Group A - Poster theme overview

Poster area	Board numbers	Theme	Set-up and take-down
Blomster salen	001-076	Open Theme	**Set-up:** Monday, 08:00-12:20 (before the lunch break) **Poster session:** Monday 18:00-20:00 **Take-Down:** Tuesday, 12:20-**12:50** (during lunch break)
Main hall	077-130	Open Theme	
Harlekin	131-206	Open Theme	
2nd floor: Arkaden 8	207-274	Open Theme	
2nd floor: Arkaden 7	275-302	Open Theme	
2nd floor: Arkaden 6	303-304	IDEA Symposium: Advancing Inclusion, Diversity, Equity, and Accessibility in Molecular Biology and Evolution	
2nd floor: Arkaden 6	305-311	Editors' Symposium	
2nd floor: Arkaden 6	312-342	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	
2nd floor: Arkaden 4+5	343-364	S05 Molecular Evolution in the Era of Genetic Diversity Decline	
2nd floor: Arkaden 2+3	365-380	S19 Causes and consequences of mutation rate variation	

Group A - Detailed poster overview

Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
001	Blomster salen	1760	Why adaptive walks can reach high-ranking peaks—a simplified Rough Mount Fuji model as a minimal example	Open Theme	Kye Hunter	CRG	United States
002	Blomster salen	1105	Bingo! Dino DNA: Chromosome-scale genome assembly of a multi-gigabase dinoflagellate protist fills a Tree-of-Life gap	Open Theme	Thomas Harvey	Norwegian University of Life Sciences	Norway
003	Blomster salen	1445	MeQTL Discovery in Admixed Human Genomes to Estimate Epistasis	Open Theme	Gillian Meeks	University Of California Davis	United States
004	Blomster salen	408	Convergence in responses to selection across two major plant pathogens	Open Theme	Jigisha	University of Neuchatel	Switzerland
005	Blomster salen	1620	Effect of incubation temperature on transposon activity in the African house snake (Boaedon fuliginosus)	Open Theme	Mariela Tenorio	Faculty of Science, Charles University	Czech Republic
006	Blomster salen	1737	An evolutionary ghost hunt: hybridisation between island endemic bird species	Open Theme	Abby Williams	University Of Oxford	United Kingdom
007	Blomster salen	242	Extremotolerance Meets Genetic Accessibility in a Non-Model Microalga from Cuatro Ciénegas Basin	Open Theme	Abril Beltran	Institute of Biotechnology, UANL	Mexico
008	Blomster salen	693	The influence of chromosomal inversions on local adaptation of Atlantic silversides, Menidia menidia	Open Theme	Adam Ziegler	University of Arizona	United States
009	Blomster salen	616	Evolution of ecological interactions in Pseudomonas aeruginosa across different stress regimes	Open Theme	Aditee Ashar	Mcgill University	Canada
010	Blomster salen	1065	Small, Isolated, and Inbred: Genomic Evidence of Strong Population Structure in the Australian humpback dolphin along the Northwestern	Open Theme	Adrien Tran Lu Y	University Of Zurich	Switzerland
011	Blomster salen	876	Specific mutation bias predicts the emergence of antibiotic resistance	Open Theme	Adrita Chakraborty	National Centre For Biological Sciences	India
012	Blomster salen	685	Examining Microbial Differences in a Cultural Context: A preliminary study of Medieval Nicaea (İznik)	Open Theme	Ahmet Berkay Demirsecen	Mersin University	Turkey
013	Blomster salen	1671	Nonhuman Primate Models for Hominin Introgression and Genetic Admixture	Open Theme	Alaina Brenner	UC Davis	United States
014	Blomster salen	1194	Inference of the distribution of fitness effects using local genealogies	Open Theme	Alan Izarraras-Gomez	International Laboratory For Human Genome Research, National Autonomous University of Mexico	Mexico
015	Blomster salen	1667	Complex and Messy Prebiotic Chemistry: Obstacles and Op-portunities for an RNA World	Open Theme	Alberto Vázquez-Salazar	Cinvestav	Mexico
016	Blomster salen	551	Ancient infectious pressures shaped the evolution of LRRK2 and PRKN	Open Theme	Alessandra Mozzi	IRCCS Eugenio Medea	Italy
017	Blomster salen	1049	Investigation of temporal changes to gene expression across the reproductive cycle of the zebra finch (Taeniopygia guttata)	Open Theme	Alexander Lawrence	Lund University	Sweden
018	Blomster salen	149	Maladaptive aphid-induced transgenerational plasticity is overcome in nature	Open Theme	Alexandra Chávez	Institute Of Organismic And Molecular Evolution, Johannes Gutenberg-universität Mainz	Germany
019	Blomster salen	1055	Evaluating the Role of Epistatic Selection in Maintaining Extended Haplotypes in the MHC	Open Theme	Alfredo Marin	Universidade De São Paulo	Brazil
020	Blomster salen	1400	Tandem Repeats in Adaptive Archaic Introgression Across the Human Genome	Open Theme	Alicia Bierly	School of Computer and Data Sciences, University of Oregon	United States
021	Blomster salen	1562	Comparison of cloacal and fecal microbiomes between two populations of sand lizards (Lacerta agilis)	Open Theme	Alina Fomin	Uppsala Universitet	Sweden
022	Blomster salen	760	Leveraging variation of matri- and patrilinear genomes reveals contrasting patterns of sex-bias dispersal in northern sea lions	Open Theme	Aliya Yakupova	University Of Munich (LMU), Max Planck Institute for Biological Intelligence (MPI-BI)	Germany
023	Blomster salen	921	Close together, far apart: does the localization of QTL impact plant domesticability?	Open Theme	Anastasia Kolesnikova	University Of Southampton	United Kingdom
024	Blomster salen	962	Insights into the genomic diversity and domestication of white lupin using pangenome graphs	Open Theme	Andrea Benazzo	University Of Ferrara	Italy
025	Blomster salen	63	The role of taxonomically restricted genes in brown algal multicellularity	Open Theme	Andrea Celeste López-Díaz	CINVESTAV Irapuato Unit	Mexico
026	Blomster salen	1638	Paralog-specific patterns of predicted pathogenicity inform functional divergence	Open Theme	Angela Dawson	Florida International University	United States
027	Blomster salen	1014	Building a Multipartite Bacterial Genome Database	Open Theme	Angelica Mariana Jara Servin	Institut de Biologia Evolutiva (IBE-CSIC)	Spain
028	Blomster salen	863	Implication of dioxygen reductase diversity on the growth physiology of Escherichia coli	Open Theme	Anjali Vijay Patil	Tata Institute Of Fundamental Research	India
029	Blomster salen	822	Assessing the potential of evolution-informed conservation in Danish butterfly populations	Open Theme	Anna Maria Langmueller	Aarhus University	Denmark
030	Blomster salen	1278	Will biofilm mutants of different Pseudomonas evolve in similar ways in similar environments?	Open Theme	Aparna Biswas	Umeå University	Sweden
031	Blomster salen	1503	Recovering genomes from museum blow flies (Diptera: Calliphoridae): a methodological comparison of low-input NGS library preparations.	Open Theme	Arianna Thomas-Cabianca	Senckenberg Natural History Collections Dresden	Germany
032	Blomster salen	1458	A within-host model of the effective population of a malaria infection	Open Theme	Ariella Gladstein	University Of California. Los Angeles	United States
033	Blomster salen	929	Delineating unconventional respiro-fermentative metabolic routes for redox homeostasis	Open Theme	Arpita Biswas	Tata Institute Of Fundamental Research	India
034	Blomster salen	1191	Alterations in hypoxia-related gene expression and physiological responses between resurrected and inhabitant obligate parthenogenetic Daphnia clones from an Arctic lake	Open Theme	Athina Karapli Petritsopoulou	Leibniz Institute of Freshwater Ecology And Inland Fisheries (IGB)	Germany
035	Blomster salen	1551	Investigating the pre- and post-colonial population structure of Khoe-San descendant populations	Open Theme	Austin Reynolds	University Of North Texas Health Science Center At Fort Worth	United States
036	Blomster salen	34	SLiM 5: Expanding the horizons of forward genetic simulation to full genomes	Open Theme	Benjamin Haller	Cornell University	United States

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
037	Blomster salen	912	UK Biobank data shows local adaptation at TLR1 in response to solar radiation	Open Theme	Bennet McComish	University of Tasmania	Australia
038	Blomster salen	1364	A systematic benchmark reveals DNA polymerase combinations for high-quality genome assembly	Open Theme	Bernhard Bein	Senckenberg – Leibniz Institution for Biodiversity and Earth System Research	Germany
039	Blomster salen	534	Comparative genomics of the weevil species of the genus Rhynchophorus in Southeast Asia	Open Theme	Bisha Shahid	New York University Abu Dhabi	United Arab Emirates
040	Blomster salen	547	Ancient shared polymorphism investigation on X and autosomes of 250 primates	Open Theme	Bjarke Pedersen	Birc Aarhus University	Denmark
041	Blomster salen	1387	CAAPA2: A diverse reference panel for improved genotype imputation in underrepresented populations	Open Theme	Caitlin Uren	Stellenbosch University	South Africa
042	Blomster salen	305	Microenvironment-regulated plasticity and genetic selection drive a two-stage evolutionary trajectory in cancer	Open Theme	Can Liu	Kunming Institute Of Zoology, Chinese Academy Of Sciences	China
043	Blomster salen	1058	Sickle-Cell Disease as a condition of African genetic origin but increasingly embedded within non-African genomes	Open Theme	Carlos Passos	Universidade De São Paulo	Brazil
044	Blomster salen	1317	A fine-grained assessment of migration into Ireland from the Early Bronze Age onwards	Open Theme	Catherine Butt	Trinity College Dublin	Ireland
045	Blomster salen	248	Adzuki bean: the genetic basis of domestication and high-latitude cultivation	Open Theme	Cheng-Ruei Lee	National Taiwan University	Taiwan
046	Blomster salen	1011	Human demography shapes patterns of language diversity across the world	Open Theme	Chiara Barbieri	University Of Cagliari	Italy
047	Blomster salen	845	Highly repeatable experimental evolution of drug resistance in yeast	Open Theme	Wen-Hsiung Li	University of Chicago	United States
048	Blomster salen	501	Population genomics of Hyaloperonospora arabidopsidis, a natural Arabidopsis thaliana pathogen	Open Theme	Ching-Yi Huang	Max Planck Institute For Biology Tübingen	Germany
049	Blomster salen	598	RNA warfare in asexual animals: pathogen-induced ribosome damage signatures correlate with upregulation of horizontally acquired RNA ligases in bdelloid rotifers	Open Theme	Chris Wilson	University Of Oxford	United Kingdom
050	Blomster salen	364	A deep learning approach to detecting negative frequency-dependent selection	Open Theme	Cindy Santander	Florida Atlantic University	United States
051	Blomster salen	635	Genetic insights into convergent acquisitions of placental phenotypes and menstruation in eutherians	Open Theme	Claire Lavergne	Institut Pasteur	France
052	Blomster salen	419	Inferring demographic histories and non-random mating dynamics in complex admixture processes related to the Trans-Atlantic Slave Trade	Open Theme	Coailinn Egan	Museum Of Natural History, Paris	France
053	Blomster salen	1494	Recovering Nuclear Genomes from Extinct Xenarthran Megafauna to Reassess Evolution, Ecology, and Physiology	Open Theme	Cole Nickason	Mcmaster Ancient Dna Centre	Canada
054	Blomster salen	1125	Rapid genomic and phenotypic change in an asexual Daphnia population	Open Theme	Dagmar Frisch	Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB)	Germany
055	Blomster salen	1101	A Chromosome-Level Genome Assembly of the coral-symbiotic gastropod Phenacovolva rosea (Mollusca: Gastropoda: Ovulidae)	Open Theme	Damin Lee	Jeonbuk National University	South Korea
056	Blomster salen	520	Phylogenomics relationships of mesquite trees based on complete chloroplast sequencing	Open Theme	Dana Lucia Aguilar	New York University Abu Dhabi	United Arab Emirates
057	Blomster salen	1309	De novo genome assembly of a lemur-infecting malaria parasite from long-read metagenomic sequencing	Open Theme	Dashiell Massey	University Of California, Los Angeles	United States
058	Blomster salen	747	Sex-Specific Ethylene Responses Drive Floral Sexual Plasticity in Cannabis	Open Theme	Davoud Torkamaneh	Université Laval	Canada
059	Blomster salen	91	Mitochondrial Heteroplasmy Reflects Maternal Lineage and Demographic History in Southern African Populations	Open Theme	Dayna Croock	Stellenbosch University	South Africa
060	Blomster salen	612	Fast and alignment-free flavivirus classification from low-coverage genomes	Open Theme	Denise Kühnert	Robert Koch Institute	Germany
061	Blomster salen	1016	Evolving waters: Contrasting the population genetics of brown trout (Salmo trutta) across the island of Ireland	Open Theme	Diarmaid Duffy	Queen's University Belfast	United Kingdom
062	Blomster salen	549	Evolutionary Dynamics of Intrinsically Disordered Regions in Eukaryotic Transposable Element Repressors	Open Theme	Diego Forni	Scientific Institute IRCCS E. Medea	Italy
063	Blomster salen	400	Reconstructing the Demographic History of a Freeze-Tolerant Frog: The Interplay Between Selection and Ne	Open Theme	Dylan Padilla	Yale University	United States
064	Blomster salen	1198	Genomic consequences of recent isolation in the Marsican brown bear	Open Theme	Elisa Desiato	University Of Ferrara	Italy
065	Blomster salen	898	Genomic erosion footprint in insects under extreme decline and isolation	Open Theme	Elisabeth Karalashvili	Leibniz Institute For The Analysis Of Biodiversity	Germany
066	Blomster salen	601	Evolution of reproductive coordination in Azolla	Open Theme	Ellen Sigourney Lorberg	Georg-August University Goettingen	Germany
067	Blomster salen	989	Molecular mechanisms of thermal adaptation in urban and forest populations of frogs	Open Theme	Emese Balogh	University Of Veterinary Medicine Budapest	Hungary
068	Blomster salen	697	Archaeogenomic reconstruction of ancient elephant ivory trade routes	Open Theme	Emily Johana Ruiz Puerta	University of Lund	Netherlands
069	Blomster salen	821	New strategies for exploring phylogenetic tree space in Bayesian inference	Open Theme	Emma Gomez	California State University, Fullerton	United States
070	Blomster salen	56	Multidisciplinary approach to study population dynamics of the Polar cod in a changing environment	Open Theme	Erica Difronzo	Ca' Foscari University Of Venice	Italy
071	Blomster salen	99	The effect of age and condition on transcript errors	Open Theme	Erik Widén	Linköpings University	Sweden
072	Blomster salen	1655	Conservation and collapse of ancestral linkage groups across Nematoda	Open Theme	Erna King	Wellcome Sanger Institute	United Kingdom
073	Blomster salen	1609	Seapill Origami: Applying RNA Secondary Structure to Improve the Sphaeromatidae Phylogeny	Open Theme	Ethan Kahn	Natural History Museum of Los Angeles County	United States
074	Blomster salen	1298	Evolution of gene expression and regulation in a haplodiploid pollinator	Open Theme	Eva Adina Baumgarten	iomE, Johannes Gutenberg University Mainz	Germany
075	Blomster salen	897	DNA repeats, sources of extremes in DNA composition in orchids?	Open Theme	Eva Hribova	Institute of Experimental Botany	Czech Republic
076	Blomster salen	1492	Characterisation of major histocompatibility complex diversity in the sand lizard (Lacerta agilis)	Open Theme	Felicia Axelsson	Uppsala University	Sweden
077	Main hall	1068	Investigating signatures of local adaptation in the ubiquitous forest ectomycorrhizal fungus Cenococcum geophilum	Open Theme	Felix Zimmermann	Swiss Federal Research Institute WSL	Switzerland
078	Main hall	1343	Genomic Architecture of Adaptation at the Range Limit: X-linked and Autosomal Divergence in Ischnura elegans	Open Theme	Fereshteh Ghadamgahi	lund university	Sweden
079	Main hall	376	Genetic Signatures Of Mitonuclear Coevolution In The Mexican Biobank.	Open Theme	Finley Grover-Thomas	University College London	United Kingdom
080	Main hall	1532	Molecular characterization of temperature tolerance in the methylotrophic yeast Komagataella phaffii (Pichia)	Open Theme	Finley Pitcock	The Ohio State University	United States
081	Main hall	215	Evolution of domesticated plasmid replication control in Pantoea.	Open Theme	Florence Muccino	Institute Of General Microbiology, CAU Kiel	Germany
082	Main hall	167	HoloTrait: A trait-based evolutionary framework for microbiome stability, dysbiosis, and recovery	Open Theme	Franceen Eshun-Wilson	University Of Copenhagen	Denmark
083	Main hall	490	Population genomics of South American Mennonites.	Open Theme	Francesc Calafell	Ibe (csic-upf)	Spain
084	Main hall	1519	A genomic snapshot of the Ottoman army in Southern Italy	Open Theme	Francesco Montinaro	University of Bari	Italy
085	Main hall	1354	Apulia at the crossroads of the Mediterranean: fine-scale population sub-structure and admixture inferred from allele-frequency and haplotype-based analyses	Open Theme	Francesco Perrone	University Of Bari	Italy

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
086	Main hall	1465	How intracellular mutualism emerges: developmental and evolutionary perspectives through an integrative study of an aphid symbiosis	Open Theme	François Gilbert	UCLouvain	Belgium
087	Main hall	818	Genomic insights into the convergent evolution of ant-eating mammals	Open Theme	Frédéric Delsuc	CNRS - Université de Montpellier	France
088	Main hall	463	Genomic adaptation to aridity in the Arabian sand boa	Open Theme	Gabriel Mochales-Riaño	New York University Abu Dhabi	United Arab Emirates
089	Main hall	1405	Using Demographic Models and Ancient European Genomes to Identify Signals of Selection due to Admixture	Open Theme	Gauri Bhide	Clemson University	United States
090	Main hall	1060	Guiding experimental design for efficient sampling of fitness landscapes	Open Theme	Georgios Kalogiannis	University of Zurich	Switzerland
091	Main hall	1382	A genomic snapshot of the Chalcolithic-Bronze Age transition from the pile-dwelling site of Ledro, Italy	Open Theme	Giacomo Villani	University Of Pavia	Italy
092	Main hall	1512	ProteomeLM: A proteome-scale language model enables accurate and rapid prediction of protein-protein interactions and gene essentiality	Open Theme	Gionata Paolo Zalaffi	EPFL	Switzerland
093	Main hall	317	Microbiome Atlas of Portuguese Aquaculture Fish	Open Theme	Gonçalo Themudo	Ciimar / Uporto	Portugal
094	Main hall	1257	Are chromosomal inversions promoting speciation in the Tyrrhenian wall lizard?	Open Theme	Guannan Wen	Max Planck Institute for Evolutionary Biology	Germany
095	Main hall	1040	Genomic and phenological variation across the geographic range of sugar maple (Acer saccharum)	Open Theme	Hanna Makowski	University Of Virginia	United States
096	Main hall	153	A pleiotropic hitchhiking model recapitulates alignments between fly wing divergence and variation	Open Theme	Haoran Cai	UCLA	United States
097	Main hall	489	Global Pathogen Analysis Platform	Open Theme	Harrison Bo Hua Zhu	Technical University of Denmark	Denmark
098	Main hall	169	The role of lncRNAs in Dryophytes arenicolor (Canyon Treefrog) metamorphosis, an evolutionary perspective	Open Theme	Héctor Herrera-Orozco	Universidad Nacional Autónoma De México	Mexico
099	Main hall	895	Towards Reconstructing the Genetic History of East Asian Goats	Open Theme	Heeseung Yeum	Seoul National University	South Korea
100	Main hall	269	Regulation of a "tripartite" Toxin Antitoxin system from the honeybee intestinal bacteria Apilactobacillus kunkeei.	Open Theme	Héléna Vassilieff	Uppsala University	Sweden
101	Main hall	1680	A Hierarchical Foundation Model for Microbial Taxonomic Prediction and Downstream Applications	Open Theme	Herui Liao	MIT	United States
102	Main hall	1066	A practical comparison of genomic prediction methods in ecology and evolution	Open Theme	Heung Ying Janet Chik	Norwegian University Of Science And Technology	Norway
103	Main hall	1578	Karyotypic analysis of established primate iPSCs by cytogenetic and M-FISH techniques	Open Theme	Hideyuki Tanabe	SOKENDAI	Japan
104	Main hall	525	Global Population Genomics of Marchantia polymorpha: Patterns of Gene Flow Across Subspecies and Continents	Open Theme	Hiromu Nakao	Gregor Mendel Institute of Molecular Plant Biology	Austria
105	Main hall	985	Tracing the spread of Celtic languages using ancient genomics	Open Theme	Hugh McColl	University of Copenhagen	Denmark
106	Main hall	808	Assessing Parental Contribution to Genetic Inheritance: Age-dependent Mutational Landscapes in Macaca fascicularis Families	Open Theme	Hye-Ri Park	KRIBB	South Korea
107	Main hall	943	Ancient genomes from the Shiveet Khairkhan archaological site reveal the genetic connectivity between Early Iron Age pastoralists	Open Theme	Hyoungmin Moon	School of Biological Sciences, Seoul National University	South Korea
108	Main hall	254	Past population structure and indicators of gene flow in a malaria parasite, Plasmodium falciparum	Open Theme	Håvard Bjerke	University Of Copenhagen	Denmark
109	Main hall	468	Evolution of the prokaryotic transcription factor repertoire	Open Theme	Inder Raj Singh	National Centre For Biological Sciences	India
110	Main hall	576	Merging evolutionary timescales to quantify adaptation	Open Theme	Ioanna Kotari	Vienna Graduate School Of Population Genetics	Austria
111	Main hall	1446	Long-read genome assemblies of museum samples	Open Theme	Ioannis Chrysostomakis	Leibniz Institute For The Analysis Of Biodiversity	Germany
112	Main hall	625	Geolocating Neanderthal Introgression using spatial simulations	Open Theme	Ioannis Patramanis	Globe Institute, University of Copenhagen	Denmark
113	Main hall	262	Comparative organoid systems for functional genomics research in primate skeletal cells	Open Theme	Irina Milicevic	Max Planck Institute for Evolutionary Anthropology	Germany
114	Main hall	517	Recombination landscape evolution in Podarcis wall lizards	Open Theme	Iris Liesbeth Ruesink Bueno	Max Planck Institute for Evolutionary Biology	Germany
115	Main hall	647	Somatic mutation signatures as markers of immune and environmental stress in Gentoo Penguins	Open Theme	Isabel Gamache	Concordia University	Canada
116	Main hall	1565	Sex-specific contemporary selection on educational attainment–associated genetic variation in Estonia	Open Theme	Ivan Kuznetsov	University of Tartu	Estonia
117	Main hall	1509	Selection on telomere homeostasis drives the adaptive evolution of TERT in Mimulus	Open Theme	Jae Young Choi	University Of Kansas	United States
118	Main hall	1541	Ancestral linkage group inference and centromere annotation elucidate rapid chromosomal evolution in the oligocentric sedges and rushes	Open Theme	James McCulloch	Wellcome Sanger Institute	United Kingdom
119	Main hall	732	Streptophyte evolution: the evolutionary origin of the plant terrestrialization toolkit	Open Theme	Jan de Vries	University of Göttingen	Germany
120	Main hall	274	Nigritella or Gymnadenia? Resolving the phylogeny of a controversial clade	Open Theme	Jan Klink	Lund University	Sweden
121	Main hall	1450	Functional characterization of casual variants and hitchhikers in recent pathogen-driven sweeps across diverse human groups	Open Theme	Jared Akers	Yale	United States
122	Main hall	1558	Breaking the yeast species barrier allows selection on recombinant hybrids	Open Theme	Jasmine Ono	University Of Nottingham	United Kingdom
123	Main hall	1499	Paragastric canal morphogenesis as a model for gut development in the ctenophore Mnemiopsis leidyi	Open Theme	Jason Presnell	University Of Kansas	United States
124	Main hall	142	Maternal effects and the expression of DNA methyltransferases in Daphnia pulex	Open Theme	Jeff Dudycha	University Of South Carolina	United States
125	Main hall	1124	(What) Can isopod genomes tell us about their ecological transitions?	Open Theme	Jessica A. Thomas Thorpe	Wellcome Sanger Institute	United Kingdom
126	Main hall	1736	Single-nucleus multi-omics analyses reveal cellular and molecular innovations in the anterior cingulate cortex during primate evolution	Open Theme	Jiamiao Yuan	Kunming Institute of Zoology, Chinese Academy of Sciences	China
127	Main hall	1747	Admixture History and Tropical Adaptation of the Cambodian Indigenous Peoples	Open Theme	Jianxin Guo	Kunming Institute of Zoology, CAS	China
128	Main hall	677	Inferences of haplotype sharing and population history across time	Open Theme	Jiaqi Yang	Max Planck Institute for Evolutionary Anthropology	Germany
129	Main hall	1215	Conserved Myosin Anchoring, Divergent C Termini: Structural Bases of Flightin/Paraflightin Functional Evolution in Pancrustacea	Open Theme	Jim Vigoreaux	University of Vermont	United States
130	Main hall	510	Population Genomics of the Asian Corn Borer (Ostrinia furnacalis) in Korea	Open Theme	Jiyeong Shin	Institute for Data Innovation in Science (IDIS), Seoul National University	South Korea
131	Harlekin	597	Exploring mitonuclear coadaptation in a Carpathian contact zone of cryptic alpine newt subspecies	Open Theme	Joanna Jakóbik	Jagiellonian University	Poland
132	Harlekin	1051	Cell culture-based approach uncovers the role of environment, evolutionary history and introgression in phenotypic plasticity in fish	Open Theme	João M Moreno	Faculdade De Ciências, Universidade De Lisboa	Portugal
133	Harlekin	1564	Genomic signatures of virulence and resistance to psittacine beak and feather disease virus (BFDV) in the echo parakeet (Alexandrinus eques)	Open Theme	Johanna Winder	University Of Kent	United Kingdom
134	Harlekin	806	Early genomic signatures of domestication in the common ostrich	Open Theme	Johanne Gottenborg	Aarhus University	Denmark
135	Harlekin	1437	Gene expression evolution across primate cardiomyocyte differentiation	Open Theme	John Hurley	University Of Texas Medical Branch	United States
136	Harlekin	566	Automation-driven Micro-Scale Spatial Metagenomics	Open Theme	Jonas Lauritsen	University Of Copenhagen	Denmark

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
137	Harlekin	751	On the limits of introgression: the early out of Africa conundrum	Open Theme	Jose Miguel Serradell Noguera	Institut Biologia Evolutiva (IBE-CSIC)	Spain
138	Harlekin	758	Mode and tempo of de novo gene birth in the brown alga Ectocarpus	Open Theme	Josué Barrera-Redondo	Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional	Mexico
139	Harlekin	887	Host associations of Borrelia afzelii ospC and ospE variants in two wild rodent reservoir species	Open Theme	Józefina Wasilewska	Adam Mickiewicz University	Poland
140	Harlekin	287	Evolutionary history and functional divergence of hydroxycarboxylic acid receptors in primates	Open Theme	Juan C. Opazo	Universidad San Sebastian	Chile
141	Harlekin	146	Differentiating Migration Rates Using Selective Sites Instead of Neutral Sites	Open Theme	Jui-hsuan Chien	Institute Of Bioinformatics And Structural Biology, National Tsing Hua University	Taiwan
142	Harlekin	714	Transcriptomic dynamics of eastern oysters under climate change stress	Open Theme	Julia McDonough	University Of Massachusetts Lowell	United States
143	Harlekin	664	A Curated Genome-Scale Nucleotide Diversity Panel of Non-Human Primates	Open Theme	Juraj Bergman	Aarhus University	Denmark
144	Harlekin	111	The molecular regulation of floral ultraviolet patterns in sunflower	Open Theme	Justin Chan	The University Of British Columbia	Canada
145	Harlekin	698	Rapid ecological diversification of Arabidopsis thaliana populations in urban environments	Open Theme	Justine Floret	University of Cologne	Germany
146	Harlekin	66	Linker histone H1.0 evolution and ferroptosis reveal new perspectives on Greenland shark longevity	Open Theme	Kaiqiao Yang	The University Of Tokyo	Japan
147	Harlekin	315	Investigating phylogenetic incongruence in wild Oryza species through genome-wide phylogenomic analysis	Open Theme	Kanako Koyanagi	Hokkaido University	Japan
148	Harlekin	1267	Beyond the Gradient: Dynamic Repression as the Architect of Developmental Precision	Open Theme	Kasım Taha Karagöz	Ihsan Dogramaci Bilkent University	Türkiye
149	Harlekin	460	Inversions facilitate parallel adaptive divergence in the wildflower Senecio lautus	Open Theme	Kathleen Mclay	University Of Queensland	Australia
150	Harlekin	282	Phased Assemblies Reveal Hybrid Genomes and Wine-Associated Hanseniaspora Yeasts Population Structure	Open Theme	Katja Doberšek	University of Ljubljana, Biotechnical Faculty, Department of Food Science and Technology	Slovenia
151	Harlekin						
152	Harlekin	477	Ancient DNA reveals long-distance population contact and dynamics in northern East Asia	Open Theme	Ke Wang	Fudan University	China
153	Harlekin	461	A Myosin Heavy Chain Gene Cluster Duplication in an Ancient Lobe-Finned Fish as a Key Event for Terrestrial Life	Open Theme	Kei Tamura	Kitasato University	Japan
154	Harlekin	997	Amylase-binding proteins as indicators of dietary adaptation in the human oral microbiome	Open Theme	Keri Burge	Harvard University	United States
155	Harlekin	1521	Diversity of sex chromosomes in seahorses and pipefish	Open Theme	Kevin Hsiung	Leibniz-Institut zur Analyse des Biodiversitätswandels	Germany
156	Harlekin	1569	Effect of past climate change events on demographic history of bats	Open Theme	Kirnalee Patel	Ashoka University, Sonipat, Haryana	India
157	Harlekin	1069	Dynamics of adaptation to slowly fluctuating environments	Open Theme	Salvatore Banno	University of Jyväskylä	Finland
158	Harlekin	733	Drivers and constraints to the recurrent evolution of a color pattern in frogs and toads	Open Theme	Sandra Goutte	NTNU	Norway
159	Harlekin	224	A multi-scale genotype-phenotype map of developmental regulatory networks	Open Theme	Santiago Herrera-Alvarez	Embl	Germany
160	Harlekin	424	Climate Change, Range Shift and Hybridization: A Genetic Investigation of P. maniculatus and leucopus	Open Theme	Sargon Yousefian Dezag Tekkie	York University	Canada
161	Harlekin	932	Dispersal history of the brown rat inferred from Asian population genomics	Open Theme	Satsuki Hirasawa	Hokkaido University	Japan
162	Harlekin	504	Population-specific signals of positive selection in the human CYP1A2 gene.	Open Theme	Sayaka Chiku	SOKENDAI	Japan
163	Harlekin	446	Longitudinal Plasma Proteomic Profiling Connects Genomic Changes to Systemic Aging Phenotypes	Open Theme	Sehee Choe	Korea Research institute of bioscience & Biotechnology, NPRC	South Korea
164	Harlekin	1054	Peculiar Pigment Pattern and Population Profile of a Poisonous Pufferfish	Open Theme	Seita Miyazawa	The University of Osaka	Japan
165	Harlekin	939	Mitochondrial support of cardiac plasticity in the high-elevation deer mouse Peromyscus maniculatus	Open Theme	Shady Kuster	Colorado State University	United States
166	Harlekin	1742	The temporal, molecular, and life-history constraints on the evolution of phenotypic plasticity	Open Theme	Shannon Snyder	University Of Oregon	United States
167	Harlekin	409	Relaxation of selective constraint on the sweet-taste receptor gene TAS1R2 in lorisiform primates	Open Theme	Shoji Kawamura	University of Tokyo	Japan
168	Harlekin	856	Evaluating data processing approaches for comparative primate functional genomics research	Open Theme	Shuanghui Chen	Department of Primate Behavior and Evolution, Max Planck Institute for Evolutionary Anthropology	Germany
169	Harlekin	1484	Origins of the wild Mustangs of North America and their genomic conservation status	Open Theme	Silas Tanderup	Aarhus University	Denmark
170	Harlekin	1471	Optimization of wet lab protocols for reference genome production of colonial ascidians	Open Theme	Simona Buonanno	University of Bari "Aldo Moro"	Italy
171	Harlekin	906	Decoding the Plantain Genome: A Complete Assembly for Structural and Evolutionary Studies	Open Theme	Simona Martikánová	Institute Of Experimental Botany	Czech Republic
172	Harlekin	1299	Detecting and characterising hybridisation between native and introduced species of Maylandia cichlid fish in Lake Malawi	Open Theme	Sing Wei Lim	University of Cambridge	United Kingdom
173	Harlekin	927	Quinone chemistry shapes NADH dehydrogenase utilization in bacterial respiratory chain evolution	Open Theme	Snehal Khairnar	Tata Institute Of Fundamental Research	India
174	Harlekin	1758	A joint Bayesian framework for identification of genotype-phenotype associations in birds	Open Theme	Sofia Stroustrup	University of Copenhagen	Denmark
175	Harlekin	599	Questioning genetic supremacy: investigating the transmission of phenotypic traits and DNA methylation patterns across three generations in	Open Theme	Stacy Rousse	Inrae	France
176	Harlekin	928	Delineating potential influence of gut microbiota on the pathophysiological outcomes of early life stress	Open Theme	Stuti Srivastava	Tata Institute Of Fundamental Research	India
177	Harlekin	694	Coding sequence evolution associated with avian beak shape diversification	Open Theme	Sze Chai Helen Wong	University of Copenhagen	Denmark
178	Harlekin	606	Structure-guided secretome analysis in a fungal plant pathogen provides insights into effector evolution and functional diversification	Open Theme	Thais Dal'Sasso	Kiel University	Germany
179	Harlekin	1189	Ancient genomics support deep divergence between Eastern and Western Mediterranean Indo-European languages	Open Theme	Tharsika Vimala	UC Berkeley	United States
180	Harlekin	337	Detecting polygenic selection signatures using tree sequences statistics	Open Theme	Thémis Lemarchand	INRAE Université Paris-Saclay	France
181	Harlekin	861	Repeat evolution of cephalic horns in vipers	Open Theme	Theo Busschau	New York University Abu Dhabi	United Arab Emirates
182	Harlekin	1675	Phenotypic and transcriptomic plasticity in the medaka gut in response to food availability	Open Theme	Tokiho Akiyama	Kitasato University School of Medicine	Japan
183	Harlekin	147	Genetic basis of innate vocalization patterns in chickens	Open Theme	Tsuyoshi Shimmura	Tokyo University Of Agriculture And Technology	Japan
184	Harlekin	1496	Phylogenomic analyses of transposable elements in simulated populations to disentangle past demographic and transpositional events	Open Theme	Valentin Grenet	Institut De Recherche Pour Le Développement	France
185	Harlekin	1377	Evolution of transposable element activity, structural variants and SNPs upon hybridisation	Open Theme	Valentina Peona	Swedish Natural History Museum	Sweden

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
186	Harlekin	817	Assessing the fitness of HIV-1 drug target protein variants through dynamical properties	Open Theme	Valeria Zoni	University Of Vigo	Spain
187	Harlekin	1041	National bioinformatics support for Evolution and Biodiversity research projects at Swedish universities	Open Theme	Verena E. Kutschera	National Bioinformatics Infrastructure Sweden	Sweden
188	Harlekin	717	Comparative investigation of style length and female self-incompatibility reaction mediated via the brassinosteroid pathway in	Open Theme	Viktoria Bednarski	Stockholm University	Sweden
189	Harlekin	607	Using Hyb-Seq (target capture sequencing) to construct a phylogenetic framework for a tropical plant family, the Calophyllaceae	Open Theme	Wei Wei Seah	Naturalis Biodiversity Center	Netherlands
190	Harlekin	1634	Continent Surfing: The First Molecular Phylogeny of A Gondwanan Isopod Suborder	Open Theme	William Farris	Natural History Museum Of Los Angeles County	United States
191	Harlekin	1195	Comparative genomics of phylum Tardigrada, based on single-specimen genomes	Open Theme	Witold Morek	Wellcome Sanger Institute	United Kingdom
192	Harlekin	633	What can we learn about speciation from high levels of allele sharing at loci subject to strong balancing selection?	Open Theme	Xavier Vekemans	University of Lille	France
193	Harlekin	1686	Why are most of the methods detecting natural selection wrong? And how to detect natural selection properly?	Open Theme	Xianfa Xie	Virginia State University	United States
194	Harlekin	1750	Uncovering the selection on non-homologous end joining and homologous recombination for genome downsizing in polyploid plants	Open Theme	Xiaotong Wang	Beijing Life Science Academy	China
195	Harlekin	1741	Brain Evolution in Lungfish: Uncovering Tetrapod Adaptations During the Water-to-Land Transition	Open Theme	Xiaoyu Meng	Kunming Institute of Zoology, CAS	China
196	Harlekin	365	Independent origin of genomic imprinting in placental fish	Open Theme	Xu Wang	Auburn University College Of Veterinary Medicine	United States
197	Harlekin	1743	A Comparative TE Annotation Framework for Bees	Open Theme	Xuejing Hu	Leibniz Institute For The Analysis Of Biodiversity Change	Germany
198	Harlekin	1137	Trimmiy: Removing erroneously aligned columns from multiple sequence alignments for improved phylogenetic inference.	Open Theme	Yi Liu	University Of Oxford	United Kingdom
199	Harlekin	831	Genomic diversity and local adaptation in the native range of the global pest Drosophila suzukii	Open Theme	Ying Zhen	Westlake University	China
200	Harlekin	306	Molecular basis of aggressive behavior in chickens	Open Theme	Yohei Yamada	Tokyo University Of Agriculture And Technology	Japan
201	Harlekin	826	Genomic diversity and population structure of Korean rice	Open Theme	Yoon Kyung Lee	Seoul National University	South Korea
202	Harlekin	926	A genome-wide association study (GWAS) reveals the molecular basis of body coloration and morphological traits in ornamental common carp	Open Theme	Yoshihiro Omori	Hiroshima University	Japan
203	Harlekin	1196	Early-onset colorectal cancer-associated driver oncogenes revealed by molecular evolutionary analysis.	Open Theme	Yosuke Seto	Japanese Foundation For Cancer Research	Japan
204	Harlekin	1573	Antimicrobial and metal resistance genes in bacteria from contaminated Moroccan soils: metal-driven co-selection revealed by metagenomics	Open Theme	Yousra Benghait	University Hassan II - Faculty of Science Ain Chock Casablanca	Morocco
205	Harlekin	255	Reconstructing phylogenetic trees with compression: Based on nested and hierarchical repetitive substructures	Open Theme	Yu Liu	Beijing Normal University	China
206	Harlekin	401	Experimental validation of phenotypic diversity associated with Jomon ancestry using blood cells and iPSCs	Open Theme	Yuka Nakamura	The University of Tokyo	Japan
207	2nd floor: Arkaden 8	303	Genomic basis of extremely long crowing in chickens	Open Theme	Yuki Matsuda	Tokyo University Of Agriculture And Technology	Japan
208	2nd floor: Arkaden 8	1083	The Most Lethal Marine Toxin: Unraveling Echotoxin’s Ecological role via Transcriptomics	Open Theme	Yukyung Kim	Jeonbuk National University	South Korea
209	2nd floor: Arkaden 8	126	Benchmarking D-statistics with forward population genetic simulations	Open Theme	Yulin Sun	The University Of Queensland	Australia
210	2nd floor: Arkaden 8	649	A Comparative Analysis of Computel and Telomerecat for Estimating Telomere Length in Macaca fascicularis using NGS Data	Open Theme	YunJung Lee	KRIBB	South Korea
211	2nd floor: Arkaden 8	122	Comparing signals of positive selection inferred by dN/dS models and mutation–selection models across mammalian genomes	Open Theme	Yuqing Peng	Queen Mary University of London	United Kingdom
212	2nd floor: Arkaden 8	784	Fruit evolution is key to ecological niches and distribution range divergence in tribe Ligustrinae (Oleaceae)	Open Theme	Yushuang Wang	The University Of British Columbia	China
213	2nd floor: Arkaden 8	1577	Uncovering the 3FTx Repertoire in Elapidae Through Reanalysis of Public Transcriptome Data	Open Theme	Yu-Wen Huang	National Yang Ming Chiao Tung University	Taiwan
214	2nd floor: Arkaden 8	748	Detecting Positive Selection Using Spatial Autocorrelation and Haplotype Structure in Populations with Limited Dispersal	Open Theme	Zachary Szpiech	Penn State University	United States
215	2nd floor: Arkaden 8	1769	Decoding the interactome of biomolecular condensates	Open Theme	Alessandro Bevilaqua	Max Planck Institute of Molecular Cell Biology and Genetics	Germany
216	2nd floor: Arkaden 8	609	Evolutionary loss of umami taste receptor gene TAS1R1 in tamarins among TAS1R gene family of ecologically diverse platyrrhine primates	Open Theme	Zhixin Wu	The University of Tokyo	Japan
217	2nd floor: Arkaden 8	177	Does the rediploidization process impact observed duplicate outcomes following the Saccharomyces whole genome duplication?	Open Theme	Zoe Vance	University Of Bath	United Kingdom
218	2nd floor: Arkaden 8	838	Population genomics of a recently expanded annual weed across its geographic range	Open Theme	Aaditya Narasimhan	University Of Lausanne	Switzerland
219	2nd floor: Arkaden 8	874	Bacterial mutators reveal a deterministic role of standing variation in streamlining evolutionary outcomes	Open Theme	Aakanksha Madhwal	National Centre For Biological Sciences	India
220	2nd floor: Arkaden 8	671	Ancient Mitogenomes from Belize Provide Insights into the Mobility and Migration of Ancient Communities in Mesoamerica and the	Open Theme	Celia Cleary	Baylor University	United States
221	2nd floor: Arkaden 8	983	Revisiting the Classification of Macro- and Microchromosomes in Vertebrates: Insights into Their Origins	Open Theme	Yuichiro Hara	Kitasato University	Japan
222	2nd floor: Arkaden 8	1511	The evolutionary origin of the Columbian mammoths from the Basin of Mexico and its implications for the Mammuthus genus	Open Theme	Rigoberto Padilla-Bustos	UNAM	Mexico
223	2nd floor: Arkaden 8	1453	Probe efficacy and an initial phylogenomic reconstruction of freshwater crayfish using anchored hybrid enrichment	Open Theme	Meng Chen Yu	George Washington University	United States
224	2nd floor: Arkaden 8	678	The Population History of Hybridisation and Local Adaptation in Previously Unknown Admixed Rice Population	Open Theme	Meng-ting Hsieh	Earlham Institute	United Kingdom
225	2nd floor: Arkaden 8	1269	Inferring shared sources of admixture among populations worldwide using a new technique	Open Theme	Mengzi Chen	University College London	United Kingdom
226	2nd floor: Arkaden 8	77	Inferring South American camelids history through the lens of whole-genome data in context of their domestication	Open Theme	Michael Orellana	University Of Colorado Boulder	United States
227	2nd floor: Arkaden 8	470	Comparative Genomic Analysis of Tandem Repeat Variations and Transcriptome Diversity across primate evolution	Open Theme	Min-gyeong Ko	Kribb	South Korea
228	2nd floor: Arkaden 8	110	Analysis of a Possible Relaxation of Natural Selection in Human Populations	Open Theme	Miriam Alejandra Jimenez Marmolejo	National Autonomous University of Mexico	Mexico
229	2nd floor: Arkaden 8	1543	Leveraging stochastic mutational mappings to estimate time-resolved, significant changes in selection along a global SARS-CoV-2 phylogeny	Open Theme	Monica Arniella	University of California Berkeley	United States
230	2nd floor: Arkaden 8	1297	A Diachronic Paleogenomic Analysis of Consanguinity from the Iron Age to the Early Middle Ages in the Roman World	Open Theme	N. Ezgi Altınışık	Hacettepe University	Türkiye
231	2nd floor: Arkaden 8	327	Persistence and Context of Human Sedimentary DNA in Modern Burial Soils: Implications for Forensic and Evolutionary Interpretation	Open Theme	Nadescha Viviane Hänggi	University Of Copenhagen, Section of Forensic Genetics, Department of Forensic Medicine	Denmark
232	2nd floor: Arkaden 8	114	Impact of a jigsaw activity on undergraduate students’ conceptual understanding: narrowing the gap between low and high performers	Open Theme	Nadia Aubin-Horth	Université Laval	Canada
233	2nd floor: Arkaden 8	853	Agmatoploidy and conserved synteny shape karyotype evolution in holocentric Cyperids	Open Theme	Natalia Castro	Max Planck Institute for Plant Breeding Research	Germany
234	2nd floor: Arkaden 8	53	Collateral fitness effects of mutation are not commonly caused by protein misfolding	Open Theme	Natalie Quan	Arizona State University	United States

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
235	2nd floor: Arkaden 8	64	Genetic variation in adrenarche-associated genes suggests shorter childhoods in Neanderthals	Open Theme	Nicholas Hartman	University Of Colorado Boulder	United States
236	2nd floor: Arkaden 8	194	Genetic Basis of Skeletal Morphology in Archaic Humans	Open Theme	Nicholas Holly	Clemson University	United States
237	2nd floor: Arkaden 8	492	Beyond static reference trees: a dynamic framework for human mtDNA phylogeny	Open Theme	Nicole Huber	Medical University Of Innsbruck	Austria
238	2nd floor: Arkaden 8	961	Assembly of megabasepair-long ribosomal DNA arrays using advanced Nanopore basecalling	Open Theme	Nikol Poláková	Masaryk University	Czech Republic
239	2nd floor: Arkaden 8	800	A ballad of Songbird and Snake: Towards T2T reference genomes for non-model species	Open Theme	Nivesh Jain	Vertebrate Genome Lab, The Rockefeller University	United States
240	2nd floor: Arkaden 8	405	Evolution of human bipedalism via genetic regulation	Open Theme	Noam Priel	Weizmann Institute Of Science	Israel
241	2nd floor: Arkaden 8	294	A Neural Network Framework Reveals Evidence of Ghost Introgression in Denisovan Introgressed Sequence in Modern Humans	Open Theme	Noel Mcallister	University Of Michigan, Ann Arbor	United States
242	2nd floor: Arkaden 8	858	Time-Series Ancient Genomes Reveal Persistence and Connectivity in Patagonia	Open Theme	Patricio Pezo	Institut de Biologia Evolutiva (IBE-CSIC)	Spain
243	2nd floor: Arkaden 8	1755	Insights from and limits to a mosaic molecular clock model for prokaryotes genomes	Open Theme	Paul Etheimer	Mines Paris Psl - Institut Curie	France
244	2nd floor: Arkaden 8	1030	Historic Overexploitation, Genetic Erosion and Local extinction: Palaeogenomic Insights into the Decline of Eubalaena glacialis in Northeast Atlantic	Open Theme	Paula F. Campos	CIIMAR, University of Porto	Portugal
245	2nd floor: Arkaden 8	862	Mutational bias in GRINS: How coding sequences accommodate intense nucleotide skews	Open Theme	Paula Thiel Pizarro	University Of Zurich	Switzerland
246	2nd floor: Arkaden 8	1752	Investigating Gene Expression Noise in Embryogenesis – Evolutionary Implications for Duplicate Gene Retention and Compensation	Open Theme	Pavol Kramár	Queen Mary University Of London	United Kingdom
247	2nd floor: Arkaden 8	145	Identifying selection in Plasmodium populations through IBD troughs rather than peaks	Open Theme	Peng-Yin Ng	National Tsing Hua University	Taiwan
248	2nd floor: Arkaden 8	366	Tracing the Evolution of Eye Pigmentation Genes in Arthropods and Identification of Such Genes in Ostracod Crustacean Skogsbergia sp.	Open Theme	Phoebe Hall	University Of California, Santa Barbara	United States
249	2nd floor: Arkaden 8	617	Comparative Genomic Analysis of Independently Miniaturised Annelids	Open Theme	Pia Merete Eriksen	University Of Copenhagen	Denmark
250	2nd floor: Arkaden 8	1497	Making the step to multiple hosts: the genomic and transcriptomic drivers of diet plasticity in Tephritis conura flies	Open Theme	Rachel Steward	Lund University	Sweden
251	2nd floor: Arkaden 8	486	Urea transporter evolution: deep conservation, recent adaptation in mammals, and maintenance of the Jka/Jkb polymorphism in the past ~110,000 years	Open Theme	Rachele Cagliani	Scientific Institute IRCCS E. Medea	Italy
252	2nd floor: Arkaden 8	1751	The genomic tug-of-war: disentangling the biological drivers of cytonuclear discordance across angiosperm.	Open Theme	Radhika Dutt	Indian Institute of Science	India
253	2nd floor: Arkaden 8	1589	Discovery and Evaluation of Molecular Mimicry between Epstein–Barr Nuclear Antigen 1 and Unrelated Human Proteins Relevant to Multiple Sclerosis	Open Theme	Raquel Battifora	Florida International University	United States
254	2nd floor: Arkaden 8	511	Protein Evolution Occurs at an Uneven Tempo: Patterns of Rate Variation Across the Tree of Life	Open Theme	Rasit Durak	Max Planck Institute For Evolutionary Biology	Germany
255	2nd floor: Arkaden 8	792	Variation in transposable element landscapes across socially parasitic and host ants	Open Theme	Raziyeh Abdilzadeh	University Of Münster	Germany
256	2nd floor: Arkaden 8	1414	A haplotype-based neutrality test, 2D-SFS, uncovers positive selection on an intergenic haplotype in the Japanese population	Open Theme	Risa L. Iwasaki	Kanazawa University	Japan
257	2nd floor: Arkaden 8	849	Investigating the utility of genome-environment association for identifying climate-adapted variation in Aegilops tauschii	Open Theme	Risha Na	Department of Ecology, Environment and Plant Sciences, Stockholm University	Sweden
258	2nd floor: Arkaden 8	1534	Paleogenomic analysis of Mongolian aurochs and cattle reveal connections to both ancient and modern bovids	Open Theme	Robin Singleton	Clemson University	United States
259	2nd floor: Arkaden 8	915	Defensive symbiosis evolves rapidly: experimental evolution reveals viral selection drives Wolbachia spread	Open Theme	Rodrigo Cogni	Universidade De Sao Paulo	Brazil
260	2nd floor: Arkaden 8	1586	Salvaging genetic data from decades-old degraded giant kelp tissue (Macrocystis pyrifera)	Open Theme	Roy Roberts	University Of California Santa Cruz	United States
261	2nd floor: Arkaden 8	78	Genetic signature reveals the impact of regional and colonial histories on Mycobacterium tuberculosis evolution in Taiwan	Open Theme	Ruo-Ya Bai	National Tsing Hua University	Taiwan
262	2nd floor: Arkaden 8	1623	Dormant immunity in bumblebees	Open Theme	Safira Moog	Institute of Organismic and Molecular Evolution (iomE), Johannes Gutenberg University Mainz	Germany
263	2nd floor: Arkaden 8	1238	Ribosome profiling for minimal (gut) consortia for novel gene finding in vivo and in vitro	Open Theme	Klaus Neuhaus	Technische Universität München	Germany
264	2nd floor: Arkaden 8	204	Retroviral OVEX genes: Evolutionary conservation and possible contribution to avian-specific gonadal functions	Open Theme	Koichi Kitao	Riken	Japan
265	2nd floor: Arkaden 8	535	Genomic Analysis of Color Pattern Polymorphism in Red Palm Weevils	Open Theme	Kripa Shrestha	New York University Abu Dhabi	United Arab Emirates
266	2nd floor: Arkaden 8	1593	HLA–KIR Interactions and Active Tuberculosis Risk in Khoe-San Descent Populations	Open Theme	Kristin Hardy	University Of California, Davis	United States
267	2nd floor: Arkaden 8	1507	Mitospecies: a novel concept for describing molecular diversity	Open Theme	Krisztián Szabó	University Of Veterinary Medicine Budapest	Hungary
268	2nd floor: Arkaden 8	414	Population genomic insights into donor site suitability for eelgrass (Zostera marina) restoration	Open Theme	Lauren Sgambelluri	Geomar Helmholtz-center For Ocean Research Kiel	Germany
269	2nd floor: Arkaden 8	373	Skin-secreted antimicrobial peptides represent a fast-acting ancestral antipredator defense system in frogs	Open Theme	Lavrans Venken	Vrije Universiteit Brussel	Belgium
270	2nd floor: Arkaden 8	413	Benchmarking Genotype Likelihoods in Ancient DNA Studies.	Open Theme	Lei Zhao	East China Normal University	China
271	2nd floor: Arkaden 8	1391	Beyond Recombination: Evaluating Mutation Clock approaches to Infer Archaic Admixture Times	Open Theme	Leonardo Nicola Martin Iasi	Max-Planck-Institute for Evolutionary Anthropology	Germany
272	2nd floor: Arkaden 8	1260	Resistance selection allows identification of druggable targets in transmission stages of the human malaria parasite P. falciparum	Open Theme	Leonie Seefeldt	Swiss TPH	Switzerland
273	2nd floor: Arkaden 8	1510	Evolutionary transcriptomic analyses identify new potential gamete recognition proteins in lungless salamanders	Open Theme	Liam Johnson	Ohio State University	United States
274	2nd floor: Arkaden 8	1201	Recombination hotspot co-regulation by Prdm9 and X-linked regulatory microRNAs during meiosis	Open Theme	Lisa-Marie Hofacker	Max-Planck Institute for Evolutionary Biology	Germany
275	2nd floor: Arkaden 7	323	Ancient and recent nuclear introgression between Fennoscandian voles	Open Theme	Lison Zunino	Czech Academy of Sciences	Czech Republic
276	2nd floor: Arkaden 7	312	On the Highroad to Reproductive Isolation: Cytonuclear Incompatibilities Between Selfing Populations of Arctic Cochlearia groenlandica (Brassicaceae)	Open Theme	Lovisa Gustafsson	The university centre in Svalbard	Svalbard and Jan Mayen
277	2nd floor: Arkaden 7	356	Characterizing the patterns of natural selection on fatty acid-related traits	Open Theme	Lu Wang	University Of Georgia	United States
278	2nd floor: Arkaden 7	273	Population genetic statistics tools for the next generation of pool sequencing	Open Theme	Lucas Czech	University Of Copenhagen	Denmark
279	2nd floor: Arkaden 7	482	Impact of compositional heterogeneity on divergence time estimation	Open Theme	Lucas Freitas	University of Bristol	United Kingdom
280	2nd floor: Arkaden 7	89	Genomic Regulatory Networks Underlying the Evolution of Avian Beak Shape	Open Theme	Lucas Rocha Moreira	Colossal Biosciences	United States
281	2nd floor: Arkaden 7	956	Warming and Hypoxia as Selective Forces Shaping Marine Bacterioplankton Functional Potential	Open Theme	Luciana Santoferrara	Hofstra University	United States
282	2nd floor: Arkaden 7	1143	Plant-Microbial Interactions: Tracing a 2-Million-Year-Old Alliance with Ancient DNA	Open Theme	Luigimaria Borruso	Free University Of Bolzano	Italy

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
283	2nd floor: Arkaden 7	430	Phylogenetic correlation between the Type IV Secretion System and HIP1 suggest an adaptation for horizontal gene transfer in cyanobacteria	Open Theme	Luis Delaye	Cinvestav	Mexico
284	2nd floor: Arkaden 7	1084	Correcting for unequal error rates in D-statistics comparisons	Open Theme	Madina Japakhova	Max Planck Institute For Evolutionary Anthropology	Germany
285	2nd floor: Arkaden 7	316	Evolution of gene regulation in the primate endometrium at single-cell resolution	Open Theme	Maëlle Daunesse	Institut Pasteur	France
286	2nd floor: Arkaden 7	1757	Repeated evolution of pink flowers in alpine Arabidopsis arenosa is driven by PAP2 alleles with pleiotropic effects on UV protection and floral thermogenesis Abstract:	Open Theme	Magdalena Bohutínská	Charles University	Czech Republic
287	2nd floor: Arkaden 7	406	Using ancient DNA to track the phenotypic history of dogs	Open Theme	Mahaut Goor	Chair of Animal Systems Genomics, Faculty of Veterinary Medicine, Ludwig-Maximilians-Universität	Germany
288	2nd floor: Arkaden 7	543	Do Living Fossils Evolve Slowly? A Comparative Analysis Across the Tree of Life	Open Theme	Manuela Cascini	University Of Sydney	Australia
289	2nd floor: Arkaden 7	847	Identifying the 'roots': development of markers for within and between species characterization of the Pinus genus.	Open Theme	Margarita Takou	Thuenen Institute Of Forest Genetics	Germany
290	2nd floor: Arkaden 7	1556	Resolving population structure and gene flow of two deep sea vestimentiferan worms from the Eastern Pacific	Open Theme	Marharyta Abashkina	University Of Copenhagen	Denmark
291	2nd floor: Arkaden 7	1217	Genomic history and ancestral origins of Afro-Mexican populations	Open Theme	Maria Fernanda Garcia Rodriguez	International Laboratory for Human Genome Research (LIIGH)	Mexico
292	2nd floor: Arkaden 7	1092	Impact of Invasion on Gonadal Microbiome Diversity in Red Palm Weevil (Rhynchophorus ferrugineus)	Open Theme	Mariam Alshamsi	New York University Abu Dhabi	United Arab Emirates
293	2nd floor: Arkaden 7	1096	Genomic signatures of local adaptation across environmental gradients in the green anole	Open Theme	Mariana Lyra	New York University Abu Dhabi	United Arab Emirates
294	2nd floor: Arkaden 7	171	Functional and genomic features shape the recombination hotspot landscape of the house sparrow	Open Theme	Marie Raynaud	University of Edinburgh	United Kingdom
295	2nd floor: Arkaden 7	1536	GEMINI: Miniaturisation, vertebrates, and the genome	Open Theme	Mark D. Scherz	Natural History Museum Denmark, University Of Copenhagen	Denmark
296	2nd floor: Arkaden 7	975	Niche conservatism during adaptive radiations	Open Theme	Martin Eriksson	Swedish Museum of Natural History	Sweden
297	2nd floor: Arkaden 7	411	A new toolbox for simulations and inference in population genetics	Open Theme	Martin Petr	Globe Institute, University of Copenhagen	Denmark
298	2nd floor: Arkaden 7	1616	Evolutionary role of ZNF492 in human neural progenitor cells	Open Theme	Marula Mathew	Freie University Berlin	Germany
299	2nd floor: Arkaden 7	458	Longitudinal multi-omics analysis of cynomolgus macaque lifespan uncovers age-related immune patterns	Open Theme	JaeWon Huh	KRIBB	South Korea
300	2nd floor: Arkaden 7	783	Effect of effective population size on the rate of Y chromosome degeneration	Open Theme	Mattéo Todaro	Université De Montpellier	France
301	2nd floor: Arkaden 7	1660	Locating genetic ancestors with ancestral recombination graphs	Open Theme	Matthew Osmond	University Of Toronto	Canada
302	2nd floor: Arkaden 7	1155	Genomic characterization of the island population of Heliconius cydno from Gorgona Island, Colombia	Open Theme	Mayelby Geraldine Rueda Muñoz	University Of Oslo	Norway
303	2nd floor: Arkaden 6	1176	La Quebrada Project: A community-engaged exploration of Afro-descendant heritage in Peru	IDEA Symposium: Advancing Inclusion, Diversity, Equity, and Accessibility in Molecular Biology and Evolution	Maria A Nieves Colón	University of Minnesota Twin Cities	United States
304	2nd floor: Arkaden 6	867	From population genomics to health equity: evolutionary insights from Indigenous populations of Taiwan	IDEA Symposium: Advancing Inclusion, Diversity, Equity, and Accessibility in Molecular Biology and Evolution	Wen-Ya Ko	National Yang Ming Chiao Tung University	Taiwan
305	2nd floor: Arkaden 6	663	Genomic architecture and reproductive trait divergence between Drosophila suzukii and its sibling species	Editors' Symposium	Aya Takahashi	Tokyo Metropolitan University	Japan
306	2nd floor: Arkaden 6	793	Higher frequency of prokaryotic low complexity regions in core and orthologous genes	Editors' Symposium	Fabia Ursula Battistuzzi	Oakland University	United States
307	2nd floor: Arkaden 6	839	Adaptation in unstable environments through genome reduction – Extending the May–Wigner theory to genomes	Editors' Symposium	Suhua Shi	Sun Yat-sen University	China
308	2nd floor: Arkaden 6	1715	Hybridization at the range margin: persistence, structure, and introgression	Editors' Symposium	Toni Gossmann	Tu Dortmund University	Germany
309	2nd floor: Arkaden 6	397	Spatial Patterns of Heterogeneity in Solid Tumors and Their Evolutionary Origins	Editors' Symposium	Weiwei Zhai	Institute of Zoology, Chinese Academy of Sciences	China
310	2nd floor: Arkaden 6	1709	Mid-trajectory transcriptome convergence and ancient gene use during plant cell differentiation	Editors' Symposium	Wenfeng Qian	Institute of Genetics and Developmental Biology, Chinese Academy of Sciences	China
311	2nd floor: Arkaden 6	371	Cross-species comparisons of the chordate digestive tract reveals conservation of pancreatic endocrine cells	Editors' Symposium	Yichen (Serena) Dai	Fudan University	China
312	2nd floor: Arkaden 6	1568	Identification of regulatory elements influencing eye evolution in cave fish	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Wynn Meyer	Lehigh University	United States
313	2nd floor: Arkaden 6	1142	Constructive neutral evolution explains the emergence of specialised ribosomes in diverse eukaryotes.	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Alan Beavan	University Of Manchester	United Kingdom
314	2nd floor: Arkaden 6	350	Epigenetics Meets Osteology: DNA Methylation and Cranial Bone Modeling in an Ontogenetic Sample of Baboons	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Alexandra Schuh	Max Planck for Evolutionary Anthropology	Germany
315	2nd floor: Arkaden 6	581	Leveraging the DNA methylation atlas of purified human cell types to detect putative metastable epialleles in humans	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Alice Balard	University College London (UCL)	United Kingdom
316	2nd floor: Arkaden 6	1479	Dissecting the molecular mechanisms and evolutionary dynamics of gene regulatory silencers	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Allison Wang	University Of California, San Francisco	United States
317	2nd floor: Arkaden 6	88	Genome-wide in-silico analysis of conserved miRNAs in aquatic and terrestrial mammals	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Beatriz Daros	University of Campinas	Brazil
318	2nd floor: Arkaden 6	118	Evolution of RNA binding in the fungal gene regulatory protein Ssd1	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Benjamin Kleinerman	University Of Edinburgh	United Kingdom
319	2nd floor: Arkaden 6	1219	Novel axes of coevolutionary innovation revealed via a cell-level study of butterfly detoxification mechanisms against mustard plants.	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Brenda Irene Medina Jiménez	Stockholm University	Sweden
320	2nd floor: Arkaden 6	1063	Introducing the Baboon Genotype-Tissue Expression Atlas (GTEx), a Community Resource for Comparative Primate Genomics	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Brittany Hazzard	University Of Chicago	United States
321	2nd floor: Arkaden 6	1266	Leveraging multimodal single-cell data of early primate development to study the evolution of regulatory elements	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Dana Lopez-Parra	University of Munich	Germany

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
322	2nd floor: Arkaden 6	1351	prime-seq2 and zUMIs-prime: an end-to-end framework for scalable cross-species transcriptomics	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Felix Pförtner	LMU Munich	Germany
323	2nd floor: Arkaden 6	766	Phylogenetic comparative analysis of single-cell transcriptomes: the evolution of gene expression noise in Saccharomyces	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Fernanda Giersdorf	Max Planck Institute For Evolutionary Biology	Germany
324	2nd floor: Arkaden 6	1658	S-LiDER: Exploiting Linkage Disequilibrium Geometry to Refine Functional Heritability Estimates	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Hannah Snell	Brown University	United States
325	2nd floor: Arkaden 6	1390	Modeling Sex-biased Gene Expression Evolution Across Firefly Phylogeny	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Haoqing Du	Ludwig-Maximilians-Universität München	Germany
326	2nd floor: Arkaden 6	622	Evolution of alpha-solenoid proteins involved in organellar gene expression	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Ingrid Lafontaine	UMR7141 CNRS/Sorbonne University	France
327	2nd floor: Arkaden 6	362	Single-stranded and non-canonical DNA formation in human and other ape cells with telomere-to-telomere genomes	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Jacob Sieg	Penn State University	United States
328	2nd floor: Arkaden 6	465	uORFs as Evolutionary Drivers of Translational Stability and Gene Expression Regulation	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Zhijuan Wang	School Of Life Sciences, Peking University	China
329	2nd floor: Arkaden 6	1188	Siphonophore genomics and mechanisms driving body polymorphism	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Namrata Ahuja	Yale Ecology And Evolutionary Biology	United States
330	2nd floor: Arkaden 6	739	A "phylogeny-in-a-dish" approach to study the evolution of context-dependent gene expression in primates	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Nelly Helmbrecht	Max Planck Institute for Evolutionary Anthropology	Germany
331	2nd floor: Arkaden 6	181	Disruption of DNA methylation in the hybrid Italian sparrow contributes to transgressive gene expression	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Nicholas Planidin	Lund University	Sweden
332	2nd floor: Arkaden 6	815	Convergent Gill Architecture, Divergent Cellular Programs: a Multi-omics Approach to Arthropod Breathing	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Polychronis Tatsis	Instituto de Biologia Evolutiva (IBE)	Spain
333	2nd floor: Arkaden 6	1663	Gene Coexpression and Microsynteny Networks Uncover Regulatory Constraints and Exaptations for C4 Evolvability in the Brassicales	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	R. Shawn Abrahams	University of Illinois, Urbana-Champaign	United States
334	2nd floor: Arkaden 6	841	Single-cell multi-omics analysis of maturation age in Atlantic salmon testes	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Rachel Carboni	Nord University	Norway
335	2nd floor: Arkaden 6	756	Conserved Secretory Programs Across Neuronal and Non-Neuronal Cell Types	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Shreejita Chatterjee	Christian-albrechts Universitat Zu Kiel	Germany
336	2nd floor: Arkaden 6	390	Breaking the Loop: Cis-Regulatory Disruption of FoxP Autoregulation during Wolf Domestication	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Tadeusz Malewski	Museum and Institute of Zoology of the Polish Academy of Sciences	Poland
337	2nd floor: Arkaden 6	1455	Regulatory Inheritance Explains Convergent Expression Patterns in Hybrids and Polyploids	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Tomáš Tichopád	South Bohemian University	Czech Republic
338	2nd floor: Arkaden 6	1181	Evolution of regulatory chromatin contacts: insights from duplicated genes	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Victor Lefebvre	Laboratory of Biometry and Evolutionary Biology (LBBE)	France
339	2nd floor: Arkaden 6	716	From SNP to function: how combinations of two large-effect locus genotypes shape maturity age through gene regulatory networks	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Xin-Di Huang	University of Helsinki	Finland
340	2nd floor: Arkaden 6	35	Integrated GWAS and Transcriptome Analyses Identify Candidate Genes for Thick-leg Trait of Vietnamese Dragon Chickens	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Xufang Ren	China Agricultural University	China
341	2nd floor: Arkaden 6	754	Hypomethylation in Oikopleura dioica genome	S22 Evolution of gene regulation: insights from novel molecular and statistical approaches	Yael Klirs	Tel-aviv University	Israel
342	2nd floor: Arkaden 6						
343	2nd floor: Arkaden 4+5	813	A century of decline: tracking genomic erosion in two endangered parrots	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Alexandra Brumwell	University Of Kent	United Kingdom
344	2nd floor: Arkaden 4+5	1448	A genomic perspective on the evolution of modern water voles (Arvicola sp.)	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Amanda Lindahl	Stockholm University	Sweden
345	2nd floor: Arkaden 4+5	353	Ultrarapid MC1R protein and associated plumage colour evolution in the domestic chicken	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Cheng Ma	Uppsala University	Sweden
346	2nd floor: Arkaden 4+5	383	Estimating Seagrass Meadow Persistence via Clone Aging	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Clara E. Winguth	Marine Evolutionary Ecology, Geomar Helmholtz Center Of Ocean Research Kiel	Germany
347	2nd floor: Arkaden 4+5	81	Historical and Recent Population Specific Bottlenecks Inflated Differentiation Measures of Louisiana Black Bear	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Emily Puckett	University of Memphis	United States
348	2nd floor: Arkaden 4+5	1695	Drought drives inbreeding and local adaptation in a rare endemic of California's Fog Belt	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Emma Steigerwald	Uc Santa Cruz	United States
349	2nd floor: Arkaden 4+5	499	Effects of fragmented landscapes on the evolution of thermal tolerance in soil arthropods.	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Fatima Jlil	Aarhus University	Denmark
350	2nd floor: Arkaden 4+5	910	Non-invasive genomic sampling uncovers novel connectivities and origins of confiscated gorillas	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Irune Ruiz-Gartzia	Institut De Bilogia Evolutiva - Upf	Spain
351	2nd floor: Arkaden 4+5	1417	Genomics of Brazilian howler monkeys reveals cryptic population structure and adaptation to folivory	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Katherine McVay	Duke University	United States
352	2nd floor: Arkaden 4+5	69	Estimates of long-term effective population size reveal the rapid decline of endangered species	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Loveday Lewin	University Of Sussex	United Kingdom
353	2nd floor: Arkaden 4+5	1381	Between isolation and invasion: the genomic fate of Antillean iguanas	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Mirte Bosse	Vrije Universiteit Amsterdam & Wageningen University	Netherlands

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Board number	Poster area	Paper number	Paper Title	Theme	Presenter name	Presenter organisation	Presenter country
354	2nd floor: Arkaden 4+5	807	Do repeat invasions have the same genetic signature: Using population genetics to manage an active invasion.	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Neve Kelly	Unsw	Australia
355	2nd floor: Arkaden 4+5	1614	Investigating the decline of a threatened Orthopteran combining ecological niche modeling and genomic analyses	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Nina Casillas	Leibniz Institute for the Analysis of Biodiversity Change (LIB)	Germany
356	2nd floor: Arkaden 4+5	1517	Global genetic structure and diversity in the widespread red fox	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Paula Gardner	University Of East Anglia	United Kingdom
357	2nd floor: Arkaden 4+5	416	From Inactive Dimers to Functional Tetramers: Evolution of Catalysis in DfrB Enzymes	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Samy Faraj	University of Montreal	Canada
358	2nd floor: Arkaden 4+5	1179	Hybridization poses challenges for the conservation of Iberian endemic freshwater fish species	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Sofia Mendes	Eawag: Swiss Federal Institute of Aquatic Science and Technology	Switzerland
359	2nd floor: Arkaden 4+5	83	The genetic diversity of seagrasses: environment, reproductive system and the nearly neutral theory	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Xinyue Teng	Zhejiang University	China
360	2nd floor: Arkaden 4+5	890	Mutation rate estimate and population genomic analysis reveals decline of koalas prior to human arrival	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Toby Kovacs	The University Of Sydney	Australia
361	2nd floor: Arkaden 4+5	230	Recent insights into the evolutionary genomics of the critically endangered aye-aye (Daubentonia madagascariensis)	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Vivak Soni	Arizona State University	United States
362	2nd floor: Arkaden 4+5	1419	Unraveling lost diversity of Arctic marine endemics - investigating ancient belugas and bowhead whales from southern Scandinavia	S05 Molecular Evolution in the Era of Genetic Diversity Decline	Wenxi Li	Globe Institute, University Of Copenhagen	Denmark
363	2nd floor: Arkaden 4+5						
364	2nd floor: Arkaden 4+5						
365	2nd floor: Arkaden 2+3	782	It's A Small World After All: The Unique Mutation Rate and Lifestyle of a Naked RNA Virus	S19 Causes and consequences of mutation rate variation	Alyssa Cenzano	Arizona State University	United States
366	2nd floor: Arkaden 2+3	735	Mutation rate evolution in cetaceans: understanding drivers of variability and observation bias in estimates of genomic mutation rate	S19 Causes and consequences of mutation rate variation	Amy Van Cise	University Of Washington	United States
367	2nd floor: Arkaden 2+3	437	Mutation and recombination in coppery titi monkeys (Plecturocebus cupreus)	S19 Causes and consequences of mutation rate variation	Cyril Versoza	Arizona State University	United States
368	2nd floor: Arkaden 2+3	701	Variation in mutation and recombination rate within and among species of Drosophilidae	S19 Causes and consequences of mutation rate variation	Darren Obbard	University Of Edinburgh	United Kingdom
369	2nd floor: Arkaden 2+3	681	The Human Mutation Spectrum Is Not Neutral	S19 Causes and consequences of mutation rate variation	David Castellano	University Of Arizona	United States
370	2nd floor: Arkaden 2+3	154	Predicting the fate of mutation rate modifiers that shift the mutation bias	S19 Causes and consequences of mutation rate variation	Diego Tenoch Morales Lopez	University of Western Ontario	Canada
371	2nd floor: Arkaden 2+3	1094	Cell type and cell division-resolved mutation rates in a hypermutating Nematode	S19 Causes and consequences of mutation rate variation	Dustin Mullaney	University Of Washington	United States
372	2nd floor: Arkaden 2+3	627	Evolutionary dynamics of DNA repair genes across primate phylogeny	S19 Causes and consequences of mutation rate variation	Emma Diepeveen	Aarhus University	Denmark
373	2nd floor: Arkaden 2+3	289	Re-assessing the correlation between mutation rates and functional elements	S19 Causes and consequences of mutation rate variation	Aaron Ragsdale	University Of Wisconsin-Madison	United States
374	2nd floor: Arkaden 2+3	506	Selection for robustness drives the evolution of the per-genome mutation rate	S19 Causes and consequences of mutation rate variation	Juliette Luiselli	Ku Leuven	Belgium
375	2nd floor: Arkaden 2+3	1361	Evolution of Mutational Susceptibility to Disease	S19 Causes and consequences of mutation rate variation	Maria Kelly	Centre For Genomic Regulation	Spain
376	2nd floor: Arkaden 2+3	32	Applications of structurally constrained substitution models of protein evolution to phylogenetic inference	S19 Causes and consequences of mutation rate variation	Miguel Arenas	University of Vigo	Spain
377	2nd floor: Arkaden 2+3	212	Accelerated evolutionary rates of Influenza A neuraminidase gene in warm climates	S19 Causes and consequences of mutation rate variation	Nina Pust	University Of Copenhagen	Denmark
378	2nd floor: Arkaden 2+3	314	How precise are mutation rate estimates? Comparison of different approaches to estimate de novo mutation rates	S19 Causes and consequences of mutation rate variation	Xi Wang	The University of Hong Kong	China
379	2nd floor: Arkaden 2+3	1135	Bias in Estimation of the Population Scaled Mutation Rate Parameter θ Under High Mutation Regimes	S19 Causes and consequences of mutation rate variation	Zahra Panahy	University of Calgary	Canada
380	2nd floor: Arkaden 2+3						