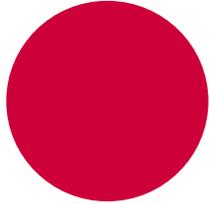


MEETING  
PROGRAM







## CONTENTS

|   |    |
|---|----|
| Committees .....                            | 05 |
| Welcome address .....                       | 06 |
| 2008 Award winners .....                    | 07 |
| Program at a glance .....                   | 08 |
| Scientific program .....                    | 09 |
| Poster presentations .....                  | 17 |
| General information .....                   | 38 |
| Social program .....                        | 41 |
| Instructions for speakers and authors ..... | 42 |
| Author Index .....                          | 45 |
| Meeting rooms' location .....               | 60 |

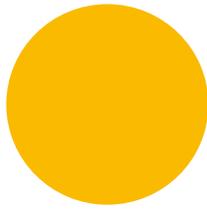
For any information regarding scientific program, registration, accommodation and social events, before or after the Meeting, please feel free to contact:

### MEETING SECRETARIAT



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## COMMITTEES

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Departament de Genètica. Universitat de Barcelona (UB), Spain

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**Lluís Serra**  
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**Laurent Duret** University of Lyon, France

**David M. Lambert** Massey University, New Zealand

**John M. Logsdon** University of Iowa, USA

**Rasmus Nielsen** University of Copenhagen, Denmark

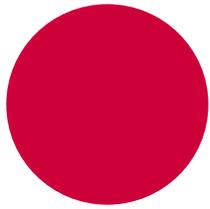
**Yoko Satta** The Graduate University for Advanced Studies, Japan

**Outi Savolainen** University of Oulu, Finland

**Wolfgang Stephan** Ludwig-Maximilians-Universität München, Germany

**George Zhang** University of Michigan, USA

and all members of the Organizing Committee.



## WELCOME ADDRESS

### BENVINGUTS A BARCELONA!

We are very pleased to welcome you to SMBE 2008. This year the Meeting has attracted more than 1,000 participants from about 40 countries. We really appreciate your attendance and hope that you enjoy the Meeting. The scientific program includes about 900 contributions that highlight the latest research at the interface of molecular biology and evolution, especially involving the analysis of genomes.

We are grateful to the members of the Organizing and Scientific Committees for their help in defining the scientific program, and to the Symposium Organizers for proposing and arranging the symposia.

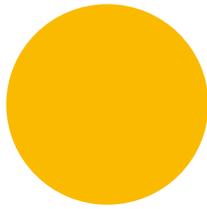
We thank the Meeting sponsors for their financial support that has made the Meeting possible.

Finally, we thank SMBE for the opportunity to host the leading Meeting in the field of molecular biology and evolution.

We hope that you enjoy the Meeting.

**Julio Rozas and Carmen Segarra**  
SMBE 2008 Organizers





## 2008 AWARD WINNERS

### CONGRATULATIONS TO SMBE 2008 AWARD WINNERS

#### Walter M. Fitch Student Award Competition Participants

|  |       |
|--|-------|
| <b>Roman Arguello</b> University of Chicago                            | WF-01 |
| <b>Frederic Chain</b> McMaster University                              | WF-03 |
| <b>Jean-Francois Gout</b> Centre National de la Recherche Scientifique | WF-06 |
| <b>Manuel Irimia</b> Universitat de Barcelona                          | WF-05 |
| <b>Lilia Perfeito</b> Instituto Gulbenkian de Ciência                  | WF-04 |
| <b>Hannah Seidel</b> Princeton University                              | WF-08 |
| <b>Taro Tsujimura</b> University of Tokyo                              | WF-07 |
| <b>Nicolas Vinckenbosch</b> University of Lausanne                     | WF-02 |

#### PostDoctoral Researcher Travel Award Recipients

|  |       |
|--|-------|
| <b>Georgii Bazykin</b> IITP-RAS                                    | O-050 |
| <b>Hubertus Beaumont</b> University of Leiden                      | O-174 |
| <b>Garrett Hellenthal</b> University of Oxford                     | O-035 |
| <b>Ryan Hernández</b> University of Chicago                        | O-027 |
| <b>Han Liang</b> University of Chicago                             | O-096 |
| <b>Judith Mank</b> Uppsala University                              | O-062 |
| <b>Lino Ometto</b> University of Lausanne                          | O-063 |
| <b>Paul Planet</b> American Museum of Natural History              | O-022 |
| <b>Nina Stoletzki</b> University of Sussex                         | O-065 |
| <b>Leslie Turner</b> Max Planck Institute for Evolutionary Biology | O-061 |

#### Graduate Student Travel Award Recipients

|  |       |
|--|-------|
| <b>Kyle Brown</b> Harvard University             | O-173 |
| <b>Tina Hu</b> University of Southern California | O-044 |
| <b>Richard Meisel</b> Penn State University      | O-067 |
| <b>George Perry</b> Arizona State University     | O-142 |
| <b>Lukasz Potrebowski</b> University of Lausanne | O-070 |
| <b>Alessia Ranciaro</b> University of Maryland   | O-052 |
| <b>Niv Sabath</b> University of Houston          | O-010 |
| <b>Timothy Sackton</b> Cornell University        | O-011 |
| <b>Jenny Tung</b> Duke University                | O-059 |
| <b>Tobia Warnecke</b> University of Bath         | O-012 |

#### Undergraduate Diversity Mentoring Program Award Recipients

|  |          |
|--|----------|
| <b>Tamar Carter</b> University of Florida              | UDMPA-08 |
| <b>Jennifer Deberardinis</b> Smith College             | UDMPA-04 |
| <b>Anna Duggan</b> Memorial University of Newfoundland | UDMPA-03 |
| <b>Wen Huang</b> Queens College                        | UDMPA-01 |
| <b>Saioa López</b> Euskal Herriko Unibertsitatea       | UDMPA-09 |
| <b>Aida Rodrigo Albores</b> Universitat de València    | UDMPA-10 |
| <b>Luisa Sánchez</b> University of Florida             | UDMPA-05 |
| <b>Christine Sharp</b> Dalhousie University            | UDMPA-06 |
| <b>Rebecca Theobald</b> University of Florida          | UDMPA-07 |
| <b>Ricardo Wilches</b> University of Munich            | UDMPA-02 |

# PROGRAM AT A GLANCE

## THURSDAY, JUNE 5

|                     |   |         |
|---------------------|---|---------|
| 09:00 am - 05:00 pm | SMBE COUNCIL MEETING (Council Members only) | ROOM 1  |
| 04:00 pm - 07:30 pm | REGISTRATION                                | LEVEL 2 |
| 06:30 pm - 07:30 pm | WELCOME DRINK                               | LEVEL 1 |

## FRIDAY, JUNE 6

|                     |   |              |
|---------------------|---|--------------|
| 07:30 am - 07:00 pm | REGISTRATION  | LEVEL 2      |
| 08:15 am - 08:30 am | OFFICIAL WELCOME  | ROOM 7       |
| 08:30 am - 09:30 am | <b>PLENARY LECTURE 1</b><br>Prof. Svante Pääbo (Max Planck Institute for Evolutionary Antropology)<br>Neandertal Genomics | ROOM 7       |
| 09:30 am - 11:00 am | MORNING SYMPOSIA & CONTRIBUTED SESSIONS (S1, S2, S3, S4)  | ROOM 7 6 5 3 |
| 11:00 am - 11:30 am | COFFEE BREAK  | LEVEL 0 1    |
| 11:30 am - 01:00 pm | MORNING SYMPOSIA & CONTRIBUTED SESSIONS (S1, S2, S5, S6)  | ROOM 7 6 5 3 |
| 01:00 pm - 03:00 pm | POSTER SESSION & LUNCH BOX  | LEVEL 0 1    |
| 03:00 pm - 05:00 pm | WALTER M. FITCH STUDENT AWARD COMPETITION   | ROOM 7       |
| 05:00 pm - 06:00 pm | UNDERGRADUATE DIVERSITY MENTORING PROGRAM - Poster Session  | LEVEL 0      |
| 05:00 pm - 07:00 pm | POSTER SESSION & COFFEE BREAK   | LEVEL 0 1    |

## SATURDAY, JUNE 7

|                     |   |                   |
|---------------------|---|-------------------|
| 07:30 am - 07:00 pm | REGISTRATION  | LEVEL 2           |
| 08:30 am - 09:30 am | <b>PLENARY LECTURE 2 - NEI LECTURE</b><br>Prof. Paul Sharp (University of Edinburgh)<br>The origins and evolution of AIDS viruses | ROOM 7            |
| 09:30 am - 11:00 am | MORNING SYMPOSIA & CONTRIBUTED SESSIONS (S7, S8, S9, S10)   | ROOM 7 6 5 3      |
| 11:00 am - 11:30 am | COFFEE BREAK  | LEVEL 0 1         |
| 11:30 am - 01:00 pm | MORNING SYMPOSIA & CONTRIBUTED SESSIONS (S7, S8, S11, S12)  | ROOM 7 6 5 3      |
| 01:00 pm - 03:00 pm | POSTER SESSION & LUNCH BOX  | LEVEL 0 1         |
| 02:15 pm - 03:00 pm | COMPANY SESSION   | ROOM 7            |
| 03:00 pm - 05:30 pm | AFTERNOON SYMPOSIA & CONTRIBUTED SESSIONS (S13, S14, S15, S16)  | ROOM 7 6 5 3      |
| 05:30 pm - 07:00 pm | POSTER SESSION & COFFEE BREAK   | LEVEL 0 1         |
| 05:45 pm - 06:45 pm | SOCIETY BUSINESS MEETING  | ROOM 6            |
| 08:30 pm            | MEETING DINNER & AWARDS   | HOTEL FIRA PALACE |

## SUNDAY, JUNE 8

|                     |  |              |
|---------------------|--|--------------|
| 07:30 am - 05:30 pm | REGISTRATION   | LEVEL 2      |
| 08:30 am - 09:30 am | <b>PLENARY LECTURE 3</b><br>Prof. Andrew G. Clark (Cornell University)<br>Genomic imprinting: An evolutionary puzzle | ROOM 7       |
| 09:30 am - 11:00 am | MORNING SYMPOSIA & CONTRIBUTED SESSIONS (S17, S18, S19, S20)   | ROOM 7 6 5 3 |
| 11:00 am - 11:30 am | COFFEE BREAK   | LEVEL 0 1    |
| 11:30 am - 01:00 pm | MORNING SYMPOSIA & CONTRIBUTED SESSIONS (S17, S18, S21, S22)   | ROOM 7 6 5 3 |
| 01:00 pm - 03:00 pm | POSTER SESSION & LUNCH BOX   | LEVEL 0 1    |
| 03:00 pm - 05:30 pm | AFTERNOON SYMPOSIA & CONTRIBUTED SESSIONS (S23, S24, S25, S26)   | ROOM 7 6 5 3 |

MEETING ENDS

# SCIENTIFIC PROGRAM

PDTA: Postdoctoral Travel Award; GSTA: Graduate Student Travel Award.

## THURSDAY, JUNE 5

|                     |  |         |
|---------------------|--|---------|
| 09:00 am - 05:00 pm | <b>SMBE COUNCIL MEETING</b> (Council Members only) | ROOM 1  |
| 04:00 pm - 07:30 pm | <b>REGISTRATION</b>                                | LEVEL 2 |
| 06:30 pm - 07:30 pm | <b>WELCOME DRINK</b>                               | LEVEL 1 |

## FRIDAY, JUNE 6

|                     |  |             |
|---------------------|--|-------------|
| 07:30 am - 07:00 pm | <b>REGISTRATION</b>  | LEVEL 2     |
| 08:15 am - 08:30 am | <b>OFFICIAL WELCOME</b>  | ROOM 7      |
| 08:30 am - 09:30 am | <b>PLENARY LECTURE 1 - Prof. Svante Pääbo</b> ( <i>Max Planck Institute for Evolutionary Anthropology</i> )<br><b>Neandertal Genomics</b><br>Chair: Jaume Bertranpetit ( <i>Universitat Pompeu Fabra</i> ) | ROOM 7      |
| 09:30 am - 01:00 pm | <b>MORNING SYMPOSIA &amp; CONTRIBUTED SESSIONS</b>   |             |
|                     | <b>S1 – Evolutionary comparative genomics</b><br>Chairs: Toni Gabaldon ( <i>Centro de Investigación Príncipe Felipe</i> )<br>and Athanasi Tzika ( <i>Université Libre de Bruxelles</i> )                   | ROOM 7      |
| 09:30 am            | O-001   Wen-Hsiung   Li   Function and Evolution fo microRNAs  |             |
| 10:00 am            | O-002   Ettema   Thijs   Mining metagenomes to trace the identity of the mitochondrial ancestor  |             |
| 10:15 am            | O-003   Huerta-Cepas   Jaime   Tissue expression complementarity after gene duplication  |             |
| 10:30 am            | O-004   Milinkovitch   Michel   Analyzing 34 metazoan full genomes in a phylogenetic framework   |             |
| 10:45 am            | O-005   Mira   Alex   Evolution of Genomic Redundancy in Bacteria  |             |
| 11:00 am - 11:30 am | <b>COFFEE BREAK</b>  | LEVEL 0   1 |
| 11:30 am            | O-006   Cáceres   Mario   Genomic regulation of gene-expression levels in the brain during human evolution   |             |
| 11:45 am            | O-007   Zhou   Qi   On the origin of new genes in <i>Drosophila</i>  |             |
| 12:00 pm            | O-008   Toft   Christina   The Evolution of Genome Redundancy in Endosymbiotic Bacteria of Insects   |             |
| 12:15 pm            | O-009   Ahmadinejad   Nahal   Shared intron positions are not always ancient - a clear independent intron gain at identical sites in the <i>nad7</i> gene  |             |
| GSTA   12:30 pm     | O-010   Sabath   Niv   Phase bias in overlapping genes reveals an association between GC content and overlap frequency   |             |
| GSTA   12:45 pm     | O-011   Sackton   Timothy   Evolution of genic content in the innate immune system of <i>Drosophila</i>  |             |
| GSTA   01:00 pm     | O-012   Warnecke   Tobias   Finding exonic islands in a sea of intronic sequence: splicing and the evolution of amino acid and codon usage   |             |
|                     | <b>S2 – Evolutionary radiations and molecular phylogeny</b><br>Chairs: Marta Riutort ( <i>Universitat de Barcelona</i> )<br>and José Castresana ( <i>Institut de Biologia Molecular de Barcelona</i> )     | ROOM 6      |
| 09:30 am            | O-013   Rokas   Antonis   The tempo and pattern of early animal evolution  |             |
| 10:00 am            | O-014   Philippe   Hervé   Resolving power and phylogenomics   |             |
| 10:30 am            | O-015   Yi   Soojin   Neutrally evolving intergenic, non-coding DNA markers to resolve a genus level phylogeny of neotropical primates (Platyrrhini)   |             |
| 10:45 am            | O-016   Cranston   Karen   Rice as a model system for plant phylogenomics  |             |
| 11:00 am - 11:30 am | <b>COFFEE BREAK</b>  | LEVEL 0   1 |
| 11:30 am            | O-017   Bryant   David   Efficient and exact algorithms for the probability of a marker under incomplete lineage sorting   |             |
| 11:45 am            | O-018   Filatov   Dmitry   Molecular adaptation and tree incongruence during rapid island adaptive radiation in Hawaiian endemics  |             |
| 12:00 pm            | O-019   Zardoya   Rafael   The radiation of the marine venomous gastropod genus <i>Conus</i> in Cape Verde   |             |
| 12:15 pm            | O-020   Castroviejo-Fisher   Santiago   Evaluating the Andean Diversification Model: Evolutionary Radiation of Neotropical Amphibians  |             |
| 12:30 pm            | O-021   Fabre   Pierre-Henri   Patterns of diversification during the rodentia radiation: a supermatrix approach   |             |
| PDTA   12:45 pm     | O-022   Planet   Paul   Total Evidence Approach to the Scaffold of Life  |             |

## SCIENTIFIC PROGRAM (continued)

|  |          |              |               |   |   |
|--|----------|--------------|---------------|---|---|
| <b>S3 – Spontaneous mutations and their evolutionary consequences</b>  |          |              |               |   | <b>ROOM 5</b>   |
| Chair: Armando Caballero ( <i>Universidad de Vigo</i> )  |          |              |               |   |   |
| 09:30 am   | O-023    | Keightley    | Peter         | Mutation accumulation in <i>D. melanogaster</i> - direct inference of mutation rates  |   |
| 10:00 am   | O-024    | Dolan        | Peter         | Genome-wide analysis of base substitution mutation processes in <i>Caenorhabditis elegans</i>   |   |
| 10:15 am   | O-025    | Hodgkinson   | Alan          | Cryptic Variation in the Mutation Rate  |   |
| 10:30 am   | O-026    | Cuevas       | José          | In-vivo mutation rate of hepatitis C virus (HCV)  |   |
| PDTA   | 10:45 am | O-027        | Hernández     | Ryan  | The Effect of Background Selection on Patterns of Human Genetic Variation |
| <b>S4 – The crossroads between prokaryotic genomics, ecology and adaptation</b>  |          |              |               |   | <b>ROOM 3</b>   |
| Chairs: Edward J. Feil ( <i>University of Bath</i> ) and Eduardo P. C. Rocha ( <i>Institut Pasteur</i> )   |          |              |               |   |   |
| 09:30 am   | O-028    | Parkhill     | Julian        | Variation detection in highly monomorphic bacteria using new sequencing technologies  |   |
| 10:00 am   | O-029    | Gosalbes     | María José    | Evolutionary analysis of the interactions between primary and secondary endosymbionts of the aphid <i>Cinara cedri</i>  |   |
| 10:15 am   | O-030    | Francino     | M. Pilar      | Comparative genomics of the gastrointestinal microbiotae of an infant/mother pair   |   |
| 10:30 am   | O-031    | Tenaillon    | Olivier       | Evolution of <i>Escherichia coli</i> genome: mutation, recombination and horizontal transfer  |   |
| 10:45 am   | O-032    | Marais       | Gabriel       | Mutation rate and genome reduction in endosymbiotic and free-living bacteria  |   |
| <b>11:00 am - 11:30 am COFFEE BREAK</b>  |          |              |               |   | <b>LEVEL 0</b>   <b>1</b>   |
| <b>S5 – Popgen in space! Theory and inference in spatial population genetics</b>   |          |              |               |   | <b>ROOM 5</b>   |
| Chairs: John Novembre ( <i>University of California, Los Angeles</i> ) and Graham Coop ( <i>University of Chicago</i> )  |          |              |               |   |   |
| 11:30 am   | O-033    | Whitlock     | Michael       | Evolution in metapopulations: Evolutionary inference with FST   |   |
| 12:00 pm   | O-034    | Francois     | Olivier       | Demographic history of European populations of <i>Arabidopsis thaliana</i>  |   |
| PDTA   | 12:15 pm | O-035        | Hellenthal    | Garrett   | Inferring Human Colonization History Using a Copying Model                |
| 12:30 pm   | O-036    | Guillot      | Gilles        | Statistical modeling in landscape genetics. Geneland, models, applications and recent developments  |   |
| 12:45 pm   | O-037    | Novembre     | John          | Spatial population structure of single nucleotide polymorphisms in human European populations   |   |
| <b>S6 – The ancestral eukaryotic cell</b>  |          |              |               |   | <b>ROOM 3</b>   |
| Chair: David Penny ( <i>Massey University</i> )  |          |              |               |   |   |
| 11:30 am   | O-038    | Roy          | Scott         | Divergence and convergence of self/minor/major/trans/alternative/mis/regulated splicing: what, when, why, and implications for the emergence of the eukaryotic genome |   |
| 12:00 pm   | O-039    | Plass        | Mireya        | Large scale comparative analysis of splicing in eukaryotes: hints on the coevolution between splicing signals and their corresponding factors                         |   |
| 12:15 pm   | O-040    | Gabaldón     | Toni          | Sub-cellular evolution: proteomes from mitochondria and peroxisomes tell different but inter-connected stories  |   |
| 12:30 pm   | O-041    | Deusch       | Oliver        | Genes of cyanobacterial origin in plant nuclear genomes point to a heterocyst-forming plastid ancestor  |   |
| 12:45 pm   | O-042    | Devos        | Damien        | Identification of key components of the eukaryotic endomembrane system in compartmentalized bacteria  |   |
| <b>01:00 pm - 03:00 pm POSTER SESSION &amp; LUNCH BOX</b>  |          |              |               |   | <b>LEVEL 0</b>   <b>1</b>   |
| <b>02:00 pm - 03:00 pm POSTER JUDGING TIME J1 (Posters: P001-P299)</b>   |          |              |               |   | <b>LEVEL 0</b>  |
| <b>03:00 pm - 05:00 pm WALTER M. FITCH STUDENT AWARD COMPETITION</b>   |          |              |               |   | <b>ROOM 7</b>   |
| Chair: Paul Sharp ( <i>University of Edinburgh</i> ) <span style="float: right;">Sponsored by </span> |          |              |               |   |   |
| 03:00 pm   | WF-01    | Arguello     | J. Roman      | Repetitive Elements and the Rise of Chimeric Genes in the <i>D. melanogaster</i> subgroup   |   |
| 03:15 pm   | WF-02    | Vinckenbosch | Nicolas       | Chromosomal Gene Movements Reflect the Recent Origin and Biology of Therian Sex Chromosomes   |   |
| 03:30 pm   | WF-03    | Chain        | Frederic      | Duplicate gene expression divergence in the wake of vertebrate allopolyploidization   |   |
| 03:45 pm   | WF-04    | Perfeito     | Lilia         | The effect of spatial structure in the adaptation of asexual populations  |   |
| 04:00 pm   | WF-05    | Irimia       | Manuel        | Convergent evolution of intron structures in reduced eukaryotes and insights into the ancestral eukaryotic splicing   |   |
| 04:15 pm   | WF-06    | Gout         | Jean-François | Translational control of intron splicing in eukaryotes  |   |
| 04:30 pm   | WF-07    | Tsujimura    | Taro          | Regulatory mechanisms for the coordinated expression of duplicated green-sensitive and red-sensitive opsin genes in zebrafish and their evolution                     |   |
| 04:45 pm   | WF-08    | Seidel       | Hannah        | Genetic incompatibility in <i>C. elegans</i> maintained by balancing selection  |   |

|                     |  |             |
|---------------------|--|-------------|
| 05:00 pm - 07:00 pm | <b>POSTER SESSION &amp; COFFEE BREAK</b>   | LEVEL 0   1 |
| 05:00 pm - 06:00 pm | <b>UNDERGRADUATE DIVERSITY MENTORING PROGRAM – Poster session and coffee break</b><br>Chairs: John Archibald ( <i>Dalhousie University</i> ) and Laura A. Katz ( <i>Smith College</i> )<br>Award recipients, mentors, supervisors, and invited guests only | LEVEL 0     |
| 05:00 pm - 06:00 pm | <b>POSTER JUDGING TIME J2</b> (Posters: P301 – P525)   | LEVEL 0     |

## SATURDAY, JUNE 7

|                     |                     |         |
|---------------------|---------------------|---------|
| 07:30 am - 07:00 pm | <b>REGISTRATION</b> | LEVEL 2 |
|---------------------|---------------------|---------|

|                     |  |       |              |          |   |
|---------------------|--|-------|--------------|----------|---|
| 08:30 am - 09:30 am | <b>PLENARY LECTURE 2 - NEI LECTURE</b><br><b>Prof. Paul Sharp</b> ( <i>University of Edinburgh</i> )<br><b>The origins and evolution of AIDS viruses</b><br>Chair: Deborah Charlesworth ( <i>University of Edinburgh</i> ) |       |              |          | ROOM 7  |
| 09:30 am - 01:00 pm | <b>MORNING SYMPOSIA &amp; CONTRIBUTED SESSIONS</b>   |       |              |          |   |
|                     | <b>S7 – Genomic evidence for natural selection and implications</b><br>Chairs: Molly Przeworski ( <i>University of Chicago</i> ) and Guy Sella ( <i>The Hebrew University of Jerusalem</i> )                               |       |              |          | ROOM 7  |
|                     | 09:30 am   | O-043 | Eyre-Walker  | Adam     | Genomic estimates of adaptive evolution   |
| GSTA                | 10:00 am   | O-044 | Hu           | Tina     | The impact of genome rearrangements on the pattern of polymorphism in <i>Arabidopsis thaliana</i>   |
|                     | 10:15 am   | O-045 | Pickrell     | Joseph   | A worldwide view of recent human adaptation   |
|                     | 10:30 am   | O-046 | Cai          | James    | Relaxed purifying selection and higher rates of adaptation in lineage-specific genes inferred from human SNP data                         |
|                     | 10:45 am   | O-047 | Elyashiv     | Eyal     | The Evolution of Functional Constraint in Yeast   |
| 11:00 am - 11:30 am | <b>COFFEE BREAK</b>  |       |              |          | LEVEL 0   1   |
|                     | 11:30 am   | O-048 | Moses        | Alan     | Evidence for large numbers of weakly selected mutations in genome-scale variation data  |
|                     | 11:45 am   | O-049 | Benger       | Etam     | Are most genomic adaptations novelties or modifications?  |
| PDTA                | 12:00 pm   | O-050 | Bazykin      | Georgii  | Estimating selection through genome-wide rate of parallel evolution   |
|                     | 12:15 pm   | O-051 | Aquadro      | Charles  | What is driving “unpreferred” synonymous substitutions in <i>Drosophila melanogaster</i> : insights from Notch                            |
| GSTA                | 12:30 pm   | O-052 | Ranciaro     | Alessia  | The evolutionary history of lactase persistence in Africa   |
|                     | 12:45 pm   | O-053 | Charlesworth | Brian    | Evidence for effects of selection on linked sites in <i>Drosophila</i>  |
|                     | <b>S8 – Evolution of gene regulation</b><br>Chair: Elvira Juan ( <i>Universitat de Barcelona</i> )   |       |              |          | ROOM 6  |
|                     | 09:30 am   | O-054 | Wittkopp     | Patricia | Genetic basis of regulatory variation within and between <i>Drosophila</i> species  |
|                     | 10:00 am   | O-055 | Ha           | Misook   | Duplicate genes increase expression diversity in polyploids   |
|                     | 10:15 am   | O-056 | Puig         | Marta    | Functional analysis of <i>CG13617</i> , a gene silenced in carriers of the widespread inversion <i>2j</i> of <i>Drosophila buzzatii</i>   |
|                     | 10:30 am   | O-057 | Torgerson    | Dara     | Comparing Patterns of Natural Selection within Protein-Coding and Candidate <i>cis</i> -Regulatory Regions in the Human Genome            |
|                     | 10:45 am   | O-058 | Khaitovich   | Philipp  | MicroRNA evolution in primates  |
| 11:00 am - 11:30 am | <b>COFFEE BREAK</b>  |       |              |          | LEVEL 0   1   |
| GSTA                | 11:30 am   | O-059 | Tung         | Jenny    | The evolutionary and functional significance of variation in a primate malaria gene   |
|                     | 11:45 am   | O-060 | Tautz        | Diethard | Microevolutionary divergence of expression levels   |
| PDTA                | 12:00 pm   | O-061 | Turner       | Leslie   | V1ar variation and its contribution to mating system variation in deer mice ( <i>Peromyscus</i> )   |
| PDTA                | 12:15 pm   | O-062 | Mank         | Judith   | Rapid turnover of sex-biased gene expression during the avian life-cycle  |
| PDTA                | 12:30 pm   | O-063 | Ometto       | Lino     | The evolution of gene expression in fire ants   |
|                     | 12:45 pm   | O-064 | Babbitt      | Gregory  | Evolution at the gateway to transcription: selective forces maintaining chromatin differences in the core promoter                        |
| PDTA                | 01:00 pm   | O-065 | Stoletzki    | Nina     | The Negative Correlation of Gene Length and Optimal Codon Use - Disentangling translational selection from compositional effects in yeast |

## SCIENTIFIC PROGRAM (continued)

|  |          |       |                 |          |  |
|--|----------|-------|-----------------|----------|--|
| <b>S9 – The X - an eXceptional chromosome!</b>   |          |       |                 |          | ROOM 5   |
| Chair: Doris Bachtrog ( <i>University of California, San Diego</i> )   |          |       |                 |          |  |
|  | 09:30 am | O-066 | Dyer            | Kelly    | Population genetics of selfish X chromosomes in <i>Drosophila</i>  |
| GSTA   | 10:00 am | O-067 | Meisel          | Richard  | Lineage specific patterns of gene duplication and relocation in <i>Drosophila</i> genomes reveal insights into the early evolution of sex chromosomes  |
|  | 10:15 am | O-068 | Vibrantovski    | Maria    | Male germline X inactivation and its consequences on the evolution of male related genes in <i>Drosophila</i>  |
|  | 10:30 am | O-069 | Jensen          | Jeffrey  | Pervasive adaptive evolution on a newly formed X chromosome  |
| GSTA   | 10:45 am | O-070 | Potrzebowski    | Lukasz   | Recruitment of new male genes to the X upon therian sex chromosome differentiation   |
| <b>S10 – What would/should we do with a million DNA barcodes?</b>  |          |       |                 |          | ROOM 3   |
| Chairs: Axel Meyer ( <i>University of Konstanz</i> ) and Stéphane Hemmerter ( <i>University of Technologie</i> ) |          |       |                 |          |  |
|  | 09:30 am | O-071 | Barracough      | Timothy  | Identifying evolutionary units of diversity using DNA barcodes   |
|  | 10:00 am | O-072 | Birmingham      | Eldredge | Barcoding communities: comparative evolutionary dynamics of regional assemblages of birds  |
|  | 10:30 am | O-073 | Austerlitz      | Frederic | Efficiency of phylogenetic and statistical classification methods for DNA barcoding  |
|  | 10:45 am | O-074 | Hadrys          | Heike    | Character-based DNA barcoding allows discrimination of genera, species and populations in Odonata  |
| 11:00 am - 11:30 am <b>COFFEE BREAK</b>  |          |       |                 |          | LEVEL 0   1  |
| <b>S11 – Evolutionary genomics of human and pathogen interactions</b>  |          |       |                 |          | ROOM 5   |
| Chairs: Gilean McVean ( <i>Oxford University</i> ) and Philip Awadalla ( <i>University of Montreal</i> )         |          |       |                 |          |  |
|  | 11:30 am | O-075 | Quintana-Murci  | Lluís    | Evolutionary immunology as a tool for exploring new frontiers of host defence: the paradigm of Toll-like receptors   |
|  | 12:00 pm | O-076 | Tishkoff        | Sarah    | Genetic variation in Africa: Implications for evolution of infectious disease resistance   |
|  | 12:30 pm | O-077 | Satta           | Yoko     | Biological implication for loss of function at Major Histocompatibility Complex loci   |
|  | 12:45 pm | O-078 | Awadalla        | Philip   | Genome-wide inferences of recombination in malaria and humans  |
| <b>S12 – RNA World: Emergence of life on earth</b>   |          |       |                 |          | ROOM 3   |
| Chair: Mauro Santos ( <i>Universitat Autònoma de Barcelona</i> )   |          |       |                 |          |  |
|  | 11:30 am | O-079 | Szathmary       | Eors     | Dynamics of RNA-like genomes   |
|  | 12:00 pm | O-080 | Caetano-Anolles | Gustavo  | Evolutionary patterns in tRNA sequence and structure: a window into early translation, the genetic code, and ancient life  |
|  | 12:15 pm | O-081 | Boussau         | Bastien  | Parallel Adaptations to High Temperatures in the Archean Eon   |
|  | 12:30 pm | O-082 | Bornberg-Bauer  | Erich    | Optimisation of latent (structural) traits facilitates phenotypic transitions and thus speeds up evolution of biomolecules   |
|  | 12:45 pm | O-083 | Johansen        | Steinar  | Why are slime molds loaded with autocatalytic introns in their ribosomal RNA genes?  |
| 01:00 pm - 03:00 pm <b>POSTER SESSION &amp; LUNCH BOX</b>  |          |       |                 |          | LEVEL 0   1  |
| 02:00 pm - 03:00 pm <b>POSTER JUDGING TIME J3</b> (Posters: P528 - P750)   |          |       |                 |          | LEVEL 0  |
| <b>COMPANY SESSION</b>   |          |       |                 |          | ROOM 7   |
| Chair: Marta Riutort ( <i>Universitat de Barcelona</i> )   |          |       |                 |          |  |
|  | 02:15 pm | CS-1  | Droege          | Marcus   | The Genome Sequencer FLX System <span style="float: right;">Sponsored by </span>  |
|  | 02:35 pm | CS-2  | Cristina        | Xavier   | Enabling New Applications with SOLiD™ System Next Generation Sequencing Platform <span style="float: right;">Sponsored by </span> |

| 03:00 pm - 05:30 pm |          |       |                   |             | AFTERNOON SYMPOSIA & CONTRIBUTED SESSIONS   |  |
|---------------------|----------|-------|-------------------|-------------|---|--|
|                     |          |       |                   |             | <b>S13 – Models of genome evolution and phylogenomics</b>   |  |
|                     |          |       |                   |             | Chair: David Posada ( <i>Universidad de Vigo</i> )  |  |
|                     |          |       |                   |             | ROOM 7  |  |
|                     | 03:00 pm | O-084 | Arvestad          | Lars        | Probabilistic analysis of gene family evolution - gene duplications and sequence evolution  |  |
|                     | 03:30 pm | O-085 | Sangaralingam     | Ajanthah    | Why do models of gene gain and loss give the incorrect phylogeny?   |  |
|                     | 03:45 pm | O-086 | Beiko             | Robert      | Genome phylogeny under different models of lateral gene transfer  |  |
|                     | 04:00 pm | O-087 | Galtier           | Nicolas     | Phylogenomic analyses: dealing with incongruence  |  |
|                     | 04:15 pm | O-088 | Cohen             | Ofir        | A Bayesian Framework to Analyze Phyletic Patterns   |  |
|                     | 04:30 pm | O-089 | Abby              | Sophie      | Evaluating prokaryotic trees in the light of gene transfers   |  |
|                     | 04:45 pm | O-090 | Sertier           | Anne-Sophie | Phylogenomics of modular proteins: relative importance of domain shuffling vs. domain innovation  |  |
|                     | 05:00 pm | O-091 | Krauss            | Veiko       | Near intron pairs and the phylogeny of holometabolous insects   |  |
|                     | 05:15 pm | O-092 | Smith             | David       | Nucleotide diversity in the mitochondrial and nuclear compartments of <i>Chlamydomonas reinhardtii</i> : investigating the origins of genome architecture   |  |
|                     |          |       |                   |             | <b>S14 – Network evolution and systems biology</b>  |  |
|                     |          |       |                   |             | Chairs: Mark L. Siegal ( <i>New York University</i> ) and Joanna Masel ( <i>University of Arizona</i> )   |  |
|                     |          |       |                   |             | ROOM 6  |  |
|                     | 03:00 pm | O-093 | Félix             | Marie-Anne  | Robustness and evolution of the signaling network underlying <i>Caenorhabditis</i> vulva development  |  |
|                     | 03:30 pm | O-094 | Rifkin            | Scott       | Probing the boundaries of stability in <i>Caenorhabditis</i> endodermal development: how genetic networks cope with stochastic variation in gene expression |  |
|                     | 03:45 pm | O-095 | Levy              | Sasha       | Network hubs buffer environmental variation   |  |
| PDTA                | 04:00 pm | O-096 | Liang             | Han         | Protein Interaction Network Architecture and Gene Duplication   |  |
|                     | 04:15 pm | O-097 | Sanjuan           | Rafael      | Network complexity determines the sign and intensity of epistasis   |  |
|                     | 04:30 pm | O-098 | Musso             | Gabriel     | The extensive and condition-dependent nature of epistasis among whole-genome-duplicates in yeast  |  |
|                     | 04:45 pm | O-099 | Rosas             | Ulises      | Microevolution of developmental networks on fitness spaces  |  |
|                     | 05:00 pm | O-100 | Borenstein        | Elhanan     | Large-scale phylogenetic analysis of inferred metabolic growth environments and the evolution of metabolic networks   |  |
|                     | 05:15 pm | O-101 | Barton            | Michael     | Systems biology of energetic and atomic costs in the yeast transcriptome, proteome, and metabolome  |  |
|                     |          |       |                   |             | <b>S15 – Transposable elements: diversity, dynamics and evolutionary impact on host genomes</b>   |  |
|                     |          |       |                   |             | Chair: Alfredo Ruiz ( <i>Universitat Autònoma de Barcelona</i> )  |  |
|                     |          |       |                   |             | ROOM 5  |  |
|                     | 03:00 pm | O-102 | Feschotte         | Cedric      | Transposon-derived transcription factors and de novo assembly of regulatory networks  |  |
|                     | 03:30 pm | O-103 | Petrov            | Dmitri      | Population genomics of transposable elements in <i>D. melanogaster</i>  |  |
|                     | 04:00 pm | O-104 | Batzer            | Mark        | L1 recombination-mediated deletions generate human structural variation   |  |
|                     | 04:15 pm | O-105 | Pritham           | Ellen       | A transposon's paradise: half of the genome of the parasitic protist, <i>Trichomonas vaginalis</i> is occupied by diverse DNA transposons                   |  |
|                     | 04:30 pm | O-106 | Maside            | Xulio       | Genome-wide estimate of the rate of horizontal transfer of transposable elements in <i>Drosophila</i>   |  |
|                     | 04:45 pm | O-107 | Charlesworth      | Deborah     | Autosomal and Y-linked transposable element frequencies in the dioecious plant <i>Silene latifolia</i>  |  |
|                     | 05:00 pm | O-108 | Boutin            | Thibaud     | Long-term evolution of transposable elements  |  |
|                     | 05:15 pm | O-109 | Landweber         | Laura       | Not all junk: a functional role for transposases in genome-wide DNA rearrangements  |  |
|                     |          |       |                   |             | <b>S16 – Molecular and evolutionary epidemiology</b>  |  |
|                     |          |       |                   |             | Chair: Fernando González-Candelas ( <i>Universitat de València</i> )  |  |
|                     |          |       |                   |             | ROOM 3  |  |
|                     | 03:00 pm | O-110 | Pybus             | Oliver      | The Phylodynamic Behaviour of RNA Viruses   |  |
|                     | 03:30 pm | O-111 | González-Candelas | Fernando    | Molecular evolution in the court-room: analysis of a large hepatitis C outbreak   |  |
|                     | 04:00 pm | O-112 | Crandall          | Keith       | Population dynamics of HIV-1 subtype B in USA estimated from data collected in a phase III AIDS vaccine trial   |  |
|                     | 04:15 pm | O-113 | Pfister           | Luz-Andrea  | How do we Estimate Bacterial Mutation rates?  |  |
|                     | 04:30 pm | O-114 | Zhai              | Weiwei      | Patterns of molecular adaptations in the Influenza Virus  |  |
|                     | 04:45 pm | O-115 | Hershberg         | Ruth        | Severely reduced selection leads to high functional diversity in <i>Mycobacterium tuberculosis</i>  |  |
|                     | 05:00 pm | O-116 | Tully             | Damien      | Understanding the diversification of Hepatitis C Virus genotypes: A major challenge for any treatment   |  |
|                     | 05:15 pm | O-117 | Janies            | Daniel      | Genomic and geographic analysis of the evolution and spread of infectious disease   |  |

## SCIENTIFIC PROGRAM (continued)

|                     |   |                   |   |
|---------------------|---|-------------------|---|
| 05:30 pm - 07:00 pm | <b>POSTER SESSION &amp; COFFEE BREAK</b><br><b>PA1. Odd Poster numbers: (i.e., P001, P003, ..., P751)</b> | LEVEL 0           | 1 |
| 05:45 pm - 06:45 pm | <b>SOCIETY BUSINESS MEETING</b>   | ROOM 6            |   |
| 08:30 pm            | <b>MEETING DINNER &amp; AWARDS</b>  | HOTEL FIRA PALACE |   |

### SUNDAY, JUNE 8

|                     |   |            |            |   |
|---------------------|---|------------|------------|---|
| 07:30 am - 05:30 pm | <b>REGISTRATION</b>   | LEVEL 2    |            |   |
| 08:30 am - 09:30 am | <b>PLENARY LECTURE 3 - Prof. Andrew G. Clark (Cornell University)</b><br><b>Genomic imprinting: An evolutionary puzzle</b><br>Chair: Montserrat Aguadé (Universitat de Barcelona) | ROOM 7     |            |   |
| 09:30 am - 01:00 pm | <b>MORNING SYMPOSIA &amp; CONTRIBUTED SESSIONS</b>  |            |            |   |
|                     | <b>S17 – Molecular phylogeography and population genetics</b><br>Chair: Carlos Juan (Universitat de les Illes Balears)  | ROOM 7     |            |   |
| 09:30 am            | O-118   | Knowles    | L. Lacey   | Phylogeography: virtues of a unified eclectic perspective   |
| 10:00 am            | O-119   | Nabholz    | Benoit     | Is mitochondrial DNA an appropriate molecular marker of biodiversity?   |
| 10:15 am            | O-120   | Carr       | Steven     | Prayers from the ArkChip: Intraspecific phylogeographic genomics of fish and mammal species in the Northwest Atlantic inferred from a multi-species DNA sequencing microarray |
| 10:30 am            | O-121   | Reich      | David      | Shotgun genome sequencing data as a tool for studying history and evidence for incomplete lineage sorting comparing chimpanzees, bonobos and humans                           |
| 10:45 am            | O-122   | Melé       | Marta      | New approach for detecting recombination events in a set of DNA sequences: towards the ancestral recombination graph  |
| 11:00 am - 11:30 am | <b>COFFEE BREAK</b>   | LEVEL 0    | 1          |   |
| 11:30 am            | O-123   | Sun        | James      | Empirical evidence that microsatellites are unbiased and precise molecular clocks   |
| 11:45 am            | O-124   | Katz       | Laura      | Phylogeography of coastal ciliates: estimates of biodiversity and effective population sizes  |
| 12:00 pm            | O-125   | Haag       | Christoph  | A bit of sex is enough: Nucleotide diversity and within-gene recombination in two partially asexual species   |
| 12:15 pm            | O-126   | Reed       | David      | Distinguishing ancient polymorphism from recent gene flow in the ectoparasitic lice of modern and archaic hominids using coalescent simulations                               |
| 12:30 pm            | O-127   | Walton     | Catherine  | Pleistocene climatic change has played a major role in shaping the genetic diversity of forest species in mainland Southeast Asia   |
| 12:45 pm            | O-128   | McGaughran | Angela     | Phylogeographic structure of maritime Antarctic populations of the springtail <i>Cryptopygus antarcticus</i>  |
|                     | <b>S18 – Genetics and molecular biology of speciation</b><br>Chair: Lluís Serra (Universitat de Barcelona)  | ROOM 6     |            |   |
| 09:30 am            | O-129   | Presgraves | Daven      | Genetics and molecular biology of speciation in <i>Drosophila</i> : the rules and the genes   |
| 10:00 am            | O-130   | Moyle      | Leonie     | Genome-wide expression analysis for detecting hybrid incompatibility interactions in <i>Lycopersicon</i>  |
| 10:15 am            | O-131   | Hollocher  | Hope       | When Genomes Collide: Microarray expression profile differences underlying female hybrid sterility in <i>Drosophila</i>   |
| 10:30 am            | O-132   | Meyer      | Axel       | Molecular approaches to understanding phenotypic diversification in the adaptive radiations of cichlid fishes   |
| 10:45 am            | O-133   | Kingan     | Sarah      | Molecular population genetics of a sex ratio distorter in <i>Drosophila simulans</i>  |
| 11:00 am - 11:30 am | <b>COFFEE BREAK</b>   | LEVEL 0    | 1          |   |
| 11:30 am            | O-134   | Coop       | Graham     | A population genetic model of the accumulation of reproductive isolation factors during parapatric speciation   |
| 11:45 am            | O-135   | Good       | Jeffrey M. | A Complex Genetic Basis to X-linked Hybrid Male Sterility During the Early Stages of Speciation in House Mice   |
| 12:00 pm            | O-136   | Yamamichi  | Masato     | No genetic evidence for complex speciation of humans and chimpanzees  |
| 12:15 pm            | O-137   | Osada      | Naoki      | Pattern of genetic admixture and differentiation between <i>Macaca fascicularis</i> and <i>M. mulatta</i> genome  |
| 12:30 pm            | O-138   | Hasselmann | Martin     | Evidence for nascence of a novel sex determination cascade by adaptive evolution  |
| 12:45 pm            | O-139   | Morán      | Tomás      | Genetic architecture of sterility in male hybrids between <i>Drosophila koepferae</i> and <i>Drosophila buzzatii</i> : the polygenic additive threshold model                 |

|  |  |                 |            |   |  |
|--|--|-----------------|------------|---|--|
| <b>S19 – Genome variation: Lessons from the human genomes</b>                                      |  |                 |            |   | <b>ROOM 5</b>  |
| Chair: Jaume Bertranpetit ( <i>Universitat Pompeu Fabra</i> )                                      |  |                 |            |   |  |
| 09:30 am   | O-140  | Helgason        | Agnar      | The study of micro-evolutionary patterns using genealogical data: Humans as a model organism  |  |
| 10:00 am   | O-141  | Jakobsson       | Mattias    | Genotype, haplotype, and copy number variation in worldwide human populations   |  |
| GSTA   | 10:15 am   | O-142           | Perry      | George  | A population genetics study of copy number variation in humans and chimpanzees |
| 10:30 am   | O-143  | Myers           | Simon      | Identification of a DNA sequence motif associated with hotspots for genome instability  |  |
| 10:45 am   | O-144  | Casals          | Ferran     | Recombination rate evolves with genetic differentiation in humans   |  |
| <b>S20 – Animal domestication genomics</b>   |  |                 |            |   | <b>ROOM 3</b>  |
| Chair: Miguel Pérez-Enciso ( <i>Universitat Autònoma de Barcelona</i> )                            |  |                 |            |   |  |
| 09:30 am   | O-145  | Larson          | Greger     | Nothing in biology makes sense except in light of domestication   |  |
| 10:00 am   | O-146  | Degenhardt      | Jeremiah   | Copy Number Variation in the Domestic Dog   |  |
| 10:15 am   | O-147  | Svensson        | Emma       | Analysis of SNPs in ancient and modern cattle reveals early selection for milk traits   |  |
| 10:30 am   | O-148  | Araki           | Hitoshi    | Genetic effects of captive breeding: A case study of the Hood River steelhead trout   |  |
| 10:45 am   | O-149  | Gray            | Melissa    | Linkage Disequilibrium and Demographic History in Wild and Domestic Canids  |  |
| 11:00 am - 11:30 am  | <b>COFFEE BREAK</b>  |                 |            | <b>LEVEL 0</b>  | <b>1</b>   |
| <b>S21 – Drosophila population genomics</b>  |  |                 |            |   | <b>ROOM 5</b>  |
| Chair: Montserrat Aguadé ( <i>Universitat de Barcelona</i> )                                       |  |                 |            |   |  |
| Sponsored by    |  |                 |            |   |  |
| 11:30 am   | O-150  | Stephan         | Wolfgang   | Mapping recent positive selection in model species  |  |
| 12:00 pm   | O-151  | Haddrill        | Penelope   | Positive and negative selection on noncoding DNA in <i>Drosophila simulans</i>  |  |
| 12:15 pm   | O-152  | Cardoso Moreira | Margarida  | Genome architecture and natural selection shape patterns of copy number polymorphism in <i>Drosophila melanogaster</i>              |  |
| 12:30 pm   | O-153  | Pool            | John       | The impact of founder events on chromosomal variability in multiply mating species  |  |
| 12:45 pm   | O-154  | Clark           | Nathaniel  | Signatures of Co-evolution in <i>Drosophila</i> Protein Networks  |  |
| <b>S22 – Genomics for crop evolution and improvement</b>   |  |                 |            |   | <b>ROOM 3</b>  |
| Chair: Pere Arús ( <i>Institut de Recerca i Tecnologia Agroalimentàries</i> )                      |  |                 |            |   |  |
| Sponsored by  |  |                 |            |   |  |
| 11:30 am   | O-155  | Morgante        | Michele    | Transposable elements and the plant pan-genomes   |  |
| 12:00 pm   | O-156  | Sakai           | Hiroaki    | Reductive genome evolution during the course of Asian rice cultivation  |  |
| 12:15 pm   | O-157  | Chen            | Z. Jeffrey | Genetic and Epigenetic Mechanisms for Gene Expression Changes in Plant Polyploids   |  |
| 12:30 pm   | O-158  | Caicedo         | Ana        | The evolutionary genomics of U.S. weedy rice  |  |
| 12:45 pm   | O-159  | Sharbel         | Timothy    | Molecular signatures of apomictic ovules: a wave of species-specific allele upregulation in the <i>Boecheira holboellii</i> complex |  |
| 01:00 pm - 03:00 pm  | <b>POSTER SESSION &amp; LUNCH BOX</b>                          |                 |            | <b>LEVEL 0</b>  | <b>1</b>   |
| 01:30 pm - 05:30 pm  | <b>PA2. Even Poster numbers: (i.e., P002, P004, ..., P752)</b> |                 |            | <b>LEVEL 0</b>  |  |
| 03:00 pm - 05:30 pm  | <b>AFTERNOON SYMPOSIA &amp; CONTRIBUTED SESSIONS</b>           |                 |            |   |  |
| <b>S23 – Bioinformatics for molecular evolution</b>  |  |                 |            |   | <b>ROOM 7</b>  |
| Chair: Roderic Guigó ( <i>Universitat Pompeu Fabra</i> )   |  |                 |            |   |  |
| Sponsored by  |  |                 |            |   |  |
| 03:00 pm   | O-160  | Notredame       | Cédric     | Recent Developments in Multiple Sequence Alignments: Growing Phylogenetic Trees on the Right Compost                                |  |
| 03:30 pm   | O-161  | Dutheil         | Julien     | Studying population genetics with genomes: a Coalescent Hidden Markov Model approach  |  |
| 03:45 pm   | O-162  | Loytynoja       | Ari        | Systematic errors in multiple sequence alignment cause bias in evolutionary analyses  |  |
| 04:00 pm   | O-163  | Scornavacca     | Celine     | PhySICIST healing source trees to infer healthy supertrees  |  |
| 04:15 pm   | O-164  | Markova-Raina   | Penka      | The choice of aligner significantly impacts the estimates of positive selection in the 12 <i>Drosophila</i> genomes                 |  |
| 04:30 pm   | O-165  | Holmes          | Ian        | Fast, accurate statistical tools for measuring substitution rates in genes, genomes and other alignments of structured features     |  |
| 04:45 pm   | O-166  | Kryukov         | Kirill     | MISHIMA - a new heuristic method of multiple sequence alignment   |  |
| 05:00 pm   | O-167  | Bastian         | Frédéric   | Bgee: Integrating Ontology and Homology for the Study of Gene Expression Evolution  |  |
| 05:15 pm   | O-168  | Vavouri         | Tanya      | Widespread conservation of genetic redundancy across a billion years of eukaryotic evolution  |  |

## SCIENTIFIC PROGRAM (continued)

| <b>S24 – Beyond scans for selection: studying the phenotypes</b>  |          |       |                 |          | ROOM 6   |
|---|----------|-------|-----------------|----------|--|
| Chair: Yoav Gilad ( <i>University of Chicago</i> )  |          |       |                 |          |  |
|   | 03:00 pm | O-169 | Fay             | Justin   | Identifying functional changes in cis-regulatory sequences   |
|   | 03:30 pm | O-170 | Nachman         | Michael  | Making the link to phenotype: the genetic basis of adaptive melanism in pocket mice  |
|   | 04:00 pm | O-171 | Montooth        | Kristi   | Relating molecular to phenotypic divergence in the context of mitochondrial-nuclear co-evolution   |
|   | 04:15 pm | O-172 | Cain            | Carolyn  | Studying the mechanisms of regulatory evolution in primates  |
| GSTA  | 04:30 pm | O-173 | Brown           | Kyle     | Epistasis and pleiotropy among naturally occurring mutations at a drug target locus in <i>Plasmodium falciparum</i> determine tradeoffs between growth rate and resistance |
| PDTA  | 04:45 pm | O-174 | Beaumont        | Hubertus | Mutations, modules & phenotypes: reverse evolution and innovation in experimental bacterial populations under alternating selection  |
|   | 05:00 pm | O-175 | Andolfatto      | Peter    | The evolution of gene regulation underlies a morphological difference between two <i>Drosophila</i> sister species   |
|   | 05:15 pm | O-176 | Everett         | Meredith | Functional genomics and the evolutionary response to hypoxia in <i>Fundulus grandis</i>  |
| <b>S25 – Dating divergence: The tower of Babel of geneticists and paleontologists?</b>  |          |       |                 |          | ROOM 5   |
| Chair: Rafael Zardoya ( <i>Museo Nacional de Ciencias Naturales</i> )   |          |       |                 |          |  |
| Sponsored by  and  |          |       |                 |          |  |
|   | 03:00 pm | O-177 | Donoghue        | Philip   | Rocks and clocks   |
|   | 03:30 pm | O-178 | Rambaut         | Andrew   | Putting time back into molecular phylogenetics   |
|   | 04:00 pm | O-179 | Steiper         | Michael  | Learning from the discordance between molecular and paleontological time estimates for the origin of primate taxa  |
|   | 04:15 pm | O-180 | Lopes           | João     | Studying Historic demographic parameters (Population size, divergence time, migration rates) using an Approximate Bayesian Computation framework                           |
|   | 04:30 pm | O-181 | Miya            | Masaki   | Mitogenomic evaluation of historical biogeography of cichlids toward reliable dating of teleostean divergences   |
|   | 04:45 pm | O-182 | Welch           | John     | Determinants of substitution rate variation in mammals: Empirically informed priors for molecular dating   |
|   | 05:00 pm | O-183 | Poux            | Céline   | Molecular phylogeny and divergence times of the endemic Malagasy tenrecs   |
|   | 05:15 pm | O-184 | Masel           | Joanna   | Quantitative predictions of molecular clock acceleration at short timescales   |
| <b>S26 – Animal molecular Evo-Devo</b>  |          |       |                 |          | ROOM 3   |
| Chair: Michel Milinkovitch ( <i>Université Libre de Bruxelles</i> ) and Denis Headon ( <i>University of Manchester</i> )  |          |       |                 |          |  |
|   | 03:00 pm | O-185 | Jernvall        | Jukka    | How many genes does it take to make mammalian dental diversity?  |
|   | 03:30 pm | O-186 | Lynch           | Vincent  | Molecular mechanisms of innovation: different from adaptation?   |
|   | 04:00 pm | O-187 | Pantalacci      | Sophie   | Conserved features and evolutionary shifts of the EDA signaling pathway involved in vertebrate skin appendage development  |
|   | 04:15 pm | O-188 | Braasch         | Ingo     | Evolutionary developmental genomics of pigmentation pathways in fish   |
|   | 04:30 pm | O-189 | Debiais Thibaud | Mélanie  | Teeth and denticles: genetic divergence in dermal skeleton modules   |
|   | 04:45 pm | O-190 | Oakley          | Todd     | The origins of novel protein interactions during animal opsin evolution  |
|   | 05:00 pm | O-191 | Ramos           | Diane    | Differential expression of <i>engrailed</i> -family members in <i>Bicyclus anynana</i> : Implications for evolution of a morphological novelty                             |
|   | 05:15 pm | O-192 | Suga            | Hiroshi  | Functional evolution of the Pax gene family in the early stage of animal evolution   |

MEETING ENDS

## POSTER PRESENTATIONS

|  | SESSION | POSTER NUMBER |          | PAGE |
|--|---------|---------------|----------|------|
| <b>Undergraduate Diversity Mentoring Program Award</b>                             | UDMPA   | UDMPA-01      | UDMPA-10 | 17   |
| <b>Posters</b>   |         |               |          |      |
| Animal domestication genomics  | S20     | P-001         | P-010    | 17   |
| Animal molecular Evo-Devo  | S26     | P-012         | P-027    | 17   |
| Beyond scans for selection: Studying the phenotypes                                | S24     | P-028         | P-048    | 18   |
| Bioinformatics for molecular evolution   | S23     | P-050         | P-093    | 18   |
| Dating divergence: The Tower of Babel of geneticists and paleontologists?          | S25     | P-094         | P-104    | 20   |
| Drosophila population genomics   | S21     | P-105         | P-119    | 20   |
| Evolution of gene regulation   | S8      | P-121         | P-171    | 20   |
| Evolutionary comparative genomics  | S1      | P-172         | P-299    | 22   |
| Evolutionary genomics of human and pathogen interactions                           | S11     | P-300         | P-315    | 25   |
| Evolutionary radiations and molecular phylogeny                                    | S2      | P-316         | P-376    | 25   |
| Genetics and molecular biology of speciation                                       | S18     | P-377         | P-413    | 27   |
| Genome variation: Lessons from the human genomes                                   | S19     | P-414         | P-430    | 28   |
| Genomic evidence for natural selection and implications                            | S7      | P-431         | P-500    | 29   |
| Genomics for crop evolution and improvement  | S22     | P-501         | P-504    | 30   |
| Models of genome evolution and phylogenomics                                       | S13     | P-505         | P-526    | 31   |
| Molecular and evolutionary epidemiology  | S16     | P-527         | P-536    | 32   |
| Molecular phylogeography and population genetics                                   | S17     | P-537         | P-641    | 31   |
| Network evolution and systems biology  | S14     | P-642         | P-652    | 34   |
| Popgen in space! Theory and inference in spatial population genetics               | S5      | P-654         | P-665    | 35   |
| Spontaneous mutations and their evolutionary consequences                          | S3      | P-666         | P-682    | 35   |
| The ancestral eukaryotic cell  | S6      | P-683         | P-687    | 35   |
| The crossroads between prokaryotic genomics, ecology and adaptation                | S4      | P-688         | P-698    | 36   |
| The X - an eXceptional chromosome!   | S9      | P-700         | P-710    | 36   |
| Transposable elements: diversity, dynamics and evolutionary impact on host genomes | S15     | P-711         | P-742    | 36   |
| What would/should we do with a million DNA barcodes?                               | S10     | P-743         | P-752    | 37   |

GS: Graduate student poster award candidate; PDF: Postdoctoral fellow poster award candidate; UG: Undergraduate student.

### UNDERGRADUATE DIVERSITY MENTORING PROGRAM AWARD (UG)

| POSTER   | LAST NAME     | FIRST NAME | STATUS | TITLE   |
|----------|---------------|------------|--------|---|
| UDMPA-01 | Huang         | Wen        | UG     | Using Shannon's index for comparative phylogeography  |
| UDMPA-02 | Wilches       | Ricardo    | UG     | Molecular evolution of two genes with male-biased expression in <i>Drosophila ananassae</i>                               |
| UDMPA-03 | Duggan        | Ana        | UG     | The ArkChip - Efficiency and Accuracy of a multi-species iterative sequencing microarray                                  |
| UDMPA-04 | De Berardinis | Jennifer   | UG     | Non-Mendelian Inheritance in the Ciliate <i>Chilodonella uncinata</i>   |
| UDMPA-05 | Sánchez       | Luisa      | UG     | Mitochondrial genetic diversity in Yemeni and Horn of Africa populations  |
| UDMPA-06 | Sharp         | Christine  | UG     | Discovery of a novel integron in the <i>Arthrobacter</i> genus: a potential agent of xenobiotic degradation? degradation? |
| UDMPA-07 | Theobald      | Rebecca    | UG     | The relationship between mutational load and oxidative damage   |
| UDMPA-08 | Carter        | Tamar      | UG     | Molecular Evidence of Male Bondedness in Ugandan Red Colobus ( <i>Procolobus rufomitratus</i> )                           |
| UDMPA-09 | López         | Saioa      | UG     | Overdominance in the human genome and olfactory receptor activity   |
| UDMPA-10 | Rodrigo       | Aida       | UG     | Phylogenomics of the <i>Legionella pneumophila</i> pan-genome   |

### POSTERS

| POSTER                                     | LAST NAME | FIRST NAME | STATUS | TITLE   |
|--|-----------|------------|--------|---|
| <b>ANIMAL DOMESTICATION GENOMICS (S20)</b> |           |            |        |   |
| P-001                                      | Berggren  | Karin T    | GS     | Weak associations between the promoter and exon 2 of the <i>DLA-DQB1</i> gene in dogs |
| P-002                                      | Chen      | Shanyuan   | PDF    | The Importance of Studying Genome-wide Variation in Local Livestock Genetic Resources |

## POSTER PRESENTATIONS (continued)

|       |              |                |     |  |
|-------|--------------|----------------|-----|--|
| P-003 | Ojeda García | Ana            |     | Nucleotide variability along a region containing a strong quantitative trait locus effect in the pig   |
| P-004 | Ramírez      | Oscar          | PDF | High Y-chromosome variation in pig and wild boar ( <i>Sus scrofa</i> )   |
| P-005 | Wiener       | Pam            |     | Patterns of genetic diversity near selected genes in cattle  |
| P-006 | Komiyama     | Tomoyoshi      |     | Elucidation of the evolutionary relationships between goldfish and human culture based on mitochondrial DNA analysis   |
| P-007 | Ferrand      | Nuno           |     | Microsatellite variation and the evolution of coat colour genes during domestication of the European rabbit ( <i>Oryctolagus cuniculus</i> )   |
| P-008 | Monteiro     | Bruno Fernando | GS  | Contrasting patterns of genetic diversity in three coat colour genes (MC1R, agouti and TYR) in wild and domestic populations of the European rabbit ( <i>Oryctolagus cuniculus</i> ) |
| P-009 | Mona         | Stefano        | PDF | Mitochondrial DNA variation in Italian <i>Bos primigenius</i> : new clues into the cattle domestication process  |

### ANIMAL MOLECULAR EVO-DEVO (S26)

|       |            |                 |     |   |
|-------|------------|-----------------|-----|---|
| P-012 | Roux       | Julien          | GS  | Developmental constraints on vertebrate gene evolution  |
| P-013 | Nicolas    | Michael         | PDF | Developmental time course in fire ants  |
| P-014 | Khadjeh    | Sara            | GS  | First Hox genes in basal winged insects   |
| P-015 | Paris      | Mathilde        | GS  | Thyroid hormones, their receptor and the evolution of metamorphosis in chordates  |
| P-016 | Negre      | Bárbara         | PDF | Evolution of the Achaete-Scute Complex in insects: recurrent duplication of proneural genes                               |
| P-017 | Wittkopp   | Patricia J.     |     | Genetic basis of pigmentation differences within and between <i>Drosophila</i> species                                    |
| P-018 | Suzuki     | Ikuo            | GS  | The Evolutionary Origin of the Laminar Structure in the Mammalian Neocortex   |
| P-020 | Sumiyama   | Kenta           |     | Cis-element evolution elucidated by genomic sequence comparison of the vertebrate <i>Dlx3-7</i> bigene clusters           |
| P-022 | Moriyama   | Hideaki         |     | Proteomic analysis of speciation barriers at the early stage of reproduction  |
| P-023 | Lott       | Susan E.        | GS  | Evolution of pattern formation without loss of precision in two <i>Drosophila</i> species as revealed by genetic analysis |
| P-024 | Clark      | Jo-Anna Barbara | GS  | Functional Genomic Analysis of Gingival Fibromatosis in Silver Foxes Using Candidate Genes and DNA Microarrays            |
| P-025 | Dell Ampio | Emiliano        | PDF | 28S rRNA and conflicting hypotheses of phylogenetic relationships among apterygote insect orders                          |
| P-026 | Maeso      | Ignacio         | GS  | Convergent evolution of clustering of <i>Iroquois</i> homeobox genes across metazoans                                     |
| P-027 | D'Aniello  | Salvatore       | PDF | Massive gene expansion but not loss leads to unprecedented Tyrosine kinase diversity and richness in amphioxus            |

### BEYOND SCANS FOR SELECTION: STUDYING THE PHENOTYPES (S24)

|       |           |               |     |   |
|-------|-----------|---------------|-----|---|
| P-028 | Kawamura  | Shoji         |     | Detection of natural selection acting to maintain allelic polymorphism of L/M opsin genes in wild populations of New World monkeys        |
| P-029 | Orsini    | Luisa         | PDF | Large-scale SNP genotyping shows overdominance at a gene associated with variation in individual performance and ecological dynamics      |
| P-030 | Heyer     | Evelyne       |     | Lactase Persistency in Central Asia: a phenotype-genotype study   |
| P-031 | Chevin    | Luis-Miguel   | GS  | Selective sweep at a quantitative trait locus in the presence of background genetic variation   |
| P-032 | Reimers   | Sabrina       | GS  | A Mouse Model for a Human-Specific Transmembrane Protein  |
| P-033 | O'Connor  | Timothy David | GS  | Microevolution vs. macroevolution in pigmentation: genes under selection in human populations evolve comparatively faster in OTH primates |
| P-034 | Magalhães | Sara          | PDF | Costless adaptation to novel host plants in herbivorous mites   |
| P-035 | Nunes     | Vera L.       | GS  | AFLPs Genome Scan To Detect Genes Under Selection In Ocellated Lizards ( <i>Lacerta lepida</i> )  |
| P-037 | Headon    | Denis J.      |     | Selection for enhanced EDAR signaling in East Asia: A mouse model to determine the phenotypic consequences                                |
| P-038 | Saito     | Shigeru       | PDF | Adaptive evolution of the sensory receptor TRPV genes in amphibians   |
| P-039 | Kaessmann | Henrik        |     | Birth and Rapid Subcellular Adaptation of a Hominoid-Specific CDC14 Protein   |
| P-040 | Kaessmann | Henrik        |     | Enhanced mitochondrial targeting of the hominoid-specific glutamate dehydrogenase through single positively selected substitution         |
| P-041 | Kronholm  | Ilkka         | GS  | Detecting local adaptation in <i>Arabidopsis thaliana</i> - Seed dormancy as a case study   |

|       |                |               |     |  |
|-------|----------------|---------------|-----|--|
| P-042 | Kuittinen      | Helmi         |     | The genetic basis of differences in flowering related traits between natural populations of <i>Arabidopsis lyrata</i> assessed in different environments |
| P-043 | Kaessmann      | Henrik        |     | Functional diversification of duplicate genes through subcellular adaptation of encoded proteins   |
| P-044 | Joron          | Mathieu       |     | Genetic characterisation of a supergene switch for mimicry in a <i>Heliconius</i> butterflies  |
| P-045 | Ehrenreich     | Ian Michael   | GS  | Network-Wide Association Mapping of Flowering Time in <i>Arabidopsis</i>   |
| P-046 | Godinho        | Raquel        | PDF | Microsatellite variation and evolution of the coat colour agouti gene in wolf ( <i>Canis lupus</i> ) and dog ( <i>Canis familiaris</i> ) populations     |
| P-047 | Rubio De Casas | Rafael        | PDF | Natural variation in germination and its underlying physiological pathways   |
| P-048 | Richards       | Christina Lee | PDF | Multi-trait phenotypic diversity of <i>Arabidopsis thaliana</i> accessions   |

## BIOINFORMATICS FOR MOLECULAR EVOLUTION (S23)

|       |                |                   |     |  |
|-------|----------------|-------------------|-----|--|
| P-050 | Robert         | Frost William     | UG  | Retroid analysis of <i>Monodelphis domestica</i> Genome  |
| P-051 | Cleveland      | Sean Bruce        | GS  | A protein disorder prediction enhanced phylogenetic reconstruction of the nucleoprotein of <i>Mononegavirales</i>  |
| P-052 | Deschavanne    | Patrik            |     | A benchmark of methods for horizontal transfer detection   |
| P-053 | Chen           | Johnny Shou-Chung | PDF | Molecular Adaptation in the Opsins of Sparidae in Varied Photic Environments   |
| P-054 | Sorimachi      | Kenji             |     | An Organelle Specific Bias Governs Codon Evolution   |
| P-055 | Dopazo         | Hernán            |     | Phylemon 2.0: New resources in a suite of web tools for molecular evolution, phylogenetics and phylogenomics   |
| P-056 | Arenas         | Miguel            | GS  | A new coalescence algorithm to simulate DNA sequences with intra-codon recombination   |
| P-057 | Penel          | Simon             |     | New release of HOGENOM, a database of homologous gene families from complete genomes   |
| P-058 | Egea           | Raquel            | GS  | Standard and Generalized McDonald-Kreitman Test: a website to detect selection by comparing different classes of DNA sites   |
| P-059 | Duprat         | Elodie            |     | A superfamily of crystallins: <i>in silico</i> prediction of the critical sites and physicochemical properties   |
| P-060 | Bornberg-Bauer | Erich             |     | Representing proteins as string of domain: evolutionary analysis of domain rearrangements and tools for rapid analysis of evolutionary scenarios over long time scales |
| P-061 | Dutheil        | Julien Yann       | PDF | Using evolutionary information to infer biochemical constraints in relation to protein structures  |
| P-062 | Gueguen        | Laurent           |     | Phylogeny reconstruction under YpR neighbour-dependence  |
| P-063 | Librado        | Pablo             | GS  | DnaSP 4.5, DNA sequence polymorphism analysis on a genome-wide scale   |
| P-064 | Palmieri       | Nicola            | GS  | Short sequence reads generated by massively parallel sequencing could lead to biased gene expression measures  |
| P-065 | Andreassen     | Morten            | PDF | The formation of a new group I intron family in nuclear ribosomal DNA  |
| P-066 | Seo            | Tae-Kun           |     | Statistical comparison of nucleotide-, amino acid-, and codon-substitution models  |
| P-067 | Papanicolaou   | Alexie            | GS  | ButterflyBase: A framework for comparative genomics in butterflies and moths   |
| P-068 | Lovell         | Simon Christopher |     | Predicting the course of HIV evolution using constraints from protein structure  |
| P-069 | Blum           | Michael           |     | Likelihood-free Bayesian inference without rejection: applications to population genetics  |
| P-070 | Squartini      | Federico          | GS  | Quantifying the Equilibrium and Time Reversibility Properties of the Nucleotide Substitution Process   |
| P-071 | Brinkworth     | Jessica Fawn      | GS  | 3Dimensional (3D) molecular modeling and comparison of primate chemokine receptors (CCR2 and CX3CR1) associated with altered progression to AIDS                       |
| P-072 | Codoñer        | Francisco Manuel  | PDF | A Graphical Approach to Understand Molecular Co-evolution  |
| P-073 | Fares          | Mario Ali         |     | The Multi-factorial Nature of Mutagenesis and the Domino Effect  |
| P-074 | Luz            | Hannes            | PDF | Parametric models of amino acid evolution  |
| P-075 | Rodrigue       | Nicolas           | PDF | Bayesian nonparametric approaches to modeling protein-coding nucleotide sequence evolution   |
| P-076 | Fischer        | Mareike           | GS  | An Equivalence of Maximum Parsimony and Maximum Likelihood revisited   |
| P-077 | Delport        | Wayne             | PDF | Modeling viral evasion of host immune response in HIV-1  |

## POSTER PRESENTATIONS (continued)

|       |                            |                   |     |   |
|-------|----------------------------|-------------------|-----|---|
| P-078 | Parker                     | Elizabeth Rose    | GS  | Molecular evolution of mammalian sperm genes based on proteomic analyses of mouse sperm   |
| P-079 | Murphy                     | Daniel N.         | GS  | Genic translocations in Primate evolution   |
| P-080 | Pesole                     | Graziano          |     | ASPIcDb: a database resource to investigate the impact of alternative splicing in the expansion of human transcriptome and proteome |
| P-081 | Ravelomanantsoa-Ratsimihah | Joël              | GS  | Modelling HIV-1 escapes from Cytotoxic T-Lymphocyte (CTL) responses   |
| P-082 | Moriyama                   | Etsuko N.         |     | Mining and Classification of Odorant Receptor Proteins from Insect Genomes  |
| P-083 | Woolley                    | Steven Mark       | GS  | Detecting crossover and gene conversion events using haplotype networks   |
| P-084 | Ridout                     | Kate Elizabeth    | GS  | Comparative functional analysis of ESTs in two familial plant species with different $N_e$ s  |
| P-085 | Nekrutenko                 | Anton Yurievich   |     | Galaxy: Bringing sequences, alignments, and polymorphism data within the reach of everyone  |
| P-086 | Ramalho                    | Rodrigo Fernandes | GS  | The frequency spectrum of polymorphisms of ESEs in constitutive and alternative exons of the human genome                           |
| P-087 | Sousa                      | Ana Margarida     | PDF | Exploring tree-building methods and distinct molecular data to recover a known asymmetric phage phylogeny                           |
| P-088 | Kumar                      | Sudhir            |     | MEGA: A biologist-centric software for evolutionary analysis of DNA and protein sequences   |
| P-089 | Donoghue                   | Mark              | GS  | Taxon restricted genes in <i>Arabidopsis thaliana</i>   |
| P-090 | Lindsay                    | Helen             | GS  | How important is sequence context to nucleotide substitution?   |
| P-091 | Endo                       | Toshinori         |     | Predicting the sequences for orphan enzymes   |
| P-092 | Hamady                     | Micah             | GS  | New insights into tRNA pool evolution and environmental distribution of microbes using UniFrac                                      |
| P-093 | Segura Mora                | Joan              | GS  | Visual Genomics   |

### DATING DIVERGENCE: THE TOWER OF BABEL OF GENETICISTS AND PALEONTOLOGISTS? (S25)

|       |                   |                     |     |  |
|-------|-------------------|---------------------|-----|--|
| P-094 | Fabre             | Pierre-Henri        | GS  | Compatibility among vertebrate paleontological calibration constraints: an evaluation from mitochondrial DNA relaxed molecular clocks  |
| P-096 | Gratton           | Paolo               | PDF | Dating Pleistocene evolutionary events in the Clouded Apollo ( <i>Parnassius mnemosyne</i> ): genetic signatures of climate cycles support the Time Dependency hypothesis of mitochondrial substitution rate |
| P-097 | San Mauro         | Diego               | PDF | Do larger sequences render narrower confidence intervals in relaxed molecular dating? A case study on the origin of living amphibians  |
| P-098 | Couvreur          | Thomas L.P.         | PDF | Dating divergences in African Annonaceae: inferring the evolutionary history of the East African rain forest biodiversity hotspot  |
| P-099 | Pisani            | Davide              |     | Timing the origin of vision  |
| P-100 | Allegrucci        | Giuliana            |     | Molecular phylogeny and historical biogeography of cave crickets from the Southern end of the world  |
| P-101 | Chevret           | Pascale             |     | Evolutionary history of murine rodents: molecular phylogeny, dating and palaeontology  |
| P-102 | Bidegaray Batista | Leticia             | GS  | A witness from the past: Did the opening of the western Mediterranean basin drive diversification of the spider genus <i>Parachtes</i> ?   |
| P-103 | Henn              | Brenna Mariah       | GS  | Time-Dependency of Human Mitochondrial DNA Mutation Rate Estimates   |
| P-104 | Gignoux           | Christopher Raymond |     | How do you date all humans at once? The use of complete genomes to date nodes of the human mitochondrial tree  |

### DROSOPHILA POPULATION GENOMICS (S21)

|       |            |                     |     |   |
|-------|------------|---------------------|-----|---|
| P-105 | Hutter     | Stephan             | PDF | A scan of gene expression variation in African and European populations of <i>Drosophila melanogaster</i>   |
| P-106 | Ponce      | Rita                | PDF | Recent origin of a gene cluster in the X chromosome of <i>Drosophila melanogaster</i>   |
| P-107 | Petit      | Natalia             | GS  | Effective population size shapes the patterns of molecular evolution in <i>Drosophila</i>   |
| P-108 | Pegueroles | Cinta               | GS  | Unexpected patterns of gene exchange among O chromosome arrangements in <i>Drosophila subobscura</i>  |
| P-109 | Conceição  | Inés Pires Carreira | GS  | Nucleotide variation at a subset of Or genes in populations of <i>Drosophila melanogaster</i> and <i>Drosophila pseudoobscura</i>                 |
| P-110 | Legrand    | Delphine            | GS  | Population genetics in the <i>Drosophila simulans</i> sibling, <i>D. sechellia</i> . New insights into its evolutionary history using ABC methods |

|       |                 |                |     |   |
|-------|-----------------|----------------|-----|---|
| P-111 | Marion De Proce | Sophie         | GS  | Comparison of coding and non-coding sequences between <i>Drosophila miranda</i> and <i>D. pseudoobscura</i>                     |
| P-112 | Findlay         | Geoffrey David | GS  | Comparative proteomics identifies novel <i>Drosophila</i> seminal fluid proteins transferred to females during mating           |
| P-113 | Orengo          | Dorcas J.      | PDF | Extended analysis of variation around 15 random fragments from an X-chromosome scan of <i>Drosophila melanogaster</i>           |
| P-115 | Singh           | Nadia D.       | PDF | Fine-scale recombination rate estimation in <i>D. melanogaster</i>  |
| P-116 | Guirao          | Sara           | GS  | Polymorphism and divergence in insulin signaling pathway genes in <i>Drosophila</i>   |
| P-117 | Betancourt      | Andrea J.      | PDF | Evolution on the dot chromosome in the <i>Drosophila virilis</i> group  |
| P-118 | Arboleda        | Carlos E.      | GS  | Divergence and adaptation after the duplication event that gave rise to the <i>Dca</i> and <i>RC</i> genes of <i>Drosophila</i> |
| P-119 | Flutre          | Timothee       | GS  | A comparative analysis of <i>de novo</i> methods for identification of transposable elements in <i>Drosophilidae</i> genomes    |

## EVOLUTION OF GENE REGULATION (S8)

|       |                  |                          |     |   |
|-------|------------------|--------------------------|-----|---|
| P-121 | Nielsen          | Johanna Fønss            |     | Evidence of multiple transcripts in <i>Drosophila</i> olfactory & gustatory receptor gene expression: a mechanism for increasing chemoreceptor diversity?   |
| P-122 | Berggren         | Karin T.                 | GS  | Functional significance of MHC promoter polymorphism in dogs  |
| P-123 | Richardson       | Dale N.                  | GS  | Promoter and protein divergence independently mediate expression divergence among <i>Arabidopsis</i> paralogs   |
| P-124 | Liu              | Qing-Xin                 | PDF | Genome-wide analysis of the <i>Drosophila tdf</i> regulation by using oligonucleotide microarrays and ChIP-chip   |
| P-125 | Finet            | Cédric Aurélien          | GS  | Evolution of ARF gene family in the Land Plants   |
| P-126 | Blanco           | Enrique                  | PDF | Conserved chromosomal clustering of genes governed by chromatin regulators in <i>Drosophila</i>   |
| P-127 | Staubach         | Fabian                   | GS  | Polymorphism on two levels - integrating sequence and expression data in natural populations of the house mouse   |
| P-128 | Budd             | Aidan Edwards Sinclair   | PDF | Systematic analysis of the evolutionary dynamics of metazoan cis-regulation   |
| P-129 | Coelho           | Maria Manuela            |     | Gene expression regulation in a polyploid context -insights from sex determination and housekeeping genes in the <i>Squalius alburnoides</i> complex        |
| P-130 | Corvelo          | André De Sousa Rodrigues | GS  | Exon creation and establishment in human genes  |
| P-131 | Carter           | Robert Andrew            | GS  | Functional divergence of the eukaryotic DNA-dependent RNA polymerases   |
| P-133 | Blekhman         | Ran                      | GS  | Shifts in diet have likely resulted in a large number of regulatory changes in the human lineage  |
| P-134 | Emblem           | Åse                      | GS  | New insight into function and evolution of mitochondrial introns in sea anemones  |
| P-135 | Kaneko           | Satoko                   | PDF | Evolution of a gene family under human-specific downregulation  |
| P-136 | Evans            | Ben Jonathan             |     | Cis- and trans- divergence between species, paralogs, and tissue types: an example from the RAG1-RAG2 heterodimer in clawed frogs                           |
| P-137 | Somel            | Mehmet                   | GS  | Large-scale primate brain transcriptome sequencing  |
| P-138 | Iwase            | Mineyo                   |     | The origin and history of <i>VCX</i> gene family in primates  |
| P-139 | Go               | Yasuhiro                 | PDF | Evolution of genomic expression and <i>trans</i> effects in the closely related <i>Drosophila</i> species   |
| P-141 | Pankova          | Victoria Vladimirovna    | PDF | Are unusual allozymic variations determined by an alternative splicing?   |
| P-142 | Takuno           | Shohei                   | PDF | Evolution of complexity in miRNA-mediated gene regulation systems   |
| P-143 | Eisen            | Michael Bruce            |     | Transcription factors bind promiscuously, but often do nothing: the importance for molecular evolution  |
| P-144 | Pavlidis         | Pavlos                   | GS  | Evolutionary conservation of BDNF gene co-expression network  |
| P-145 | Farré            | Domènec                  | GS  | Effect of gene duplication on gene expression regulatory sequence evolution   |
| P-146 | Carretero-Paulet | Lorenzo                  | PDF | Evidences of functional diversification in plant DXS, a family of genes involved in the first step of the plastidial mep pathway of isoprenoid biosynthesis |
| P-147 | Nicolas          | Vinckenbosch             | GS  | Segmental copy number variation shapes tissue transcriptomes  |
| P-148 | Piganeau         | Gwenael                  |     | Unraveling promoter structure in distant unicellular eukaryotes using phylogenetic footprinting   |
| P-149 | Lang             | Michael                  | GS  | Evolution of ADF-1 binding sites in the <i>Adh</i> upstream region of <i>Drosophilidae</i>  |

## POSTER PRESENTATIONS (continued)

|       |                 |                 |     |  |
|-------|-----------------|-----------------|-----|--|
| P-151 | Franchini       | Lucía F.        |     | Birth of the mammalian proopiomelanocortin (POMC) gene neuron-specific enhancers: a story of exaptation  |
| P-152 | Nakagawa        | So              | GS  | Comparative genomic analysis of the nucleotide sequences upstream of the translation initiation codon in prokaryotes   |
| P-153 | Carlini         | David B.        |     | Experimental increase of codon bias in the <i>Drosophila</i> Adh gene has no effect on ADH protein expression  |
| P-154 | Bellora         | Nicolas         | GS  | Regulatory motif conservation on eukariotic promoters  |
| P-155 | Ishibashi       | Minaka          | GS  | Highly conserved non-coding sequences in ParaHox clusters drive reporter gene expression similar to endogenous ParaHox Gsh genes   |
| P-156 | Bainer          | Russell         | GS  | Speciation and Adaptation of Primate DNA Damage Response Pathways  |
| P-157 | Mckay           | John K.         |     | Molecular Evolution of the DREB/CBF transcription factor sub-family in Arabidopsis   |
| P-158 | Chan            | Yingguang Frank | GS  | Parallel evolution of pelvic reduction by repeated <i>de novo</i> regulatory mutations at <i>Pitx1</i> in threespine sticklebacks  |
| P-159 | Scott           | Cinda Pitts     | GS  | The effect of genetics and environmental variation on gene expression in the teleost fish, <i>Fundulus heteroclitus</i>  |
| P-160 | He              | Bin             | GS  | Studying evolutionary constraints in transcription factor binding sites and spacers using <i>Drosophila</i> polymorphism data  |
| P-161 | Lassig          | Michael         |     | Repeat sequence and the evolution of regulatory modules in <i>Drosophila</i>   |
| P-162 | Exum            | Amy             | GS  | Proximal promoter sequence analysis of a tightly regulated gene, Ras associated with diabetes  |
| P-163 | Loftus          | Katherine J.    | GS  | Evolution of Regulation of Large Oxidative Phosphorylation Enzyme Complex  |
| P-164 | Scannell        | Devin           | PDF | Gene regulatory network rewiring after whole genome duplication: Comparison of gene regulatory elements between four <i>Saccharomyces sensu stricto</i> and four <i>Zygosaccharomyces</i> yeasts |
| P-165 | Riehle          | Kevin Paul      | GS  | MotiX: A Computational Tool for Single Species Evaluation of Short DNA Sequences Based on Clustering and Frequency Biases  |
| P-167 | Elango          | Navin           | GS  | Organismal Complexity and Tissue-specificity Shape Evolution of Vertebrate Promoters   |
| P-168 | Rest            | Joshua S.       | PDF | Evolution and condition-specificity of non-coding transcription in yeast   |
| P-169 | Ogura           | Atsushi         |     | Evolution of gene regulation from the viewpoint of vertebrates eye formation   |
| P-170 | Pérez-Farrerons | Alejandro       | GS  | Evolution of Adult Enhancer Factor 1 (AEF-1) in <i>Drosophilidae</i> and its regulatory activity on Adh gene expression  |
| P-171 | Yi              | Soojin          |     | Gene expression and developmental plasticity in social wasps   |

### EVOLUTIONARY COMPARATIVE GENOMICS (S1)

|       |                 |                |     |  |
|-------|-----------------|----------------|-----|--|
| P-172 | Eirin-López     | José María     | PDF | The sperm proteins from amphioxus mirror its 'basal' position among chordates and set the origin of vertebrate protamines a step back from tunicates   |
| P-174 | Lu              | Jian           | GS  | The birth and death of microRNA genes in <i>Drosophila</i>   |
| P-175 | Vamathevan      | Jessica        | GS  | Natural Selection of Disease and Drug Targets in Mammalia  |
| P-176 | Bekaert         | Michael        | PDF | The evolution and specialisation of visual perception in Bats  |
| P-177 | Fischer         | Anne           | PDF | Sequencing the bonobo genome   |
| P-178 | Webster         | Matthew Thomas |     | Hotspots of biased nucleotide substitutions in human genes   |
| P-179 | González-Romero | Rodrigo        | GS  | Birth-and-death evolution with strong purifying selection in the histone H2A multigene family  |
| P-180 | Su              | Bing           |     | Molecular evolution of a primate-specific microRNA family  |
| P-181 | Zhang           | Liqing         |     | Burst of young retrogenes and independent retrogene formation in mammals   |
| P-182 | Backstrom       | Niclas         | GS  | A gene-based genetic linkage map of the collared flycatcher ( <i>Ficedula albicollis</i> ) reveals extensive synteny and gene order conservation during 100 million years of avian evolution |
| P-183 | Guillet         | Claire         | GS  | Evolution of CpG island methylation in Primates  |
| P-184 | Arndt           | Peter F.       |     | Unraveling Mutagenic Processes Associated with Transcription   |
| P-185 | Arbiza          | Leonardo       | GS  | Evolution of Human Tissue-Specific Genes. Rates, Expression, and Interactions  |
| P-186 | Rensing         | Stefan A.      |     | Prediction of dual protein targeting to plant organelles   |
| P-188 | Huh             | Jae-Won        | PDF | Evolutionary dissection of Williams-Beuren syndrome: comparative analysis of 7q11.23 region in human, chimpanzee, and rhesus macaque   |
| P-189 | Oulion          | Silvan         | GS  | A survey of the transcription of Hox clusters of the shark <i>Scyliorhinus canicula</i>  |

|       |              |                         |     |   |
|-------|--------------|-------------------------|-----|---|
| P-190 | Caballero    | Armando                 |     | Evaluation of AFLP fragment size homoplasmy in 14 whole genomes using in silico AFLP  |
| P-191 | Vieira       | Jorge                   |     | Chemical evolution of ANTP and PRD homeobox genes   |
| P-192 | Schneeweiss  | Gerald M.               |     | Heteroplasmy and horizontal gene transfer in a non-photosynthetic flowering plant: Where do the two distinct plastid large single copy regions come from? |
| P-193 | Kordis       | Dusan                   |     | Genome evolution after mass extinctions   |
| P-194 | Wicke        | Susann                  | GS  | From the exception to the rule: the co-localisation of the nuclear ribosomal DNA (nrDNA) in land plants represents the ancestral state                    |
| P-195 | Wicke        | Susann                  | GS  | Plastid genome evolution in a group of non-photosynthetic angiosperms   |
| P-196 | O'Connell    | Mary J.                 |     | Molecular Evolution of the Mammalian imprintome   |
| P-197 | Chuang       | Trees-Juen              |     | Different Alternative Splicing Patterns Are Subject to Opposite Evolutionary Effects  |
| P-198 | Emery        | Laura                   | GS  | The strength of selected codon usage bias in Archaea  |
| P-199 | Vieira-Silva | Sara                    | GS  | An assessment of the role of molecular oxygen in protein evolution  |
| P-200 | Treangen     | Todd James              | GS  | The impact of neisserial DNA uptake sequences on genome evolution and stability   |
| P-201 | Corral       | José María              | PDF | Multiplexed Differential Gene Expression Analysis between Apomictic and Sexual <i>Boechera</i>  |
| P-202 | Schierup     | Mikkel Heide            |     | Demographic inference in the human-chimp ancestor   |
| P-203 | Martin       | Fergal James            | GS  | The mess of YESS: A phylogenetic analysis of the YESS group   |
| P-204 | Zimmer       | Andreas David           | GS  | Tandemly arrayed genes in the green lineage   |
| P-205 | Sémon        | Marie                   |     | Preferential subfunctionalization of slow-evolving genes after allopolyploidization in <i>Xenopus laevis</i>  |
| P-206 | Lang         | Daniel                  | GS  | Tandem duplications and concerted evolution shape the LHC superfamily in the green lineage  |
| P-207 | Breines      | Ragna                   | GS  | Duplication of OriL and flanking tRNA genes within the Polar cod mitochondrial genome   |
| P-208 | Cortez       | Diego                   | GS  | A hidden viral reservoir is the major source of foreign genes and ORFans in archaeal and bacterial genomes  |
| P-209 | Toll Riera   | Macarena                | GS  | How do novel genes arise? Insights from mammalian genome sequence comparisons   |
| P-210 | Loughran     | Noeleen                 | GS  | The Phylogeny of the Mammalian Heme Peroxidases: insights into their functional specificity from comparative genomic analyses                             |
| P-211 | Heidel       | Andrew Jay              | PDF | Mitochondrial Genome Evolution in the Social Amoebae  |
| P-212 | Li           | Jingjing                | GS  | MicroRNAs preferentially regulate duplicate genes in mammals  |
| P-213 | McCann       | Angela Josephine        | GS  | Steps Towards the Tree of 100 Percent   |
| P-214 | Vieira       | Filipe Garrett          | GS  | Evolutionary dynamics of the Odorant-Binding Protein multigene family across Arthropods   |
| P-215 | Hughes       | David Allen             | GS  | Evaluating the Evolution of Thermogenesis through the Protein Evolution of UCP1   |
| P-216 | Esser        | Christian               | GS  | Lateral gene transfer in intra-species scale: analysis gene distribution patterns within nine <i>Escherichia coli</i> strains                             |
| P-217 | Gil          | Rosario                 |     | Massive presence of insertion sequences in the genome of SOPE, the primary endosymbiont of the rice weevil <i>Sitophilus oryzae</i>                       |
| P-218 | Burger       | Gertraud                |     | Unorthodox genome and gene structure in mitochondria of early diverging eukaryotes  |
| P-219 | Babra        | Bobby A.                | GS  | Evolution of Eukaryotic Mismatch Repair Pathways  |
| P-220 | Viljakainen  | Lumi                    | GS  | Comparative evolutionary genomics of insect immune system   |
| P-221 | Eilertson    | Kirsten Elise           | GS  | Detecting Genes Under Selection using Log-linear Models   |
| P-222 | Wlasiuk      | Gabriela                | GS  | Patterns of DNA sequence variation at Toll-like receptors in humans and chimpanzees   |
| P-223 | Yi           | Soojin                  |     | Comparative Analysis of Index of Dispersion Provides New Insights into Molecular Evolution of Synonymous and Nonsynonymous Sites in Mammalian Genomes     |
| P-224 | Jørgensen    | Frank Grønlund          | PDF | Causes of Temporal and Spatial Substitution Rate Variation in Mammals   |
| P-225 | Necsulea     | Anamaria                | GS  | Nucleotide substitution patterns in human microsatellites   |
| P-226 | Haggerty     | Leanne Sarah            | UG  | A Supertree Analysis of 27 Complete YESS Group Genomes  |
| P-227 | Brites       | Daniela Silva Henriques | GS  | The diversification of Dscam: the evolution of an extensively alternatively spliced gene used by the nervous and immune systems                           |
| P-228 | Gaidos       | Eric                    |     | Non-nuclear genomes in Placozoa: Big genomes for a small animal   |

## POSTER PRESENTATIONS (continued)

|       |                  |                |     |  |
|-------|------------------|----------------|-----|--|
| P-229 | Fawcett          | Jeffrey Andrew | GS  | Estimating the ages of ancient whole genome duplications in plants: is there a link between polyploidization and the Cretaceous-Tertiary extinction event? |
| P-230 | Moum             | Truls          |     | Mitochondrial genome variation in stronglycentrotid sea urchins  |
| P-231 | Wilke            | Claus O.       |     | Contact density affects protein evolutionary rate from bacteria to animals   |
| P-232 | Matz             | Mikhail        |     | How to study adaptive processes in non-model organisms at the whole-genome level   |
| P-234 | Lefebure         | Tristan        | PDF | Phylogenomic assessment of adaptation in <i>Streptococcus pyogenes</i> based on comparative analysis with its sister group <i>Streptococcus canis</i>      |
| P-235 | Woolfit          | Meg            | PDF | Horizontal gene transfer from mosquito to its endosymbiotic bacterium <i>Wolbachia pipientis</i>   |
| P-236 | Wang             | Shi            | PDF | Development of improved Diversity Arrays Technology (iDART) for whole-genome genotyping in non-model organisms   |
| P-237 | Byrnes           | Jake Kelly     | GS  | A Generalized Hidden Markov Model for the Comparative Analysis of Tiling Microarray Data   |
| P-238 | Niimura          | Yoshihito      |     | Similar numbers but different repertoires of olfactory receptor genes in humans and chimpanzees  |
| P-239 | Zhao             | Zhongming      |     | CpG island density, its correlations with genomic features in mammalian genomes and its implications for genome sequence evolution                         |
| P-240 | Vinkler          | Michal         | GS  | Structure and expression of TLR4 in zebra finch ( <i>Taeniopygia guttata</i> ), the first Toll-like receptor in passerine birds                            |
| P-241 | Oota             | Hiroki         |     | Are genes that are highly diversified between human populations also variable in the medaka populations?   |
| P-242 | Brawand          | David          | GS  | Detection and evolutionary analysis of ancient mammalian pseudogenes   |
| P-243 | Doucet Beupré    | Hélène         | GS  | Complete genomes for a complete story: male and female transmitted mitochondrial genome of <i>Pyganodon</i> (Bivalvia: Unionidae)                          |
| P-244 | Ledda            | Alice          | GS  | Patterns of conservation of human amino acid tandem repeats in vertebrate proteins   |
| P-245 | Patricio         | Mateus         | GS  | Pipeline for dynamic genetic code prediction   |
| P-246 | Eory             | Lel            | GS  | Selective constraint and the genomic deleterious mutation rate in hominids   |
| P-247 | Hayden           | Sara Orla      | GS  | Olfaction at the Molecular level: Trade-Offs between Echolocating and Non-Echolocating Bats  |
| P-248 | Cummins          | Carla Ann      | UG  | Phylogenetic Super-Network of $\alpha$ -Proteobacteria   |
| P-249 | Kuraku           | Shigehiro      |     | Timing of two-round (2R) genome duplications in early vertebrates  |
| P-250 | Suzuki           | Rumiko         | GS  | New kind of constraint for synonymous substitution in gene groups  |
| P-251 | González Knowles | David          | GS  | Origin of new human genes through exaptation of non-coding sequences   |
| P-252 | Mower            | Jeffrey P.     | PDF | Mitochondrial genome architecture in a plant with a highly accelerated substitution rate   |
| P-253 | Takahashi        | Mahoko         | GS  | Identification of non-coding regions conserved specifically in primates  |
| P-254 | Galiana-Arnoux   | Delphine       |     | Evolutionary dynamics of the SOX gene family in fish   |
| P-255 | Boehne           | Astrid         | GS  | Sexy evolution: A new type of vertebrate sex-determining gene candidate on the Y chromosome of the platyfish   |
| P-256 | Schultheis       | Christina      | PDF | Differential duplication, inactivation and loss of a gonad-specific gene on vertebrate sex chromosomes   |
| P-258 | Armisen          | David          | GS  | Evolution and specificities of unique genes in plants  |
| P-259 | Gissi            | Carmela        |     | High genome plasticity of ascidian mtDNA as exemplified by comparison of congeneric species  |
| P-260 | Gissi            | Carmela        |     | Mitochondrial genomics demonstrate the existence of two cryptic species in <i>Ciona intestinalis</i>   |
| P-261 | Lai              | Yu-Ting        | GS  | Compaction and deletional bias in the chloroplast genomes of Gnetophyta (gymnosperms)  |
| P-262 | Douzery          | Emmanuel       |     | Evolutionary dynamics and phylogenetic content of coding sequences in mammalian genomes  |
| P-263 | Urrutia          | Araxi O.       | PDF | Is linkage among negatively co expressed genes in yeast functionally relevant?   |
| P-264 | Denoeud          | France         |     | Genome sequence of <i>Oikopleura dioica</i> , an extremely fast evolving chordate  |
| P-265 | Gazave           | Elodie         | PDF | Copy Number Variation in the Great Apes  |
| P-266 | Krause           | Johannes       | GS  | Sequencing and analysis of a complete Neandertal mitochondrial genome  |
| P-267 | Wicke            | Susann         | GS  | Structure and evolution of the <i>trnL<sub>UUA</sub></i> -intron in Monilophytes   |

|       |               |               |     |  |
|-------|---------------|---------------|-----|--|
| P-268 | Lorenc        | Anna          | PDF | Within-species diversity and between-species differences in gene expression in two closely related species of <i>Mus</i>   |
| P-270 | Farré         | Marta         | GS  | Distribution of tandem repeats in the human genome and its evolutionary implications   |
| P-271 | Thiel         | Thomas        | GS  | Influence of gene copy number variation on candidate apomixis gene expression in hybrids of <i>Boecheera</i>   |
| P-272 | Larracuent    | Amanda Marie  | GS  | Translocation of the ancestral <i>Drosophila</i> Y chromosome to the dot chromosome in <i>D. pseudoobscura</i>   |
| P-274 | Donaher       | Natalie A.    | GS  | Pyrosequencing the A+T-rich nucleomorph genomes of the cryptophyte algae <i>Rhodomonas</i> sp. 1178 and <i>Cryptomonas paramecium</i> : insight into the pattern and process of nuclear genome reduction |
| P-275 | Ruiz Trillo   | Iñaki         |     | The origin of metazoan multicellularity: a comparative genomics approach   |
| P-276 | Archibald     | John M.       |     | Endosymbiotic gene transfer and genome evolution in nucleomorph-containing microalgae  |
| P-277 | Dean          | Matthew David | PDF | Proteomic analyses reveal signatures of adaptive evolution in male accessory proteins in house mice ( <i>Mus</i> )   |
| P-278 | Betran        | Esther        |     | Recurrent recruitment of retrogenes involved in nuclear transport in <i>Drosophila</i>   |
| P-279 | Carson        | Andrew R.     | GS  | Identification of Duplicated Genes that have Undergone Concerted Evolution in Multiple Mammalian Lineages  |
| P-280 | Assis         | Raquel        | GS  | Increasing organizational complexity of metazoan genomes   |
| P-281 | Pérez-Bercoff | Ása           | GS  | The molecular mechanisms of genome rearrangements in primates  |
| P-282 | Zhang         | Jianzhi       |     | Null mutations in human and mouse orthologs frequently result in different phenotypes  |
| P-283 | Fonseca       | Miguel M.     | GS  | Inverted replication of vertebrate mitochondria  |
| P-284 | Makino        | Takashi T.    | PDF | Interacting Gene Clusters and the Evolution of the Vertebrate Immune System  |
| P-285 | Ardell        | David H.      |     | tRNA Identity Element Divergence between Proteobacteria and Cyanobacteria  |
| P-286 | Kelley        | Joanna L.     | GS  | Evolution and functional diversification of antifreeze proteins in the Antarctic fish <i>Lycodichthys dearborni</i>  |
| P-287 | Lavrov        | Dennis V.     |     | An alternative evolution of animal mitochondrial DNA - insights from a comparative analysis of 22 demosponge mitochondrial genomes   |
| P-289 | Emerson       | J.J.          | PDF | Copy number detection at a basepair resolution using comparative genomics  |
| P-290 | Gojobori      | Takashi       |     | An Evolutionary Study of Nervous System by Comparative Gene Expressomics   |
| P-291 | Ogura-Noda    | Akiko         | PDF | The origins and innovative events of the tissues coincide with evolutionary origins of human tissue-specific genes   |
| P-292 | Frank         | Carolin       |     | Integration of killer plasmids and killer viruses in yeast genomes   |
| P-293 | Bakewell      | Margaret A.   | GS  | Comparative genomic analysis of positive selection in fungi, insects and mammals   |
| P-294 | Prachumwat    | Anuphap       | PDF | Gene number expansion and contraction in vertebrate genomes with respect to invertebrate genomes   |
| P-295 | Huang         | Yao-Ting      |     | A comparative study of human and mouse haplotype maps  |
| P-296 | Stapley       | Jessica       | PDF | A linkage map of the zebra finch <i>Taeniopygia guttata</i> provides new insights into avian genome evolution  |
| P-297 | Bratke        | Kirsten       | GS  | Phyletic patterns of poxvirus proteins   |
| P-298 | Gotzek        | Dietrich Axel | PDF | Preliminary analysis of odorant binding proteins in <i>Solenopsis invicta</i>  |
| P-299 | García        | Juan Antonio  | GS  | Ecophysiological Significance of Scale-Dependent Patterns in Prokaryotic Genomes Unveiled by Combination of Statistic and Genometric Analyses  |

#### EVOLUTIONARY GENOMICS OF HUMAN AND PATHOGEN INTERACTIONS (S11)

|       |                 |            |     |   |
|-------|-----------------|------------|-----|---|
| P-300 | Wilder          | Jason A.   |     | Molecular Evolution of GYPC: Strong Natural Selection and Pervasive Structural Alteration at a Malaria Resistance Locus                       |
| P-301 | Ferrer Admetlla | Anna       | GS  | Worldwide variation in glycosylation genes  |
| P-302 | Gray            | Rebecca R. | GS  | HIV-1 Evolutionary and Population Dynamics are Predictors of Progression to AIDS  |
| P-303 | Gophna          | Uri        |     | The contribution of lateral gene transfer and convergent evolution to the emergence of eukaryotic like genes in <i>Legionella pneumophila</i> |
| P-304 | Gerrard         | Dave T.    | PDF | Primate CEACAM3: 25 Million Years on the front line against bacterial attack  |
| P-305 | Sikora          | Martin     | GS  | Genetic susceptibility to placental malaria infection: An integrated approach combining evolutionary analysis and case-control studies        |
| P-306 | Piontkivska     | Helen      |     | Evolution of quorum-sensing system in <i>Burkholderia</i> and adaptive diversification  |

## POSTER PRESENTATIONS (continued)

|       |           |                       |     |   |
|-------|-----------|-----------------------|-----|---|
| P-307 | Bravo     | Ignacio González      |     | Evolution of antiretroviral APOBEC3 proteins: gene duplication, gene loss and subfunctionalisation events |
| P-308 | Pereira   | Susana Rodrigues      | PDF | The evolutionary dynamics of the protein phosphatases in the Metazoan                                     |
| P-309 | Shah      | Seena                 | GS  | Elucidating the mechanisms of papillomavirus evolution  |
| P-310 | Burstein  | David                 | GS  | Predicting secreted virulent proteins based on evolutionary signatures                                    |
| P-311 | Keebler   | Jonathan Edward Myers | GS  | Inferring the demographic history of <i>Plasmodium falciparum</i>   |
| P-313 | Francis   | Jedidiah Eli          | GS  | A model-based approach for mapping associations between human HLA genotype and HIV evolution              |
| P-314 | Knight    | Rob                   |     | Evolution of the human gut microbiome   |
| P-315 | Boissinot | Stéphane              |     | Long-term balancing selection at the anti-viral OAS1 gene in chimpanzees                                  |

### EVOLUTIONARY RADIATIONS AND MOLECULAR PHYLOGENY (S2)

|       |                    |                        |     |  |
|-------|--------------------|------------------------|-----|--|
| P-316 | Feulner            | Philine Gabriele Doris | PDF | Electric signalling facilitates reproductive isolation in an adaptive radiation of African weakly electric fish (genus: <i>Campylomormyrus</i> )                 |
| P-317 | Shitenberg         | Amir                   | GS  | Recurrent horizontal gene transfer in the mitochondrial genome of Tetillid sponges (order Spiroborida)   |
| P-318 | Belinky            | Frida                  | GS  | Indel Analysis Supports Ecdysozoa and a Basal Position of Porifera   |
| P-319 | Bon                | Céline                 | UG  | The mitochondrial genome of the extinct cave bear  |
| P-320 | Emadzade           | Khatere                | GS  | Phylogenetic Relationships, Evolution and Biogeography of <i>Ranunculus</i> (Ranunculaceae) in the Northern Hemisphere   |
| P-321 | Zaldivar-Riverón   | Alejandro              | PDF | Evolution of the parasitic wasp subfamily Rogadinae (Braconidae): phylogeny and evolution of lepidopteran host ranges and mummification                          |
| P-322 | Burki              | Fabien                 | GS  | Phylogenomics reveals a new "megagroup" of photosynthetic eukaryotes   |
| P-323 | Mayer              | Werner Eugen           |     | Phylogeny of the nematode genus <i>Pristionchus</i> (Family Diplogastridae) and implications for biodiversity, biogeography and the evolution of hermaphroditism |
| P-324 | Weinert            | Lucy                   | GS  | Phylogeny, life history evolution and recombination in intracellular <i>Rickettsia</i> bacteria  |
| P-325 | Espegueira Themudo | Gonçalo                | GS  | Resolving a rapid radiation of newts: A boost from multiple nuclear markers  |
| P-326 | Coucheron          | Dag H.                 |     | Molecular evolution of mitochondrial encoded protein genes and proteins in Gadidae   |
| P-327 | Marcet-Houben      | Marina                 | GS  | The tree versus the forest: the fungal tree of life and the topological diversity within the yeast phylome   |
| P-328 | Blösch             | Cordula                | GS  | Phylogeny and chromosomal evolution of the genus <i>Melampodium</i>  |
| P-329 | Lang               | B. Franz               |     | Monophyly of primary photosynthetic eukaryotes from a mitochondrial and plastid genome perspective   |
| P-330 | Mcgowen            | Michael R.             | GS  | The Vestigial Olfactory Receptor Subgenome of Odontocete Whales: Pseudogenes in Phylogenetic Reconstruction  |
| P-331 | Fondi              | Marco                  | GS  | The origin of phenylpropanoid metabolism: the evolutionary puzzle of phenylalanine ammonia lyase   |
| P-332 | Ornelas García     | Claudia Patricia       | GS  | Lineage turnover and radiation in the characid fish genus <i>Astyanax</i> (Baird and Girard, 1854) from Mesoamerica  |
| P-333 | Pedraza            | Carlos                 | GS  | Molecular Phylogeny of the crayfish subfamily Cambarellinae (Decapoda:Cambaridae) from North America   |
| P-334 | Ayoub              | Nadia Antoine          | PDF | Evolutionary implications of gene duplication in the diversification of spider silks   |
| P-335 | Muschick           | Moritz                 | GS  | Parallelism in pharyngeal jaws of cichlid fishes from Lake Tanganyika, East Africa   |
| P-336 | Nevado             | Bruno                  | GS  | Are the evolutionary origins of two lamprologine cichlid species ( <i>Lamprologus callipterus</i> and <i>Neolamprologus fasciatus</i> ) connected?               |
| P-337 | Poux               | Céline                 | PDF | Towards a comprehensive molecular phylogeny of the endemic cottoid species flock from Lake Baikal (Siberia)  |
| P-338 | Rea                | Alethea Mary           | GS  | NeighborNets the statistical way   |
| P-339 | Markova            | Michaela               | GS  | The GISH method used in plant phylogenetics  |
| P-340 | Ebersberger        | Ingo                   | PDF | An EST-based Phylogeny of Eukaryotes   |
| P-341 | Holton             | Therese Anne           | GS  | Genome-wide investigations in the phylogeny of animals   |
| P-342 | Bechsgaard         | Jesper                 | PDF | Extensive intergeneric trans-specific polymorphism and evolution of sporophytic self-incompatibility specificities   |

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|-------|------------------|---------------------------|-----|--|
| P-343 | Cabezas Padilla  | Patricia                  | GS  | A phylogenetic and phylogeographic approach of the genus <i>Paramunida</i> (Galatheidae, Crustacea, Decapoda) in the Indo-Pacific Oceans   |
| P-344 | Marinho          | Marco Antonio Tonus       | GS  | Evaluation of the internal transcribed spacer 2 (ITS2) as a molecular marker for phylogenetic inference using sequence and secondary structure information: an example for the myiasis-causing flies of the Calliphoridae family (Diptera: Brachycera) |
| P-345 | Rota-Stabelli    | Omar                      | GS  | A perfect polytomy in the tree of life (?)   |
| P-346 | Gribaldo         | Simonetta                 |     | Mesophilic crenarchaeota: proposal for a third archaeal phylum, the Thaumarchaeota   |
| P-347 | Desmond          | Elie                      | UG  | Evolution of the mitochondrial ribosomal proteome  |
| P-348 | Thomas           | Jessica A.                | GS  | The Palaeoptera problem: Resolving deep splits in the winged insects   |
| P-350 | Hidalgo          | Amparo                    | GS  | Early Miocene origin of species, and Pleistocene origin of phylogeographic variation, in West Mediterranean Hydrochidae water beetles  |
| P-351 | Morgan           | Katy J.                   | GS  | Pleistocene radiation of the forest-dependent <i>Leucosphyrus</i> group of <i>Anopheles</i> mosquitoes across Southeast Asia   |
| P-352 | Simon            | Sabrina                   | GS  | New markers and bioinformatics tools to reconstruct the phylogeny of winged insects (Pterygota)  |
| P-353 | Elias            | Marianne                  | PDF | Mimicry, community ecology and adaptive diversification of butterflies   |
| P-354 | Soria-Carrasco   | Víctor                    | GS  | Rates and patterns of mammalian species diversification using molecular phylogenies  |
| P-355 | Chaw             | Shu-Miaw                  |     | Evolution of Pinaceous chloroplast genomes (cpDNAs) and insights into the phylogenetic positions of the genus <i>Cedrus</i>  |
| P-356 | Pérez-Losada     | Marcos                    |     | The Tempo and Mode of Barnacle Evolution   |
| P-357 | Delsuc           | Frédéric                  |     | More data and better models provide further evidence than tunicates are the closest living relatives of vertebrates  |
| P-358 | Igea             | Javier                    | GS  | Fast evolving introns to study the phylogeny of closely related mammalian species  |
| P-359 | Teeling          | Emma Caroline             |     | Molecular Phylogenetics informs Bat Biogeographic Origins and the Missing Fossil Record  |
| P-360 | Russo            | Claudia Augusta De Moraes |     | Molecular phylogeny, divergence times and the invasion of freshwater environments by ancestral marine lineages of Gobioidaei   |
| P-361 | Voloch           | Carolina Moreira          | GS  | Hoatzin's place among the Birds  |
| P-362 | Junqueira        | Ana Carolina Martins      | GS  | Mitochondrial genomics and phylogenetic inferences with single genes and concatenated sequences in Diptera order   |
| P-363 | Musilová         | Zuzana                    | GS  | Incongruence in phylogenetic signals - real conflict or just insufficient data?  |
| P-364 | Álvarez Álvarez  | Raquel                    | GS  | Phylogeographic analysis of mitochondrial DNA variation in two sympatric vitrinid semislugs of Tenerife (Canary Islands)   |
| P-365 | Parent           | Christine                 | GS  | Intraspecific phenotypic variation in <i>Bulimulus reibischi</i> parallels the adaptive radiation of Galapagos endemic bulimulid land snails   |
| P-366 | Macías-Hernández | Nuria                     | GS  | The phylogeographic and demographic basis of among-lineage variation in diversification rates in woodlouse-hunter spiders <i>Dysdera</i> from the Canary Islands   |
| P-367 | Nasrallah        | Chris A.                  | GS  | Quantifying the impact of nonindependent evolution among sites on phylogenetic analyses  |
| P-368 | Joy              | Jeffrey B.                | GS  | Historical gene flow during intra-host adaptive radiation of gall-inducing insects   |
| P-369 | Townsend         | Jeffrey Peter             |     | A theoretical framework for assessing power to resolve polytomies in molecular phylogenetics   |
| P-370 | López-Giraldez   | Francesc                  | PDF | Profiling phylogenetic information content of genes across time: fungal phylogeny  |
| P-371 | Rubio De Casas   | Rafael                    | PDF | Drifting away: molecular and morphological evolution in <i>Cakile</i> (Brassicaceae)   |
| P-372 | Prasad           | Arjun B.                  | GS  | Using Large Comparative Genomic Sequence Datasets to Refine the Mammalian Phylogeny  |
| P-373 | Paps Montserrat  | Jordi                     | GS  | The radiation of the Bilateria: a novel tree using a multigenic approach and a comprehensive taxon sampling  |
| P-375 | López Pancorbo   | Alberto                   | GS  | Tracking the origin and distribution of mediterranean nesticids (Arachnida: Araneae)   |
| P-376 | Montgelard       | Claudine                  |     | Fast-evolving positions and multigene phylogeny of Rodentia  |

## GENETICS AND MOLECULAR BIOLOGY OF SPECIATION (S18)

|       |           |                   |     |  |
|-------|-----------|-------------------|-----|--|
| P-377 | Becquet   | Céline            | GS  | Learning about modes of speciation by computational approaches |
| P-379 | Stemshorn | Kathryn Christina | PDF | The Genomic Make-Up of a Hybrid Fish Species                   |

## POSTER PRESENTATIONS (continued)

|       |                    |                     |     |   |
|-------|--------------------|---------------------|-----|---|
| P-380 | Lexer              | Christian           |     | The genetic architecture of barriers to gene flow within and between European species of <i>Populus</i>   |
| P-381 | Macholan           | Milos               |     | Genetic Conflict Outweighs Heterogametic Incompatibility in the Mouse Hybrid Zone?  |
| P-383 | Geraldes           | Armando             | PDF | Patterns of polymorphism and divergence among three species of house mice at autosomal, X-linked, Y-linked and mitochondrial genes  |
| P-384 | Chang              | Audrey S.           | GS  | Epistasis modifies dominance of loci causing hybrid male sterility  |
| P-385 | Aboim              | Maria Ana           | PDF | Introgressive hybridization between two Iberian endemic Cyprinidae species <i>Pseudochondrostoma duriense</i> and <i>Achondrostoma oligolepis</i> : a comparison between two independent hybrid zones |
| P-386 | Fierst             | Janna L.            | GS  | Genetic Architecture in Reproductive Isolation  |
| P-388 | Leppälä            | Johanna             | GS  | Mapping speciation genes in <i>Arabidopsis lyrata</i>   |
| P-389 | Legrand            | Delphine            | GS  | Divergent populations of <i>Drosophila mauritiana</i> - incipient speciation in the melanogaster subgroup   |
| P-390 | Da Lage            | Jean-Luc            |     | Ecological adaptation retraced by molecular changes in Odorant Binding Proteins (OBP) in the <i>Drosophila simulans</i> complex   |
| P-391 | Agorreta           | Ainhoa              | GS  | Phylogenetic relationship of the genus <i>Heterandria</i> (Poeciliidae: Osteichthyes) in Mesoamerica based on mitochondrial and nuclear genes   |
| P-393 | Mavarez            | Jesús A.            | PDF | Ecological divergence drives disruption of gene expression in hybrids between two sympatric populations of Brook Trout ( <i>Salvelinus fontinalis</i> )   |
| P-394 | Milana             | Valentina           | GS  | Differential distribution of an intergenic spacer in <i>Atherina boyeri</i> mtDNA   |
| P-395 | Barluenga          | Marta               | PDF | Parallel evolution in Nicaraguan crater lake cichlids   |
| P-396 | Fukova             | Iva                 | PDF | Comparative molecular cytogenetics: extending the toolkit for evolutionary studies  |
| P-397 | Muenzel            | Frauke Maria        | GS  | A single nucleotide polymorphism (SNP) assay for East African cichlid fishes: development and application   |
| P-398 | Sans-Fuentes       | Maria Assumpció     | PDF | Patterns of genetic variation at male reproductive genes in house mouse   |
| P-399 | Toups              | Melissa Anne        | GS  | Are head lice and clothing lice genetically distinct? A coalescent approach   |
| P-400 | Springer           | Stevan A.           | GS  | Extraordinary intra-specific diversity in oyster sperm bindin   |
| P-401 | Scavetta           | Rick Joey           | GS  | Novel and Unexpected Destabilization of Structural Genome Variation in Hybrid <i>Mus Musculus</i> ssp. Individuals  |
| P-402 | Semina             | Alisa V.            | GS  | Homoploid Hybrid Speciation: A New Cyprinid Species in the Northwest Pacific Marginal Sea   |
| P-403 | Carneiro           | Miguel Jorge Pinto  | GS  | Divergence with gene flow between parapatric subspecies of the European rabbit: Multilocus analysis of nucleotide variation shows striking contrasts between centromeric and telomeric loci           |
| P-404 | Martínez-Fernández | Mónica              | GS  | Differential gene expression in two sympatric ecotypes of <i>Littorina saxatilis</i> by transcriptomics and proteomics  |
| P-405 | Vyskocilova        | Martina             | GS  | The role of MHC in sexual selection in European bitterling ( <i>Rhodeus amarus</i> )  |
| P-406 | Cizkova            | Dagmar              | GS  | Genetic structuring at two MHC genes in two subspecies of the house mouse   |
| P-407 | Vekemans           | Xavier              |     | Repeated adaptive introgression at a gene under multiallelic balancing selection  |
| P-408 | Delneri            | Daniela             |     | Fitness profiling of yeast natural isolates: identifying negative epistatic interactions using microarrays  |
| P-409 | Vilà               | Carles              |     | Hybridization Between European Quail ( <i>Coturnix coturnix</i> ) and Released Japanese Quail ( <i>Coturnix japonica</i> )  |
| P-410 | Cooper             | Elizabeth Armstrong | GS  | Genetic variation at nuclear loci fails to distinguish two morphologically distinct species of <i>Aquilegia</i>   |
| P-411 | Cunha Almeida      | Francisca           | PDF | Molecular evolution of accessory gland protein (Acp) genes and divergence in a case of incipient speciation   |
| P-412 | Bailey             | Richard Ian         | PDF | Gene networks involved in sexual isolation between Zimbabwean and Cosmopolitan races of <i>Drosophila melanogaster</i>  |
| P-413 | Puechmaile         | Sebastien           | GS  | Does sensory ecology drive speciation?  |

### GENOME VARIATION: LESSONS FROM THE HUMAN GENOMES (S19)

|       |                |          |     |   |
|-------|----------------|----------|-----|---|
| P-414 | Duret          | Laurent  |     | The Impact of Recombination on Nucleotide Substitutions in the Human Genome |
| P-415 | Coghlan        | Avril L. | PDF | Factors determining triplet repeat instability in the human population      |
| P-416 | Gallego Romero | Irene    | GS  | Ascertainment Bias in Genome-Wide Studies of Human Populations              |
| P-417 | Cruz Rodríguez | Fernando | PDF | Identification of Balancing Selection in the Human Genome                   |

|       |            |             |     |   |
|-------|------------|-------------|-----|---|
| P-418 | Przeworski | Molly       |     | Constraints on broad-scale recombination rates in humans  |
| P-419 | Scott      | Nicole M.   | GS  | A test that two individuals are from the same Hardy Weinberg Equilibrium (HWE) population   |
| P-420 | Sjödín     | Per         | PDF | Increased efficacy of selection against deletions in the hominan lineage  |
| P-421 | Loire      | Etienne     | GS  | Hypermutable genes in Homo sapiens  |
| P-422 | Martínez   | Urko        | GS  | The effect of population genetic differentiation on the replicability of association studies  |
| P-423 | Verdu      | Paul        | GS  | History and sociocultural barriers structure the autosomal genetic diversity of Central African Pygmies.                            |
| P-424 | Kim        | Hielim      | GS  | Darwinian evolution of <i>ASAH1</i> gene associated with mental activity in modern humans   |
| P-425 | Ohshima    | Kazuhiko    |     | Possible selective pressure for an exon-shuffled gene, PIPSL, in human population   |
| P-426 | Fuselli    | Silvia      |     | Evolution of detoxifying systems: the role of environment and population history in shaping genetic diversity at human CYP2D6 locus |
| P-427 | Colonna    | Vincenza    | PDF | Validating inference of human population structure using genealogical information   |
| P-428 | Wall       | Jeffrey D.  |     | Evidence of ancient admixture in multiple human populations   |
| P-429 | Lohmueller | Kirk Edward | GS  | Effects of demographic history on the distribution of deleterious SNPs in human populations   |
| P-430 | Lorente    | Belén       | GS  | SYSNPs (Select Your SNPs): a web tool for automatic/massive SNP selection   |

#### GENOMIC EVIDENCE FOR NATURAL SELECTION AND IMPLICATIONS (S7)

|       |                  |                 |     |  |
|-------|------------------|-----------------|-----|--|
| P-431 | Oleksyk          | Taras K.        |     | Evolution and worldwide distribution of <i>APOL1</i> , <i>APOL2</i> , <i>APOL3</i> , <i>APOL4</i> and <i>MYH9</i> in human populations |
| P-432 | Moreno Estrada   | Andres          | GS  | Interrogating fast evolving genes for signatures of local positive selection in worldwide human populations                            |
| P-433 | Boitard          | Simon           |     | Detection of selective sweeps using Hidden Markov Models   |
| P-434 | Li               | Haipeng         |     | Recent Positive Selection Enriched in Regions near Brain-related Genes in the Human Lineage  |
| P-435 | Drummond         | David Allan     | PDF | Pervasive natural selection for translational accuracy   |
| P-436 | Zaldivar-Riverón | Alejandro       | PDF | Evolutionary genetics of adaptation to hypersalinity in the brine shrimp <i>Artemia</i> (Crustacea)                                    |
| P-437 | Andolfatto       | Peter           |     | Signatures of positive selection in coding and noncoding DNA in <i>Drosophila</i>  |
| P-438 | Caballero        | Armando         |     | Efficiency of the DFDIST software in detecting selective loci using AFLP markers   |
| P-439 | Vieira           | Cristina P.     |     | Recombination at Prunus S-locus region SLFL1 gene  |
| P-440 | Ferreira         | Zélia           | GS  | Searching for evidences of natural selection on the human WFDC cluster located in the 20q13 region                                     |
| P-441 | Ivanova          | Nevyana Ivanova | PDF | Loss and gain of gene function in human SERPINB11  |
| P-443 | Fernando         | Olga            | GS  | Introns as neutrally evolving sequences: How far?  |
| P-444 | Chevin           | Luis-Miguel     | GS  | Molecular signature of two interfering selective sweeps  |
| P-445 | Studer           | Romain          | GS  | Pervasive positive selection on duplicated and non duplicated vertebrate protein coding genes  |
| P-446 | Amills           | Marcel          |     | Evolutionary analysis of the mammalian major histocompatibility complex class II DQA and DQB genes                                     |
| P-447 | Corbi            | Jonathan        | GS  | Molecular evolution of AGPase multigenic family in Angiosperms   |
| P-448 | Coll             | Marta           | GS  | Directional selection in <i>Fagus sylvatica</i> in response to temperature changes over geographical gradients                         |
| P-449 | Promerova        | Marta           | GS  | The role of MHC Class I in mate choice in a socially monogamous songbird, the Scarlet Rosefinch ( <i>Carpodacus erythrinus</i> )       |
| P-451 | Zivkovic         | Daniel          | GS  | Second order moments of segregating sites under variable population size   |
| P-453 | Vieira Chelo     | Ivo Manuel      | PDF | Reverse evolution reveals natural selection on standing genetic variation  |
| P-454 | Oleksyk          | Taras K.        |     | Identifying selected regions from heterozygosity and divergence using a light-coverage genomic dataset from two human populations      |
| P-455 | Glemin           | Sylvain GM      |     | Interaction between selection and biased gene conversion: consequences for recombining genomes and mating system evolution             |
| P-456 | Kaiser           | Vera Barbara    | GS  | Hill-Robertson interference among strongly selected sites reduces their effects on linked neutral sites                                |

## POSTER PRESENTATIONS (continued)

|       |                 |                          |     |  |
|-------|-----------------|--------------------------|-----|--|
| P-457 | Vitalis         | Renaud                   |     | A MCMC-based approach for detecting and measuring selection from gene frequency data   |
| P-458 | Fares           | Mario Ali                |     | Different Fates Different Rates: Three-dimensionality of Mutational dynamics   |
| P-459 | Thornton        | Kevin Richard            |     | Deleterious mutations, the McDonald-Kreitman test, and inferring adaptive evolution in <i>Drosophila</i>   |
| P-460 | Lobell          | Amanda S.                | GS  | Molecular evolution of placental invasion in primates  |
| P-461 | Hanada          | Kousuke                  | PDF | Different level of genetic redundancy throughout duplicated genes among various phenotypes in <i>Arabidopsis thaliana</i>  |
| P-462 | Tsaur           | Shun-Chern               |     | Adaptive protein evolution drives functional diversification of fatty acid desaturases in <i>Drosophila</i>  |
| P-463 | Ramírez-Soriano | Anna                     | GS  | Correcting Estimators of theta and Tajima's D for ascertainment biases caused by the SNP discovery process   |
| P-464 | Kondo           | Rumi                     |     | Evolution of <i>Drosophila</i> gustatory receptor gene family  |
| P-465 | Innan           | Hideki                   |     | Signature of neofunctionalization of duplicated genes under the pressure of gene conversion  |
| P-466 | Vetter          | Monika Madlen            | GS  | Life history influences the evolution of FLS2 immunity   |
| P-467 | Archetti        | Marco                    | PDF | Synonymous codon usage bias as an adaptation to minimize errors at the protein level   |
| P-468 | Lazzaro         | Brian P.                 |     | Population genetics of the APL1 malaria resistance gene cluster of <i>Anopheles gambiae</i>  |
| P-469 | Nygaard         | Sanne                    | GS  | Selective Constraint in the Small and Compact Genomes of Malaria Parasites ( <i>Plasmodium sp.</i> )   |
| P-470 | Pauwels         | Maxime                   | PDF | How large is the genomic region linked to the self-incompatibility locus in <i>Arabidopsis halleri</i> ?   |
| P-471 | Alves           | Isabel María             | GS  | Patterns of microsatellite variation within Kit Ligand (KITLG) and Tyrosinase Related Protein-1 (TYRP1) genes and the evolutionary history of skin pigmentation in human populations |
| P-472 | Foll            | Matthieu                 | PDF | A genome scan method to identify selected loci appropriate for both dominant and codominant markers: A Bayesian perspective  |
| P-474 | Higgs           | Paul                     |     | Coevolution of Codon Usage and tRNA Gene Content in Bacterial Genomes  |
| P-475 | Higgs           | Paul                     |     | Codon Usage in Mitochondrial Genomes: Distinguishing Context-Dependent Mutation from Translational Selection   |
| P-476 | Allen           | Julie                    | GS  | Dramatic Decrease in Substitution Rates Over Time in Obligate Endosymbionts: the role of selection in tempering Muller's Ratchet   |
| P-477 | Innocenti       | Paolo                    | GS  | Effects of mating on gene expression patterns in fruitflies: evidence for natural and sexually antagonistic selection  |
| P-478 | Williams        | Larissa Moriarty         | GS  | Genome-wide scan in a non-model species using 454 pyrosequencing   |
| P-479 | Poncet          | Bénédicte Nelly          | GS  | New insights in local adaptation study using genome scan: application to the alpine plant <i>Arabidopsis alpina</i>  |
| P-480 | Campbell        | Michael Colin            | PDF | Patterns of Genetic Diversity at TAS2R38, a Bitter-Taste Receptor Gene, in Diverse African Populations from Cameroon and Kenya   |
| P-481 | Pereira-Leal    | Jose B.                  |     | Detecting selective gene loss in intracellular pathogens   |
| P-482 | Jones           | Felicity Clare           | PDF | Genomic evidence for repeated adaptation in threespine sticklebacks from signatures of selection and hybrid zone studies   |
| P-483 | Simões          | Pedro Miguel             | PDF | Temporal Genetic Changes During Laboratory Evolution in <i>Drosophila subobscura</i>   |
| P-484 | Kosiol          | Carolin                  | PDF | The dynamics of positive selection on the mammalian tree   |
| P-485 | Oleksiak        | Marjorie Frances         |     | Genomic Analyses of Individual Variation   |
| P-486 | Sánchez-Donoso  | Inés                     | GS  | Genetical aspects of the mating behaviour in the Common quail ( <i>Coturnix coturnix</i> )   |
| P-487 | Dickins         | Benjamin James Alexander | PDF | Sifting genetic change: fine-grained analysis of selective sweeps in a bacteriophage   |
| P-488 | Kim             | Yuseob                   |     | Population genetic signature of recent adaptive niche expansion  |
| P-489 | Da Fonseca      | Rute R.                  | GS  | Molecular evolution of mammalian glutathione transferases: the alpha family  |
| P-490 | Santos          | Josiane Miranda Sales    | GS  | Are changes in laboratory adaptation driven by temporal genetic variation?   |
| P-492 | Mallick         | Swapan                   |     | Stringent multiple sequence alignment to avoid false-positives in genome-wide scans for selection  |
| P-493 | Tomasco         | Ivanna H.                | GS  | Positive Darwinian selection at mitochondrial DNA genes associated to the invasion of the subterranean niche in caviomorph rodents   |

|       |           |                  |     |  |
|-------|-----------|------------------|-----|--|
| P-494 | Toomajian | Christopher      | PDF | Genome-wide patterns of recombination in <i>Arabidopsis thaliana</i> and their impact on the efficacy on natural selection |
| P-495 | Wheat     | Christopher West | PDF | Functional Genomics of Dispersal: developing and using molecular tools in an ecological model system                       |
| P-497 | Mano      | Shuhe            |     | Ancestral process and diffusion model with selection   |
| P-498 | Tsaur     | Shun-Chern       |     | Molecular Adaptation of the <i>Drosophila simulans</i> clade   |
| P-499 | Kondo     | Rumi             |     | Tempo and mode of evolution in <i>Drosophila</i> gustatory receptor gene family  |
| P-500 | Bazin     | Eric             | PDF | Quantifying levels of adaptive divergence between populations from frequency data  |

### GENOMICS FOR CROP EVOLUTION AND IMPROVEMENT (S22)

|       |            |            |     |   |
|-------|------------|------------|-----|---|
| P-501 | Manicacci  | Domenica   |     | Epistatic interaction between the transcription activator <i>Opaque2</i> and its target <i>CyPPDK</i> associated with grain filling traits in maize |
| P-502 | Aranzana   | María José | PDF | DNA Sequence Variability in Peach ( <i>Prunus persica</i> (L) Batsch) Commercial Varieties  |
| P-503 | Rubinstein | Samara     | PDF | The Molecular Origins of Basmati Rice   |
| P-504 | Talianova  | Martina    | GS  | Analysis of the efficacy of selection in <i>Silene</i> species with different breeding systems and its implication for the evolution of dioecy      |

### MODELS OF GENOME EVOLUTION AND PHYLOGENOMICS (S13)

|       |                   |                       |     |  |
|-------|-------------------|-----------------------|-----|--|
| P-505 | Tsai              | Isheng Jason          | GS  | Practical uses of estimating population recombination rates: quantifying the life cycle of wild yeast <i>Saccharomyces paradoxus</i> and its effect in yeast evolution |
| P-506 | Bakker            | Freek T.              |     | DNA sequence evolution in fast evolving mitochondrial DNA in Geraniaceae and Plantaginaceae  |
| P-507 | Aguileta          | Gabriela              | PDF | Assessing the Performance of Single-Copy Genes for Recovering Robust Phylogenies: fungal genomes as case study   |
| P-508 | Roettger          | Mayo                  | GS  | Inference of lateral gene transfer from phylogenetic trees is sensitive to size and evolutionary rate of the protein family  |
| P-510 | Svinti            | Victoria              | GS  | A Phylogenetic Approach to Detecting Reassortment in Influenza Viruses   |
| P-511 | Rusin             | Leonid                |     | Phylogenomic pipeline and construction of a multi-gene dataset for Metazoa   |
| P-512 | Shavit Grievink   | Liat                  | GS  | Lineage specific sequence evolution  |
| P-513 | Scofield          | Douglas Glen          | PDF | Evolution of DNA repair mechanisms in plants: are there consequences of meristematic growth?   |
| P-514 | Pankova           | Victoria Vladimirovna | PDF | Boring - non-boring - so boring! Whether two life styles can be realized by one polychaete species (Annelida, Spionidae)   |
| P-515 | Kassahn           | Karin Sonja           | PDF | Retention and functional divergence of duplicate gene loci following whole-genome duplication in teleost fishes  |
| P-516 | Fernández-Sánchez | Jesús                 | PDF | Performance of a new invariants method for phylogenetic reconstruction   |
| P-517 | Bernardi          | Giorgio               |     | The neo-selectionist theory of genome evolution  |
| P-518 | Sella             | Guy                   |     | A Theoretical Upper Bound on the Number of Genes in the Genome   |
| P-519 | Teruel            | María                 | GS  | Non-concerted ITS evolution among X and B chromosomes of the grasshopper <i>Eyprepocnemis plorans</i>  |
| P-520 | Bedford           | Trevor B.C.           | GS  | Mutational robustness stabilizes protein evolution in yeast, <i>Drosophila</i> and mammals   |
| P-521 | Roure             | Béatrice              | GS  | Qualitative heterogeneity in the evolutionary process and its impact on the phylogenetic inference   |
| P-522 | Hallsworth        | Christopher Andrew    | GS  | Approximate Genealogical Inference   |
| P-523 | Weissman          | Daniel Benjamin       | GS  | The Dynamics of Crossing Fitness Valleys   |
| P-524 | Zhang             | Zhang                 | PDF | Maximum-Likelihood Estimation of Substitution Heterogeneity through Clustering   |
| P-525 | Dean              | Jed                   | PDF | Pervasive and Persistent Redundancy among Duplicated Genes in Yeast  |
| P-526 | Allman            | Elizabeth S.          |     | Identifiability of covarion models of sequence evolution   |

### MOLECULAR AND EVOLUTIONARY EPIDEMIOLOGY (S16)

|       |         |             |     |  |
|-------|---------|-------------|-----|--|
| P-527 | Dennehy | John Joseph |     | The Peer Pressure of Sex: Greater Clonal Diversity in Clonally-Evolved Populations |
| P-528 | Lao     | Oscar       | PDF | In silico genome-wide association mapping of complex traits                        |
| P-529 | Alda    | Fernando    | GS  | Evolutionary history of rabbit haemorrhagic disease virus in Spain                 |

## POSTER PRESENTATIONS (continued)

|       |                |                 |     |   |
|-------|----------------|-----------------|-----|---|
| P-530 | Laayouni       | Hafid           | PDF | Stratification bias in association studies involving the Spanish population                         |
| P-531 | Wilbur         | Alicia K.       | PDF | Mycobacterial Disease in the Pre-Columbian New and Old Worlds: A Paleoepidemiological Analysis      |
| P-533 | Kolokotronis   | Sergios-Orestis | GS  | Molecular evolutionary dynamics of elephant tuberculosis  |
| P-534 | Piccinali      | Romina Valeria  | PDF | Lack of gene flow between peridomestic and sylvatic <i>Triatoma infestans</i> from Chaco, Argentina |
| P-535 | López Labrador | Xavier          |     | Molecular epidemiology of hepatitis c virus NS3/4A protease polymorphisms in worldwide isolates     |
| P-536 | Oleksyk        | Taras K.        |     | Genome wide admixture mapping identifies a major effect risk gene for renal disease                 |

### MOLECULAR PHYLOGEOGRAPHY AND POPULATION GENETICS (S17)

|       |                  |                           |     |   |
|-------|------------------|---------------------------|-----|---|
| P-537 | Bataille         | Arnaud                    | GS  | Natural colonisation and adaptation of a mosquito species in Galápagos: implications for disease threats to endemic wildlife                  |
| P-538 | Chamutpong       | Siriphatr                 | GS  | Isolation and characterization of microsatellite markers for Thai Great Hornbill ( <i>Buceros bicornis</i> )                                  |
| P-539 | Jordan           | Mark A.                   |     | Island fragmentation drives evolutionary diversification of populations of Galápagos lava lizards ( <i>Microlophus albemarlensis</i> complex) |
| P-540 | Takezaki         | Naoko Nt                  |     | Empirical Tests of the Reliability of Phylogenetic Trees Constructed with Microsatellite DNA  |
| P-541 | Wolff            | Kirsten                   |     | The battle of the genomes in gynodioecious plants: Mitochondrial DNA variation in <i>Plantago</i>   |
| P-542 | Orsini           | Luisa                     | PDF | Genetic spatial structure in a butterfly metapopulation correlates better with past than present demographic structure                        |
| P-543 | Seddon           | Jennifer Mary             |     | Incorporating spatial data into analysis of koala populations in South-East Queensland  |
| P-544 | Keinan           | Alon                      | PDF | Accelerated genetic drift on chromosome X suggests greater participation of men in the dispersal out of Africa                                |
| P-545 | Khang            | Tsung Fei                 | GS  | Molecular data analysis in diploids using multilocus dominant DNA markers   |
| P-546 | Sotelo           | Graciela                  | GS  | Genetic variation of the spiny spider crab <i>Maja brachydactyla</i> in the northeastern Atlantic   |
| P-547 | Segurel          | Laure                     | GS  | Influence of social organization on the sex-specific genetic structure in Central Asia  |
| P-548 | Goyache          | Félix                     |     | Cattle phylogeography inferred from Y-specific microsatellite systems   |
| P-549 | Mendizábal       | Isabel                    | GS  | Genetic origin, admixture, and asymmetry in maternal and paternal human lineages in Cuba  |
| P-550 | Knapp            | Michael                   | PDF | The complex biogeography of extinct Eurasian cave bears   |
| P-551 | Palero           | Ferran                    | GS  | Population genetic structure of the European spiny lobster ( <i>Palinurus elephas</i> ) inferred using microsatellite markers                 |
| P-552 | Beans Picón      | Gabrielle Angela          | GS  | Is mitochondrial diversity a reliable indicator of population size?   |
| P-553 | Mestres          | Francesc                  |     | Molecular analysis of a colonization: <i>Odh</i> gene variability in Mediterranean and American populations of <i>D. subobscura</i>           |
| P-554 | Hemmerter        | Stéphane                  | GS  | A curious coincidence: mosquito biodiversity and the limits of the Japanese encephalitis virus in Australasia                                 |
| P-555 | Aliyu            | Olawale Mashood           | PDF | Quantitative variation for apomictic seed production in <i>Boechera holboellii</i>  |
| P-556 | Cicconardi       | Francesco                 | GS  | Comparative phylogeography of the genus <i>Lepidocyrtus</i> (Hexapoda: Collembola) in the north-western Mediterranean basin                   |
| P-557 | Puente-Molins    | Marta                     | PDF | Biogeographic variation for apomixis expression in St. John's wort ( <i>Hypericum perforatum</i> L.)  |
| P-558 | Falahati-Anbaran | Mohsen                    | GS  | Patterns of genetic variation in Norwegian <i>A. lyrata</i> seed bank populations   |
| P-559 | Coelho           | Margarida Cardoso Reis Sá | GS  | On the edge of the Bantu expansions: mtDNA, Y-chromosome and lactase genetic variation in the Namibe desert of Angola                         |
| P-560 | Fadhlaoui-Zid    | Karima                    | PDF | Genetic heterogeneity in human Tunisian populations shown by paternal lineages  |
| P-561 | Toupance         | Bruno                     |     | A new estimate of site-specific mutation rate variability in the D-loop region using complete human mitochondrial DNA                         |
| P-562 | Bauzá-Ribot      | María del Mar             | GS  | Origin and phylogeography of the subterranean amphipod crustacean <i>Metacrangonyx</i> in islands   |
| P-563 | Sandoval Mendoza | Karla                     | GS  | Insights into the genetic diversity of indigenous Mexican populations   |
| P-564 | Foucaud          | Julien                    | PDF | Sex and Clonality in the Little Fire Ant  |

|       |                   |                  |     |  |
|-------|-------------------|------------------|-----|--|
| P-565 | Badaoui           | Bouabid          | GS  | Genetic relationships amongst Iberian, Canarian and African goat populations   |
| P-566 | Puerma            | Eva              | GS  | Nucleotide variation at six genes involved in salt tolerance in <i>Arabidopsis thaliana</i>  |
| P-567 | Rebernik          | Carolin Anna     | GS  | <i>Melampodium cinereum</i> (Heliantheae, Asteraceae) - phylogeography and polyploidization  |
| P-568 | Pinheiro          | Fabio            | GS  | Hybridization and introgression between Neotropical orchids, <i>Epidendrum fulgens</i> and <i>E. puniceoluteum</i>   |
| P-569 | Fàbrega Vidal     | Oriol            | PDF | Genetic analysis of the endangered anole <i>Anolis quadriocellifer</i> from three locations of the Guanahacabibes Peninsula (Cuba)   |
| P-570 | Serra Pérez       | Alexandra        | GS  | Sex determination in the pyrenean desman ( <i>galemys pyrenaicus</i> ) through the amplification of dbx and dby genes  |
| P-572 | Delfin            | Frederick Cortez | GS  | Y-chromosome genetic affinities of nine Filipino ethno-linguistic groups   |
| P-573 | Villacorta Martín | José Carlos      | GS  | The dark ages: phylogenies and molecular evolution in surface and subterranean populations of <i>Palmorchestia cavehoppers</i>   |
| P-574 | Navascués         | Miguel           | PDF | Discrimination between ancestral polymorphism and recent introgression as causes of shared polymorphic sites between species   |
| P-575 | Burgarella        | Concetta         | PDF | Demographic expansions in conifer and human populations characterized by linked microsatellite data  |
| P-576 | Pascual           | Marta            |     | Phylogeography of the widespread marine invader <i>Microcosmus squamiger</i> (Asciacea) using mtDNA and microsatellites  |
| P-577 | Da Silva          | Clarisse Palma   | GS  | Phylogeography and genetic diversity of nuclear and plastid markers in a Neotropical forest species, <i>Vriesea gigantea</i> (Bromeliaceae)  |
| P-579 | Batini            | Chiara           | GS  | Complete mitochondrial genome variation in African Pygmies: a population-based approach  |
| P-580 | Trucchi           | Emiliano         | GS  | Chronicles of an age-old invader: genetic and demographic parameters of past and present crested porcupine ( <i>Hystrix cristata</i> ) European populations  |
| P-581 | Matschiner        | Michael          | GS  | Gene flow and adaptive radiations: The population genetic structure of the humped rockcod ( <i>Gobionotothen gibberifrons</i> )  |
| P-582 | Degnan            | James H.         | PDF | Distributions of gene tree branch lengths under coalescence  |
| P-583 | Álvarez Presas    | Marta            | GS  | Phylogeographical analysis of land planarians (Platyhelminthes) from the Brazilian Atlantic Forest   |
| P-584 | Gante             | Hugo F           | GS  | Tempo and mode of speciation in a polytypic species  |
| P-586 | Campos            | Paula F.         | GS  | Musk ox ( <i>Ovibos moschatus</i> ) Ancient DNA: The hairy survivors of Pleistocene climate change tell their story  |
| P-587 | D'Anatro          | Alejandro Daniel | GS  | Genetic structure of <i>Micropogonias furnieri</i> in Uruguay  |
| P-589 | Uyenoyama         | Marcy K.         |     | Effect of interspecific incompatibility factors on the pattern of neutral divergence at linked and unlinked sites  |
| P-590 | Semina            | Alisa V.         | GS  | Molecular Phylogeography and Population Genetics of Tribolodon Species (Pisces: Cyprinidae)  |
| P-591 | Lázaro            | Eva              | GS  | Phylogeography and genetic variability of populations of the specie <i>Schmidtea mediterranea</i> (Tricladida, Platyhelminthes)  |
| P-592 | Lorenzen          | Eline            | GS  | Hybridization between subspecies of waterbuck ( <i>Kobus ellipsiprymnus</i> ) in East Africa with limited introgression  |
| P-593 | Mila              | Borja            | PDF | Multilocus analysis of genetic variation reveals the role of vicariance and selection in structuring populations of a polymorphic endemic bird ( <i>Zosterops borbonicus</i> ) on the islands of Reunion and Mauritius |
| P-594 | Abellán           | Pedro            |     | Comparative phylogeography of beetles from Western Mediterranean saline inland waters: the effect of habitat preferences   |
| P-595 | Montero-Pau       | Javier           | GS  | A multigene approach to assess the evolutionary history of the rotifer <i>Brachionus plicatilis</i> in the Iberian Peninsula   |
| P-596 | Naveira           | Horacio Fachal   |     | Chronicle of an extinction not genetically foretold  |
| P-597 | Kornobis          | Etienne          | GS  | Underneath the glaciers... Amphipods?!   |
| P-598 | Faria             | Rui Miguel       | PDF | Evolutionary history of Eurasian shads ( <i>Alosa</i> spp.)  |
| P-599 | Alves             | Maria Judite     |     | Evolutionary history of the genus <i>Lampetra</i> (Petromyzontidae) in the Iberian glacial refugium as inferred from mtDNA phylogeography  |
| P-600 | Halvarsson        | Peter            | GS  | Characterization of MHC class IIB in the Siberian Jay  |
| P-601 | Hobolth           | Asger            |     | Importance sampling for the infinite sites model   |
| P-602 | Bosch             | Montserrat       | PDF | Nuclear sequences for Eurasian badger phylogeographic studies  |
| P-603 | Muir              | Graham           | PDF | 'Porous species boundary' between <i>Silene latifolia</i> and <i>S. dioica</i> isolates Y and nuclear genes but not adaptive mutations in the cytoplasm  |

## POSTER PRESENTATIONS (continued)

|       |                   |                   |     |  |
|-------|-------------------|-------------------|-----|--|
| P-604 | Gentile           | Gabriele          |     | The lizard that Darwin missed: A new land iguana lineage in the Galápagos  |
| P-605 | Vyskocilova       | Martina           | GS  | The microsatellite variability and parasitism in native and introduced populations of four <i>Neogobius</i> species (Gobiidae)   |
| P-606 | Perdices          | Anabel            |     | Phylogeography and evolutionary history of the Neotropical catfish <i>Rhamdia quelen</i> (Teleostei: Heptapteridae)  |
| P-607 | Vyskocilova       | Martina           | GS  | Genetic diversity, phylogeography and parasitism among European populations of chub ( <i>Leuciscus cephalus</i> Linnaeus, 1758)  |
| P-608 | Simões            | Bruno Fonseca     | GS  | Phylogenetics and phylogeographic patterns in <i>Myotis daubentonii daubentonii</i> and <i>Myotis d. nathlinae</i> based in mtDNA and nDNA data  |
| P-609 | Simon             | Andrea            | GS  | Immunogenetic deficiency and the susceptibility to Whirling Disease in introduced rainbow trout ( <i>Oncorhynchus mykiss</i> ) populations   |
| P-611 | Gonçalves         | Helena Aguiar     | PDF | Inferring ancient patterns of lineage diversification and extinction in the common midwife toad ( <i>Alytes obstetricans</i> ) based on mtDNA and nuclear genealogies  |
| P-612 | Vila              | Carles            |     | Hybridization between wolves and dogs: impact on a wolf population   |
| P-613 | Muñoz-Fuentes     | Violeta           | PDF | Ecological Factors Drive Differentiation in British Columbia Gray Wolves   |
| P-615 | Mesquita          | Natacha           | PDF | Microsatellite analysis of introduced populations of red swamp crayfish, <i>Procambarus clarkii</i> (Crustacea, Cambaridae)  |
| P-616 | Stiller           | Mathias           | GS  | Wolverine ( <i>Gulo gulo</i> ) population dynamics throughout time and space   |
| P-617 | Hickerson         | Michael J.        |     | Testing comparative phylogeographic models of marine community assembly using a hierarchical Bayesian approach   |
| P-618 | Horn              | Susanne           | GS  | Genetic diversity and phylogeography of ancient Scandinavian beavers ( <i>Castor fiber</i> )   |
| P-619 | Macholan          | Milos             |     | Mitochondrial DNA sequence variation and evolution of Old World house mice: A new deep lineage from Socotra (Yemen)  |
| P-620 | Alexandrino       | João              |     | Comparative phylogeography of amphibians widespread in the Brazilian Atlantic Forest: contrasting the hypotheses of glacial refugia versus neotectonics as agents of biological diversification  |
| P-621 | Madeira           | María José García | PDF | Genetic diversity and structure of brown trout ( <i>Salmo trutta</i> ) populations from North of Iberian Peninsula   |
| P-623 | Cardia            | Pedro Miguel      | GS  | Exploring the properties of non-recombinant (Cytb) and recombinant ( $\beta$ -fibin7) haplotypes in phylogeographical studies: Evidence for the early split and recent admixture of populations of the Eurasian woodcock ( <i>Scolopax rusticola</i> ) |
| P-624 | Flowers           | Jonathan M.       | PDF | Genetic variation and natural selection in the flowering-time network of <i>Arabidopsis thaliana</i>   |
| P-625 | Vallinoto         | Marcelo           | PDF | Conflicting phylogeographic patterns of mitochondrial and nuclear markers in the neotropical toad <i>Rhinella marina</i> species complex   |
| P-626 | Sequeira          | Fernando          | PDF | Contrasting patterns of nuclear and mitochondrial phylogenetic relationships among the Neotropical treefrogs of the <i>Phyllomedusa burmeisteri</i> species complex  |
| P-627 | Schoville         | Sean Dennis       | GS  | Comparative Phylogeography of Alpine Insects in the California Sierra Nevada   |
| P-628 | Carvalho          | Dulcinéia De      | PDF | Patterns of genomic diversity in <i>Populus tremula</i> in the western portion of its native range   |
| P-629 | Papadopoulou      | Anna              | GS  | Comparative phylogeography in the Aegean archipelago: the effect of habitat stability  |
| P-631 | Oliveira          | Rita Isabel       | GS  | Towards a genome-wide approach for detecting hybrids: assembling microsatellites and SNPs to detect hybridisation between wild and domestic cats   |
| P-632 | Oliveira          | Rita Isabel       | GS  | Interrogating hybridisation: towards a genome-wide approach for wildcat conservation   |
| P-633 | Chen              | Hua               | PDF | The polymorphism pattern after a selective sweep   |
| P-634 | Cibrian Jaramillo | Angelica          | PDF | Spatial genetics of an understory Mexican palm, <i>Chamaedorea ernesti-augustii</i> ; scale matters  |
| P-635 | Huang             | Yu                | GS  | Self-fertilization and population structure in <i>Arabidopsis thaliana</i>   |
| P-636 | Hribova           | Eva               | PDF | Phylogenetic relationships in family Musaceae based on the nucleotide sequence of ITS1-5.8S-ITS2 region  |
| P-637 | Kruckenhauser     | Luise             | PDF | When do cave fish get blind? Genetic analysis of the cyprinid fish <i>Garra barreimiae</i> from cave and surface populations in Oman   |
| P-638 | Kruckenhauser     | Luise             | PDF | Genetic differentiation of selected Alpine land snails in Austria  |
| P-639 | Haring            | Elisabeth         |     | Distinct phylogeographic patterns in widespread corvid birds revealed by mitochondrial sequences   |
| P-640 | Naydenov          | Krassimir Dakov   |     | Genetic structure in Scots pine ( <i>Pinus sylvestris</i> L.) provenances from Bulgaria - implications for future local gene pool conservation   |
| P-641 | Naydenov          | Krassimir Dakov   |     | Structure of <i>Pinus nigra</i> Arn. populations in Bulgaria revealed by nuclear microsatellites and electrophoretic total protein profiles: Provenance tests  |

| NETWORK EVOLUTION AND SYSTEMS BIOLOGY (S14) |                 |                    |     |  |
|---|-----------------|--------------------|-----|--|
| P-642                                       | Álvarez-Ponce   | David              | GS  | Systems-level evolutionary analysis of the insulin/TOR signaling pathway in 12 <i>Drosophila</i> genomes   |
| P-643                                       | Bornberg-Bauer  | Erich              |     | Phylogenetic analysis of the evolution of interaction networks in four different eukaryotic transcription factor families: different evolutionary fates lead to different local topologies |
| P-644                                       | Merritt         | Thomas James Smyth |     | Empirical Analysis of Metabolic Control and Complexity in the <i>Drosophila melanogaster</i> NADP(H) Enzyme Network  |
| P-645                                       | Dagan           | Tal                | PDF | Modular networks and cumulative impact of lateral transfer in prokaryote genome evolution  |
| P-646                                       | Caetano-Anolles | Gustavo            |     | The role of enzymatic recruitment in evolution of modern metabolic networks  |
| P-647                                       | Mezey           | Jason G.           |     | A Bayesian approach for identifying robust topologies in genetic networks  |
| P-648                                       | Ikeo            | Kazuho             |     | Large Scale screening of human transcriptome: An Introduction of Human Genome Network platform   |
| P-649                                       | Gros            | Pierre-Alexis      | GS  | Evolution of costly genetic robustness at low mutation rate  |
| P-650                                       | Atchley         | William R.         |     | Evolution of Two Myc-Max-Mad Transcription Factor Networks   |
| P-651                                       | Tzika           | Athanasia C.       | GS  | A phylogenetic framework for the analysis of the evolvability and robustness of protein interaction networks   |
| P-652                                       | Kim             | Kerry Justin       | PDF | Computational modeling of vulval cell fate patterning in <i>Caenorhabditis</i>   |

| POPGEN IN SPACE! THEORY AND INFERENCE IN SPATIAL POPULATION GENETICS (S5) |                  |            |     |  |
|---|------------------|------------|-----|--|
| P-654   | Leblois          | Raphael    |     | Inference of demographic parameters using importance sampling on coalescence history   |
| P-655   | Ray              | Nicolas    | PDF | Inference of patterns of long distance dispersal during past human expansions  |
| P-657   | Lundemo          | Sverre     | GS  | Local scale genetic structuring and clonality in <i>Arabidopsis lyrata</i>   |
| P-658   | Bierne           | Nicolas    |     | Associative selection in subdivided populations  |
| P-659   | Robledo-Arnuncio | Juan José  |     | Isolation by Distance in Continuous Populations under Stochastic Demographic Fluctuations  |
| P-660   | Eldon            | Bjarki     | GS  | Population subdivision with migration and skewed offspring distribution among individuals in a population  |
| P-662   | Non              | Amy L.     | GS  | Synthesis of genetic and GIS distance data   |
| P-663   | Teixeira         | José Alves | PDF | Comparison between mitochondrial and nuclear DNA phylogeography patterns of <i>Bosca's newt</i> ( <i>Lissotriton boscai</i> ) based on explicit spatial models: concordance, admixture and implications for species delimitation |
| P-664   | Gauffre          | Bertrand   | GS  | Spatial genetic structure of a small rodent in a heterogeneous landscape   |
| P-665   | Barbará          | Thelma     | GS  | Microevolution in terrestrial islands: fine-scale spatial population genetics of plant species on neotropical inselberg rock outcrops  |

| SPONTANEOUS MUTATIONS AND THEIR EVOLUTIONARY CONSEQUENCES (S3) |                |                  |     |  |
|--|----------------|------------------|-----|--|
| P-666  | Wang           | Jinkai           | GS  | A common SNP of MCPH1 is associated with cranial volume variation in Chinese population                                  |
| P-667  | Lu             | Zhixiang         | GS  | Functional Characterization of the Human-specific Form (Type II) of Kallikrein 8, a Gene Involved in Learning and Memory |
| P-668  | Rogers         | Rebekah L.       | GS  | Formation and Longevity of Chimeric and Duplicate Genes in <i>Drosophila melanogaster</i>                                |
| P-669  | Duffy          | Siobain          | PDF | Chemistry, not biology: Evidence for polymerase-independent mutation in single-stranded DNA viruses                      |
| P-670  | Chuang         | Jeffrey H.       |     | What Silent Sites Tell Us about Regional Mutation Rates and Selection  |
| P-671  | Pérez-Figueroa | Andrés           | PDF | Impact of epistasis of deleterious mutations on the genetic variance components after a bottleneck                       |
| P-672  | Kvikstad       | Erika Marit      | GS  | Ride The Wavelet: Scale-Specific Dynamics Of Genomic Contexts Flanking Small Insertions And Deletions                    |
| P-673  | Trindade       | Sandra Gonçalves | GS  | Pervasive positive epistasis between mutations conferring antibiotic resistance  |
| P-674  | Gordo          | Isabel           |     | Sex, stress and Muller's ratchet   |
| P-676  | Chuang         | Jeffrey H.       |     | Do Orthologous Mammalian Loci Have Similar Neutral Mutation Rates?   |
| P-677  | Misawa         | Kazuharu         | PDF | The universal trend of amino acid gain-loss is caused by CpG hypermutability   |

## POSTER PRESENTATIONS (continued)

|       |             |              |     |  |
|-------|-------------|--------------|-----|--|
| P-678 | Polak       | Paz          | GS  | Transcription induced mutations vary across eukaryote species                                      |
| P-679 | Lucas Lledó | José Ignacio | PDF | Less evolutionary constrained photolyase genes are not preferentially lost                         |
| P-682 | Maclean     | Craig        |     | Fitness effects of spontaneous beneficial mutations in the bacterium <i>Pseudomonas aeruginosa</i> |

### THE ANCESTRAL EUKARYOTIC CELL (S6)

|       |                 |           |     |  |
|-------|-----------------|-----------|-----|--|
| P-683 | Hurtz           | Christian | GS  | Distribution and evolution of core carbon metabolism enzymes among microbes  |
| P-684 | Dagan           | Tal       | PDF | The evolutionary history of the eukaryotic glycolytic pathway - eubacterial origin and fluid bacterial chromosomes |
| P-685 | Caetano-Anolles | Gustavo   |     | The origins of modern proteomes and the ancestral eukaryotic cell  |
| P-686 | Grant           | Jessica   |     | Multigene Approach in Placing Unknown Taxa on the Eukaryotic Tree of Life  |
| P-687 | Penny           | David     |     | The ancestral Eukaryote Cell   |

### THE CROSSROADS BETWEEN PROKARYOTIC GENOMICS, ECOLOGY AND ADAPTATION (S4)

|       |                   |                 |     |   |
|-------|-------------------|-----------------|-----|---|
| P-688 | Smith             | Noel Henry      |     | Ecotypes of the <i>M. tuberculosis</i> complex and the uses and abuses of bacterial genome sequences                |
| P-689 | Maughan           | Heather         | PDF | The relationship between transformability and recombination in natural populations of <i>Haemophilus influenzae</i> |
| P-690 | Silva             | Francisco J.    |     | Re-annotation and analysis of <i>Sodalis glossinidius</i> , the endosymbiont of tsetse flies                        |
| P-692 | González-Candelas | Fernando        |     | Non-vertical inheritance in the evolution of <i>Legionella pneumophila</i>  |
| P-694 | Balbi             | Kevin Jon       | GS  | Contrasting purifying selection in the <i>Shigellae</i> and <i>E. coli</i> at synonymous and non-synonymous sites   |
| P-695 | Yafremava         | Liudmila        | PDF | Primordial strategy hypothesis for the evolution of tripartite world  |
| P-696 | Neef              | Alexander       | PDF | The genome of <i>Blattabacterium</i> sp., the bacterial cockroach endosymbiont                                      |
| P-697 | Lamelas           | Araceli Cabello | GS  | <i>Serratia symbiotica</i> , secondary endosymbiont of aphids: two evolutionary histories                           |
| P-698 | Johnson           | Philip L.       | GS  | Estimating recombination rate in microbial populations from metagenomic data  |

### THE X - AN EXCEPTIONAL CHROMOSOME! (S9)

|       |               |           |     |  |
|-------|---------------|-----------|-----|--|
| P-700 | Kejnovsky     | Eduard    | PDF | Structure and evolution of young sex chromosomes in <i>Silene latifolia</i>  |
| P-701 | Parsch        | John      |     | Effects of X-linkage and sex-biased gene expression on the rate of adaptive protein evolution in <i>Drosophila</i>                                     |
| P-702 | Garrido-Ramos | Manuel A. |     | The genus <i>Rumex</i> as a study model of sex chromosome evolution in plants  |
| P-704 | Gurbich       | Tatiana   | GS  | Effect of X-linkage on rates of evolution of sex-biased genes in <i>Drosophila</i>   |
| P-705 | Boursot       | Pierre    |     | Sex chromosomes, genetic conflicts and reproductive isolation in mice  |
| P-706 | Nam           | Kiwoong   | GS  | Identification of Three Evolutionary Strata, Formed by the Serial Chromosomal Inversions of Chicken W  |
| P-707 | Melo Ferreira | José      | GS  | Gender issues in Iberia: a genomic enquiry about an Xtraordinary legacy from the cold past in hares  |
| P-708 | Bachtrog      | Doris     |     | The evolution of dosage compensation in <i>Drosophila</i>  |
| P-709 | Popkova       | Anna      | PDF | Expression of candidate genes for sex-ratio drive in <i>Drosophila simulans</i>  |
| P-710 | Fouvry        | Lucie     | GS  | Sex-ratio meiotic drive in <i>Drosophila simulans</i> : functional analysis of a 2-locus system combining fine genetic mapping and population genomics |

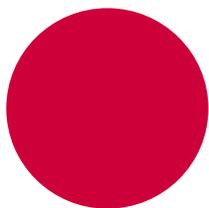
### TRANSPOSABLE ELEMENTS: DIVERSITY, DYNAMICS AND EVOLUTIONARY IMPACT ON HOST GENOMES (S15)

|       |               |            |     |  |
|-------|---------------|------------|-----|--|
| P-711 | Mccole        | Ruth       | GS  | Evolutionary fates of retrotransposed imprinted genes  |
| P-712 | Poncet        | Valérie    |     | Allelic variations of the MITE Alex in <i>Coffea canephora</i> Pierre: towards a novel phylogenetic tool for <i>Coffea</i> species       |
| P-713 | Crease        | Teresa J.  |     | The effect of transposon <i>Pokey</i> insertions on sequence variation in the 28S rRNA genes of <i>Daphnia pulex</i>                     |
| P-714 | Kim           | Young-Hyun | GS  | In silico analysis and experimental validation of recently exonized Alu in <i>Macaca fascicularis</i>                                    |
| P-715 | Kim           | Hyoungwoo  | GS  | Comparative analysis of human placenta specific genes using various primates   |
| P-716 | Morales-Hojas | Ramiro     | PDF | The fixation of a <i>bilbo</i> -like non-LTR retroelement in the <i>virilis</i> phylad of the <i>Drosophila virilis</i> group of species |

|       |                  |                    |     |   |
|-------|------------------|--------------------|-----|---|
| P-717 | Zerjal           | Tatiana            | PDF | Large-scale survey using M-SAP (Methylation-Sensitive Amplification Polymorphism) technique to estimate the level of cytosine methylation in four MITE families in the maize genome |
| P-718 | Steinbauerova    | Veronika           | GS  | Splicing of intron-containing transcripts of plant LTR-retrotransposon Ogre   |
| P-719 | García Guerreiro | María Pilar        |     | The impact of <i>Drosophila</i> colonisation on genomic distribution and molecular structure of transposable elements   |
| P-720 | Delprat Obeaga   | Alejandra          | PDF | The Galileo transposon promotes chromosomal inversions in <i>Drosophila</i>   |
| P-721 | Llorens          | Carlos             | GS  | The Polyphyletic Recurrence of Vertebrate Retroviruses into the Ty3/Gypsy Bio-distribution within the LTR retroelement Big Bang and the Three Kings Hypothesis                      |
| P-722 | Leclercq         | Sébastien          |     | Dynamics of microsatellites within polyA tails of Alu elements  |
| P-723 | Metcalfe         | Cushla Jane        | PDF | The structure and evolution of the Australian lungfish genome   |
| P-724 | García           | Koldo              | GS  | Intergenic recombination, gene conversion and selection in bovine endogenous retroviruses   |
| P-725 | Schaack          | Sarah              | GS  | Inter-element variation in patterns of gain and loss in recombining and non-recombining genomic backgrounds   |
| P-726 | Hua-Van          | Aurélié            |     | Mariner landscape within the 12 <i>Drosophila</i> sequenced genomes   |
| P-727 | Feschotte        | Cédric             |     | Space Invaders! Repeated horizontal transfers of a DNA transposon in mammals and OTH tetrapods  |
| P-728 | González         | Josefa             | PDF | High rate of recent transposable elements induced adaptations in <i>Drosophila melanogaster</i>   |
| P-729 | Privman          | Eyal               | GS  | Selection constraints on selfish homing endonucleases facilitate their use in gene therapy  |
| P-730 | Muñoz-López      | Martín             | GS  | A novel mariner from the ant, <i>Messor bouvieri</i> , is capable of efficient transposition in vitro   |
| P-731 | Naveira          | Horacio Fachal     |     | The long walk to extinction of five families of human endogenous retroviruses (ERVs)  |
| P-732 | Pereira          | Vini               | PDF | The effect of new transposable element insertions on gene expression profiles in murids   |
| P-733 | Calvete Torres   | Oriol              | GS  | Breakpoint characterization of three chromosomal inversions fixed in <i>Drosophila buzzatii</i>   |
| P-734 | Montiel          | Eugenia Elisabeth  | GS  | Characterization of an R2 retrotransposon, in the grasshopper <i>Eyprepocnemis plorans</i>  |
| P-735 | Tubío            | José Manuel Castro | GS  | Fixation of transposable elements in the genome of the Malaria mosquito <i>Anopheles gambiae</i>  |
| P-736 | Ganko            | Eric               | PDF | Identification and characterization of transposons and OTH repeats in the wildflower <i>Mimulus guttatus</i>  |
| P-739 | Casacuberta      | Josep M.           |     | Different strategies to persist: the pogo-like Lemi1 transposon produces MITEs or typical defective elements in different plant genomes   |
| P-740 | Casacuberta      | Josep M.           |     | Analysis of class II transposons in grapevine ( <i>Vitis vinifera</i> L.)   |
| P-741 | Quesneville      | Hadi               |     | When repeats meet chromatin: Relationship between repeats and heterochromatin dynamics  |
| P-742 | Novick           | Peter Anthony      | GS  | Evolution and diversity of non-LTR retrotransposons in the genome of <i>Anolis carolinensis</i>   |

#### WHAT WOULD/SHOULD WE DO WITH A MILLION DNA BARCODES? (S10)

|       |            |             |     |   |
|-------|------------|-------------|-----|---|
| P-743 | Hajibabaei | Mehrdad     |     | From one to one million DNA barcodes per reaction: environmental barcoding using massively parallelized pyrosequencing        |
| P-744 | Lohse      | Konrad      | GS  | Kinks in the tree- reproductive isolation vs. population structure  |
| P-745 | Fehrer     | Judith      |     | DNA barcodes: the need for taxonomic and phylogenetic validation  |
| P-747 | Magnacca   | Karl        | PDF | Mitochondrial heteroplasmy: avoiding pitfalls and finding positives   |
| P-748 | Kim        | Choong-Gon  |     | DNA barcoding of the Korean Marine Organisms  |
| P-749 | Semina     | Alisa V.    | GS  | Analysis of COI Sequences Helps Infer Phylogenetic Relationships in Mugilids (Pisces: Mugilidae) and Solve Taxonomic Problems |
| P-750 | Aliabadian | Mansour     | PDF | Performance of distance-based DNA barcoding in the molecular identification of Birds  |
| P-751 | Charlat    | Sylvain     |     | SymBicode: a DNA barcode approach to symbiosis  |
| P-752 | Alansari   | Aliya Saleh |     | DNA-barcoding mammals in Oman   |



## GENERAL INFORMATION

All the events are held at the Recinte Montjuïc - Palau de Congressos de Barcelona unless otherwise noted.

**Venue:** Recinte Montjuïc - Palau de Congressos de Barcelona  
Fira de Barcelona  
Hall 5  
Avda. Reina Maria Cristina, s/n  
E-08014 Barcelona

### Registration Fee:

|                       | Until March 10** | After March 10 |
|-----------------------|------------------|----------------|
| <b>SMBE member</b>    |                  |                |
| Regular               | 420 €            | 520 €          |
| Student*              | 220 €            | 350 €          |
| <b>Not a member</b>   |                  |                |
| Regular               | 520 €            | 620 €          |
| Student*              | 320 €            | 450 €          |
| <b>Meeting Dinner</b> | <b>50 €</b>      |                |

16% VAT included.

\*Student (graduate and undergraduate): Certificate-letter signed by the research supervisor is needed.

\*\*Reduced fee only is applied if both the registration form and payment have been received at the Meeting Secretariat until March 10, 2008.

### Your registration fee includes:

- Admission to all sessions and poster presentations.
- Admission to exhibition area.
- Welcome drink on Thursday 5 June, Palau de Congressos de Barcelona.
- Meeting documentation and program.
- Coffee breaks (Friday 6 to Sunday 8 June).
- Lunch box (Friday 6 to Sunday 8 June).
- Certificate of attendance.

### SECRETARIAT AND REGISTRATION DESK

#### Opening hours:

|          |        |                     |
|----------|--------|---------------------|
| Thursday | June 5 | 04:00 pm - 07:30 pm |
| Friday   | June 6 | 07:30 am - 07:00 pm |
| Saturday | June 7 | 07:30 am - 07:00 pm |
| Sunday   | June 8 | 07:30 am - 05:30 pm |

**BADGES** Your personal badge is your entrance ticket to the Meeting Venue and all scientific sessions  
Badges will be issued to all participants on registration and will be colour coded as follows:  
**Orange label: Local Organizing Committee.**  
**Blue label: Participants.**  
**Red label: Exhibitors.**

Due to security regulations, badges must be worn throughout the Meeting venue and social events. Only those participants wearing badges will be admitted to scientific sessions and exhibition.

**BOOK OF ABSTRACTS** The book of abstracts is available on-line from the SMBE 2008 web site.

**CLOAKROOM** Cloakroom is located on Level 2 during Meeting hours.

**COFFEE BREAK & LUNCH BOX** Coffees are served at poster and exhibition area during coffee-break scheduled time.

A lunch box is provided to registered participants at the exhibition area (Level 1) on Friday, Saturday and Sunday at scheduled times.

**COMPUTER ROOM** Computers with access to Internet are available for Meeting participants in Room 4.

**EXHIBITION** Exhibition area is located on Level 1.

Exhibitors are:

|             |   |
|-------------|---|
| Stand 1     | Oxford University Press / Oxford Journals |
| Stand 2     | Delphi Genetics                           |
| Stand 3     | Roche Diagnostics GmbH                    |
| Stand 4 & 5 | Wiley-Blackwell                           |
| Stand 6     | Royal Society Publishing                  |

Opening time:

|          |        |                     |
|----------|--------|---------------------|
| Thursday | June 5 | 06:00 pm - 07:30 pm |
| Friday   | June 6 | 08:30 am - 07:00 pm |
| Saturday | June 7 | 08:30 am - 07:00 pm |
| Sunday   | June 8 | 08:30 am - 05:30 pm |

## GENERAL INFORMATION (continued)

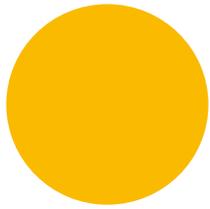
### MEETING HOTELS

|                     | Address                         | Telephone   |
|---------------------|---------------------------------|-------------|
| Hotel Fira Palace   | Avinguda de Rius i Taulet, 1-3  | 934 262 223 |
| Hotel AC Vilamarí   | Vilamarí, 34-36                 | 932 890 909 |
| Hotel Barceló Sants | Plaça dels Països Catalans, s/n | 935 035 300 |
| Hotel NH Numancia   | Numància, 74                    | 933 224 451 |
| Hotel NH Les Corts  | Travessera de les Corts, 292    | 933 220 811 |
| Hotel NH Angelo     | Consell de Cent, 74             | 934 234 647 |
| Hotel Onix Fira     | Llançà, 30                      | 934 260 087 |
| Hotel Paral.lel     | Cabanyes, 5-7                   | 933 291 104 |

**LANGUAGE** English is the official language of the Meeting.  
No simultaneous translation is provided.

**LIABILITY** The organizers accept no liability for personal injuries sustained, or loss or damage to property belonging to Meeting participants or accompanying persons, either during or as a result of the Meeting.

**MESSAGE BOARD** A message board is located next to the Registration Area to be used by participants.



## SOCIAL PROGRAM

**Event:** WELCOME DRINK

**Date:** Thursday, June 5 at 06:30 pm

**Place:** Recinte Montjuïc - Palau de Congressos de Barcelona Level 1.

**Access:** Badge required.

**Event:** MEETING DINNER

**Date:** Saturday, June 7 at 08:30 pm

**Place:** Hotel Fira Palace  
Avda. Rius i Taulet, 1-3 Barcelona

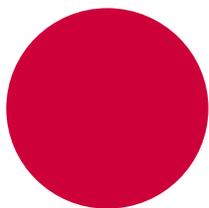
**Access:** Tickets will be requested at the entrance.

Tickets were available in advance by means of the registration form at a cost of 50 €.

Extra tickets are sold on-site, only if available, at the Registration Area.

No transportation is provided.

Music entertainment will take place after dinner.



## INSTRUCTIONS FOR SPEAKERS AND AUTHORS

### ORAL PRESENTATION GUIDELINES

**PROJECTION** All presentations are to be in PowerPoint, PDF or Keynote formats.

All lecture rooms are equipped with two computers (one PC and one Macintosh) and a LCD-video projector.

**Software:** **PC:** Microsoft Windows XP and Office 2007.  
**Macintosh:** Leopard, Office 2008 and Keynote 2008.

You need to bring a copy of your presentation on a CD or Flash drive (USB Drive, memory stick) and have it loaded onto the speaker's room at least 60 minutes before your session. If you are speaking in the first session of the day, we encourage you to load your presentation preferably the day before.

It is not allowed to use your own computer for the presentation.

A technician specifically designated for receiving oral presentations will assist you at the speaker's room. Please inform him if your presentation is PC or Macintosh.

Speakers' room (Room 4) opening hours:

|          |        |                     |
|----------|--------|---------------------|
| Thursday | June 5 | 04:00 pm - 07:30 pm |
| Friday   | June 6 | 07:30 am - 06:00 pm |
| Saturday | June 7 | 07:30 am - 06:30 pm |
| Sunday   | June 8 | 07:30 am - 05:30 pm |

If your presentation needs to call up additional files (e.g., a video file embedded in your PowerPoint presentation), please make sure with the technician that these files work properly and are available for transfer as well.

The allocated time to each talk is usually 30 minutes for invited speakers (25 minutes for presentation plus 5 minutes for discussion) or 15 minutes for contributed talks (12 minutes for presentation plus 3 minutes for discussion). Please gauge the length of your presentation according to your allocated time.

### THE GENERAL PROCEDURE OF THE ORAL SESSIONS WILL BE

- The chairperson opens the session and introduces the first symposium invited speaker.
- After each symposium invited talk, the chairman may allow short questions.
- After the invited talks, the chairman introduces the contributed talk speakers.
- If there is available time, the chairperson may conduct a general discussion at the end of the session.
- The chairperson closes the session.

## POSTER PRESENTATION

- Poster area location: Level 0.
- Materials for assembling posters (tape) are provided in the Level 0. Posters can be fixed on the poster boards from Thursday, June 5 at 04.00 pm. Posters have to be removed on Sunday, June 8 before 05.30 pm. Posters are displayed during all the Meeting.
- Materials for assembling posters (tape) are provided in the Level 0.
- The Meeting is not responsible for any loss or damage occurred to posters left on the panel beyond Sunday, June 8, at 05.30 pm. Posters left on the panel will not be mailed to the authors after the Meeting.
- The code of a poster presentation in the program is identical to the poster board number (see page 17).

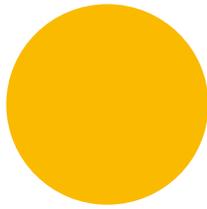
## POSTER PRIZES

- All posters presented by graduate students and postdoctoral fellows are considered for prizes, 6 prizes for each category.
- Judging time. There are three judging times.  
J1. Posters: P001 - P299 Friday, June 6 from 02.00 pm to 03.00 pm  
J2. Posters: P301 - P525 Friday, June 6 from 05.00 pm to 06.00 pm  
J3. Posters: P528 - P750 Saturday, June 7 from 2.00 pm to 03.00 pm
- Please be sure to stand by your poster during the designated judging time in case the judges have specific questions. If the author is not present at the scheduled time, the poster might be not considered.

## POSTER SESSIONS

- There are five posters sessions (see the scientific program) and in two of these sessions the authors are expected to be present to answer questions.  
PA1. Odd Poster numbers: (i.e., P001, P003, ..., P751).  
Saturday, June 7 from 05.30 pm to 07.00 pm  
PA2. Even Poster numbers: (i.e., P002, P004, ..., P752).  
Sunday, June 8 from 01.30 pm to 03.00 pm
- Please remember that the poster sessions are different than the poster judging time.





## AUTHOR INDEX

CS: Company Session.

O: Oral.

P: Poster.

PL: Plenary.

UDMPA: Undergraduate Diversity Mentoring Program Award Recipient.

WF: Walter M. Fitch Student Award Competitor Participant.

The book of abstracts is available on-line from the SMBE 2008 web site.

### A

|                     |                                   |                     |                            |
|---------------------|-----------------------------------|---------------------|----------------------------|
| Aagaard, J.         | P-286                             | Anderson, D.        | P-136                      |
| Abby, S.            | O-089                             | Anderson, N.        | P-153                      |
| Abellán, P.         | P-594                             | Anderson, O.        | P-686                      |
| Abelló, P.          | P-551                             | Andersson, G.       | P-122                      |
| Aboim, M.A.         | P-385                             | Andolfatto, P.      | O-151, O-175, P-437        |
| Abramov, A.         | P-616                             | Andreassen, M.      | P-65                       |
| Absher, D.          | P-158, P-482                      | Andrew, B.          | O-059                      |
| Abt, D.             | O-171                             | Anselmo, A.         | P-080                      |
| Achaz, G.           | P-421                             | Antelo, B.          | P-735                      |
| Achituv, Y.         | P-356                             | Antunes, A.         | P-308, P-489               |
| Adams, S.           | P-400                             | Aponte, J.          | P-305                      |
| Affourtit, J.       | PL-1                              | Aquadro, C.         | O-051, O-154, P-108, P-115 |
| Aglyamova, G.       | P-236                             | Araki, H.           | O-148                      |
| Agorreta, A.        | P-391                             | Aranzana, M.J.      | P-502                      |
| Aguadé, M.          | P-109, P-113, P-116, P-566, P-642 | Arauz, P.           | P-553                      |
| Aguileta, G.        | P-507                             | Arbiza, L.          | P-055, P-185               |
| Ahmadinejad, N.     | O-009                             | Arboleda, C.        | P-118                      |
| Aid-Pavlidis, T.    | P-144                             | Archer, J.          | P-068                      |
| Alansari, A.        | P-752                             | Archetti, M.        | P-467                      |
| Alasentie, A.       | P-542                             | Archibald, J.       | P-276                      |
| Albà, M.            | P-145, P-154, P-209, P-244        | Arctander, P.       | P-592                      |
| Alberts, S.         | O-059                             | Ardell, D.          | P-285                      |
| Albrecht, T.        | P-240, P-449                      | Ardren, W.          | O-148                      |
| Alda, F.            | P-529                             | Arenas, M.          | P-056                      |
| Al-Dafry, K.        | P-752                             | Arguello, J.R.      | WF-01                      |
| Alegre, J.          | P-430                             | Arkhas, S.          | P-017                      |
| Alexandre, P.       | P-189                             | Armengol, L.        | O-006, P-209               |
| Alexandrino, J.     | P-620, P-626                      | Armisen, D.         | P-258                      |
| Alexandrino, P.     | P-598                             | Arndt, P.F.         | P-070, P-184, P-414, P-678 |
| Aliabadian, M.      | P-750                             | Arnedo, M.          | P-102, P-366               |
| Alieva, N.          | P-236                             | Arnold, L.          | P-017                      |
| Alix-Jenczewski, K. | P-717                             | Arntzen, J.         | P-325                      |
| Aliyu, O.           | P-555, P-557                      | Artiguenave, F.     | P-264                      |
| Allard, M.          | P-372                             | Artzy-Randrup, Y.   | P-645                      |
| Allegrucci, G.      | P-100                             | Arús, P.            | P-502                      |
| Allen, J.           | P-476, UDMPA-08                   | Arvestad, L.        | O-084                      |
| Allman, E.          | P-526                             | Asaoka, Y.          | P-241                      |
| Al-Meeri, A.        | P-662, UDMPA-05                   | Assis de Faria, D.  | P-565                      |
| Almeida, P.R.       | P-599                             | Assis, R.           | P-280                      |
| Alonso, S.          | UDMPA-09                          | Atchley, W.         | P-650                      |
| Alonso-Blanco, C.   | P-041                             | Aubin, L.D.         | P-640, P-641               |
| Altmann, J.         | O-059                             | Aubourg, S.         | P-258                      |
| Álvarez Álvarez, R. | P-364                             | Audet, C.           | P-393                      |
| Álvarez, I.         | P-548                             | Aulchenko, Y.       | P-528                      |
| Álvarez-Ponce, D.   | P-642                             | Aureli, F.          | P-028                      |
| Álvarez-Presas, M.  | P-583                             | Aury, J.            | P-264, WF-06               |
| Alves, A.           | P-606                             | Ausió, J.           | P-172, P-179               |
| Alves, I.           | P-471                             | Austerlitz, F.      | O-073, P-030, P-423        |
| Alves, M.J.         | P-584, P-599, P-615               | Auton, A.           | O-035, O-143               |
| Alves, P.C.         | P-631, P-632, P-707               | Awadalla, P.        | O-078, O-144, P-311        |
| Al-Zadjali, S.      | P-752                             | Aymerich, P.        | P-570                      |
| Ambur, O.H.         | P-200                             | Ayoub, N.           | P-334                      |
| Amills, M.          | P-004, P-446, P-565               | Azeredo-Espin, A.M. | P-344, P-362               |
| Ananda, G.          | P-085                             | Azevedo, M.         | P-002                      |
| Andersen, A.        | P-230                             | Azuma, Y.           | O-181                      |

## AUTHOR INDEX (continued)

### B

|                    |                                   |                          |  |                      |                            |
|--------------------|-----------------------------------|--------------------------|--|----------------------|----------------------------|
| Babbitt, G.        | O-064                             | Bekaert, M.              | P-176, P-608                             | Boehne, A.           | P-255                      |
| Babra, B.          | P-219                             | Belda, E.                | P-217, P-690                             | Boersma, A.          | P-032                      |
| Babteste, E.       | P-216                             | Beleza, S.               | P-471, P-559                             | Böhne, A.            | P-254, P-256               |
| Bachtrog, D.       | O-151, P-704, P-708               | Belinky, F.              | P-318                                    | Boissinot, S.        | P-315, P-742               |
| Backstrom, N.      | P-182                             | Belkhir, K.              | P-262                                    | Boitard, S.          | P-433                      |
| Badaoui, B.        | P-565                             | Bell, M.                 | P-158, P-482                             | Bokma, V.            | P-042                      |
| Baer, C.           | O-024, UDMPA-07                   | Bello, X.                | O-106                                    | Bon, C.              | P-319                      |
| Baguña, J.         | P-373, P-591                      | Bellora, N.              | P-154, P-209                             | Bonizzoni, P.        | P-080                      |
| Bahuchet, S.       | P-423                             | Belokobylskij, S.        | P-321                                    | Borday Birraux, V.   | O-189                      |
| Bailey, R.         | P-412                             | Beltrán, J.              | P-612                                    | Borenstein, E.       | O-100                      |
| Bainer, R.         | O-172, P-156                      | Beltran, S.              | P-126                                    | Borevitz, J.         | O-152, P-237, P-494, P-635 |
| Baines, J.         | P-701, UDMPA-02                   | Ben Ammar Elgaaeid, A.   | P-560                                    | Bornberg-Bauer, E.   | O-082, P-060, P-643        |
| Baird, S.J.        | P-381                             | Benger, E.               | O-049                                    | Boronat, A.          | P-146                      |
| Bakewell, M.       | P-293                             | Benjak, A.               | P-740                                    | Boscato, P.          | P-009                      |
| Bakker, F.         | P-506                             | Benoit, G.               | O-187                                    | Bosch, E.            | O-144, P-301, P-422, P-432 |
| Balanya, J.        | P-719                             | Berard, J.               | P-062                                    | Bosch, M.            | P-270, P-602               |
| Balbi, K.          | P-694                             | Beraud-Colomb, E.        | P-319                                    | Bosch, N.            | P-209                      |
| Balloux, F.        | P-416                             | Bered, F.                | P-577                                    | Boto, L.             | P-436                      |
| Banta, J.          | P-048                             | Bergelson, J.            | P-494, P-635                             | Bouhouche, K.        | WF-06                      |
| Barbadilla, A.     | P-058, P-107                      | Berggren, K.             | P-001, P-122                             | Boulesteix, M.       | P-705                      |
| Barbará, T.        | P-577, P-628, P-665               | Berglund, J.             | P-178                                    | Bourlat, S.          | P-345                      |
| Barbujani, G.      | P-426, P-427                      | Bergman, C.              | O-101                                    | Boursot, P.          | P-705, P-707               |
| Barfuss, M.        | P-328                             | Bergmann, S.             | O-037                                    | Boussau, B.          | O-081, P-346               |
| Barker, D.         | P-121                             | Berman, P.               | O-112                                    | Boutin, T.           | O-108                      |
| Barluenga, M.      | P-395                             | Bermingham, E.           | O-072, P-332, P-391                      | Bouzaid, E.          | P-319                      |
| Barraclough, T.    | O-071                             | Bernardi, G.             | P-517                                    | Boyko, A.            | O-037, O-057, O-149, P-429 |
| Barrie, A.         | O-105                             | Bernardi, R.             | P-625                                    | Braasch, I.          | O-132, O-188               |
| Barros, F.         | P-568                             | Bernard-Samain, S.       | P-189, P-255, P-256                      | Bracho, M.A.         | O-111                      |
| Bartolomé, C.      | O-106                             | Bernatchez, L.           | P-385, P-393                             | Bradic, M.           | P-453                      |
| Barton, K.J.       | P-552                             | Berne-Dedieu, A.         | P-125                                    | Braendle, C.         | O-093                      |
| Barton, M.         | O-101                             | Berniell-Lee, G.         | P-549                                    | Brajković, D.        | P-266                      |
| Barton, N.         | P-744                             | Berriman, M.             | P-469                                    | Bras, J.             | O-141                      |
| Bartumeus, F.      | P-299                             | Berry, A.                | P-469                                    | Brask, A.            | O-161, P-202               |
| Barua, D.          | P-047                             | Berry, V.                | O-163                                    | Bratke, K.           | P-297                      |
| Baryshnikov, G.    | P-550, P-616                      | Bertorelle, G.           | P-009                                    | Braunstein, A.       | P-469                      |
| Barzel, A.         | P-729                             | Bertrand, S.             | P-027                                    | Bravo, I.            | P-307                      |
| Bassan, A.         | P-482                             | Bertranpetit, J.         | O-122, O-144, P-301, P-305, P-530, P-579 | Brawand, D.          | P-043, P-242               |
| Basset, P.         | P-383                             | Betancourt, A.           | P-117                                    | Brazier, L.          | P-030                      |
| Basta, H.          | P-742                             | Bétermier, M.            | WF-06                                    | Breines, R.          | P-207, P-326               |
| Bastian, F.        | O-167                             | Betran, E.               | P-278                                    | Breslin, P.          | P-480                      |
| Batada, N.         | P-263                             | Beye, M.                 | O-138                                    | Bretagnolle, V.      | P-664                      |
| Bataille, A.       | P-537                             | Bidegaray, L.            | P-102                                    | Briggs, A.           | PL-1, P-266                |
| Bataillon, T.      | P-420                             | Bierne, N.               | P-658                                    | Brindefalk, B.       | O-002                      |
| Bates, P.          | P-413                             | Biggin, M.               | P-143                                    | Brinkworth, J.       | P-071                      |
| Batini, C.         | P-579                             | Biggs, P.                | P-687                                    | Brites, D.           | P-227                      |
| Batzler, M.        | O-102, O-104                      | Billiard, S.             | P-444                                    | Britton, A.          | O-141                      |
| Bauer DuMont, V.   | O-051                             | Bimova, B.               | P-381                                    | Brochier-Armanet, C. | P-346, P-347               |
| Bauzá -Ribot, M.M. | P-562                             | Birkhead, T.             | P-296                                    | Bromham, L.          | P-348                      |
| Bazin, E.          | P-500                             | Bischerour, J.           | P-730                                    | Brown, K.            | O-173                      |
| Bazykin, G.        | O-050                             | Bizuayehu, T.            | P-230                                    | Brown, M.            | P-747                      |
| Beakert, M.        | P-247                             | Blanchet, E.             | P-034                                    | Brtko, J.            | P-015                      |
| Beans Picón, G.    | P-552                             | Blanco, E.               | P-126                                    | Brudno, M.           | O-050                      |
| Beaumont, H.       | O-174                             | Blankenberg, D.          | P-085                                    | Brunes, T.           | P-620, P-626               |
| Beaumont, M.       | O-180, P-035, P-457, P-500, P-551 | Blanquart, S.            | O-081                                    | Brunet, F.           | P-015, P-254, P-255, P-256 |
| Bechsgaard, J.     | P-342, P-407                      | Bleakley, K.             | O-073                                    | Brunstrom, B.        | O-062                      |
| Becq, J.           | P-052                             | Blekhman, R.             | P-133                                    | Bryant, D.           | O-017, O-085, P-338        |
| Becquet, C.        | P-377                             | Blier, P.                | P-243                                    | Bryc, K.             | O-037                      |
| Bedford, T.        | P-520, P-668                      | Blöch, C.                | P-328                                    | Bryja, J.            | P-240, P-406, P-449        |
| Beebe, N.          | P-554                             | Blouin, M.               | O-148                                    | Bryjova, A.          | P-240                      |
| Behar, D.          | P-579                             | Blum, M.                 | O-034, P-069                             | Brykov, V.           | P-402, P-590, P-749        |
| Beiko, R.          | O-086                             | Blum, T.                 | P-186                                    | Bucan, M.            | O-141                      |
| Beja-Pereira, A.   | P-002, P-548                      | Bobbe, J.                | P-255                                    | Buckley, D.          | P-663                      |
| Bejcek, V.         | P-619                             | Bodanese-Zanettini, M.H. | P-577                                    | Buckling, A.         | P-682                      |
|                    |                                   |                          |  | Budd, A.             | P-128                      |

|                    |   |                        |                                   |                       |   |
|--------------------|---|------------------------|-----------------------------------|-----------------------|---|
| Buentello-Malo, L. | P-563                                       | Carson, A.             | P-279                             | Chinen, A.            | WF-07   |
| Buikstra, J.       | P-531                                       | Carter, R.             | P-131                             | Chiva, M.             | P-172   |
| Bujnicki, J.       | P-241                                       | Carter, T.             | UDMPA-08                          | Choi, E.              | P-748   |
| Bullaughay, K.     | O-047                                       | Carthew, R.            | P-174                             | Chourrout, D.         | P-264   |
| Büntge, A.         | O-060                                       | Carvalho, D.           | P-628                             | Christine, L.M.       | P-013   |
| Burgarella, C.     | P-575                                       | Casacuberta, J.        | P-739, P-740                      | Chuang, J.            | P-670, P-676                                      |
| Burger, G.         | P-218, P-329                                | Casals, F.             | O-144, P-301, P-305, P-422        | Chuang, T.            | P-197, P-295                                      |
| Burke, T.          | P-296                                       | Casamayor, E.          | P-299                             | Chung, W.             | P-085   |
| Burke, W.D.        | P-734                                       | Casane, D.             | O-189, P-189, P-319, P-723        | Churlaud, C.          | P-052   |
| Burki, F.          | P-322                                       | Casanellas, M.         | P-516                             | Cibrian Jaramillo, A. | P-634   |
| Burstein, D.       | P-310, P-729                                | Casillas, S.           | P-058                             | Cicconardi, F.        | P-556   |
| Burt, A.           | P-505                                       | Casola, C.             | O-102                             | Ciesielski, F.        | P-015   |
| Bustamante, C.     | O-037, O-057, O-146,<br>O-149, P-221, P-429 | Casoli, A.             | P-009                             | Cipriani, R.          | O-072   |
| Butarbutar, A.     | P-177                                       | Castelo, R.            | P-209                             | Ciullo, M.            | P-427   |
| Butler, C.         | P-047                                       | Castresana, J.         | P-354, P-358                      | Cizkova, D.           | P-406   |
| Butlin, R.         | P-035, P-121                                | Castric, V.            | P-407, P-470                      | Cizkova, J.           | P-636   |
| Byrnes, J.         | P-237                                       | Castrignanò, T.        | P-080                             | Clark, A.             | PL-3, O-011, O-054, O-057,<br>P-115, P-272, P-429 |
|                    |   | Castroviejo-Fisher, S. | O-020                             | Clark, J.             | P-024   |
|                    |   | Caswell, J.            | O-121                             | Clark, N.             | O-154, P-277                                      |
|                    |   | Catalano, G.           | P-009                             | Clark, R.             | O-044, P-494                                      |
|                    |   | Caudy, N.              | P-319                             | Cleveland, S.         | P-051   |
|                    |   | Cazaux, B.             | P-705                             | Clifton, R.           | P-089   |
|                    |   | Ceballos, L.           | P-534                             | Cobolli, M.           | P-100   |
|                    |   | Cenci, A.              | P-455                             | Codoñer, F.           | P-072   |
|                    |   | Cermak, T.             | P-700                             | Coelho, M.            | P-129, P-559                                      |
|                    |   | Cerny, R.              | P-022                             | Coelho, M.M.          | P-385   |
|                    |   | Chabarría, C.          | P-156                             | Coen, E.              | O-099   |
|                    |   | Chabot, A.             | O-172, P-133, P-156               | Coghlan, A.           | P-415   |
|                    |   | Chahal, M.             | P-711                             | Cohen, J.             | WF-06   |
|                    |   | Chaignat, E.           | P-147                             | Cohen, O.             | O-088   |
|                    |   | Chain, F.              | WF-03                             | Cole, J.              | P-686   |
|                    |   | Chalmel, F.            | WF-02                             | Coll, M.              | P-448   |
|                    |   | Chalmers, R.           | P-730                             | Collins, L.           | P-687   |
|                    |   | Chamberlain, N.        | P-044                             | Colonna, V.           | P-427   |
|                    |   | Chamutpong, S.         | P-538                             | Comandi, S.           | O-128   |
|                    |   | Chan, Y.F.             | P-158, P-482                      | Comas, D.             | O-144, P-549, P-560, P-563, P-579                 |
|                    |   | Chang, A.              | P-384                             | Comas, I.             | P-692, UDMPA-10                                   |
|                    |   | Chang, K.              | P-188, P-714, P-715               | Comesaña Martínez, G. | P-072   |
|                    |   | Chao, L.               | P-527                             | Conceição, I.C.       | P-109   |
|                    |   | Chapman, C.            | UDMPA-08                          | Congiu, L.            | P-394   |
|                    |   | Charcosset, A.         | P-501                             | Constantin, S.        | P-616   |
|                    |   | Charlat, S.            | P-751                             | Convey, P.            | O-128   |
|                    |   | Charlebois, R.         | O-086                             | Coop, G.              | O-045, O-134, P-418                               |
|                    |   | Charles, W.            | P-371                             | Cooper, B.            | O-148   |
|                    |   | Charlesworth, B.       | O-053, O-106, P-111, P-117, P-456 | Cooper, E.            | O-044, P-410                                      |
|                    |   | Charlesworth, D.       | O-107, O-125, P-504               | Copsey, L.            | O-099   |
|                    |   | Chatrou, L.            | P-098                             | Corander, J.          | P-542   |
|                    |   | Chaumot, A.            | O-187                             | Coraor, N.            | P-085   |
|                    |   | Chavez-Sandoval, B.E.  | P-719                             | Corbi, J.             | P-447   |
|                    |   | Chaw, S.               | P-261, P-355                      | Cordaux, R.           | O-102   |
|                    |   | Chelo, I.M.            | P-453                             | Cordula, B.           | P-567   |
|                    |   | Chen, F.               | P-197                             | Corominas, M.         | P-126   |
|                    |   | Chen, H.               | P-633                             | Corral, J.            | P-557   |
|                    |   | Chen, J.               | P-053                             | Corral, J.M.          | P-201, P-271                                      |
|                    |   | Chen, K.               | P-633                             | Correia, A.M.         | P-615   |
|                    |   | Chen, S.               | P-002, P-548                      | Cortez, D.            | P-208   |
|                    |   | Chen, W.               | P-137                             | Corvelo, A.           | P-130   |
|                    |   | Chen, Z.J.             | O-055, O-157                      | Coscolla, M.          | P-692, UDMPA-10                                   |
|                    |   | Chenel, T.             | P-389                             | Cosson, J.            | P-664   |
|                    |   | Chevin, L.             | P-031, P-444                      | Costa, A.             | P-194   |
|                    |   | Chevret, P.            | P-101                             | Costa, V.             | P-002   |
|                    |   | Chiang, G.             | P-047                             | Costanzo, M.          | O-098, O-173                                      |
|                    |   | Chiapello, H.          | O-031, P-507                      | Costas, B.            | O-124   |
|                    |   | Chiaromonte, F.        | P-672                             |                       |   |

## AUTHOR INDEX (continued)

|                        |   |                       |                                   |                         |  |
|------------------------|---|-----------------------|-----------------------------------|-------------------------|--|
| Costas, J.             | P-731   | De Villiers, D.       | P-543                             | Du, L.                  | PL-1                                     |
| Cotton, J.             | P-510   | Dean, J.              | P-525                             | Dubchak, I.             | O-050                                    |
| Cottrell, J.           | P-628   | Dean, M.              | P-277                             | Dufayard, J.F.          | P-057                                    |
| Coucheron, D.          | O-083, P-134, P-207, P-326                      | Dean, M.D.            | O-135                             | Duffy, S.               | P-527, P-669                             |
| Couloux, A.            | P-255, P-256                                    | DeBerardinis, J.      | UDMPA-04                          | Dufkova, P.             | P-381                                    |
| Couvreur, T.           | P-098   | Debiais Thibaud, M.   | O-189, P-189                      | Duggan, A.              | O-120, UDMPA-03                          |
| Cox, A.                | P-469   | Degenhardt, J.        | O-146                             | Dumont, B.              | P-337                                    |
| Cozzolino, S.          | P-568   | Degnan, J.            | O-141, P-582                      | Duprat, E.              | P-059, P-119                             |
| Crandall, K.           | O-112, P-333                                    | Del Cerro, I.         | P-602                             | Durbin, R.              | O-048, P-415                             |
| Crandall, K.A.         | P-356   | Delabie, J.           | P-564                             | Duret, C.               | P-712                                    |
| Cranston, K.           | O-016   | Delaye, L.            | P-217                             | Duret, L.               | P-057, P-183, P-225, P-414, P-445, WF-06 |
| Cravedi, J.            | P-015   | Delfin, F.            | P-572                             | Dutheil, J.             | O-161, P-061, P-202, P-447               |
| Crawford, D.           | O-176, P-159, P-163                             | Delgado, J.D.         | P-364                             | Duvaux, L.              | P-101, P-705                             |
| Crease, T.             | P-713   | Dell'Ampio, E.        | P-025                             | Duveau, F.              | P-652                                    |
| Creely, H.             | P-268   | Delneri, D.           | O-101, P-408                      | Dvora, S.               | P-315                                    |
| Crespi, B.             | P-368   | Delport, W.           | P-077                             | Dyer, K.                | O-066                                    |
| Cristina, X.           | CS-2  | Delprat, A.           | P-720                             |                         |  |
| Cruz Rodríguez, F.     | P-417   | Delsuc, F.            | O-187, P-262, P-357               | <b>E</b>                |  |
| Cuevas, J.             | O-026   | Denamur, E.           | O-031                             | Ebersberger, I.         | P-340                                    |
| Cui, Y.                | P-285   | Dennehy, J.           | P-527                             | Ebert, D.               | P-227                                    |
| Cummins, C.            | P-248   | Denoeud, F.           | P-264                             | Echegaray, J.           | P-409, P-486, P-612                      |
| Cunha Almeida, F.      | P-411   | Denver, D.            | O-024, P-219                      | Ecker, J.               | O-044, P-494                             |
| Cunningham, A.         | P-537   | Depaulis, F.          | P-574                             | Edwards, S.             | P-527                                    |
| Curik, I.              | P-548   | Dermitzakis, E.       | P-469                             | Egas, M.                | P-034                                    |
| Cusack, B.             | P-183   | Derome, N.            | P-710                             | Egea, R.                | P-058                                    |
|                        |   | Desai, M.             | P-523                             | Egholm, M.              | PL-1, P-177, P-266                       |
| <b>D</b>               |   | DeSalle, R.           | O-022, P-411, P-533, P-634        | Ehrenreich, I.          | P-045, P-048                             |
| D'Anatro, A.           | P-587   | Deschavanne, P.       | P-052                             | Eichler, E.             | P-265                                    |
| D'Aniello, S.          | P-027   | Desmond, E.           | P-347                             | Eickbush, T.H.          | P-734                                    |
| D'Antonio, M.          | P-080   | Destro-Bisol, G.      | P-426, P-579                      | Eilertson, K.           | P-221                                    |
| D'Aubenton-Carafa, Y.  | P-189   | Deusch, O.            | O-041                             | Eirin-López, J.M.       | P-172, P-179                             |
| D'Erchia, A.           | P-080   | Devos, D.             | O-042                             | Eisen, M.               | P-143, P-164                             |
| D'Onorio De Meo, P.    | P-080   | Dickins, B.           | P-487                             | Eisenhardt, C.          | O-091                                    |
| Da Fonseca, R.         | P-484, P-489                                    | Dickson, M.           | P-158                             | Eisler, H.              | O-131                                    |
| Da Lage, J.            | P-390   | Ding, L.              | O-102                             | Ekman, J.               | P-600                                    |
| Da Silva, C.           | O-138, P-189, P-264                             | Ding, Y.              | O-007                             | Elalouf, J.             | P-319                                    |
| Dagan, T.              | O-009, O-041, P-216, P-508, P-645, P-683, P-684 | Dionisio, F.          | P-673                             | Elango, N.              | P-167                                    |
| Damerval, C.           | P-447, P-501                                    | Doadrio, I.           | P-332, P-333, P-391, P-529, P-584 | Eldon, B.               | P-660                                    |
| Danneman, M.           | P-268   | Doepkes, D.           | P-616                             | Elias, M.               | P-353                                    |
| Darimont, C.           | P-613   | Doherty, M.           | O-124                             | Ellegren, H.            | O-062, P-182, P-706                      |
| Darras, A.             | P-254   | Dolan, P.             | O-024                             | Ellis, W.               | P-543                                    |
| Darré - Toulemonde, F. | P-265   | Dolezel, J.           | P-636                             | Elyashiv, E.            | O-047                                    |
| Daubin, V.             | O-089, O-090, P-751                             | Domiguez-Domiguez, O. | P-332                             | Emadzade, K.            | P-320                                    |
| David, J.              | P-455   | Dominguez, O.         | P-391                             | Emblem, Å.              | P-134                                    |
| David, O.              | O-073   | Donaher, N.           | P-274                             | Emerson, B.             | P-366, P-556                             |
| David, R.              | P-476   | Donald, H.            | O-102                             | Emerson, J.             | O-152, P-289                             |
| Davies, J.             | P-051   | Donnelly, P.          | O-143                             | Emery, L.               | P-198                                    |
| Davies, N.             | P-751   | Donoghue, M.          | P-089, P-196                      | Emes, R.                | P-175                                    |
| Davis, J.              | P-525   | Donoghue, P.          | O-177                             | Emili, A.               | O-098                                    |
| Davis, R.              | P-525   | Donohue, K.           | P-47, P-371                       | Emiliani, G.            | P-331                                    |
| Dawson, K.             | P-457, P-500                                    | Doolittle, F.         | UDMPA-06                          | Enard, D.               | P-732                                    |
| De Dieuleveult, M.     | P-319   | Dopazo, H.            | P-055, P-185                      | Enard, W.               | PL-1, P-032                              |
| De Filippo, C.         | P-426   | Dopazo, J.            | O-003, P-055, P-430               | Endo, T.                | P-091                                    |
| De Kochko, A.          | P-712   | Dörtschuck, E.        | P-307                             | Engelhardt, B.          | P-104                                    |
| De la Mare, M.         | P-712   | Dorus, S.             | P-078                             | Eory, L.                | P-246                                    |
| De la Rúa, C.          | UDMPA-09  | Doucet Beaupré, H.    | P-243                             | Escriva, H.             | P-015                                    |
| De La Vega, F.         | P-454   | Douzery, E.           | O-021, O-187, P-094, P-262        | Espregueira Themudo, G. | P-325                                    |
| De Matos Simoes, R.    | P-340   | Douzery, E.J.         | O-163                             | Esser, C.               | P-216                                    |
| De Meaux, J.           | P-041, P-466                                    | Dowling, T.           | P-584                             | Estenban, P.            | P-471                                    |
| De Neergaard, R.       | P-592   | Drayna, D.            | P-480                             | Estivill, X.            | O-006, P-209                             |
| De Souza, J.           | P-086   | Droege, M.            | CS-1                              | Estoup, A.              | P-564, P-664                             |
| De Souza, S.           | P-086, P-151                                    | Drummond, A.          | O-178                             | Ettema, T.              | O-002                                    |
| De Ungria, M.C.        | P-572   | Drummond, D.          | P-231, P-435                      | Ettwiller, L.           | P-128                                    |
|                        |   | Du Pasquier, L.       | P-227                             | Evans, B.               | P-136, WF-03                             |

|                       |   |                     |                                   |                                |  |
|-----------------------|---|---------------------|-----------------------------------|--------------------------------|--|
| Evans, J.             | P-220   | Foll, M.            | P-472                             | García Guerreiro, M.P.         | P-719  |
| Evelyne, H.           | P-547   | Fondi, M.           | P-331                             | García, J.A.L.                 | P-299  |
| Everett, M.           | O-176   | Fonseca, M.M.       | P-283                             | García, K.                     | P-724  |
| Excoffier, L.         | P-655   | Fonseca, N.         | P-191                             | García-Dorado, A.              | P-671  |
| Exum, A.              | P-162   | Fontanillas, P.     | P-139                             | García-Fernández, J.           | P-026, P-027   |
| Eyras, E.             | O-039, P-130  | Fontdevila, A.      | O-139, P-719                      | García-Paris, M.               | P-611, P-663   |
| Eyre-Walker, A.       | O-025, O-043, P-732   | Forest, A.          | P-504                             | García-Verdugo, J.M.           | P-697  |
| Eyun, S.              | P-082   | Forget, L.          | P-329                             | Gardiner, A.                   | P-121  |
|                       |   | Fornek, A.          | P-740                             | Garrido-Ramos, M.              | P-702  |
| <b>F</b>              |   | Forterre, P.        | P-208, P-346, P-347               | Gatesy, J.                     | P-330  |
| Fabiani, A.           | P-604   | Fortunato, A.       | P-100                             | Gauffre, B.                    | P-664  |
| Fabre, P.             | O-021, P-094  | Fosse, P.           | P-319                             | Gaut, B.                       | O-044, P-494   |
| Fadhlaoui-Zid, K.     | P-560   | Foucaud, J.         | P-564                             | Gavory, F.                     | P-189  |
| Fagan, C.             | P-210   | Fournier, D.        | P-564                             | Gazave, E.                     | P-265  |
| Falahati-Anbaran, M.  | P-558   | Fournier, E.        | P-507                             | Gebauer-Jung, S.               | P-067  |
| Falush, D.            | O-035   | Fouvry, L.          | P-709, P-710                      | Gehring, W.                    | O-192  |
| Fanciulli, P.P.       | P-556   | Fox, A.             | P-670                             | Gempe, T.                      | O-138  |
| Fang, S.              | P-462   | Fragata, I.         | P-490                             | Gendrault-Jacquemard, A.       | P-507  |
| Fani, R.              | P-331   | Franchini, L.       | P-151                             | Gentile, G.                    | P-604  |
| Fardella, G.          | P-427   | Francino, M.P.      | O-030                             | Georges, M.                    | P-030  |
| Fares, M.             | O-008, O-116, P-072, P-073, P-458                             | Francis, J.         | P-313                             | Georgi, F.                     | O-091  |
| Faria, R.             | P-598   | Francois, O.        | O-034, P-069                      | Geraldes, A.                   | P-383  |
| Farré, D.             | P-145   | Frank, C.           | P-292                             | German Mouse Clinic Consortium | P-032  |
| Farré, M.             | P-270   | Franke, J.          | O-042                             | Germon, I.                     | O-189  |
| Faruk, S.             | O-112   | Frati, F.           | O-128, P-025, P-556               | Germonpré, M.                  | P-616  |
| Fawcett, J.           | P-229   | Frederic, B.        | WF-01                             | Gerrard, D.                    | P-304  |
| Fay, J.               | O-169   | Freedman, B.        | P-536                             | Gharizadeh, B.                 | P-743  |
| Fay, M.               | P-665   | Freeman, C.         | O-143                             | Giaever, G.                    | O-098  |
| Fayard, J.            | P-034   | Frehlick, L.        | P-172                             | Giannini, R.                   | P-331  |
| Fedigan, L.           | P-028   | French-Constant, R. | P-044                             | Gibbs, R.                      | O-141  |
| Fehrer, J.            | P-745   | Freyhult, E.        | P-285                             | Gibson, B.                     | P-383  |
| Feil, E.              | P-694   | Friberg, U.         | P-412                             | Gignoux, C.                    | P-104  |
| Feldman, M.           | O-045, O-100, O-115, P-523                                    | Frilander, M.       | P-029, P-495                      | Gil, R.                        | P-217  |
| Félix, M.             | O-093, P-652  | Froment, A.         | O-052, P-480                      | Gilad, Y.                      | O-172, P-133, P-156                                    |
| Ferguson, W.          | P-315   | Froschauer, A.      | P-255, P-256                      | Gilbert, D.                    | P-454  |
| Fernández, I.         | P-548   | Frost, R.           | P-050                             | Giovanelli, J.                 | P-620  |
| Fernández, L.         | P-546   | Froula, J.          | O-030                             | Giraldo, J.                    | P-299  |
| Fernández-Sánchez, J. | P-516   | Fuchs, H.           | P-032                             | Giraud, T.                     | P-507  |
| Fernando, O.          | P-443   | Fukova, I.          | P-396                             | Gissi, C.                      | P-259, P-260   |
| Ferrand, N.           | P-007, P-008, P-046, P-403, P-611, P-623, P-625, P-663, P-707 | Fukumoto, S.        | P-464, P-499                      | Glass, S.                      | P-713  |
| Ferrand, Y.           | P-623   | Fung, H.            | O-141                             | Glemin, S.                     | O-119, P-455   |
| Ferrando, A.          | P-565   | Fuselli, S.         | P-426, P-426                      | Glöckner, G.                   | P-211  |
| Ferreira, Z.          | P-440, P-441  | Fuss, J.            | P-186                             | Glos, J.                       | O-183  |
| Ferrer-Admetlla, A.   | P-301, P-305  | Futschik, A.        | P-433                             | Gnerre, S.                     | O-121, P-492   |
| Ferro, J.             | P-569   |                     |                                   | Go, Y.                         | O-077, P-139, P-238                                    |
| Feschotte, C.         | O-102, P-727  | <b>G</b>            |                                   | Godinho, R.                    | P-007, P-008, P-046, P-631, P-632                      |
| Fescymere, H.         | P-495   | Gabalón, T.         | O-003, O-009, O-040, P-055, P-327 | Gojobori, T.                   | O-166, P-006, P-018, P-124, P-152, P-290, P-291, P-648 |
| Feulner, P.           | P-316   | Gadagkar, S.        | P-165                             |                                |  |
| Fierst, J.            | P-386   | Gaggiotti, O.       | P-472                             | Golding, B.                    | O-085  |
| Filatov, D.           | O-018, P-084, P-603   | Gagneux, S.         | O-115                             | Goldstein, R.                  | P-309  |
| Findlay, G.           | P-112   | Gaidos, E.          | P-228                             | Gómez, A.                      | P-595  |
| Finet, C.             | P-125   | Gailus-Durner, V.   | P-032                             | Gómez, F.                      | O-076  |
| Finet, S.             | P-059   | Gaitero, T.         | P-529                             | Gómez-Moliner, B.              | P-621  |
| Fiore-Donno, A.       | P-065   | Galán, P.           | P-596                             | Gompert, Z.                    | P-353  |
| Fischer, A.           | P-177   | Galewski, T.        | O-021                             | Goncalves, D.                  | P-623  |
| Fischer, M.           | P-076   | Galiana Arnoux, D.  | P-254, P-255, P-256               | Gonçalves, H.                  | P-611  |
| Fisher, D.            | P-523   | Gallego Romero, I.  | P-416                             | González Candelas, F.          | O-111, P-535, P-692, UDMA-10                           |
| Fiston-Lavier, A.     | P-741   | Gallie, J.          | O-174                             |                                |  |
| Fledel-Alon, A.       | P-418   | Galtier, N.         | O-087, O-119, P-094, P-262, P-455 | González Knowles, D.           | P-251  |
| Floumanhaft, M.       | P-742   | Gamauf, A.          | P-639                             | González, F.                   | O-026  |
| Flowers, J.           | P-624   | Gamón, M.Á.         | P-072                             | González, J.                   | O-103, P-728, P-733                                    |
| Flutre, T.            | P-119   | Ganko, E.           | P-736                             | González-Martínez, S.          | P-628  |
| Folch, J.             | P-003   | Gansner, M.         | P-300                             | González-Romero, R.            | P-179  |
|                       |   | Gante, H.           | P-584                             | Good, J.                       | O-135, P-177, P-266                                    |

## AUTHOR INDEX (continued)

|                     |                            |                  |  |                      |                     |
|---------------------|----------------------------|------------------|--|----------------------|---------------------|
| Goodenow, M.M.      | P-302                      | Halligan, D.     | P-111                                    | Higueta, D.          | P-421               |
| Goodisman, M.       | P-171                      | Hallsworth, C.   | P-522                                    | Hill, D.             | P-306               |
| Goodman, S.         | P-537                      | Halos, S.        | P-572                                    | Hirai, M.            | P-461               |
| Goodwin, L.         | O-104                      | Halvarsson, P.   | P-600                                    | Hiramatsu, C.        | P-028               |
| Gophna, U.          | P-303, P-729               | Hamady, M.       | P-092, P-314                             | Hirata, T.           | P-018               |
| Gordo, I.           | P-673, P-674, WF-04        | Hamon, P.        | P-712                                    | Hirbo, J.            | O-052               |
| Gordon, J.          | P-314                      | Hamon, S.        | P-712                                    | Hirose, S.           | P-124               |
| Gosalbes, M.J.      | O-029, P-217, P-697        | Han, K.          | O-104                                    | Hishiki, T.          | P-291               |
| Gosálbez, J.        | P-570                      | Han, L.          | P-239                                    | Hiwatashi, T.        | P-028               |
| Götherström, A.     | O-147                      | Han, M.          | O-067                                    | Höber, B.            | P-177               |
| Gotzek, D.          | P-298                      | Hanada, K.       | P-461                                    | Hobolth, A.          | O-161, P-202, P-601 |
| Goudet, J.          | P-416                      | Hanel, R.        | P-581                                    | Hobza, R.            | P-700               |
| Gout, J.            | WF-06                      | Hanna, W.        | P-567                                    | Hodges, S.           | P-410               |
| Gouy de Bellocq, J. | P-406                      | Hansen, T.       | P-386                                    | Hodgkinson, A.       | O-025               |
| Gouy, M.            | O-081, O-089, P-057        | Hanski, I.       | P-029, P-495, P-542                      | Hoede, C.            | O-031               |
| Goyache, F.         | P-548                      | Hanzawa, Y.      | P-045, P-624                             | Høeg, J.T.           | P-356               |
| Grandbastien, M.    | P-717                      | Hardouin, E.     | O-060                                    | Hoeglund, A.         | P-186               |
| Granka, J.          | O-149                      | Hardy, J.        | O-141                                    | Hoeh, W.             | P-243               |
| Grant, J.           | P-686                      | Haring, E.       | P-637, P-638, P-639                      | Hoekstra, H.         | O-061               |
| Grant, P.           | O-184                      | Harper, A.       | P-603                                    | Hoerandl, E.         | P-320               |
| Grath, S.           | UDMPA-02                   | Harris, D.J.     | P-283                                    | Hoffman, E.          | P-171               |
| Gratton, P.         | P-096                      | Harris, J.       | P-608                                    | Höffner, B.          | P-177               |
| Graur, D.           | O-010                      | Harrison, R.     | P-408                                    | Hofreiter, M.        | P-550, P-616, P-618 |
| Gray, M.            | O-149                      | Harrod, C.       | P-395                                    | Hokamp, K.           | P-072               |
| Gray, R.R.          | P-302                      | Hartl, D.        | O-133, O-173, P-139, P-520, P-668, P-701 | Holbrook, J.         | P-175               |
| Graziussi, D.       | O-192                      | Hasselmann, M.   | O-138                                    | Holland, B.          | P-512               |
| Green, E.           | P-372                      | Haubold, B.      | P-123                                    | Holland, N.          | P-015               |
| Green, R.           | PL-1, P-266                | Hauck, C.        | P-304                                    | Holland, P.          | P-191               |
| Gribaldo, S.        | P-208, P-331, P-346, P-347 | Haudry, A.       | P-455                                    | Hollocher, H.        | O-131               |
| Griggio, F.         | P-259                      | Haugen, P.       | P-065                                    | Holmes, E.           | P-669               |
| Grimwood, J.        | P-158, P-482               | Haugli, K.       | O-083, P-065                             | Holmes, I.           | O-165               |
| Gros, P.            | P-649                      | Hautier, L.      | O-021                                    | Holton, T.           | P-341               |
| Gruenheit, N.       | O-009, O-041               | Hayashi, C.      | P-334                                    | Homolka, S.          | O-115               |
| Gueguen, L.         | P-062                      | Hayden, S.       | P-247                                    | Horn, S.             | P-618               |
| Guermonprez, H.     | P-739                      | He, B.           | P-160, P-174                             | Horton, M.           | P-635               |
| Guerreiro, R.       | O-141                      | Headon, D.       | P-037                                    | Hosoya, T.           | WF-07               |
| Guigo, R.           | P-126                      | Hebert, P.       | P-743                                    | Hospital, F.         | P-031, P-444        |
| Guiguen, Y.         | P-255                      | Heckel, D.G.     | P-067                                    | Howad, W.            | P-502               |
| Guillet, C.         | P-183                      | Heddi, A.        | P-217                                    | Howe, D.             | O-024               |
| Guillot, G.         | O-036                      | Heeb, P.         | P-593                                    | Hoyle, D.            | P-408               |
| Guirao, S.          | P-116                      | Hegay, T.        | P-030                                    | Hoyos, E.            | P-652               |
| Gunnarsdottir, E.   | P-572                      | Heidel, A.       | P-211                                    | Hrabe de Angelis, M. | P-032               |
| Gurbich, T.         | P-704                      | Heinze, B.       | P-628                                    | Hribova, E.          | P-636               |
| Gürtler, R.         | P-534                      | Helaers, R.      | P-651                                    | Hu, H.               | O-058               |
| Gušić, I.           | PL-1, P-266                | Helgason, A.     | O-140                                    | Hu, T.               | O-044, P-494        |
| Gutiérrez-Gil, B.   | P-005                      | Hellenthal, G.   | O-035                                    | Hu, X.               | O-057               |
| Guyomard, R.        | P-621                      | Hemmerter, S.    | P-554                                    | Huang, Q.            | P-667               |
| Guyot, R.           | P-712                      | Hendy, M.        | P-512                                    | Huang, W.            | UDMPA-01            |
|                     |                            | Henk, B.         | P-476                                    | Huang, Y.            | P-295, P-635        |
| <b>H</b>            |                            | Henn, B.         | P-103, P-104                             | Hua-Van, A.          | P-726               |
| Ha, M.              | O-55, O-157                | Henrichsen, C.N. | P-147                                    | Hubisz, D.           | P-429, P-484        |
| Haag, C.            | O-125, P-029, P-044        | Henrik, K.       | O-070                                    | Huchon, D.           | P-317, P-318        |
| Haag-Liautard, C.   | O-023                      | Hense, W.        | P-153                                    | Huelsenbeck, J.      | P-367               |
| Habib, K.A.         | P-748                      | Hernández, D.    | O-141                                    | Huerta Cepas, J.     | O-003, P-055        |
| Haddad, C.          | P-620, P-626               | Hernández, R.    | O-027, O-057, P-429                      | Hufthammer, A.K.     | P-618               |
| Hadrill, P.         | O-151                      | Herrmann, M.     | P-323                                    | Hughes, D.           | P-215               |
| Hadrys, H.          | O-074, P-014, P-352        | Hershberg, R.    | O-115                                    | Huh, J.              | P-188, P-714, P-715 |
| Haerum, B.          | O-054, P-017               | Heuertz, M.      | P-665                                    | Huisman, J.          | P-409               |
| Haggerty, L.        | P-203, P-226               | Hewett, E.       | P-300                                    | Hunt, B.             | P-171               |
| Hahn, B.            | P-634                      | Heyer, E.        | P-030, P-423, P-561                      | Hurles, M.           | P-572               |
| Hahn, M.            | O-067                      | Hickerson, M.    | P-617, UDMPA-01                          | Hurst, L.            | O-012, P-263        |
| Hailer, F.          | P-409                      | Hidalgo, A.      | P-350                                    | Hurtz, C.            | P-683, P-684        |
| Hajibabaei, M.      | P-743                      | Higgins, B.      | O-109                                    | Hurwitz, B.          | O-016               |
| Hall, J.            | P-371                      | Higgs, P.        | P-474, P-475                             |                      |                     |

|                     |                                   |                       |  |                   |                                   |
|---------------------|-----------------------------------|-----------------------|--|-------------------|-----------------------------------|
| Hutter, S.          | P-105, P-153                      | Jónsson, B.           | P-158                                    | Kim, K.           | P-652                             |
| Huttley, G.         | P-090                             | Jordan, M.            | P-539                                    | Kim, M.           | P-714, P-715                      |
| Huynen, M.          | O-003                             | Jordan, W.            | P-121                                    | Kim, S.           | P-223                             |
| Hwang, J.           | P-290                             | Jordana, J.           | P-565                                    | Kim, Y.           | O-064, P-188, P-488, P-714, P-715 |
| <b>I</b>            |                                   |                       |  |                   |                                   |
| Iannelli, F.        | P-259, P-260                      | Jorde, L.             | P-579                                    | King, K.          | O-037                             |
| Ibrahim, M.         | O-052                             | Jørgensen, F.G.       | P-224                                    | Kingan, S.        | O-133                             |
| Igarashi, K.        | P-425                             | Joron, M.             | P-044                                    | Kingsley, D.      | P-158, P-482                      |
| Igea, J.            | P-358                             | Joseph, J.            | P-628                                    | Kin-Ichiro, M.    | P-152                             |
| Ikeo, K.            | O-166, P-6, P-124, P-290, P-648   | Joss, J.              | P-723                                    | Kirilchik, S.     | P-337                             |
| Ilan, M.            | P-317                             | Joy, J.               | P-368                                    | Kirschbaum, F.    | P-316                             |
| Imamura, H.         | P-676                             | Joyner-Matos, J.      | UDMPA-07                                 | Kishino, H.       | P-066                             |
| Imanishi, T.        | P-291                             | Juan, C.              | P-562, P-573                             | Kitchen, A.       | P-399                             |
| Indap, A.           | O-037, O-057, P-429               | Juan, E.              | P-149, P-170                             | Kitron, U.        | P-534                             |
| Ingle, C.           | P-469                             | Jubin, C.             | P-264                                    | Klingenspor, M.   | P-215                             |
| Ingvarsson, P.      | P-628                             | Juenger, T.           | P-236                                    | Knapp, M.         | P-550                             |
| Innan, H.           | O-136, P-028, P-142, P-465        | Jugo, B.              | P-724                                    | Knight, J.        | PL-1                              |
| Innocenti, P.       | P-477                             | Jump, A.              | P-448                                    | Knight, R.        | P-092, P-314                      |
| Inoko, H.           | P-006                             | Junqueira, A.C.       | P-344, P-362                             | Knowles, L.L.     | O-118                             |
| Irimia, M.          | P-0026, P-027, WF-05              | <b>K</b>              |  |                   |                                   |
| Ishibashi, M.       | P-155                             | Kaboli, M.            | P-750                                    | Ko, W.            | O-076                             |
| Itoh, T.            | O-156                             | Kadam, S.             | P-168                                    | Kobayashi, H.     | P-006                             |
| Iturbe-Ormaetxe, I. | P-235                             | Kaessmann, H.         | P-039, P-040, P-043, P-147, P-242, WF-02 | Koblmueller, S.   | P-336                             |
| Ivanoff, D.         | P-616                             | Kahn, D.              | O-090                                    | Koenig, J.        | UDMPA-06                          |
| Ivanova, N.         | P-440, P-441                      | Kaiser, V.            | P-456                                    | Kohl, G.          | P-567                             |
| Iwase, M.           | P-138                             | Kamari, S.            | P-640, P-641                             | Kohlbacher, O.    | P-186                             |
| Izagirre, N.        | UDMPA-09                          | Kameoka, Y.           | O-137                                    | Kolokotronis, S.  | P-533                             |
| <b>J</b>            |                                   |                       |  |                   |                                   |
| Jaillon, O.         | P-264, WF-06                      | Kaneko, S.            | P-135                                    | Komiyama, T.      | P-006                             |
| Jakobsson, M.       | O-034, O-141                      | Kaplan, Z.            | P-745                                    | Kondo, R.         | P-464, P-499                      |
| Jamba, M.           | P-431                             | Kapralov, M.          | O-018                                    | Kondrashov, A.    | O-050, P-280                      |
| Janies, D.          | O-117                             | Karl, S.              | P-196                                    | Kondrashov, F.    | O-050, P-280                      |
| Janko, K.           | P-363                             | Karlins, E.           | O-146                                    | Konnno, T.        | P-648                             |
| Janousek, B.        | P-339                             | Karlsen, B.O.         | P-134                                    | Konopinski, M.    | P-096                             |
| Janssen, A.         | P-034                             | Karr, T.              | O-068, P-078                             | Koonin, E.        | P-280                             |
| Jaris, H.           | O-124                             | Karro, J.             | P-676                                    | Koornneef, M.     | P-041                             |
| Jarne, P.           | P-722                             | Karyadi, D.           | O-146                                    | Kopp, J.          | P-536                             |
| Jastroch, M.        | P-215                             | Kassahn, K.           | P-515                                    | Kordis, D.        | P-193                             |
| Jaume, D.           | P-562, P-573                      | Katz, L.              | O-124, P-686, UDMPA-04                   | Kornobis, E.      | P-597                             |
| Jeffares, D.        | P-469                             | Kawamura, S.          | P-028, P-241, WF-07                      | Kosintsev, P.     | P-616                             |
| Jégou, B.           | WF-02                             | Kayser, M.            | P-528, P-572                             | Kosiol, C.        | P-484                             |
| Jensen, J.          | O-069                             | Keebler, J.           | P-311                                    | Kost, C.          | O-174                             |
| Jeong, D.           | P-748                             | Kefi, R.              | P-319                                    | Koufopanou, V.    | P-505                             |
| Jeong, S.           | O-175                             | Keightley, P.         | O-023                                    | Kovner, A.        | UDMPA-04                          |
| Jernvall, J.        | O-185                             | Keinan, A.            | P-544                                    | Krahulcova, A.    | P-745                             |
| Jia, W.             | P-475                             | Kejnovsky, E.         | P-700                                    | Krak, K.          | P-745                             |
| Jiggins, C.         | P-044, P-353                      | Keller, L.            | O-063                                    | Kramer, E.        | P-371                             |
| Jiggins, C.D.       | P-067                             | Kelley, J.            | P-286                                    | Krause, J.        | PL-1, P-266                       |
| Jiménez-Delgado, S. | P-027                             | Kelley, T.            | P-227                                    | Krauss, V.        | O-091                             |
| Jiménez-Lozano, N.  | P-093                             | Kelso, J.             | PL-1, O-058, P-266                       | Kreitman, M.      | P-023, P-160, P-494               |
| Jin, L.             | P-572                             | Kergoat, G.           | P-564                                    | Kremer, K.        | O-115                             |
| Jobs, D.            | O-112                             | Khadjeh, S.           | P-014                                    | Krishna, S.       | P-469                             |
| Joets, J.           | P-717                             | Khaitovich, P.        | O-058, P-137                             | Kristjánsson, B.  | P-597                             |
| Johan, V.           | O-002                             | Khanaev, I.           | P-337                                    | Krogh, A.         | P-469                             |
| Johansen, S.        | O-083, P-065, P-134, P-207, P-326 | Khang, T.F.           | P-545                                    | Kronholm, I.      | P-041                             |
| Johnson, P.         | P-266, P-698                      | Khodjet Ell Khill, H. | P-560                                    | Kruckenhauser, L. | P-637, P-638                      |
| Johnson, R.         | P-536, P-536                      | Kiethega, G.          | P-218                                    | Kryukov, A.       | P-639                             |
| Johnson, T.         | O-037                             | Kim, C.               | P-748                                    | Kryukov, K.       | O-166                             |
| Johnson, P.         | PL-1                              | Kim, D.               | P-188                                    | Kubat, Z.         | P-700                             |
| Johnston, S.        | P-543                             | Kim, E.               | O-055                                    | Kubatko, L.       | P-582                             |
| Jones, D.           | P-356                             | Kim, G.E.             | P-748                                    | Kučan, Z.         | PL-1, P-266                       |
| Jones, F.           | P-482                             | Kim, H.               | P-188, P-424, P-714, P-715               | Kucera, H.        | P-368                             |
|                     |                                   | Kim, H.S.             | P-646                                    | Kudaravalli, S.   | O-045                             |
|                     |                                   |                       |  | Kuehl, J.         | O-030                             |
|                     |                                   |                       |  | Kuittinen, H.     | P-042                             |
|                     |                                   |                       |  | Kumar, S.         | P-088, P-174, P-511               |
|                     |                                   |                       |  | Kumazawa, Y.      | O-181                             |

## AUTHOR INDEX (continued)

|                    |                                   |                    |   |                      |                     |
|--------------------|-----------------------------------|--------------------|---|----------------------|---------------------|
| Kumlehn, J.        | P-201                             | Lenkov, K.         | O-103, P-728                                    | Lovell, S.           | P-068               |
| Kupiec, M.         | O-100, P-729                      | Leonard, J.        | P-613   | Loytynoja, A.        | O-162               |
| Kuraku, S.         | P-249                             | Leonid, K.         | WF-08   | Lozano, E.           | P-436               |
| Kuremiya, E.       | P-499                             | Lepère, G.         | WF-06   | Lozupone, C.         | P-092, P-314        |
| Kuromori, T.       | P-461                             | Leppälä, J.        | P-042, P-388                                    | Lu, J.               | P-174               |
| Kutalik, Z.        | O-37                              | Lessa, E.          | P-493, P-587                                    | Lu, X.               | P-498               |
| Kvikstad, E.       | P-672                             | Levy, S.           | O-095   | Lu, Z.               | P-667               |
| Kvist, J.          | P-029, P-495                      | Lexer, C.          | P-380, P-577, P-628, P-665                      | Lucas Lledó, J.I.    | P-679               |
| Kyes, S.           | P-469                             | Ley, R.            | P-314   | Ludwig, M.           | P-023               |
| <b>L</b>           |                                   |                    |   |                      |                     |
| Laayouni, H.       | O-144, P-301, P-530               | Li, H.             | P-434   | Luikart, G.          | P-002               |
| Lachaise, D.       | P-110, P-389                      | Li, J.             | P-212   | Luis, S.             | P-553               |
| Lachman, M.        | P-268                             | Li, W.             | O-001, O-096, P-168, P-237, P-239, P-289, P-294 | Lundemo, S.          | P-558, P-657        |
| Lachmann, M.       | P-137, P-518                      | Li, X.             | O-007, P-143                                    | Lurie-Weinberger, M. | P-303               |
| Ladoukakis, E.     | O-025                             | Li, Y.             | P-494, P-635, P-666                             | Luz, H.              | P-74                |
| Lagergren, J.      | O-084                             | Liang, H.          | O-096   | Lynch, M.            | P-679, P-725        |
| Lai, Y.            | P-261                             | Liao, B.           | P-282   | Lynch, V.            | O-186               |
| Lalueza-Fox, C.    | P-009                             | Liao, K.           | P-295   | Lyons, L.            | P-631, P-632        |
| Lambert, D.M.      | P-552                             | Librado, P.        | P-063   | Lyubetsky, V.        | P-511               |
| Lambert, N.        | P-039                             | Licciulli, F.      | P-080   | Lyver, P.            | P-552               |
| Lambot, M.         | P-039                             | Liedtke, D.        | O-188   | <b>M</b>             |                     |
| Lamelas, A.        | O-029, P-697                      | Lienau, E.K.       | O-022   | Mabuchi, K.          | O-181               |
| Landan, G.         | O-010, O-041                      | Light, J.          | P-399, P-476                                    | MacArthur, S.        | P-143               |
| Landweber, L.      | O-109                             | Lin, C.            | P-355   | Macas, J.            | P-700, P-718        |
| Lane, C.           | P-276                             | Lin, R.            | O-102   | MacCoss, M.          | P-112, P-277        |
| Lang, B.F.         | P-329                             | Lindsay, H.        | P-090   | MacHolán, M.         | P-381, P-619        |
| Lang, D.           | P-204, P-206                      | Linton, Y.         | P-351   | MacHordom Barbé, A.  | P-343               |
| Lang, M.           | P-149, P-170                      | Lipatov, M.        | O-103, O-115, P-728                             | MacHordom, A.        | P-621               |
| Lao, O.            | P-422, P-528                      | Liu, J.            | O-157   | Macías, J.           | P-093               |
| Lari, M.           | P-009                             | Liu, Q.            | P-124   | Macías-Hernández, N. | P-366               |
| Larracuenta, A.    | P-272                             | Liu, Z.            | P-092   | MacLean, C.          | P-682               |
| Larson, G.         | O-145                             | Lixín, P.          | WF-01   | Macpherson Mayol, E. | P-343               |
| Lartillot, N.      | O-081, P-357, P-521               | Llaneza, L.        | P-046, P-612                                    | Macpherson, E.       | P-551               |
| Lassig, M.         | P-161                             | Llorens, C.        | P-721   | Macpherson, J.       | O-103               |
| Latkolik, S.       | P-638                             | Lobell, A.         | P-460   | Macpherson, M.       | P-728               |
| Latorre, A.        | O-029, P-217, P-553, P-696, P-697 | Lobry, J.          | P-225   | Madani, K.           | P-255               |
| Laudet, V.         | O-187, P-015                      | Lockhart, P.       | P-512   | Madeira, M.J.        | P-621               |
| Laugier, C.        | P-319                             | Loftus, K.         | P-163   | Madsen, O.           | O-183               |
| Laurent, K.        | P-013                             | Lodgson, B.        | P-647   | Maere, S.            | P-229               |
| Laurenti, P.       | O-189                             | Lohmueller, K.     | P-428, P-429                                    | Maeso, I.            | P-026, P-027        |
| Lavrov, D.         | P-287                             | Lohse, K.          | P-744   | Magalhães, S.        | P-034               |
| Lawson Handley, L. | P-416                             | Loire, E.          | P-421   | Magnacca, K.         | P-747               |
| Lázaro, E.         | P-591                             | Loiseau, A.        | P-564   | Mahé, S.             | P-255               |
| Lazzaro, B.        | P-468                             | Long, A.D.         | P-453   | Mailund, T.          | O-161, P-202        |
| Le Breton, J.      | P-564                             | Long, J.           | P-419   | Makino, T.           | P-284               |
| Le Mouél, A.       | WF-06                             | Long, M.           | O-068, O-152                                    | Makova, K.           | P-672               |
| Le Rouzic, A.      | O-108                             | Loot, C.           | P-739   | Maksud, F.           | P-319               |
| Leblois, R.        | O-073, P-654                      | Lopes, H.          | O-068   | Malaspinas, S-A.     | PL-1                |
| Lebrun, M.         | P-507                             | Lopes, J.          | O-180   | Malats, N.           | P-430               |
| Lecharny, A.       | P-258                             | Lopes, S.          | P-046   | Mallick, S.          | O-121, P-492        |
| Leclercq, S.       | P-722                             | López Labrador, X. | P-535   | Manchenko, G.        | P-141               |
| Lecompte, E.       | P-101                             | López, A.          | P-375   | Manel, S.            | P-479               |
| Ledda, A.          | P-244                             | López, S.          | P-217, UDMA-09                                  | Mangiulli, M.        | P-080               |
| Lee, C.            | O-142, P-462, P-498               | López-Fanjul, C.   | P-671   | Manica, A.           | P-416               |
| Lee, J.            | O-104                             | López-Giráldez, F. | P-270, P-370                                    | Manicacci, D.        | P-447, P-501        |
| Lee, K.            | P-543                             | López-Leal, R.     | P-151   | Mank, J.             | O-062               |
| Lee, S.            | P-044, P-714, P-715, P-715        | López-León, M.D.   | P-734   | Mano, S.             | P-497               |
| Lee, Y.            | P-748, P-748                      | López-Sánchez, M.  | P-696   | Manyuan, L.          | WF-01               |
| Lefebure, T.       | P-234                             | López-Sánchez, P.  | P-731   | Manzke, L.           | P-215               |
| Legrand, D.        | P-110, P-389, P-390               | Lorenc, A.         | P-268   | Maquilan, G.         | O-109               |
| Lehmann, J.        | O-091                             | Lorente, B.        | P-430, P-530                                    | Marais, G.           | O-032, P-504, P-700 |
| Lehner, B.         | O-168                             | Lorenzen, E.       | P-592   | Marande, W.          | P-218               |
| Leinonen, P.       | P-042                             | Lorite, P.         | P-730   | Marcelino, V.        | P-620               |
|                    |                                   | Lott, S.           | P-023   | Marcet-Houben, M.    | P-327               |
|                    |                                   | Loughran, N.       | P-196, P-210                                    |                      |                     |

|                        |  |                      |                     |                   |  |
|------------------------|--|----------------------|---------------------|-------------------|--|
| Marden, J.             | P-495  | Medina, I.           | P-055, P-430        | Morgante, M.      | O-155  |
| Marec, F.              | P-396  | Megarry, M.          | P-117               | Moriyama, E.      | P-082  |
| Maričić, T.            | PL-1, P-266  | Meiklejohn, C.       | O-171               | Moriyama, H.      | P-022  |
| Marinho, M.A.          | P-344  | Meisel, R.           | O-067               | Morris, G.        | P-168  |
| Marion de Proce, S.    | P-111  | Melé, M.             | O-122, O-144        | Morrow, E.        | P-412  |
| Marjoram, P.           | O-044, P-494                                       | Melin, A.            | P-028               | Moses, A.         | O-048  |
| Markova, M.            | P-339  | Melo-Ferreira, J.    | P-707               | Moszczynska, A.   | P-713  |
| Markova-Raina, P.      | O-164  | Méndez, J.           | P-179               | Motiwale, M.      | P-278  |
| Marlétaz, F.           | P-125  | Mendizábal, I.       | P-549, P-560        | Mou, C.           | P-037  |
| Marmi, J.              | P-602  | Mendonça, A.         | P-481               | Moum, T.          | P-230  |
| Maron, J.              | P-557  | Merchán, T.          | P-529               | Mountain, J.      | P-103, P-104   |
| Marquès Bonet, T.      | P-265, P-432                                       | Merritt, T.          | P-644               | Mower, J.         | P-252  |
| Marques, A.            | P-039, P-040, P-043                                | Mesquita, N.         | P-615               | Moy, G.           | P-400  |
| Marques, A.C.          | WF-02  | Mestres, F.          | P-108, P-553        | Moya, A.          | O-026, O-029, O-111, P-217, P-535,<br>P-690, P-696, P-697, P-721 |
| Marquez, C.            | P-604  | Metcalfe, C.         | P-723               | Moyle, L.         | O-130  |
| Marshall, D.           | P-024, UDMA-03                                     | Meyer, A.            | O-132, P-304, P-395 | Mu, J.            | O-078  |
| Marshall, H.           | O-120  | Meyer, B.            | P-014               | Mueller, S.       | P-396  |
| Marthey, S.            | P-507  | Meyer, C.            | P-617               | Muenzel, F.       | P-397  |
| Martin, F.             | P-203, P-226                                       | Meyer, D.            | P-086, P-568        | Muir, G.          | P-603  |
| Martin, W.             | O-009, O-041, P-216, P-508,<br>P-645, P-683, P-684 | Meyer, E.            | P-232, P-236, WF-06 | Mularoni, L.      | P-244  |
| Martinelli, G.         | P-665  | Meyer, M.            | P-266               | Mulligan, C.J.    | P-662, UDMA-05   |
| Martínez Camacho, J.P. | P-734  | Meyer, T.            | O-104               | Mullikin, J.      | PL-1, O-123, P-177, P-544  |
| Martínez-Cruz, B.      | P-560  | Mezey, J.            | P-647               | Munclinger, P.    | P-381, P-449   |
| Martínez-Fernández, M. | P-404  | Micael, J.           | P-584               | Mundy, N.         | P-033  |
| Martínez-Fuentes, A.   | P-549  | Michaux, J.          | P-101               | Münk, C.          | P-307  |
| Martínez-Marigorta, U. | P-422  | Michiel, M.          | P-059               | Muñoz, J.         | P-194  |
| Martínez-Solano, I.    | P-663  | Michu, E.            | P-339, P-504        | Muñoz-Fuentes, V. | P-613  |
| Martinho, C.           | P-471  | Mignone, F.          | P-080               | Muñoz-López, M.   | P-730  |
| Masel, J.              | O-184  | Mila, B.             | P-593               | Munro, E.         | P-652  |
| Maside, X.             | O-106  | Milana, V.           | P-394               | Murigneux, A.     | P-501  |
| Masuda, R.             | WF-07  | Milinkovitch, M.     | O-004, P-651        | Murphy, D.        | P-079  |
| Matarin, M.            | O-141  | Millán, A.           | P-594               | Muschick, M.      | P-335, P-395   |
| Matos, M.              | P-483, P-490                                       | Millar, C.D.         | P-552               | Musilová, Z.      | P-363  |
| Matschiner, M.         | P-581  | Miller, M.           | O-072               | Musso, G.         | O-098, P-212   |
| Matsumoto, M.          | P-022  | Milloz, J.           | O-093, P-652        | Myers, R.         | O-045, O-078, P-158, P-482                                       |
| Matsumoto, Y.          | P-028, P-241                                       | Mineta, K.           | P-091, P-290        | Myers, S.         | O-143  |
| Matsuo, T.             | P-390  | Minhós, T.           | P-007, P-008        | Myoga, F.         | P-461  |
| Matthee, C.C.          | P-376  | Mira, A.             | O-005               |                   |  |
| Matz, M.               | P-232, P-236                                       | Miranda, R.          | P-391               |                   |  |
| Maughan, H.            | P-689  | Miro, A.             | O-126               | <b>N</b>          |  |
| Mavárez, J.            | P-385  | Misawa, K.           | P-677               | Nabholz, B.       | O-119, P-094   |
| Mavarez, J.            | P-393  | Mitani, H.           | P-241               | Nachman, M.       | O-170, P-222, P-277, P-383, P-398, P-403                         |
| Mayer, W.              | P-323  | Mitschke, J.         | P-186               | Nachman, M.W.     | O-135  |
| Mayo, S.               | P-665  | Mittenthal, J.       | P-646, P-685, P-695 | Nagel, D.         | P-550  |
| Mayor, A.              | P-305  | Miya, M.             | O-181               | Nakachi, M.       | P-022  |
| Mazan, S.              | P-189  | Miyamoto, S.         | P-648               | Nakagawa, S.      | P-152  |
| McAuliffe, J.          | P-469  | Mona, S.             | P-009, P-426        | Nam, K.           | P-706, P-748   |
| McCann, A.             | P-213  | Montchamp-Moreau, C. | P-709, P-710        | Nardi, F.         | O-128, P-556   |
| McClure, M.            | P-050, P-051, P-742                                | Monteiro, A.         | O-191               | Naruya, S.        | P-250, P-253   |
| McCole, R.             | P-711  | Monteiro, B.         | P-007, P-008        | Nasrallah, C.     | P-367  |
| McDonald, J.           | O-056  | Montero-Pau, J.      | P-595               | Naughton, B.      | P-104  |
| McGaughran, A.         | O-128  | Montgelard, C.       | P-376               | Navajas-Pérez, R. | P-702  |
| McGee, K.              | O-144, P-311                                       | Montiel, E.          | P-734               | Navarro, A.       | O-144, P-265, P-422, P-430,<br>P-432, P-443, P-530               |
| McGowen, M.            | P-330  | Montooth, K.         | O-171               | Navascués, M.     | P-574, P-575   |
| McGraw, E.             | P-235  | Mooers, A.           | P-368               | Naveira, H.       | P-596, P-731   |
| McInerney, J.          | P-203, P-226, P-510                                | Morales-Hojas, R.    | P-716               | Naydenov, K.      | P-640, P-641   |
| McKay, J.              | P-157  | Morán, P.            | P-546               | Nebot, M.         | O-097  |
| Mclysaght, A.          | P-251, P-281, P-297                                | Morán, T.            | O-139               | Necsulea, A.      | O-081, P-225   |
| McManus, G.            | O-124  | Morcillo, C.         | P-422, P-430        | Neef, A.          | P-696  |
| McMillan, O.           | P-067  | Moreau, H.           | P-148               | Negre, B.         | P-016, P-720   |
| McTaggart, S.          | O-125, P-227                                       | Moreno-Estrada, A.   | P-432               | Nei, M.           | P-540  |
| McVean, G.             | O-143  | Moretti, S.          | O-167               | Neidert, A.       | P-017  |
| Médigue, C.            | O-031  | Morgan, J.           | O-030               | Neinhuis, C.      | P-194  |
|                        |  | Morgan, K.           | O-127, P-351        |                   |  |

## AUTHOR INDEX (continued)

|                                     |  |                      |                                   |                       |  |
|-------------------------------------|--|----------------------|-----------------------------------|-----------------------|--|
| Nekrutenko, A.                      | P-085, P-487                             | Oliveira, R.         | P-046, P-360, P-631, P-632        | Patterson, D.         | P-686  |
| Nelson, G.                          | P-431, P-536                             | Oliver, S.           | O-101                             | Patterson, N.         | PL-1, O-123, P-492, P-544  |
| Nelson, M.                          | O-037                                    | Olivieri, I.         | P-034                             | Pattyn, P.            | O-044, P-494   |
| Nemcova, P.                         | P-636                                    | Olsen, E.            | O-148                             | Paulo, O.S.           | P-035  |
| Netter, P.                          | P-421                                    | Olteanu, M.          | O-073                             | Pauwels, M.           | P-470  |
| Neubauer, J.                        | O-121                                    | Omar, S.             | O-052                             | Pavesi, G.            | P-080  |
| Neumann, P.                         | O-718                                    | Ometto, L.           | O-063                             | Pavlidis, P.          | P-144  |
| Nevado, B.                          | P-336                                    | Ondrackova, M.       | P-605                             | Pawlowski, J.         | P-322  |
| Newbold, C.                         | P-469                                    | Oota, H.             | P-241                             | Pedraza, C.           | P-333  |
| Nguyen, N.                          | O-105, O-133                             | Opazo, J.            | O-015                             | Pegueroles, C.        | P-108  |
| Nicholas, M.                        | P-504                                    | Opiyo, S.            | P-082                             | Peñalosa-Espinosa, R. | P-563  |
| Nicolas, M.                         | P-013                                    | Orengo, D.           | P-113                             | Penel, S.             | P-057, P-445   |
| Nielsen, J.                         | P-121                                    | Orivel, J.           | P-564                             | Penny, D.             | P-512, P-687   |
| Nielsen, R.                         | O-057, O-114, O-153, P-429, P-463, P-484 | Ornelas-García, C.P. | P-332                             | Peñuelas, J.          | P-448  |
| Niemann, S.                         | O-115                                    | Oromí, P.            | P-366, P-562, P-573               | Perdices, A.          | P-332, P-606   |
| Niimura, Y.                         | P-152, P-238                             | Orsini, L.           | P-029, P-542                      | Perdigon, H.          | P-572  |
| Nijman, V.                          | P-750                                    | Osada, N.            | O-137, P-465                      | Pereira, M.           | WF-04  |
| Nilsson, O.                         | P-285                                    | Oshlack, A.          | P-133                             | Pereira, S.           | P-308  |
| NISC Comparative Sequencing Program | P-372                                    | Osman, M.            | O-052                             | Pereira, V.           | P-732  |
| Nishida, M.                         | O-181                                    | Ostrander, E.        | O-146, O-149                      | Pereira-Leal, J.      | P-481  |
| Nishina, H.                         | P-241                                    | Otte, M.             | O-138                             | Pérez, E.             | P-569  |
| Nislow, C.                          | O-098                                    | Oulion, S.           | P-189                             | Pérez-Bercoff, A.     | P-281  |
| Noda-Ogura, A.                      | P-290                                    | Ozawa, N.            | P-028                             | Pérez-Enciso, M.      | P-003, P-004   |
| Noel, B.                            | P-264, WF-06                             | Ozouf-Costaz, C.     | P-256                             | Pérez-Farrerons, A.   | P-149, P-170   |
| Nolte, A.                           | P-379                                    |                      |                                   | Pérez-Figueroa, A.    | P-671  |
| Non, A.L.                           | P-662                                    | <b>P</b>             |                                   | Pérez-Losada, M.      | O-112, P-356   |
| Noor, M.                            | P-272                                    | Pääbo, S.            | PL-1, O-058, P-032, P-177, P-266  | Pérez-Pardal, L.      | P-548  |
| Nordborg, M.                        | O-044, P-410, P-494, P-635               | Pace, J.             | P-727                             | Pérez-Serra, A.       | P-569, P-570   |
| Notredame, C.                       | O-160                                    | Padial, J.           | O-020                             | Perfectti, F.         | P-519  |
| Nourmohammad, A.                    | P-161                                    | Pae, S.              | P-748                             | Perfeito, L.          | WF-04  |
| Novembre, J.                        | O-037, O-045                             | Paffetti, D.         | P-331                             | Peris-Bondia, F.      | P-553  |
| Novick, P.                          | P-742                                    | Paggi, G.            | P-577                             | Permar, A.            | O-170  |
| Nowacki, M.                         | O-109, WF-06                             | Pain, A.             | P-469                             | Perotti, A.           | P-476  |
| Nunes, V.L.                         | P-035                                    | Paiva, S.            | P-565                             | Perriere, G.          | P-057  |
| Nussbaumer, M.                      | P-616                                    | Pajpachova, V.       | P-339                             | Perry, G.             | O-142  |
| Nutile, T.                          | P-427                                    | Pala, I.             | P-129                             | Pesole, G.            | P-080, P-259, P-260  |
| Nygaard, S.                         | P-469                                    | Palero, F.           | P-551                             | Petit, M.             | O-031  |
| Nymark, M.                          | P-207, P-326                             | Palma-Silva, C.      | P-568, P-577                      | Petit, N.             | P-107  |
|                                     |  | Palmer, J.           | P-252                             | Petrov, D.            | O-049, O-046, O-103, O-115, O-164,<br>P-158, P-482, P-525, P-728 |
| <b>O</b>                            |  | Palmieri, N.         | P-064                             |                       |  |
| O'Brien, S.                         | P-454                                    | Palomeque, T.        | P-730                             | Pfister, L.           | O-113, P-531   |
| O'Connell, M.                       | P-196, P-210                             | Pálsson, S.          | P-597                             | Pham, J.              | O-105  |
| O'Connor, B.                        | P-210                                    | Pan, D.              | P-181                             | Phelps, S.            | O-061  |
| O'Connor, T.                        | P-033                                    | Pankova, V.          | P-141, P-514                      | Philippe, H.          | O-014, P-357, P-521  |
| O'Keefe, K.                         | P-527                                    | Pantalacci, S.       | O-187                             | Philippe, M.          | P-319  |
| O'Loughlin, S.                      | O-127                                    | Papadopoulou, A.     | P-629                             | Pialek, J.            | P-381, P-406   |
| O'Neill, S.                         | P-235                                    | Papanicolaou, A.     | P-067, P-396                      | Picardi, E.           | P-080  |
| Oakey, R.                           | P-711                                    | Papp, B.             | O-101                             | Piccinali, R.         | P-534  |
| Oakley, T.                          | O-190                                    | Paps, J.             | P-373                             | Pickrell, J.          | O-045  |
| Ober, C.                            | P-418                                    | Paquet, P.           | P-613                             | Piganeau, G.          | P-148  |
| Ochman, H.                          | O-030                                    | Parent, C.           | P-365                             | Pignatelli, M.        | P-126, P-696   |
| Oda, S.                             | P-241                                    | Parfrey, L.          | P-686                             | Pils, S.              | P-304  |
| Ogereau, D.                         | P-709, P-710                             | Parida, L.           | O-122                             | Pinhasi, R.           | P-550  |
| Ogura, A.                           | P-169                                    | Paris, M.            | P-015                             | Pinheiro, F.          | P-568  |
| Ogura-Noda, A.                      | P-291                                    | Park, H.             | P-748                             | Piontkivska, H.       | P-306  |
| Ohshima, K.                         | P-425                                    | Parker, E.           | P-078                             | Pisani, D.            | P-099, P-341   |
| Ojeda García, A.                    | P-003, P-004                             | Parkhill, J.         | O-028                             | Pisano, D.G.          | P-430  |
| Okabe, Y.                           | P-028                                    | Parmentier, G.       | O-167                             | Pita, G.              | P-430  |
| Okayasu, T.                         | P-054                                    | Parsch, J.           | P-105, P-153, P-701, UDMPA-02     | Piyapan, P.           | P-413  |
| Okuloff, A.                         | P-042                                    | Pascual, M.          | P-108, P-483, P-490, P-551, P-576 | Pla, C.               | P-569, P-570   |
| Oleksiak, M.                        | P-162, P-478, P-485                      | Pascual-Anaya, J.    | P-027                             | Plachetzki, D.        | O-190  |
| Oleksyk, T.                         | P-431, P-454, P-536                      | Pasquet, P.          | P-030                             | Plagnol, V.           | P-428, P-494   |
| Oliva-Paterna, F.                   | P-584                                    | Pass, G.             | P-025                             | Planet, P.            | O-022  |
| Oliveira, C.                        | P-606                                    | Patricio, M.         | P-245                             | Plass, M.             | O-039  |

|                      |                                   |                                |                                  |                          |   |
|----------------------|-----------------------------------|--------------------------------|----------------------------------|--------------------------|---|
| Platt, A.            | P-635                             | Radovic, S.                    | O-155                            | Rivals, E.               | P-722   |
| Pokorny, P.          | P-638                             | Rafferty, I.                   | O-141                            | Rizzi, R.                | P-080   |
| Polak, P.            | P-184, P-678                      | Ragan, M.                      | P-515                            | Roach, J.                | O-115   |
| Poliakov, A.         | O-050                             | Rainey, P.                     | O-174                            | Robatzek, S.             | P-466   |
| Pollard, K.          | P-178                             | Raj, A.                        | O-094                            | Robertson, D.            | P-068   |
| Polyakova, N.        | P-402, P-590, P-749               | Rajabi-Maham, H.               | P-705                            | Robinson-Rechavi, M.     | O-167, P-012, P-417, P-445                      |
| Ponce de Leon, A.    | P-548                             | Ralf, R.                       | P-204, P-206                     | Robinson-Willmott, J.    | P-353   |
| Ponce, R.            | P-106                             | Ramalho, R.                    | P-086                            | Robledo-Arnuncio, J.J.   | P-659   |
| Poncet, B.           | P-479                             | Rambaut, A.                    | O-178, P-348                     | Rocha, E.                | O-031, P-199, P-200, P-694                      |
| Poncet, V.           | P-712                             | Ramirez, O.                    | P-004, P-446                     | Rocha, G.                | P-529   |
| Ponglikitmongkol, M. | P-538                             | Ramirez-Soriano, A.            | P-463                            | Rocha, J.                | P-007, P-008, P-440, P-441, P-471, P-559, P-707 |
| Pons, J.             | P-562                             | Ramos, D.                      | O-191                            | Roche, D.                | P-299   |
| Ponsà, M.            | P-270                             | Ramos, S.                      | P-217                            | Rockman, M.              | WF-08   |
| Pool, J.             | O-153                             | Ran, W.                        | P-474                            | Roderick, G.             | P-627   |
| Poonswad, P.         | P-538                             | Ranciaro, A.                   | O-052, P-480                     | Rodolphe, F.             | P-507   |
| Popkova, A.          | P-709, P-710                      | Rand, D.                       | O-171                            | Rodrigo, A.              | P-692, UDMPA-10                                 |
| Porcel, B.           | P-264, WF-06                      | Randi, E.                      | P-631, P-632                     | Rodrigue, N.             | P-075   |
| Posada, D.           | O-112, P-056, P-245, P-283, P-546 | Ranwez, S.                     | P-262                            | Rodríguez-Piñeiro, A.M.  | P-404   |
| Posto, A.            | O-130                             | Ranwez, V.                     | O-163, P-262                     | Rodríguez-Teijeiro, J.D. | P-409, P-486                                    |
| Potrzebowski, L.     | O-070, WF-02                      | Ratray, M.                     | O-101                            | Roecklin, D.             | P-015   |
| Poux, C.             | O-183, P-337                      | Ravelomanantsoa-Ratsimihah, J. | P-081                            | Roettger, M.             | O-041, P-508                                    |
| Powell, K.           | O-502                             | Ray, N.                        | P-655                            | Roger, A.                | P-275   |
| Prachumwat, A.       | P-294                             | Rea, A.                        | P-338                            | Rogers, R.               | P-668   |
| Pradervand, S.       | P-147                             | Reagon, M.                     | O-158                            | Rohland, N.              | P-550   |
| Prasad, A.           | P-372                             | Rebeiz, M.                     | O-175                            | Rokas, A.                | O-013   |
| Praz, F.             | P-421                             | Rebelo, H.                     | P-608                            | Rokhsar, D.              | O-044, P-494                                    |
| Preece, H.           | P-543                             | Rebernic, C.                   | P-328, P-567                     | Rolán-Alvarez, E.        | P-404, P-438                                    |
| Presgraves, D.       | O-129                             | Redfield, R.                   | P-689                            | Romero-Severson, J.      | O-131   |
| Preuss, T.           | O-006                             | Reed, D.                       | O-126, P-399, UDMPA-08           | Römpler, H.              | O-061   |
| Primus, A.           | O-059                             | Reed, F.                       | O-052, O-076                     | Ronaghi, M.              | P-743   |
| Prioul, J.           | P-501                             | Reich, D.                      | PL-1, O-121, O-123, P-492, P-544 | Ronald, F.               | P-427   |
| Pritchard, J.        | O-045, P-418                      | Reichard, M.                   | P-405                            | Ronan, M.                | P-266   |
| Pritham, E.          | O-105                             | Reimers, S.                    | P-032                            | Rosas, U.                | O-099   |
| Privman, E.          | P-729                             | Reina, R.                      | P-391                            | Rose, M.                 | P-483   |
| Promerova, M.        | P-449                             | Reis, M.                       | P-716                            | Rose, M.R.               | P-453   |
| Pruefer, K.          | PL-1, P-177                       | Reis, S.                       | P-606                            | Rosenberg, M.            | O-113   |
| Przeworski, M.       | P-377, P-418                      | Remedios, P.                   | O-104                            | Rosenberg, N.            | O-017, O-034, O-141                             |
| Ptak, S.             | PL-1, P-177                       | Remón, N.                      | P-596                            | Rosenfeld, J.            | O-022   |
| Puechmaile, S.       | P-413                             | Renate, O.                     | P-567                            | Ross, K.                 | O-063   |
| Puente-Molins, M.    | P-557                             | Renaud, J.                     | P-015                            | Rossi, A.R.              | P-394   |
| Puerma, E.           | P-566                             | Renaud, V.                     | P-547                            | Rosso, L.                | P-039, P-040                                    |
| Puig, M.             | O-056, P-720                      | Rensing, S.                    | P-186                            | Rota Stabelli, O.        | P-345   |
| Puigcerver, M.       | P-409, P-486                      | Reski, R.                      | P-186                            | Rothberg, J.             | PL-1  |
| Pupko, T.            | O-088, P-310, P-729               | Rest, J.                       | P-168                            | Rotter, B.               | P-201   |
| Purugganan, M.       | P-045, P-048, P-503, P-624        | Reymond, A.                    | P-147                            | Rottschaefer, S.         | P-468   |
| Pybus, O.            | O-110                             | Rhodes, J.                     | P-526                            | Roure, B.                | P-521   |
| <b>Q</b>             |                                   | Ribera, C.                     | P-375                            | Rousseau, B.             | P-319   |
| Quail, M.            | P-469                             | Ribera, I.                     | P-350, P-594                     | Rousset, F.              | P-654, P-659                                    |
| Quandt, D.           | P-194, P-195, P-267               | Richard, R.                    | O-142                            | Rout, M.                 | O-042   |
| Quesada, H.          | P-190, P-404, P-438               | Richards, C.                   | P-048                            | Roux, C.                 | P-470   |
| Quesneville, H.      | P-119, P-741                      | Richardson, D.                 | P-123                            | Roux, J.                 | O-167, P-012                                    |
| Quicke, D.           | P-321                             | Richardson, J.                 | P-098                            | Roy, J.                  | P-218   |
| Quilot, B.           | P-42                              | Richter, D.                    | O-121                            | Roy, S.                  | O-038, O-173                                    |
| Quintana-Murci, L.   | O-075, P-030, P-423, P-579        | Ricklefs, R.                   | O-072                            | Roy, S.W.                | WF-05   |
| Quintella, B.        | P-599                             | Ridout, K.                     | P-084                            | Royo, L.                 | P-548   |
| Qvarnström, A.       | P-412                             | Riehle, K.                     | P-165                            | Rozas, J.                | P-063, P-214, P-583, P-642                      |
| <b>R</b>             |                                   | Riehle, M.                     | P-468                            | Rubinstein, M.           | P-151   |
| Raaum, R.L.          | P-662, UDMPA-05                   | Rifkin, S.                     | O-094                            | Rubinstein, S.           | P-503   |
| Rabeder, G.          | P-550                             | Rio, J.                        | P-278                            | Rubio de Casas, R.       | P-047, P-371                                    |
| Rach, J.             | O-074                             | Ripoll, D.                     | O-102                            | Rudan, P.                | PL-1, P-266                                     |
| Radashevsky, V.      | P-514                             | Ritchie, M.                    | P-121                            | Ruedi, M.                | P-147   |
|                      |                                   | Rius, M.                       | P-576                            | Ruggiero, M.V.           | P-470   |
|                      |                                   | Riutort, M.                    | P-373, P-583, P-591              | Ruiz Rejón, M.           | P-702   |
|                      |                                   | Riva, A.                       | P-080                            |                          |   |

## AUTHOR INDEX (continued)

|                       |                                   |                       |                                   |                     |                           |
|-----------------------|-----------------------------------|-----------------------|-----------------------------------|---------------------|---------------------------|
| Ruiz, A.              | O-056, P-720, P-733               | Schartl, M.           | O-188, P-255, P-256               | Sharp, C.           | UDMPA-06                  |
| Ruiz Herrera, A.      | P-270                             | Scheet, P.            | O-141                             | Sharp, P.           | PL-2, P-198               |
| Ruiz Trillo, I.       | P-275                             | Scheffler, K.         | P-077                             | Shartl, M.          | P-129                     |
| Ruoping, Z.           | WF-01                             | Scherer, S.           | P-279                             | Shavit Grievink, L. | P-512                     |
| Ruppin, E.            | O-100                             | Schierup, M.          | O-161, P-202, P-224, P-407, P-420 | Shaw, M.            | P-321                     |
| Rusin, L.             | P-511                             | Schierwater, B.       | O-074                             | Sheffer, H.         | O-115                     |
| Russo, C.             | P-360, P-361                      | Schiller, D.          | P-192                             | Shen, Y.            | P-174                     |
| Russo, C.A.M.         | P-362                             | Schillerova, L.       | P-636                             | Sher, A.            | P-550, P-616              |
| Ruvolo, M.            | P-460                             | Schioett, M.          | O-138                             | Sherwin, W.         | UDMPA-01                  |
| <b>S</b>              |                                   | Schirmer, C.          | O-121                             | Shi, S.             | P-174                     |
| Sabath, N.            | O-010                             | Schlötterer, C.       | P-064, P-433                      | Shimada, M.         | P-464, P-499              |
| Sackton, T.           | O-011                             | Schluter, D.          | P-158, P-482                      | Shingai, R.         | P-038                     |
| Sadier, A.            | O-187                             | Schmid, K.            | P-196                             | Shinozaki, K.       | P-461                     |
| Sález, A.             | P-321, P-436                      | Schmid, V.            | O-192                             | Shitenberg, A.      | P-317                     |
| Sagot, M.             | P-751                             | Schmidt, C.           | P-255, P-256                      | Shoemaker, D.       | O-063                     |
| Saito, D.             | P-538                             | Schmidt, H.A.         | P-550                             | Shriver, M.         | P-471                     |
| Saito, K.             | P-461                             | Schmidt, S.           | P-429                             | Shuang, Y.          | WF-01                     |
| Saito, S.             | P-038                             | Schmutz, J.           | O-044, P-158, P-482, P-494        | Siddique, A.        | P-730                     |
| Saitou, N.            | O-166, P-155                      | Schneeweiss, G.M.     | P-192, P-195                      | Siegel, M.          | O-095                     |
| Sajantila, A.         | P-426                             | Schneider, H.         | P-267, P-625                      | Siegismund, H.      | P-592                     |
| Sakai, H.             | O-156                             | Schnitzer, J.         | P-449                             | Siepel, A.          | P-484                     |
| Salas, A.             | P-549                             | Scholz, S.            | O-141                             | Sikora, M.          | P-301, P-305              |
| Salatino, A.          | P-568                             | Schoville, S.         | P-627                             | Sillanpää, M.       | P-042                     |
| Salazar-Ciudad, I.    | O-185                             | Schrago, C.           | P-361                             | Silva, B.           | P-046                     |
| Salemi, M.            | P-302                             | Schubert, M.          | P-015                             | Silva, F.J.         | P-217, P-690              |
| Sali, A.              | O-042                             | Schultheis, C.        | P-255, P-256                      | Silva, P.           | P-087                     |
| Salvador, J.          | P-572                             | Schulz, R.            | P-711                             | Simkova, A.         | P-405, P-605, P-607       |
| Salzburger, W.        | O-132, P-335, P-395, P-397, P-581 | Schymick, J.          | O-141                             | Simões, B.          | P-608                     |
| Saminadin-Peter, S.   | P-105                             | Scofield, D.          | P-513                             | Simoes, P.          | P-483, P-490, P-751       |
| Sampaio, I.           | P-625                             | Scornavacca, C.       | O-163                             | Simon, A.           | P-609                     |
| San Mauro, D.         | P-097                             | Scott, C.             | P-159                             | Simon, S.           | P-352                     |
| Sánchez, L.F.         | P-662, UDMA-05                    | Scott, N.             | P-419                             | Simons, J.          | PL-1                      |
| Sánchez-Donoso, I.    | P-486                             | Scutt, C.             | P-125                             | Simon-Sanchez, J.   | O-141                     |
| Sánchez-Fernández, D. | P-594                             | Seddon, J.            | P-001, P-122, P-543               | Simpson, P.         | P-016                     |
| Sánchez-Gracia, A.    | P-214                             | Sedivy, C.            | P-628                             | Sineo, L.           | P-009                     |
| Sanderson, M.         | O-016                             | Segal, G.             | P-310                             | Singer, G.          | P-743                     |
| Sandoval, K.          | P-549, P-563                      | Segarra, C.           | P-118                             | Singh, N.           | O-051, P-115              |
| Sangaralingam, A.     | O-085                             | Segura, J.            | P-093                             | Singleton, A.       | O-141                     |
| Sangrós, R.           | P-430                             | Segurel, L.           | P-030, P-547                      | Sistonen, J.        | P-426                     |
| Sanjuán, R.           | O-026, O-097                      | Ségurens, B.          | P-255, P-256, P-264, WF-06        | Siv, A.             | O-002                     |
| Sans-Fuentes, M.      | P-398                             | Seidel, H.            | WF-08                             | Sjödín, P.          | P-420                     |
| Santos, J.            | P-483, P-490                      | Seifertova, M.        | P-607                             | Skouri-Panet, F.    | P-059                     |
| Saperas, N.           | P-172                             | Seixas, S.            | P-440, P-441                      | Ślapeta, J.         | P-554                     |
| Sapfo-Malaspinas, A.  | P-266                             | Sella, G.             | O-047, O-049, P-518               | Slate, J.           | P-296                     |
| Sarkar, I.N.          | O-022                             | Semina, A.            | P-402, P-590, P-749               | Slatkin, M.         | PL-1, O-114, P-266, P-698 |
| Satasook, C.          | P-413                             | Sémon, M.             | P-205, P-254, P-256               | Small, P.           | O-115                     |
| Satta, Y.             | O-077, P-135, P-138, P-424        | Semple, J.            | O-168                             | Smith, D.           | O-092                     |
| Sattath, S.           | O-047                             | Sennblad, B.          | O-084                             | Smith, K.           | P-383                     |
| Sattmann, H.          | P-637, P-638                      | Seo, T.               | P-066                             | Smith, M.           | P-431, P-454              |
| Saudermont, B.        | WF-06                             | Seoighe, C.           | P-077, P-081                      | Smith, N.           | P-688                     |
| Savolainen, O.        | P-042, P-388, P-657               | Sequeira, F.          | P-620, P-625, P-626               | Smith-Winberry, G.  | P-017                     |
| Sawada, Y.            | P-461                             | Sera, M.              | P-648                             | Smyth, G.           | P-133                     |
| Sawai, H.             | O-077                             | Serra, E.             | P-305                             | Snell, H.           | P-539, P-604              |
| Sawyer, S.            | P-701                             | Serra, F.             | P-055                             | Sninsky, J.         | O-057, P-429              |
| Sbordoni, V.          | P-096, P-100, P-580, P-604        | Serra, L.             | P-719                             | Snoeks, J.          | P-336                     |
| Scanlan, T.           | P-015                             | Serra, M.             | P-595                             | Sodré, D.           | P-625                     |
| Scannell, D.          | P-164                             | Serrano, V.           | WF-06                             | Sola, L.            | P-394                     |
| Scarpelli, C.         | P-264                             | Serras, F.            | P-126                             | Somel, M.           | P-137                     |
| Scavetta, R.          | P-401                             | Sertier, A.           | O-090                             | Sommer, R.          | P-323, P-616              |
| Schaack, S.           | P-725                             | Severson, T.          | O-059                             | Sordino, P.         | P-260                     |
| Schächter, V.         | WF-06                             | Shah, S.              | P-309                             | Soria-Carrasco, V.  | P-354                     |
| Schaeffer, B.         | O-073                             | Shalchian-Tabrizi, K. | P-322                             | Soriano, M.         | P-697                     |
| Schaffner, C.         | P-028                             | Shao, N.              | O-058                             | Sorimachi, K.       | P-054                     |
|                       |                                   | Sharbel, T.F.         | O-159, P-201, P-271, P-555, P-557 | Sosef, M.           | P-098                     |

|                   |                                   |                |                                   |                     |                            |
|-------------------|-----------------------------------|----------------|-----------------------------------|---------------------|----------------------------|
| Sotelo, G.        | P-546                             | Szpiech, Z.    | O-141                             | Touchon, M.         | O-031                      |
| Sotnikova, M.     | P-616                             | Szucsich, N.   | P-025                             | Toupance, B.        | P-561                      |
| Sousa, A.         | P-087                             |                |                                   | Toups, M.           | O-126, P-399               |
| Southwick, A.     | P-158, P-482                      | <b>T</b>       |                                   | Townsend, J.        | P-369                      |
| Spedini, G.       | P-579                             | Tabbada, K.    | P-572                             | Townsend, J.P.      | P-370, P-524               |
| Spencer, M.       | O-085                             | Takahashi, I.  | O-137                             | Tracy, C.           | P-278                      |
| Sperling, L.      | WF-06                             | Takahashi, M.  | P-253                             | Traore, A.          | P-548                      |
| Spillane, C.      | P-089, P-196                      | Takahata, N.   | P-135, P-138, P-424               | Traynor, B.         | O-141                      |
| Spitz, F.         | P-128                             | Takezaki, N.   | P-540                             | Treangen, T.        | P-200                      |
| Springer, S.      | P-400                             | Takuno, S.     | P-142                             | Tremblay, F.        | P-640, P-641               |
| Squartini, F.     | P-070                             | Talianova, M.  | P-504                             | Trindade, S.        | P-673                      |
| Stadler, P.       | O-091                             | Tamames, J.    | O-029, P-696                      | Trucchi, E.         | P-580                      |
| Stalker, J.       | P-469                             | Tamura, M.     | O-124                             | True, J.            | O-175                      |
| Stanhope, M.      | P-234                             | Tang, K.       | P-432                             | Trueman, J.         | P-348                      |
| Stanley, H.E.     | P-299                             | Tao, Y.        | O-133                             | Tsagkogeorga, G.    | P-357                      |
| Stapley, J.       | P-296                             | Tapia, W.      | P-604                             | Tsai, I.            | P-505                      |
| Stastny, K.       | P-619                             | Tardieu, A.    | P-059                             | Tsaur, S.           | P-462, P-498               |
| Staubach, F.      | P-127                             | Tarraga, J.    | P-055                             | Tschopp, P.         | O-192                      |
| Stefan, R.        | P-204, P-206                      | Tarrosó, P.    | P-663                             | Tsujimura, T.       | WF-07                      |
| Stein, L.         | O-016                             | Tateno, Y.     | P-006                             | Tsutsui, T.         | P-028                      |
| Steinacher, A.    | P-025                             | Tautz, D.      | O-060, P-127, P-379, P-401        | Tubío, J.M.         | P-735                      |
| Steinbauerova, V. | P-718                             | Taylor, J.     | P-085                             | Tuch, B.            | P-670                      |
| Steiner, G.       | P-025                             | Teeling, E.    | P-176, P-247, P-359, P-413, P-608 | Tully, D.           | O-116                      |
| Steiper, M.       | O-179                             | Teijeiro, S.   | P-218                             | Tully, S.           | P-024                      |
| Stemshorn, K.     | P-379                             | Teixeira, J.   | P-663                             | Tung, J.            | O-059                      |
| Stenøien, H.K.    | P-558, P-657                      | Tekle, Y.      | P-686                             | Turcotte, C.        | P-177                      |
| Stenzel, U.       | PL-1, P-266                       | Telford, M.    | P-345                             | Turnbaugh, P.       | P-314                      |
| Stephan, W.       | O-150, P-105                      | Templeton, A.  | P-083                             | Turner, L.          | O-061                      |
| Stephens, M.      | O-037                             | Tenaillon, M.  | P-110, P-447, P-717               | Turner, P.          | P-527                      |
| Stern, A.         | O-088                             | Tenaillon, O.  | O-031, O-032, P-649               | Turon, X.           | P-576                      |
| Stevens, M.       | O-128                             | Tenreiro, R.   | P-087                             | Tzika, A.           | O-004, P-651               |
| Stewart, E.       | P-017                             | Teotónio, H.   | P-453                             |                     |                            |
| Stierwald, M.     | O-192                             | Terao, K.      | O-137                             | <b>U</b>            |                            |
| Stiller, M.       | P-616                             | Terry, P.      | P-022                             | Ueno, K.            | P-091                      |
| Stoletzki, N.     | O-065                             | Teruel, M.     | P-519                             | Uhlemann, A.        | P-469                      |
| Stone, A.         | O-113, O-142, P-531               | Teschke, M.    | O-060                             | Uhler, C.           | P-266                      |
| Stone, A.C.       | P-315                             | Teshima, K.    | P-465                             | Upadhyay, A.        | UDMPA-07                   |
| Stoneking, M.     | P-215, P-572                      | Thatte, B.     | P-076                             | Urrutia, A.         | P-263                      |
| Strauss, S.       | P-340                             | Thebaud, C.    | P-593                             | Ursvik, A.          | P-207                      |
| Strope, P.        | P-082                             | Theobald, R.   | UDMPA-07                          | Uyenoyama, M.       | P-589, P-601               |
| Studer, R.        | P-445                             | Thermes, C.    | P-189                             |                     |                            |
| Stuessy, T.       | P-328, P-567                      | Thiel, T.      | P-271                             | <b>V</b>            |                            |
| Sturmbauer, C.    | P-336                             | Tholleson, M.  | O-002                             | Vacquier, V.        | P-400                      |
| Su, B.            | P-180, P-239, P-666, P-667        | Thomas, A.     | P-469                             | Vaishampayan, P.    | O-030                      |
| Su, X.            | O-078                             | Thomas, J.     | O-006, P-348                      | Vallinoto, M.       | P-625                      |
| Suárez, M.        | P-529                             | Thomason, H.   | P-037                             | Vamathevan, J.      | P-175                      |
| Suga, H.          | O-192                             | Thomé, M.T.    | P-620                             | van de Leemput, J.  | O-141                      |
| Sumiyama, K.      | P-020, P-155                      | Thompson, B.   | P-017                             | Van de Peer, Y.     | O-044, P-148, P-229, P-494 |
| Sun, F.           | O-080                             | Thornton, K.   | P-459                             | Van der Plicht, J.  | P-319                      |
| Sun, J.           | O-123                             | Thümmel, C.    | O-091                             | Van Der Veen, L.    | P-579                      |
| Sundqvist, A.     | P-612                             | Tiedemann, R.  | P-316                             | Van Loo, M.         | P-628                      |
| Sunyaev, S.       | P-429                             | Tilak, M.      | P-262                             | Van Oudenaarden, A. | O-094                      |
| Susann, W.        | P-192                             | Timmusk, T.    | P-144                             | Vandepoele, K.      | P-148                      |
| Susko, E.         | O-085                             | Ting, C.       | P-462, P-498                      | Vanderhaeghen, P.   | P-039                      |
| Sutter, N.        | O-149                             | Tisdale, T.    | P-047, P-371                      | VanLiere, J.        | O-141                      |
| Suzuki, I.        | P-018                             | Tishkoff, S.   | O-052, O-076, P-480               | Varshney, A.        | P-201                      |
| Suzuki, R.        | P-250                             | Toft, C.       | O-008                             | Vasconcelos, V.     | P-308, P-489               |
| Svavarsson, J.    | P-597                             | Toll-Riera, M. | P-154, P-209                      | Vavouri, T.         | O-168                      |
| Svensson, E.      | O-147                             | Tomas, A.      | P-446                             | Vejnar, C.          | P-741                      |
| Svinti, V.        | P-510                             | Tomasco, I.    | P-493                             | Vekemans, X.        | P-407, P-470               |
| Swanson, W.       | O-154, P-112, P-277, P-286, P-400 | Tonjum, T.     | P-200                             | Velasco, J.         | P-594                      |
| Symonova, R.      | P-396                             | Toomajian, C.  | O-044, P-494                      | Vellalta, G.        | P-430                      |
| Szathmary, E.     | O-079                             | Torgerson, D.  | O-057                             | Vences, M.          | O-183, P-750               |
| Szekeres, E.      | P-177                             | Torres, M.     | O-026                             | Vera, C.            | P-495                      |

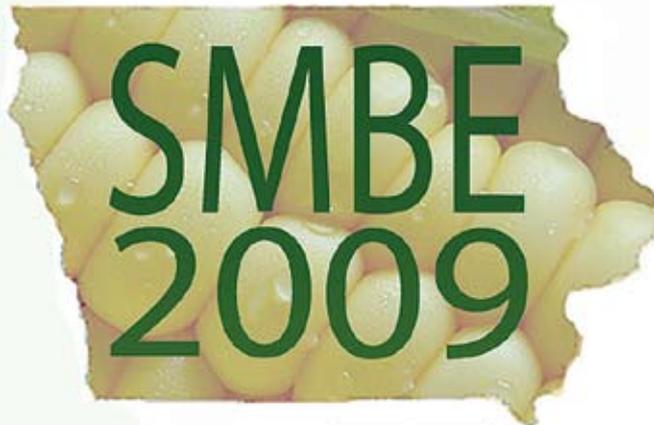
## AUTHOR INDEX (continued)

|                    |                                   |                       |                     |                      |                            |
|--------------------|-----------------------------------|-----------------------|---------------------|----------------------|----------------------------|
| Verdu, P.          | P-423                             | Wayne, R.             | O-149, P-613        | <b>Y</b>             |                            |
| Verheyen, E.       | P-336, P-337                      | Webster, M.           | P-178               | Yafremava, L.        | P-646, P-685, P-695        |
| Vernick, K.        | P-468                             | Weier, M.             | P-039               | Yamamichi, M.        | O-136                      |
| Verrelli, B.       | O-142                             | Weigel, D.            | O-044, P-494        | Yan, H.              | P-053                      |
| Vetter, M.M.       | P-466                             | Weihmann, A.          | P-177               | Yang, F.             | O-142                      |
| Veuille, M.        | O-073, P-030                      | Weinert, L.           | P-324               | Yang, Z.             | P-175                      |
| Vibransovski, M.   | O-068                             | Weinstock, J.         | P-550               | Yap, V.B.            | P-545                      |
| Vidal, O.          | P-446, P-565, P-569, P-570        | Weissenbach, J.       | P-264               | Yatsusenko, T.       | P-314                      |
| Vieira, C.         | P-191, P-439                      | Weissman, D.          | P-523               | Yi, S.               | O-015, P-167, P-171, P-223 |
| Vieira, C.P.       | P-716                             | Weiss-Schneeweiss, H. | P-328               | Yi, X.               | P-112, P-277               |
| Vieira, F.         | P-214                             | Welch, J.             | O-182               | Ying, C.             | WF-01                      |
| Vieira, J.         | P-191, P-439, P-716               | Wen, W.               | P-418, WF-01        | Yokubol, M.          | P-413                      |
| Vieira-Silva, S.   | P-199                             | Werner, T.            | O-175               | Young, A.            | O-061                      |
| Vilà, C.           | O-020, P-409, P-486, P-612        | Wheat, C.             | P-029, P-495        | Young, N.            | O-179                      |
| Vilhjálmsson, B.   | O-044                             | White, T.             | O-057, P-429        | Yue, Z.              | WF-01                      |
| Viljakainen, L.    | P-220                             | Whitlock, M.          | O-033               | Yun, D.              | WF-01                      |
| Villacorta, C.     | P-573                             | Whittall, J.          | P-410               |                      |                            |
| Villamor, L.       | P-572                             | Wicke, S.             | P-194, P-195, P-267 | <b>Z</b>             |                            |
| Villarreal Jr., G. | P-158                             | Widmann, J.           | P-092               | Zaldivar-Riverón, A. | P-321, P-436               |
| Villasenor, J.L.   | P-328, P-567                      | Widmer, A.            | P-700               | Zardoya, R.          | O-019, P-364, P-529        |
| Vinar, T.          | P-484                             | Wiebe, V.             | P-032               | Zerjal, T.           | P-717                      |
| Vinckenbosch, N.   | O-070, P-043, P-147, WF-02        | Wiehe, T.             | P-123, P-434, P-451 | Zé-Zé, L.            | P-087                      |
| Vinkler, M.        | P-240, P-449                      | Wiener, P.            | P-005               | Zhai, W.             | O-114                      |
| Visagie, J.        | PL-1                              | Wilbe, M.             | P-122               | Zhang, G.            | O-007                      |
| Visheshakul, N.    | P-538                             | Wilbur, A.            | P-531               | Zhang, J.            | P-282, P-293               |
| Vision, T.         | P-736                             | Wilches, R.           | UDMPA-02            | Zhang, L.            | P-181, P-236               |
| Vitalis, R.        | P-457                             | Wilder, J.            | P-300               | Zhang, R.            | P-180                      |
| Vitkova, M.        | P-396                             | Wildman, D.           | O-015               | Zhang, X.            | P-237                      |
| Vivat-Hannah, V.   | P-015                             | Wilfried, D.J.        | O-183               | Zhang, Z.            | O-098, P-212, P-524        |
| Vlahov, D.         | P-536                             | Wilhelm, L.           | O-024, P-219        | Zhao, K.             | P-454                      |
| Vogel, H.          | P-067, P-201                      | Wilke, C.             | P-231               | Zhao, R.             | O-007                      |
| Vogler, A.         | P-629                             | Wilkinson, P.         | P-044               | Zhao, Z.             | P-239                      |
| Voigt, M.          | P-201, P-271                      | Willerslev, E.        | P-616               | Zhou, Q.             | O-007, P-255, P-256        |
| Volff, J.          | O-188, P-254, P-255, P-256, P-264 | Williams, D.          | P-159               | Zhou, T.             | P-231                      |
| Voloch, C.         | P-361                             | Williams, L.          | P-478, P-485        | Zhou, Y.             | O-109                      |
| Von Haeseler, A.   | P-340                             | Williams, S.          | P-068               | Zhu, L.              | O-149                      |
| Von Kuster, G.     | P-085                             | Willmott, K.          | P-353               | Zidi, A.             | P-565                      |
| Vretemark, M.      | O-147                             | Wincker, P.           | P-189, P-264, WF-06 | Zielonka, J.         | P-307                      |
| Vujovic, Z.        | P-408                             | Wing, R.              | O-016               | Zimmer, A.           | P-204, P-206               |
| Vyskocilova, M.    | P-405, P-605, P-607, P-619        | Winkler, C.           | P-431, P-536        | Zivkovic, D.         | P-451                      |
| Vyskot, B.         | P-339, P-700                      | Wittbrodt, J.         | P-128               | Zluvova, J.          | P-339, P-504               |
|                    |                                   | Wittkopp, P.          | O-054, P-017        | Zollner, S.          | P-147                      |
| <b>W</b>           |                                   | Wiuf, C.              | P-601               |                      |                            |
| Wagner, G.         | O-186                             | Wlasiuk, G.           | O-170, P-222        |                      |                            |
| Wahli, W.          | P-242                             | Wolfe, K.             | P-205, P-252, P-292 |                      |                            |
| Wall, J.           | P-428                             | Wolff, K.             | P-541               |                      |                            |
| Walton, C.         | O-127, P-351                      | Wood, A.              | P-711               |                      |                            |
| Wang, C.           | P-053                             | Woolfit, M.           | P-235               |                      |                            |
| Wang, D.           | P-053                             | Woolley, S.           | P-083               |                      |                            |
| Wang, H.           | O-102                             | Wray, G.              | O-059               |                      |                            |
| Wang, J.           | P-013, P-666                      | Wróbel, B.            | O-111               |                      |                            |
| Wang, K.           | O-141                             | Wu, C.                | P-174, P-261, P-355 |                      |                            |
| Wang, M.           | P-685, P-695                      | Wu, Q.                | P-174               |                      |                            |
| Wang, S.           | P-232, P-236                      | Wurm, Y.              | P-013               |                      |                            |
| Wang, S.M.         | P-174                             |                       |                     |                      |                            |
| Wang, T.           | P-053                             | <b>X</b>              |                     |                      |                            |
| Wang, W.           | O-007                             | Xin, L.               | WF-01               |                      |                            |
| Wang, X.           | P-287                             | Xu, A.G.              | P-137               |                      |                            |
| Wang, Y.           | P-180, P-261                      | Xu, H.                | P-640, P-641        |                      |                            |
| Wapinski, I.       | P-520                             | Xu, S.                | O-007, P-572        |                      |                            |
| Ward, H.           | P-682                             | Xu, W.                | O-173               |                      |                            |
| Ware, D.           | O-016                             |                       |                     |                      |                            |
| Warnecke, T.       | O-012                             |                       |                     |                      |                            |
| Watanabe, K.       | P-241                             |                       |                     |                      |                            |

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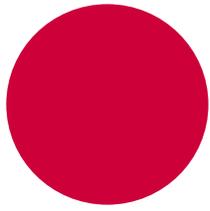


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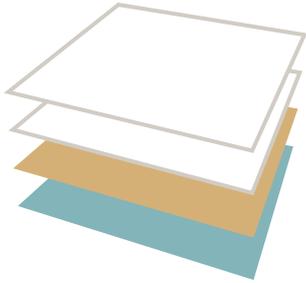


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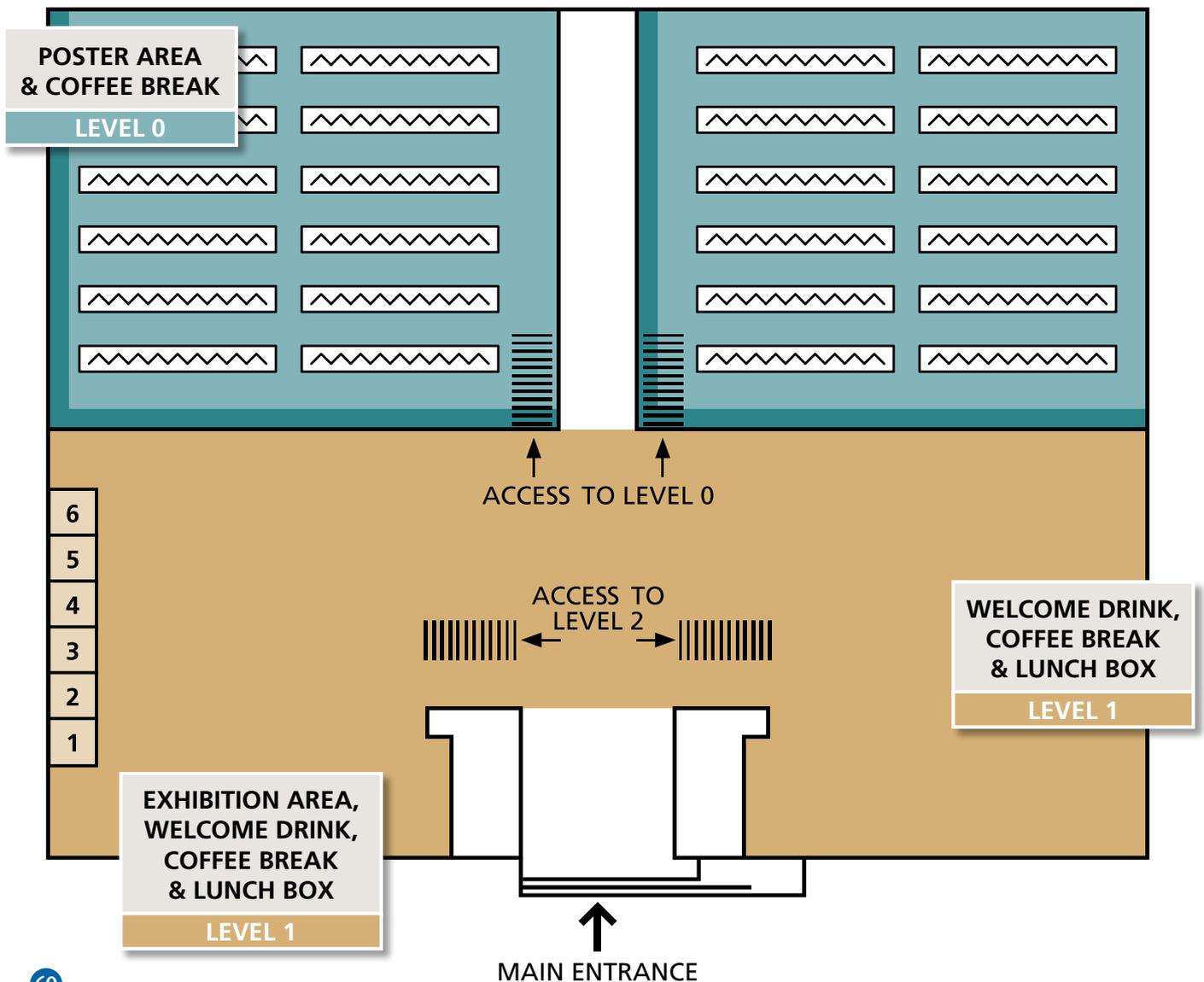


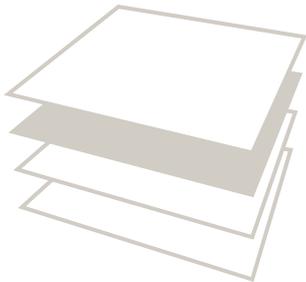


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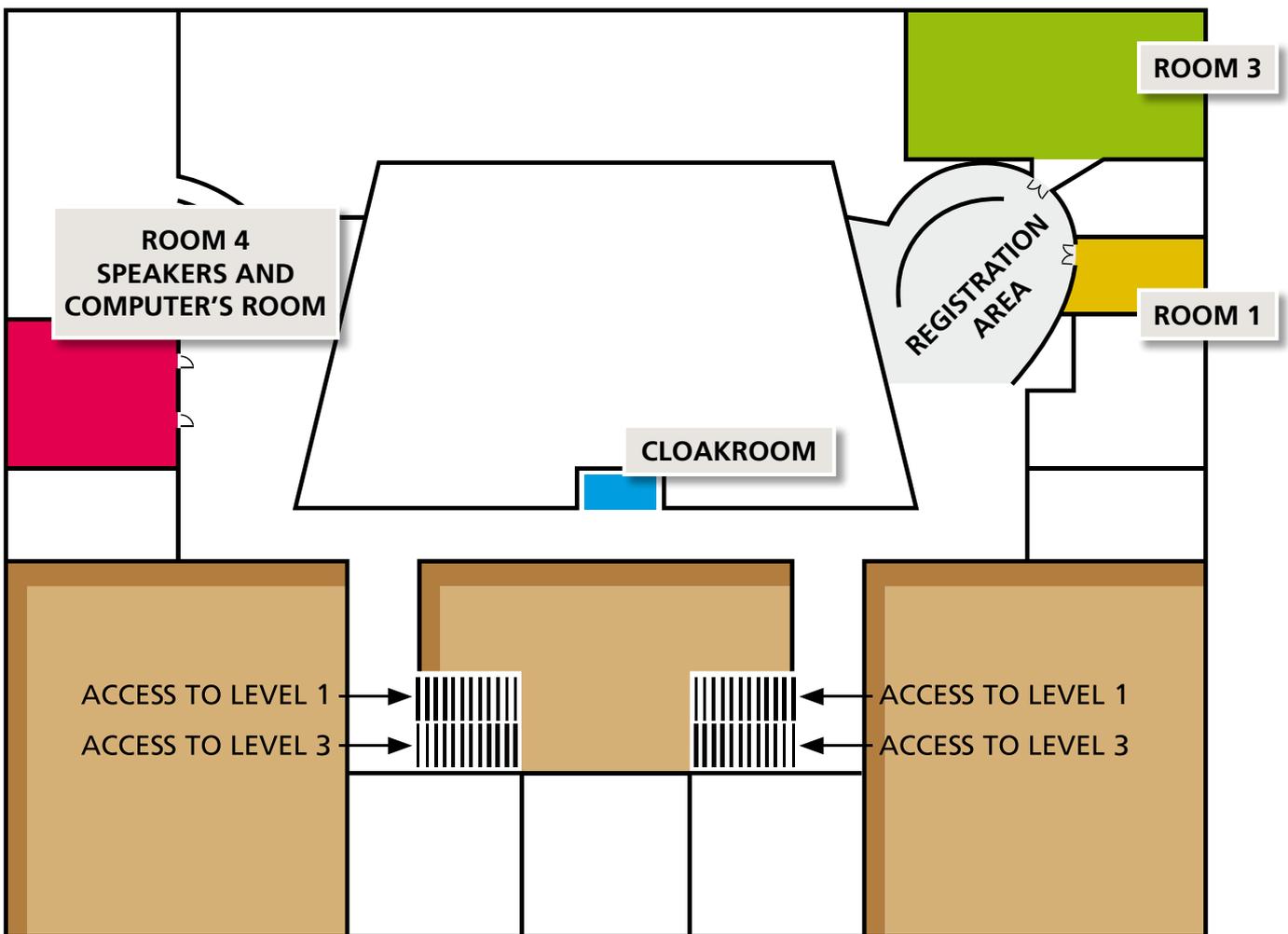


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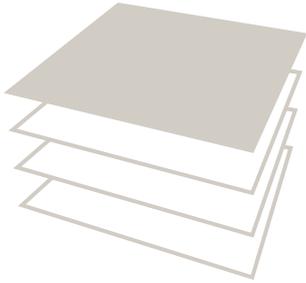




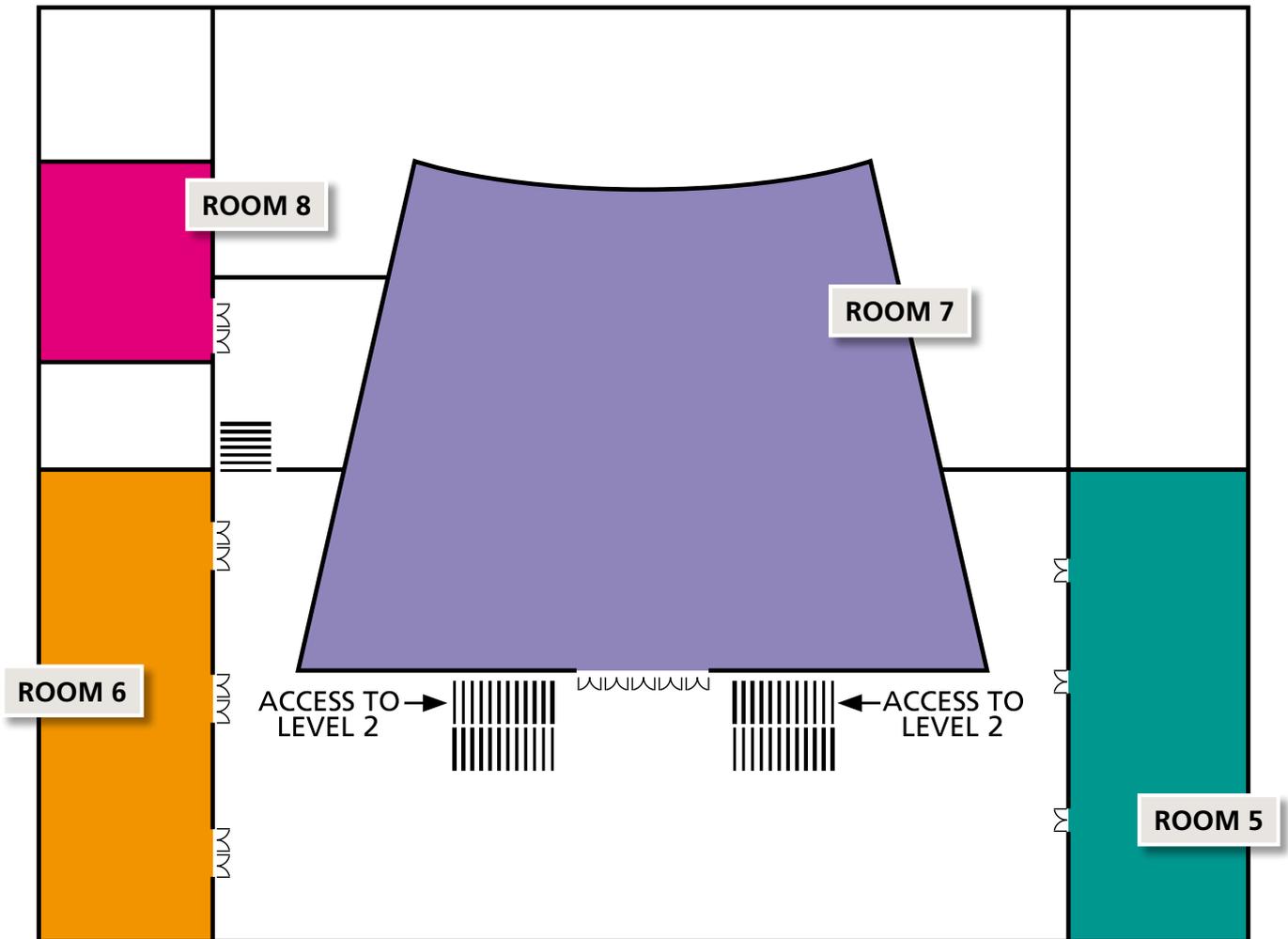
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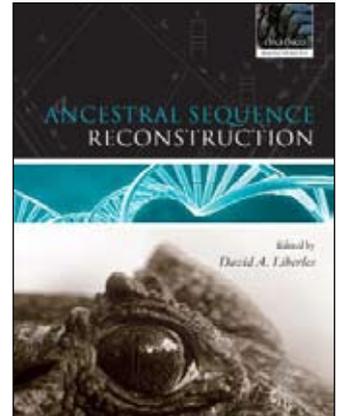
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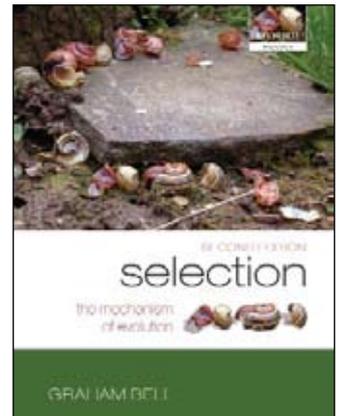
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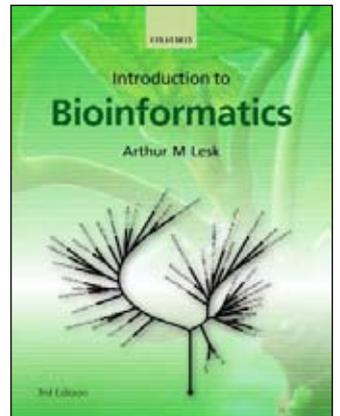
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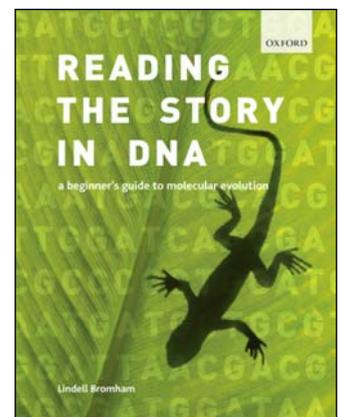
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