pig
Victoria	Caudill	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25		990 43	3U Cracking Coevolution: Consequences of Space Dynamics on Coevolving Polygenic Traits
Vanessa	Cunha	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25		997 42	27 The impact of selection in contrasting environments on behavior, gene expression and polymorphisms in a facultative parasitic blowfly
Leah	Darwin	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25		998 112	20 Using replicate experimental Drosophila populations to test for mitoruclear co-adaptation
Archana	Devi	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25		999 81	17 Adaptation of polygenic traits in finite populations
Sara	Duarri	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	1 10	1000 61	8 Unraveling dynamics of long-term polygenic adaptation in D. simulans
Giulia	Ferraretti	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1001 24	45 Investigating the evolution of polygenic traits through the reconstruction of adaptive gene-networks able to modulate related functional pathways
Francesc	Ganau Penella	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1003 109	0 Can GWAS data be used to detect adaptation on human complex phenotypes?
Olivia	Ghosh	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1004 88	31 Modularity and pleiotropy in multiple steps of adaptation
Mateus	Gouveia	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1005 61	17 Subcontinental admixture in Europeans and European Americans: Implications for genome-wide association studies (GWAS)
Matthew	Hansen	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1006 89	99 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	10	1007 148	35 The effect of selection on predicting the direction of phenotypic difference in polygenic traits
Petri	Kemppainen	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1008 47	73 Epistatic shielding AC how ancestral genetic variation for local adaptation can be preserved across multiple habitats
Ivan	Kuznetsov	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1009 102	26 Contrasting patterns of present-day and historical natural selection for educational attainment in the Estonian population
Juan	Li	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1010 163	35 The canalization of direct selection and epistasis during adaptation
Davide	Marnetto	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1011 99	1 Prehistoric ancestries are consistently associated to the complex trait landscape in European Biobanks
Diogo	Melo	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1012 77	78 Longitudinal sequencing reveals polygenic and epistatic nature of genomic response to selection
Richard	Nichols	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1013 4	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	10	1014 67	Vector of Domestication Signals through the Analysis of the Full Distribution of Fitness Effects using Forward Simulations and Polygeric Adaptation
Bao-Hua	Song	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1015 73	33 Genetic basis and selection of phytochemical variation in wild soybean
Ann Maud	Tate	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1016 10	3 The evolution and maintenance of developmental pleiotropy in insect immune systems
Maud	Tenaillon	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	10	1017 53	31 Exploration of phenotypic space as evidenced in maize divergent selection experiments
Henrique	Teotonio	13 - Polygenic Adaptation – Predictability and Pleiotropy	SP_25	10	1018 2	28 Selection and the direction of phenotypic evolution
Benjamin	Wölfi	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	10	1019 165	58 A theory of oligogenic adaptation of a quantitative teat
Changyi	Xiao	13 - Polygenic Adaptation - Predictability and Pleiotropy	SP_25	10	1020 34	Subtle-genomic differences could result in distinct genomic responses to temperature adaptation
Josué	Barrera Redondo	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1021 14	47 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	10	1022 161	11 independent recruitments of different types of phospholipases A2 to the venom of Caenophidian snakes
Frederic	Brunet	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1023 53	36 Translational readthrough of the long Mat gene in Drosophilidae nests a universal Eukaryote domain
Claudio	Casola	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1024 44	16 Low stability may affect functionality of human microproteins
Carolin	Freye	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1025 37	73 Substrate Specificity and Conformational Historogeneity in Ancestral and Extant Glucokinases
Dusan	Kordis	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1026 7	77 The origin and early diversification of eukacyotic retroelements
Victor	Luria	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1027 159	23 Novel genes enable protein structural innovation and function in the brain
Josep	Marti-Solans	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1028 135	33 Functional divergence in the DEG/ENAC/ASIC protein family: the quest for proton-sensing determinants
José Carlos	Montañés Domínguez	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1029 37	78 Uncovering evolutionary trajectories of newly arisen genes
Edmund	Moody	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1030 34	14 The nature of LUCA and its impact on the early Earth system
Petar	Pajic	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1031 5	54 A mechanism of gene evolution generating mucin function
Christos	Papadopoulos	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1032 39	34 Hgh novel gene diversity across Saccharomyces cerevisiae strains
Carolina	Rocha	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1033 83	36 Interactions of ancient coensymes reflect a reduced repertoire of amino acida
Paul	Roginski	14 - Novel proteins and their emergence from LUCA until today	SP_25	10	1034 34	15 Impact of GC content on the hove gene birth
Duncan	Sussfeld	14 - Novel proteins and their emergence from LUCA until today	SP_25		1035 105	A multi-mainter network approach to uncover highly divergent groups of environmental variants in ancient gene tamilies
Emilios	Tassios	14 - Novel proteins and their emergence from LUCA until today	SP 25	10	1036 140	12 Tracing the birth and evolution of novel genes across the entries budding yeast subphysim.
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