THE 28th CONGRESS OF THE INTERNATIONAL SOCIETY FOR FORENSIC GENETICS

9 – 13th SEPTEMBER 2019
PRAGUE CONGRESS CENTRE, THE CZECH REPUBLIC

PROGRAMME BOOK
Flexible Nucleic Acid Solutions for forensic laboratories

With preloaded methods for sample preprocessing and post-purification applications, the Maxprep™ Liquid Handler easily integrates wherever you need it in your laboratory workflow. There are no methods to create or protocols to write—the Maxprep™ Liquid Handler is ready to do the tedious work for you.

- **Flexible**: Process 1 to 48 samples.
- **Reliable**: Consistent yields of high-quality DNA from casework samples.
- **Intuitive Software**: Preprogrammed protocols get you up and running quickly.

Personal Automation for the Forensic Lab
www.promega.com/MaxprepForensics
ISFG 2019

28th Congress of the International Society for Forensic Genetics

9 – 13th September 2019
Prague Congress Centre, the Czech Republic

Hosted by
International Society for Forensic Genetics

Czechoslovak Society for Forensic Genetics
Unlock the Power of DNA Sequencing

And See More Than CE

Visit us at Booth 2 to learn more
## Content

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Welcome Words</td>
<td>4</td>
</tr>
<tr>
<td>Committees</td>
<td>5</td>
</tr>
<tr>
<td>Programme at a Glance</td>
<td>7</td>
</tr>
<tr>
<td>Guidelines for Authors</td>
<td>8</td>
</tr>
<tr>
<td>Pre-Congress Workshops</td>
<td>10</td>
</tr>
<tr>
<td>Scientific Prize Lecture</td>
<td>20</td>
</tr>
<tr>
<td>Keynote Speakers</td>
<td>21</td>
</tr>
<tr>
<td>Detailed Scientific Programme</td>
<td>24</td>
</tr>
<tr>
<td>Company Symposia</td>
<td>32</td>
</tr>
<tr>
<td>ISFG Working Groups Meetings</td>
<td>33</td>
</tr>
<tr>
<td>Social Programme</td>
<td>34</td>
</tr>
<tr>
<td>Floorplans</td>
<td>36</td>
</tr>
<tr>
<td>Exhibition Floorplan</td>
<td>39</td>
</tr>
<tr>
<td>Acknowledgment</td>
<td>40</td>
</tr>
<tr>
<td>Company Profiles</td>
<td>41</td>
</tr>
<tr>
<td>General Information</td>
<td>48</td>
</tr>
<tr>
<td>List of Orals</td>
<td>52</td>
</tr>
<tr>
<td>List of Posters</td>
<td>57</td>
</tr>
</tbody>
</table>
Dear Colleagues,

preparation for the 28th International Congress of International Society for Forensic Genetics (ISFG) is approaching its climax. Online registration is running, promising to beat the record from Seoul in number of participants. Program is ready, featuring hands-on and ear-on workshops, meetings of national or topical societies, lectures from renowned and rising scientists, austere and lavish posters, and last but not least, accompanying social programme.

It is possible that for ISFG executive committee and professional congress organiser C-IN it is just another event in the row. However, for me and members of local organizing committee it was so far thrilling experience, different in quantity and quality from our biannual Forensica conference. We hope that congress itself will be not only thrilling, but also congenial and seminal experience for all of you.

What can you expect?

Pre-congress workshop leaders will teach you, how to use software flawlessly, semicontinuously, continuously, FAMILiarly, or STRUCTURally, how to handle mixture, pristine, and canine samples in seamless workflow, how to recognize body fluid or phenotype, how to publish your findings using correct nomenclature, how to do everything while networking, and with high quality and ethics mark.

Keynote speakers Drs. Erlich, Kayser, Metcalf, van Oorschot, Pouyet, Roewer, Šimková will set the pace and roll the canvas out, on which 60+ other speakers will glue their stone to create the final scientific mosaic where topics of Forensic DNA Phenotyping, Probabilistic Reasoning, Genealogy, DNA transfer, Population Genetics, and Microbiome will have chance to shine like gem. For those whom auditory stimulation does not suffice, hundreds of posters will feed and please their eyes. Sponzoring companies will try to catch your attention to secure future deals, musicians and chefs will try to evoke cordial and cooperative atmosphere. If you will be attentive, you may be rewarded by topics of voodoo or mammoths that sneaked into the program as well.

In epitome, we tried to blend cornucopian cuvée that will make alchemy of Prague memorable and will stay on your palate for long time.

It is my great honour to welcome you in Prague, to greet you all!

Jiří Drábek  
ISFG2019 Congress President
Committees

Local Organizing Committee

Jiří Drábek
Andrea Cignová
Veronika Gazdová
Marie Korabečná
Jana Matoušková
Martina Novotná
Tomáš Pexa
Halina Šimková
Petra Škapová
Kateřina Štaffová
Zuzana Štaffová
Pavel Tomek

ISFG Board and Scientific Committee

Walther Parson
Peter M. Schneider
John Butler
Mechthild Prinz
Leonor Gusmão

About ISFG

The International Society for Forensic Genetics is an international association promoting scientific knowledge in the field of genetic markers analyzed for forensic purposes. The ISFG has been founded in 1968 and represents more than 1100 members from over 60 countries. Regular meetings are held at a regional and international level. Scientific recommendations on relevant forensic genetic issues are developed and published by expert commissions of the ISFG.
DEPAarray™NxT digital sorting enables the use of single cell analysis in forensic genetic to resolve the most complex mixtures of two or more contributors. Samples containing homogenous mixes of cells of the same type (blood/blood, sperm/sperm, epithelial/epithelial) are resolved isolating multiple single cells and profiling each one independently, to finally in-silico reconstruct the full, 100% concordant profile of each contributor. Never a forensic mix could be resolved so sharply.

Visit us at booth #4
www.siliconbiosystems.com/forensics
For research use only. Not for use in diagnostic procedures.
# Programme at a Glance

<table>
<thead>
<tr>
<th>Time</th>
<th>Monday</th>
<th>Tuesday</th>
<th>Wednesday</th>
<th>Thursday</th>
<th>Friday</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:30</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>9:00</td>
<td>Pre-Congress Workshops</td>
<td>Pre-Congress Workshops</td>
<td>Scientific Session 1</td>
<td>Scientific Session 5</td>
<td>Scientific Session 9</td>
</tr>
<tr>
<td>9:30</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>10:00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>10:30</td>
<td>Coffee Break</td>
<td>Coffee Break</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>11:00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>11:30</td>
<td>Pre-Congress Workshops</td>
<td>Pre-Congress Workshops</td>
<td>Scientific Session 2</td>
<td>Scientific Session 6</td>
<td>Scientific Session 10</td>
</tr>
<tr>
<td>12:00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>13:00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>13:30</td>
<td>Lunch</td>
<td>Lunch</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>14:00</td>
<td>Pre-Congress Workshops</td>
<td>Pre-Congress Workshops</td>
<td>Company Symposium – QIAGEN (13:30 – 14:20)</td>
<td>Lunch</td>
<td>Lunch</td>
</tr>
<tr>
<td>14:30</td>
<td>Pre-Congress Workshops</td>
<td>Pre-Congress Workshops</td>
<td>Scientific Session 3</td>
<td>Scientific Session 7</td>
<td>Scientific Session 11</td>
</tr>
<tr>
<td>15:00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>15:30</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Scientific Session 11</td>
</tr>
<tr>
<td>16:00</td>
<td>Coffee Break</td>
<td>Coffee Break</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>16:30</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>17:00</td>
<td>Pre-Congress Workshops</td>
<td>Pre-Congress Workshops</td>
<td>Scientific Session 4</td>
<td>Scientific Session 8</td>
<td>Scientific Session 12</td>
</tr>
<tr>
<td>17:30</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>18:00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>18:30</td>
<td></td>
<td>Opening Ceremony</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>19:00</td>
<td></td>
<td>&amp; Scientific Prize Lecture</td>
<td>Working Groups Meetings</td>
<td>General Assembly</td>
<td></td>
</tr>
<tr>
<td>19:30</td>
<td>Welcome Cocktail</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>20:00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>20:30</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>21:00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>21:30</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>22:00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>22:30</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>23:00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Closing Ceremony &amp; Congress Dinner</td>
</tr>
<tr>
<td>23:30</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Guidelines for Authors

The ISFG board and the local organizing committee have carefully reviewed a lot of abstracts of high quality. All authors of oral and poster presentations are kindly required to follow the instruction as below.

Oral Presentation Guidelines

Oral presentations are always accompanied by PowerPoint presentations. The speakers are entirely responsible for the presentation content (order, graphics etc…). All presentations and questions must be delivered in English. Time reserved for scientific presentation is:

- **Keynote presentation** 40 min + 5 min discussion
- **Presentation** 12 min + 3 min discussion
- **Presentation** 10 min + 2 min discussion

Presentation format

Please prepare your presentation preferably using up to date version of Microsoft PowerPoint; however older versions are also supported. Screens’ aspect ratio will be 16:9.

Please note that Apple Keynote and Prezi presentations are not supported and they have to be converted into PDF files.

When saving your final presentation to the USB stick, do not forget to make sure to include your video files and all links to these multimedia files.

As no presentation template is prepared, you are welcome to use your own. Please restrain inviting to other scientific conferences, if any, to the last slide of your presentation.

Depositing the File

Presentations must be handed over to the personnel in the SPEAKERS’ PREVIEW ROOM, with USB stick, as far in advance as possible and **TWO hours before the start of entire session**, where the presentation is to be displayed. The presentation for an early morning session should be handed over the evening before.

SPEAKERS’ PREVIEW ROOM will be located in **on 1st floor in room 1.1**, clearly marked and will be available in following times:

<table>
<thead>
<tr>
<th>Date</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>Monday 9th, September</td>
<td>8:00 – 18:00</td>
</tr>
<tr>
<td>Tuesday 10th, September</td>
<td>8:00 – 20:00</td>
</tr>
<tr>
<td>Wednesday 11th, September</td>
<td>7:30 – 19:00</td>
</tr>
<tr>
<td>Thursday 12th, September</td>
<td>7:30 – 19:00</td>
</tr>
<tr>
<td>Friday 13th, September</td>
<td>7:30 – 17:00</td>
</tr>
</tbody>
</table>
In the Lecture Room

All presentations will be sent directly to the lecture room through the internal computer network. Please, we kindly ask all authors NOT to come at the last minute with their own computer into the lecture room. All presentations must be downloaded in the SPEAKERS’ PREVIEW ROOM beforehand.

Poster Dimensions, Mounting & Removing

The presenting authors are entirely responsible for the poster content (order, graphics etc…). All posters must be delivered in English.
Kindly note the posters should not exceed the given dimensions, which are 120 × 90 cm, portrait orientation. Posters will be hanged on a standard poster boards. The organizer will provide suitable fixing material.

Poster Mounting

**Tuesday, 11th September 2019, 17:30 – 21:30**
**Wednesday, 12th September 2019, 7:30 – 10:00**

Each poster board was given a specific number. Authors are kindly asked to make sure to mount their poster on the poster board with the number corresponding to the number assigned to their poster presentation (e.g. P 01, P 02 etc…).

Poster Dismantling

**Friday, 13th September 16:30 – 19:00**

Poster shall remain displayed within the whole meeting period and be removed by their authors at the end of the meeting. Posters left behind after 19:00, Friday 13th September will be discarded by organizers without notice. Organizing committee is not responsible for any loss or damage to your poster if it is not removed by the notified time. Posters not dismantled by their authors by the end of the Congress will be removed by the organizers and discarded.
Storage for poster cases is not available.

Poster Sessions

Presenting authors should be available at their poster (Poster Area, South Hall 2) to explain and discuss their work to interested participants during the attended poster sessions listed below:

<table>
<thead>
<tr>
<th>Date</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wednesday 11th, Sept.</td>
<td>10:00 – 11:00</td>
</tr>
<tr>
<td>Thursday 12th, Sept.</td>
<td>10:00 – 11:00</td>
</tr>
<tr>
<td>Friday 13th, Sept.</td>
<td>10:00 – 11:00</td>
</tr>
</tbody>
</table>
Pre-Congress Workshops

FW1 – Interpretation of complex DNA profile mixtures using open-source software including LRmix and EuroForMix

Organisers: Peter Gill & Corina Benschop & Oyvind Bleka
Type: Full Day Workshop, Hands-on
Room: Club B
Date & Time: Monday, 9th September 2019 (9:00 – 18:00)

Aim: To provide participants with necessary skills to carry out probabilistic genotyping of complex mixtures using open-source programs to calculate the strength of evidence of complex mixtures.

Target Group: Law enforcement forensic experts – experienced reporting officers who deal routinely with DNA profiling evidence and are required to interpret complex mixtures in casework.

General Learning Outcomes:
- Understand the theory behind using likelihood ratios to interpret evidence
- Discuss the theory used to interpret complex mixtures of two or more contributors where the samples may be compromised - partial, degraded
- Describe best practice in relation to the ISFG DNA commission recommendations
- Be proficient in the use of open source software in order to carry out the calculations (LRmix Studio, EuroForMix)
- Write court going statements
- Describe the limitations of methods
- New developments will be presented, including DNAxs, a new package for reporting officers
- Participants will be provided with necessary tools to carry out cascade training at a national level

Organisation of the course:
The course is practically orientated. The participants must bring their own laptop. Approximately one month before the course, participants will be provided with pre-course material and links that will enable them to download necessary software. Participants are encouraged to view the training videos on the EuroForMix website

Software:
All softwares are open-source and freely available for users. Free support is provided to users via help desks found on the web-sites.

LRmix studio is a commonly used qualitative program that utilises the peak designation only http://lrmixstudio.org/.

EuroForMix is a more complicated quantitative program. Its development was supported by a EU-FP7 initiative (EuroForGen-NOE). Peak height, stutter and degradation are incorporated into the model. This package is ‘state of the art’, and is also used for analysis of massive parallel sequencing data http://www.euroformix.com/.
DNAxs is a new program under development by the NFI. EuroForMix will be integrated into this package, along with a host of features designed to assist the reporting officer to interpret complex DNA profiles. Corina Benschop will provide feedback and demonstrate program features.

FW2 – Kinship statistics using Familias and FamLink

**Organisers:** Thore Egeland & Daniel Kling  
**Type:** Full Day Workshop, Hands-on  
**Room:** Club B  
**Date & Time:** Tuesday, 10th September (9:00 – 18:00)

The workshop provides the necessary background for relationship inference using autosomal markers. Statistical methods are introduced and the likelihood ratio based approach is emphasized. Models for linked markers are discussed and their relevance for recent forensic applications are illustrated. The freely available softwares Familias and FamLink are exemplified. The former software is restricted to unlinked autosomal markers. However, the functionality goes beyond standard kinship problems and includes modules for simulation, disaster victim identification and familial searching. The program FamLink has recently been extended to deal with any number of linked markers (STR-s or SNP-s). The open software R is introduced, and the relevance for plotting of pedigrees and estimation of haplotype frequencies is demonstrated. The participants should bring a laptop with the mentioned software installed.

FW3 – Population analysis of forensic DNA data using Snipper and STRUCTURE

**Organisers:** Christopher Phillips & Leonor Gusmao  
**Type:** Full Day Workshop, Hands-on  
**Room:** Club E  
**Date & Time:** Monday, 9th September (14:00 – 18:00), Tuesday, 10 September (9:00 – 13:00)

This workshop will cover the preparation of reference population data and forensic profile data for analysis with Snipper-based Bayes likelihood ratio tests and Principal Component Analysis; and STRUCTURE-based genetic cluster analysis. Such tests are gaining increasing interest as a way to estimate the possible bio-geographical ancestry of DNA recovered from forensic samples. Students will run all three analyses with autosomal STR and SNP genotypes generated from both capillary electrophoresis and massively parallel sequencing assays typing established forensic panels. STRUCTURE tests of medium-scale population data will be run ‘overnight’ between the pm and am sessions of the workshop, which is divided across two half-days. Students will be required to pre-install STRUCTURE software and allow their laptops to run STRUCTURE in the background overnight. Students are invited to bring their own data, which could be analysed during the workshop.
HW1 – NGS Workflows for forensic genetics

Organiser: Pete Vallone  
Type: Half Day Workshop, Lecture  
Room: Club E  
Date & Time: Monday, 9th September (9:00 – 13:00)

This workshop aims to review and explore the details of various NGS/MPS sequencing methods. Common sequencing methods and platforms that may be applied to forensic genetic analyses will be discussed. The laboratory workflow steps involved in library preparation and their specific purposes will be presented. Examples of the process will be illustrated through forensically-relevant workflows for the sequencing of STRs, SNPs and the mitochondrial genome. Examination of the resulting sequence data will be demonstrated by the instructor using open source and commercial software tools.

This workshop is intended as an introduction to those attendees interested in the basic and practical aspects of carrying out sequencing experiments and considerations in adopting this method of genetic analysis in their laboratory. Questions related to the scope of the workshop can be directed to the instructor (peter.vallone@nist.gov)

HW2 – Y chromosome: YHRD, mixture interpretation, kinship, population differentiation

Organisers: Lutz Roewer & Sascha Willuweit  
Type: Half Day Workshop, Hands-on  
Room: Club C  
Date & Time: Monday, 9th September (9:00 – 13:00)

Program:

09:00 – 09:15  Introduction
09:15 – 10:30  Current national and international guidelines on interpretation of Y-STRs and reporting to court (Germany, USA, ISFG)
10:30 – 11:30  Use of YHRD to generate match statistics (Augmented counting, Discrete Laplace method, Meta- and Suspect population)
11:30 – 11:45  Break
11:45 – 13:00  Casework challenge (Match probability, Mixture and Kinship analysis, Ancestry inference using Y-SNPs)

Note: We will bring casework examples, but please bring your own and enter discussion!
HW3 – Body fluid identification through mRNA profiling or DNA methylation analysis

**Organisers:** Titia Sijen & Hwan Young Lee  
**Type:** Half Day Workshop, Lecture  
**Room:** Club H  
**Date & Time:** Monday, 9th September (9:00 – 13:00)

Human DNA profiling has the potential to present strong evidence for placing a suspect at a crime scene. Increasingly, forensic questions that go beyond the identity of the donor of a sample are asked. Knowledge regarding the cell types residing in an evidentiary trace can facilitate inference of activities. Body fluids such as blood, saliva, semen, vaginal mucosa and menstrual secretion are mostly assessed in both sexual assaults and violent crimes. The inference of organ tissues such as brain, lung, kidney, liver, heart and skeletal muscle can also be useful. Tissue identification may be achieved through various marker types: mRNAs, miRNAs, DNA methylation or microbial markers.

In this workshop, we will focus on mRNA profiling and DNA methylation analysis. mRNA profiling has been studied at the Netherlands Forensic Institute since 2009 and the mRNA assays have been applied to over 250 forensic cases. Around the same time, research on tissue-specific DNA methylation begun in several research groups, and the multiplex assays developed by Lee’s group have been validated for practical application in forensic casework samples.

We will explain the foundations of assay design, share how the assays were developed and demonstrate the basic procedures regarding the application of the assays. We will discuss technical issues that may occur with compromised forensic samples and explain how data interpretation is achieved considering an accompanying DNA profile and the context of a case. Through casework examples we will illustrate the forensic possibilities and opportunities. Issues that were raised in court will also be discussed.

Participants will actively work with exemplar results to gain hands-on experience. An interactive format will be used throughout the session to stimulate discussions.

HW4 – Forensic mitochondrial DNA analysis:  
Alignment and interpretation using the EMPOP database

**Organiser:** Walther Parson  
**Type:** Half Day Workshop, Hands-on  
**Room:** Club C  
**Date & Time:** Monday, 9th September (14:00-18:00)

This is a practical workshop using EMPOP tools to better understand the mitochondrial phylogeny in the context of
- database queries for frequency estimations
- retrieving statistical information on common and rare haplotypes
- forensic reporting of mtDNA data
We try to make the workshop as practical as possible and present/discuss forensic examples. You are invited to contribute to the workshop by bringing your own mtDNA sequences. These can involve haplotypes from research projects, from practical forensic work or your own mtDNA. Also feel free to bring challenging haplotypes that you would like to have discussed at the workshop. You can bring your own laptop but it is not necessary! In case you plan to use your own laptop, please make sure you are a registered EMPOP user (via https://empop.online).

Please send questions that you may have also before the meeting to walther.parson@gmail.com

HW5 – ISO/IEC 17025:2017

Organiser: Jiri Drabek
Type: Half Day Workshop, Lecture
Room: Club H
Date & Time: Monday, 9th September (14:00 – 18:00)

The basic requirements for a management system for forensic genetics laboratories are based on the international standard ISO/IEC 17025. This standard is used for the assessment and accreditation of laboratories worldwide by Accreditation Bodies in order to enhance the confidence of the clients for the competence, impartiality, and consistently high performance of these laboratories, producing high quality results.

The ISO/IEC 17025 was revised in 2017 in order to reflect the risk-based thinking, the latest version of ISO9001 norm stressing process approach in quality management, changes in IT and other technologies available for laboratories, and changes in client requirements. Laboratories already accredited to ISO/IEC 17025:2005 will need to transition their processes to the new version till November 2020.

Workshop on accreditation according to ISO/IEC 17025:2017 norm in forensic genetics laboratory is aimed at all levels of competent personnel, involved with establishing, implementing and maintaining laboratory quality and technical systems.

Workshop will cover topics of:
• Terminology, scope, definition, and normative references
• Requirements regarding management, training, and laboratory work
• Records, documents and procedures
• Internal Audit Assessment and Proficiency Testing / Interlaboratory Programs
• Method validation and conducting testing.

Upon successful completion of the course, learners will be able to:
• Identify and understand the general requirements of ISO/IEC 17025:2017, its principles and concepts
• Understand processes for controlling risks associated with the laboratory’s testing processes
• Plan method validation
• Apply the requirements of ISO/IEC 17025 to their laboratory systems.
HW6 – Scientific publication: Reading, writing, and reviewing

Organiser: John Butler  
Type: Half Day Workshop, Lecture  
Room: Club C  
Date & Time: Tuesday, 10th September (9:00 – 13:00)

Science benefits from effective communication of ideas. Research results are shared with others through publications and presentations. Scientific publication involves efforts in reading, writing, and reviewing the literature. Editors of peer-reviewed journals rely on input from scientific colleagues to judge the merits of submitted manuscripts. Knowledgeable reviewers providing timely feedback are important for a successful peer-review process. This workshop will share insights based upon editorial experience with Forensic Science International: Genetics as well as extensive writing practice in preparing five textbooks and over 170 research articles and invited book chapters. Reviewing manuscripts is a chance to provide an important service and to influence the scientific community for good. In addition to discussing approaches to reading, writing, and reviewing relevant literature, some recent articles covering forensic genetics will be considered and examined.

HW7 – CaDNAP Meeting – Canine DNA Profiling group

Organisers: CaDNAP Group  
Type: Half Day Workshop  
Room: Club H  
Date & Time: Tuesday, 10th September (9:00 – 13:00)

Preliminary Agenda:
CaDNAP - a brief historical sketch  
Walther Parson1,5 on behalf of the CaDNAP group

The CaDNAP 13-STR panel: a tool for identification and breed assignment  
Burkhard Berger1, Cordula Berger1, Josephin Heinrich1, Andreas Hellmann3, Uwe Schleenbecker3, Udo Rohleder3, Werner Hecht2, Nadja V. Morf4, Walther Parson1,5

The CaDNAP proficiency test  
Werner Hecht2, Burkhard Berger1, Cordula Berger1, Andreas Hellmann3, Uwe Schleenbecker3, Udo Rohleder3, Nadja V. Morf4, Walther Parson1,5

Population structure, mating strategies and generation interval in dogs: Implications for forensic profiling?  
Werner Hecht2

Detecting the DNA from poached and poachers  
Adrian Linacre6

Forensic genetics and taxonomic identification  
Antonio Amorim7,8
Dog attacks, voodoo and mammoth cases at Zurich Institute of Forensic Medicine
Nadja V. Morf4, Pamela Voegeli4, Adelgunde Kratzer4

History of origins of the non-human DNA department of the Bundeskriminalamt Wiesbaden (BKA)
Andreas Hellmann3, Uwe Schleenbecker3, Udo Rohleder3

Canine mitochondrial DNA analysis – casework tool of last resort and reference databases
Cordula Berger1, Werner Hecht2, Walther Parson1,5

Genetic drawing of dog identikit pictures – Canine DNA phenotyping for forensic applications
Cordula Berger1, Josephin Heinrich1, Werner Hecht2, Burkhard Berger1, Walther Parson1,5

Affiliations:
1 Institute of Legal Medicine, Medical University of Innsbruck, Austria
2 Institute of Veterinary Pathology, Justus-Liebig-University Giessen, Germany
3 Bundeskriminalamt, Kriminaltechnisches Institut, Wiesbaden, Germany
4 Zurich Institute of Forensic Medicine, University of Zurich, Switzerland
5 Forensic Science Program, The Pennsylvania State University, University Park, PA, USA
6 School of Biological Sciences, Flinders University, Adelaide, Australia
7 Faculdade de Ciências da Universidade do Porto, Instituto de Investigação, Portugal
8 Inovação em Saúde, Universidade do Porto, Portugal

HW8 – Autosomal STR Genomics 101: Sequence variation and nomenclature

Organiser: Katherine Gettings
Type: Half Day Workshop, Lecture
Room: Club H
Date & Time: Tuesday, 10th September (14:00 – 18:00)

This workshop will introduce attendees to autosomal STR sequences, with a target audience of students and practitioners having minimal sequencing experience or background knowledge. The workshop will be divided into three modules: 1) Anatomy of an STR Locus, 2) Historical and Modern STR Sequencing, and 3) STR Sequencing Quality Control and Nomenclature.

In the first module, we will begin by dissecting the sequences of autosomal STR loci in the traditional categories of simple, compound, and complex repeat motifs. We will use these example loci to explore the concept of bracketing (e.g. [GATA]8), considering historical precedent, modern guidance, and issues of CE backward compatibility. Then we will venture out into the flanking regions to find examples of SNPs and Indels, exemplifying their role in concordance between both length- and sequence-based assays.

In the second module, we will consider historical STR sequencing challenges and the benefits of modern sequencing platforms. We will review commercial STR sequencing assays and bioinformatic tools designed specifically for the forensic community, as well as bioinformatics geared toward STR analysis in whole genome sequence data. Lastly in this module, we will discuss
the proliferation of STR population sequence data, following an example of how a lab could implement such data to generate match statistics.

Finally, in the third module, we will explore interpretation issues specific to STR sequencing, and additional quality control measures which may be useful. Quality control and guidance initiatives expected to be discussed in the congress session will be described and contextualized so that attendees will have a firm foundation for the coming days. Lastly, we will discuss examples of early adopter casework implementation.

HW9 – Forensic DNA Phenotyping: basics of data acquisition and interpretation

Organiser: Wojciech Branicki
Type: Half Day Workshop, Lecture
Room: Club E
Date & Time: Tuesday, 10th September (14:00 – 18:00)

Forensic DNA Phenotyping (FDP) is a relatively new area in the filed of forensic genetics that utilizes the potential of DNA to predict ancestry, appearance and age. The obtained predictions can be used for intelligence purposes to track unknown individuals and speed up the investigation. This workshop will introduce the entire concept of FDP including theoretical aspects of marker selection, prediction modelling and practical application. Participants will get acquainted with technologies, assays and mathematical models available for predictive DNA analysis in forensics. They will also learn about the principles of data interpretation, accuracy parameters like AUC and MAE and prediction error related to different FDP methods. Much attention will be placed to the prediction of pigmentation traits and forensic implementation of the new system HlrisPlex-S for simultaneous prediction of eye, hair and skin colour. The workshop will also address the issue of epigenetic age prediction in the forensic field. Participants will learn about the current problems of age estimation by DNA methylation analysis including tissue specificity of age markers, sensitivity of the assays and sources of prediction errors. The available methods of age prediction will be reviewed and the concept of biological age and age acceleration will be introduced. Participants will get acquainted with the importance of combining information about gender, ancestry, and age for appearance prediction. The lectures will be illustrated with practical examples and participants will have opportunity to familiarize themselves with the methods currently used in FDP.
HW10 – Making sense of Ethical, Legal & Social Aspects of forensic genetics

Organisers: Matthias Wienroth & Gabrielle Samuel
Type: Half Day Workshop, Lecture
Room: Club C
Date & Time: Tuesday, 10th September (14:00 – 18:00)

The aim of the workshop is to make accessible to forensic stakeholders the concept of ‘ethical, legal and social aspects’ of science and technology. We will not discuss ethics approval procedures or health & safety concerns, but instead look at the type of knowledge that ethical, legal and social aspects represent. The ideas of anticipation and responsibility will guide this workshop. In order to equip participants with the tools to explore how such understanding can be applied in making forensic genetics research and technology uses societally and ethically more robust, participants will be supported in engaging in case study work, exploring two very topical emerging forensic technologies and applications in (1) forensic DNA phenotyping, and (2) the searching of public and private genetic databases for investigative purposes.

Methods:
• Introductory lectures
• Case study work

Objectives:
• To provide participants with tools for understanding and assessing ethical, legal and social aspects of the development and use of forensic genetics technologies.
• To encourage participants to adopt the principles of anticipation and responsibility
• To support the management of dilemmas in researching and applying new technologies.

HW11 – Bayesian reasoning in the framework of Bayesian Networks

Organiser: Tomas Furst
Type: Half Day Workshop, Lecture
Room: Club D
Date & Time: Tuesday, 10th September (14:00 – 18:00)

Bayesian networks represent a universal framework for almost any inference tasks. BN is a network of nodes connected by directed links such that the resulting graph contains no loops. The nodes represent random variables (e.g. an action of a suspect, or the presence of a trace) whose state may be either known or unknown.

The links represent causal relations (e.g. the presence of the suspect causes the occurrence of a trace). In each node, a probability distribution conditional on the parent nodes is given (e.g. the presence of a suspect leads to the occurrence of a particular trace with the probability of 0.7).

The network is used for making inference about unobserved nodes (e.g. on the activity level
on hierarchy of propositions) conditional on the values of observed nodes (usually the evidence nodes).

In the workshop, fundamentals of Bayesian inference will be explained and various examples of their usage in forensic context will be given. The examples will be illustrated in freely available software (unbbayes.sourceforge.net), so that the participants may explore the behavior of the network themselves. The examples will go from a really trivial case all the way to a rather involved illustration of BN usage in forensic practice.
Scientific Prize Lecture

Prof. Dr. Manfred Kayser

Department of Genetic Identification, Erasmus MC University Medical Center Rotterdam

ROTTERDAM, THE NETHERLANDS

Date & time of the presentation: 10th September 2019, 18:45 – 19:30, Forum Hall

Manfred Kayser is (full) Professor of Forensic Molecular Biology at Erasmus University Rotterdam and (founding) Head of the Department of Genetic Identification at Erasmus University Medical Center. He obtained his diploma in biology with magna cum laude from University of Leipzig, his doctorate degree in biology/genetics with summa cum laude from Humboldt University Berlin, and his habilitation in genetics from University of Leipzig. After postdoctoral research at the Department of Anthropology, Pennsylvania State University, he was staff scientist, later Heisenberg Fellow of the German Research Council, at the Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology Leipzig, before he accepted his professorship appointment in Rotterdam. His research interest is in various aspects of forensic and anthropological genetics. In the forensic field, he is well known for his pioneering work on forensic DNA phenotyping and his contributions to the introduction and further development of forensic Y-chromosome analysis, while also published on various other forensic genetic topics. As of early 2019, he authored 240 articles (60 % as leading author) in peer-reviewed scientific journals that were cited 14,000 times; his h-index is 67. He received the Scientific Price 1998 of the German Society of Legal Medicine and the Biennial Scientific Price 2017 of the International Society for Forensic Genetics. He serves/d as editor-in-chief, academic editor, section editor, guest editor, and editorial board member of several forensic and human genetic journals, and is regular ad-hoc reviewer for various scientific journals and research funding agencies in different countries and the EU.
Keynote Speakers

Prof. Dr. Lutz Roewer, PhD
Institute of Legal Medicine and Forensic Sciences, Charité -Universitätsmedizin
BERLIN, GERMANY

Date & time of the presentation: 11th September 2019, 08:30 – 09:15, Forum Hall

Lutz Roewer studied biochemistry in Leipzig and received his PhD in molecular biology in 1990 at the Charité in Berlin. His early work encompassed the application of oligonucleotide probes for forensic DNA fingerprinting and the development of PCR-based methods to analyze autosomal and Y-chromosomal microsatellites. Since 2008 he is professor for forensic genetics at the Institute of Legal Medicine and Forensic Sciences, Charité -Universitätsmedizin Berlin, Germany and head of the Department of Forensic Genetics. His laboratory with 14 staff members processes several thousand crime cases per year. Lutz was awarded the scientific prize of the DGRM (Deutsche Gesellschaft für Rechtsmedizin) in 1990 and 1998 and the scientific prize of the ISFG (International Society of Forensic Genetics) in 1999 for the development of the Y chromosome STR haplotyping method. Lutz Roewer is founder and curator of the largest forensic reference database for Y chromosome profiles, the YHRD (https://yhrd.org). His major research interest is the molecular and population genetics of the Y chromosome with regard to its forensic application. Another research line is the evolution and demography of world populations. He studied indigenous populations in Europe, Asia and the Americas and authored large multi-centred studies on this topic. He is co-beneficiary of a grant of the European Union to develop autosomal/Y-chromosomal STR prototypes for massive parallel sequencing analysis (MPS) in forensics.

Mgr. Halina Šimková
Faculty of Science, Charles University
PRAGUE, THE CZECH REPUBLIC

Date & time of the presentation: 11th September 2019, 14:30 – 15:15, Forum Hall

Forensic geneticist, lecturer and science popularizer.

Halina Šimková graduated in Anthropology and Human Genetics at the Faculty of Science at Charles University in Prague and in Scenography at Master School of Art Design in Prague. During her studies at the Faculty of Science, Charles University, she became a civilian intern at the Institute of Criminalistics in Prague, later she started working there as an expert in the field of DNA analysis. She co-founded the Czechoslovak Society for Forensic Genetics, and has been Vice-Chair since 2008. In order to demonstrate her generally declared love of uncertainty, she left her stable position to become freelancer in 2016 and her interest gradually shifted mainly to promote the use of Bayesian inference in the field of forensic expertise and within other disciplines working with probabilistic conclusions.
She enjoys lecturing and popularization very much, emphasizing the use of non-verbal and combined teaching tools. She is the author of the educational book *Breviary of Forensic Genetics*, in 2016 she won the Neuron Prima ZOOM award for the best popular science video. She regards Bayesian inference as beautiful, brilliant and logical, and it bothers her that the vast majority of people do not know Bayesian inference at all – not even those whose decisions cannot be properly made without it. She wants to change it.

**Dr. Yaniv Erlich**

Data Science Institute, Colombia University  
NEW YORK, USA

*Date & time of the presentation: 12th September 2019, 08:30 – 09:15, Forum Hall*

Dr. Yaniv Erlich is the Chief Science Officer of MyHeritage.com and an Associate Professor of Computer Science and Computational Biology at Columbia University (leave of absence). Prior to these positions, he was a Fellow at the Whitehead Institute, MIT. Dr. Erlich received his bachelor’s degree from Tel-Aviv University, Israel (2006) and a PhD from the Watson School of Biological Sciences at Cold Spring Harbor Laboratory (2010). Dr. Erlich’s research interests are computational human genetics. Dr. Erlich is a TEDMED speaker (2018), the recipient of DARPA’s Young Faculty Award (2017), the Burroughs Wellcome Career Award (2013), Harold M. Weintraub award (2010), the IEEE/ACM-CS HPC award (2008), and he was selected as one of 2010 Tomorrow’s PIs team of Genome Technology.

**Assoc. Prof. Roland van Oorschot**

School of Molecular Sciences, La Trobe University  
MELBOURNE, AUSTRALIA

*Date & time of the presentation: 12th September, 14:30 – 15:15, Forum Hall*

After acquiring an Agricultural science and engineering degree in the Netherlands, a PhD from Macquarie University in Australia on marsupial genetics, postdoctoral positions at the Southwest Foundation for Biomedical Research in San Antonio, Texas on genemapping and at the Centre for Animal Biotechnology at Melbourne University in Australia on genetics of disease resistance in sheep, Roland started working, in 1992, at the Forensic Services Department of Victoria Police where he is currently a Principal RD&I Specialist. He is also an Adjunct Professor in the School of Molecular Sciences at La Trobe University.

Roland has over 160 publications in scientific journals and books. Including an article in *Nature* (in 1997) regarding the ability to retrieve directly and indirectly deposited DNA from touched objects that helped revolutionise forensic investigations. Roland has supervised over 90 postgraduate students, examined several theses, sits on University course advisory committees and has reviewed manuscripts for several journals. His current interests include the areas of: ‘DNA transfer, persistence prevalence, and recovery’, ‘contamination minimisation’ and ‘acquiring more information from available biological samples to assist investigations of criminal activity’. 
Fanny Pouyet, PhD
Institute of Ecology and Evolution, University of Bern
BERN, SWITZERLAND

Date & time of the presentation: 13th September, 08:30 – 09:15, Forum Hall

Fanny Pouyet received a MSc degree in Biology from the Ecole Normale Supérieure de Lyon and a MSc in Bioinformatics from the University of Paris VI. During my PhD in Lyon, I quantified the importance of both adaptive and non-adaptive processes on the evolution of codon usage in genes in Human.

I have currently a postdoctoral position at the University of Bern since October 2016 in the laboratory of Prof. Laurent Excoffier. My research focus on disentangling the impact of evolutionary mechanisms that constrain the genome-wide diversity in humans as a population geneticist. I am particularly interested in understanding the links between such evolutionary processes and recombination across the genome.

Dr. Jessica Metcalf
Department of Animal Sciences, Colorado State University
FORT COLLINS, COLORADO, USA

Date & time of the presentation: 13th September, 14:30 – 15:15, Forum Hall

Dr. Jessica L. Metcalf is a microbiome scientist who leads highly interdisciplinary, innovative research projects that span the fields of forensics, animal science, and health by combining experimental ecology, large genomic datasets, and bioinformatics tools. Her lab studies the complex suite of microorganisms (bacteria, archaea, fungi, protists, etc) driving decomposition of post-mortem vertebrate animals. Over the past several years, she has been developing a microbial clock to estimate how long vertebrate (including human) remains have been decomposing. Along with several collaborators, she is developing the microbial clock into a new forensic science tool to help investigators estimate the postmortem interval (PMI) for cases with unknown PMIs. She also studies the gastrointestinal tract of vertebrate animals with a focus on the effects of captivity and domestication on animal health. In a similar vein, she also studies the loss of microbial diversity in the human gastrointestinal tract associated with the industrialization/urbanization of human populations.

Metcalf earned a Bachelor of Science in chemistry from University of Georgia and a Ph.D. in ecology and evolution from University of Colorado Boulder. She completed postdoctoral positions in ancient DNA at the University of Adelaide in South Australia and in microbiome science at UC San Diego. She joined Colorado State University in 2016 as part of the Microbiome Systems Cluster Hire Initiative. She is an Associate Professor in the Department of Animal Sciences.
Detailed Scientific Programme

Tuesday 10th September 2019, Forum Hall

18:30  OPENING CEREMONY

19:00  OPENING CEREMONY & SCIENTIFIC PRIZE LECTURE
FORENSIC APPEARANCE PREDICTION FROM DNA: A JOURNEY THROUGH
10 YEARS OF SCIENTIFIC CONTRIBUTIONS
Kayer, Manfred

20:00  WELCOME COCKTAIL (FOYER)

Wednesday 11th September, Forum Hall

Session 1
Chairs: Walther Parson, Marie Korabečná

08:30  KEYNOTE LECTURE
THE WHITE ELEPHANT IN THE FIELD – WHAT MEANS “POPULATION”
IN FORENSIC GENETICS?
Roewer, Lutz

09:15  DEVELOPMENT AND OPTIMIZATION OF THE VISAGE PROTOTYPE TOOLS
FOR BIO-GEOGRAPHIC ANCESTRY AND APPEARANCE TRAITS INFERENCE
USING TARGETED MPS
Xavier, Catarina

09:30  APPROACHES TO EXPLAIN AND POTENTIALLY PREDICT THE COMPLEX
ARCHITECTURE OF THE HUMAN FACE
Walsh, Susan

09:45  INTRODUCTION OF A PREDICTIVE DNA TEST FOR THE OCCURRENCE
OF FRECKLES
Branicki, Wojciech

10:00  COFFEE BREAK (FOYER) & POSTER SESSION (SOUTH HALL 2)
Session 2
Chairs: Walther Parson, Marie Korabečná

11:00  FORENSIC DNA PHENOTYPING: A SERVICE PROVIDER TRIAL
       Raymond, Jennifer

11:12  COMPARISON OF CE- AND MPS-BASED ANALYSES OF FORENSIC MARKERS WITH SINGLE CELL AFTER WHOLE GENOME AMPLIFICATION
       Chen, Man

11:24  PRESENTATION OF THE HUMAN PIGMENTATION (HUPI) AMPLISEQ CUSTOM PANEL
       Meyer, Olivia Strunge

11:36  PREDICTIVE DNA ANALYSIS OF HUMAN HEAD HAIR GREYING USING WHOLE-EXOME AND TARGETED NGS DATA EXAMINED WITH DEEP LEARNING METHODS
       Pośpiech, Ewelina

11:48  A COMPARISON OF DNA METHYLATION TECHNOLOGIES AND PERFORMANCE OF AGE PREDICTION MODELS
       Freire-Aradas, Ana

12:00  A COMING OF AGE TALE
       Aliferi, Anastasia

12:12  IN SEARCH OF CENTRAL- AND EASTERN EUROPEAN- SPECIFIC ANCESTRY INFORMATIVE MARKERS
       Woźniak, Marcin

12:30  COMPANY SYMPOSIUM BY THERMO FISHER SCIENTIFIC

13:00  LUNCH

13:30  COMPANY SYMPOSIUM BY QIAGEN (SOUTH HALL 1B)

Session 3
Chairs: John Butler, Manfred Kayser

14:30  KEYNOTE LECTURE
       EXPLAINING BAYESIAN INFERENC PRINCIPLES NONVERBALLY: HOW TO HELP NON-MATHMATICIANS UNDERSTANDING THE WEIGHT OF EVIDENCE
       Šimková, Halina

15:15  HOW TO AVOID DRIVING DNA CASEWORKERS CRAZY: CASESOLVER, AN EXPERT SYSTEM TO INVESTIGATE COMPLEX CRIME SCENES
       Prieto, Lourdes
15:30 COMPARISON OF CE AND MPS BASED ANALYSIS FOR THE PROBABILISTIC INTERPRETATION OF MIXED STR PROFILES
Benschop, Corina

15:45 USING GENETIC COMPLEXITY TO SOLVE FORENSIC COMPLEXITY: A NEW CLASS OF COMPLEX HYPERVARIABLE STR MARKERS FOR DECONVOLUTION OF COMPLEX DNA MIXTURES
Ralf, Arwin

16:00 COFFEE BREAK (FOYER)

Session 4
Chairs: John Butler, Manfred Kayser

16:30 THE FIRST MPS-STR BASED CONVICTION IN A CRIMINAL CASE?
De Knijff, Peter

16:42 ENHANCING STR SEQUENCE ALLELE REPRESENTATION FOR PROBABILISTIC GENOTYPING
Just, Rebecca

16:54 A MASSIVELY PARALLEL SEQUENCING ASSAY OF MICROHAPLOTYPES FOR MIXTURE DECONVOLUTION
Oldoni, Fabio

17:06 A TOP-DOWN APPROACH TO MIXTURE EVALUATION
Slooten, Klaas

17:18 FROM REFERENCE TO MIXTURE TO MIXTURE TO MIXTURE AND BEYOND
Kruijver, Maarten

17:30 EXPLORING DNA INTERPRETATION SOFTWARE USING THE PROVEDIT DATASET
Riman, Sarah

17:42 ARE REPORTED LIKELIHOOD RATIOS WELL CALIBRATED?
Hannig, Jan

18:00 WORKING GROUPS MEETINGS
Thursday 12\textsuperscript{th} September 2019, Forum Hall

Session 5
Chairs: Mechthild Prinz, Jiří Drábek

8:30  
**KEYNOTE LECTURE**  
FORENSIC GENETICS AND DTC GENOMICS: FRIEND OR FOE?  
Erlich, Yaniv

9:15  
**DEVELOPING PRIORITIES FOR DISCUSSION AND OVERSIGHT OF THE RAPIDLY EVOLVING FIELD OF GENETIC GENEALOGY**  
Phillips, Christopher

9:30  
**THE EFFECTIVENESS OF FORENSIC GENEALOGY TECHNIQUES IN THE UNITED KINGDOM – AN EXPERIMENTAL ASSESSMENT**  
Thomson, Jim

9:45  
**FORENSIC GENEALOGY – PERFORMANCE OF DENSE SNP DATA TO TRACE DISTANT RELATIVES**  
Kling, Daniel

10:00  
**COFFEE BREAK (FOYER) & POSTER SESSION (SOUTH HALL 2)**

Session 6
Chairs: Mechthild Prinz, Jiří Drábek

11:00  
**AN INTERNATIONAL CONSIDERATION OF A STANDARDS-BASED APPROACH TO FORENSIC GENETIC GENEALOGY**  
Scudder, Nathan

11:12  
**WHOLE GENOME SEQUENCING OF HUMAN REMAINS TO ENABLE GENEALOGY DNA DATABASE SEARCHES – A CASE REPORT**  
Tillmar, Andreas

11:24  
**ETHICAL, SOCIAL AND LEGAL ISSUES OF FAMILIAL SEARCHING: NEW AND OLD DEBATES**  
Granja, Rafaela

11:36  
**THE GENETIC IDENTIFICATION OF DEAD MIGRANTS IN THE MEDITERRANEAN SEA: THE LAMPEDUSA 2013 SHIPWRECK**  
Bertoglio, Barbara

11:48  
**RE-EVALUATION OF DNA BASED IDENTIFICATION RESULTS OF VICTIMS OF A TERRORIST ATTACK 25 YEARS LATER**  
Corach, Daniel
12:00 NEW ISO STANDARDS FOR FORENSICS: DNA “FREE” CONSUMABLES AND THE FORENSIC PROCESS
Bastisch, Ingo

12:12 REFLECTIONS AND EXAMPLES OF PROBLEMATIC REPORTING IN DNA CASES: THE NEED FOR ACCREDITED FORMATS AND CERTIFIED REPORTING COMPETENCE
Hicks, Tacha

12:30 COMPANY SYMPOSIUM BY PROMEGA

13:00 LUNCH

---

Session 7

Chairs: Peter Schneider, Titia Sijen

14:30 KEYNOTE LECTURE
DNA TRANSFER: ASPECTS RELEVANT TO FORENSIC INVESTIGATIONS
van Oorschot, Roland

15:15 TRANSFER, PERSISTENCE AND RECOVERY OF EPITHELIAL CELLS ON THE SKIN IN DIRECT AND SECONDARY TRANSFER SCENARIOS
Fonneløp, Ane Elida

15:30 MODELLING DNA TRANSFERS IN COMPLEX SCENARIOS
Taylor, Duncan

15:45 ASSIGNING FORENSIC BODY FLUIDS TO DNA DONORS IN MIXED SAMPLES BY TARGETED RNA/DNA DEEP SEQUENCING OF CODING REGION SNPS USING ION TORRENT TECHNOLOGY
Ballantyne, John

16:00 COFFEE BREAK (FOYER)

---

Session 8

Chairs: Peter Schneider, Titia Sijen

16:30 VISUALISING DNA TRANSFER: LATENT DNA DETECTION USING DIAMOND DYE
Champion, Jessica

16:42 IN AND OUT OF TOUCH: RELATIVE ACCUMULATION OF CELLULAR AND ACELLULAR “TOUCH DNA” FROM ENDOGENOUS AND EXOGENOUS SOURCES ON HANDS OVER TIME
Burrill, Julie
CHARACTERIZATION OF TISSUE-SPECIFIC BIOMARKERS WITH THE EXPRESSION OF CIRC RNAs IN FORENSICALLY RELEVANT BODY FLUIDS
Yang, Qinrui

BODY FLUID IDENTIFICATION USING mRNA – BETTER, FASTER, CHEAPER – WHAT METHOD IS BEST OR SHOULD A COMBINATION OF TECHNIQUES BE USED?
Harbison, Sallyann

PREDICTING THE ORIGIN OF FORENSICALLY RELEVANT BIOLOGICAL MATERIAL USING A MACHINE LEARNING APPROACH
Iacob, Diana

DEVELOPMENT OF A MIRNA BODY FLUID PREDICTION SYSTEM USING PROBABILISTIC APPROACHES
Li, Zhilong

PROTEOMIC GENOTYPING: USING MASS SPECTROMETRY TO INFER SNP GENOTYPES IN A FORENSIC CONTEXT
Parker, Glendon

GENERAL ASSEMBLY

Friday 13th October 2019, Forum Hall

Session 9
Chairs: Leonor Gusmão, Halina Šimková

KEYNOTE LECTURE
BACKGROUND SELECTION AND BIASED GENE CONVERSION AFFECT MORE THAN 95% OF THE HUMAN GENOME AND BIAS DEMOGRAPHIC INFERENCES
Pouyet, Fanny

Y-PROFILE EVIDENCE: CLOSE PATERNAL RELATIVES AND MIXTURES
Andersen, Mikkel Meyer

INFERENCE OF ADMIXED ANCESTRY WITH ANCESTRY INFORMATIVE MARKERS
Tvedebrink, Torben

THE IMPACT OF IGNORING INBREEDING IN KINSHIP EVALUATIONS
Kjelgaard Brustad, Hilde

COFFEE BREAK (FOYER) & POSTER SESSION (SOUTH HALL 2)
### Session 10
**Chairs:** Leonor Gusmão, Halina Šimková

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Speaker</th>
</tr>
</thead>
<tbody>
<tr>
<td>11:00</td>
<td>STR SEQUENCE NOMENCLATURE: PROGRESS REPORT FROM THE STRAND WORKING GROUP</td>
<td>Gettings, Katherine</td>
</tr>
<tr>
<td>11:24</td>
<td>ADVANCING MITOCHONDRIAL GENOME DATA INTERPRETATION IN MISSING PERSONS CASEWORK</td>
<td>Marshall, Charla</td>
</tr>
<tr>
<td>11:36</td>
<td>CSY? A PANEL-BASED MPS APPROACH INCLUDING 12,523 Y-CHROMOSOME POLYMORPHISMS</td>
<td>Claerhout, Sofie</td>
</tr>
<tr>
<td>11:48</td>
<td>ANALYSIS OF RECOMBINATION AND MUTATION EVENTS FOR 12 X-CHR STR LOCI: A COLLABORATIVE FAMILY STUDY OF THE ITALIAN SPEAKING WORKING GROUP GE.F.I.</td>
<td>Bini, Carla</td>
</tr>
<tr>
<td>12:00</td>
<td>GENETIC PEOPLING OF PAKISTAN AND THE IMPACT OF HISTORICAL MIGRATIONS, ETHNIC CULTURES AND THE PRACTICE OF ENDOGAMY ON THE FORENSIC MATCH PROBABILITIES</td>
<td>Anwar, Ijaz</td>
</tr>
<tr>
<td>12:12</td>
<td>THE SCOPE AND LIMITATIONS OF THE LIKELIHOOD RATIO METHOD APPLIED TO STR DATA FOR DETERMINING GENETIC KINSHIP IN ANCIENT OR ISOLATED HUMAN POPULATIONS</td>
<td>Zvenigorosky, Vincent</td>
</tr>
<tr>
<td>12:30</td>
<td>LUNCH</td>
<td></td>
</tr>
</tbody>
</table>

### Session 11
**Chairs:** Adrian Linacre, Eugenia D’Amato

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Speaker</th>
</tr>
</thead>
<tbody>
<tr>
<td>14:00</td>
<td>KEYNOTE LECTURE USING MICROBIOME TOOLS TO ESTIMATE THE POSTMORTEM INTERVAL OF HUMAN REMAINS</td>
<td>Metcalf, Jessica</td>
</tr>
<tr>
<td>14:45</td>
<td>ENVIRONMENTAL DNA TO ASSIST FORENSIC INVESTIGATIONS, COUNTER-TERRORISM, FRAUDULENT MEDICINES AND DRUG SEIZURES</td>
<td>Young, Jennifer</td>
</tr>
</tbody>
</table>
15:00 TAXONOMY-INDEPENDENT DEEP LEARNING MICROBIOME APPROACH FOR ACCURATE CLASSIFICATION OF FORENSICALLY RELEVANT HUMAN BIOMATERIALS USING TARGETED MPS
Díez López, Celia

15:15 PERFORMANCE OF ENVIRONMENTAL DNA METABARCODING IN SOIL TRACE MATCHING AND PROVENANCING
Frøslev, Tobias Guldberg

15:30 COFFEE BREAK (FOYER)

---

Session 12
Chairs: Adrian Linacre, Eugenia D’Amato

16:00 COLLABORATION ACROSS BORDERS TO IMPLEMENT A EUROPEAN DATABASE FOR CANINE STR IDENTIFICATION MARKERS
Giangasparo, Federica

16:12 MULTI-LOCUS DNA METABARCODING FOR AUTHENTICATION OF HIGHLY PROCESSED MEAT PRODUCTS COLLECTED IN SOUTH AFRICA
Pietroni, Carlotta

16:24 SPECIES IDENTIFICATION USING MASSIVELY PARALLEL SEQUENCING – DETECTING MULTIPLE SPECIES IN MIXED SOURCES
Dellamico, Barbara

16:36 SPECIES IDENTIFICATION IN ROUTINE CASEWORK SAMPLES USING THE SPINDEL KIT
Pereira, Filipe

16:48 WHOLE-GENOME SEQUENCING OF NEISSERIA GONORRHOEAE IN A FORENSIC TRANSMISSION CASE
Gonzalez-Candelas, Fernando

17:00 WHOLE TRANSCRIPTOME ANALYSIS OF AGED BIOLOGICAL CRIME SCENE TRACES
Salzmann, Andrea

17:12 PREVALENCE OF DNA IN VEHICLES: OPTIMIZING SAMPLING STRATEGY AND ACTIVITY LEVEL EVALUATION OF DNA TYPING RESULTS
Kokshoorn, Bas

19:30 CLOSING CEREMONY & CONGRESS DINNER (MUNICIPAL HOUSE – SMETANA HALL)
Company Symposia

Thermo Fisher Scientific

Date: Wednesday, 11th September, 2019
Time: 12:30–13:20
Location: Forum Hall, 2nd floor

Validation of the latest forensic genetic technologies for the solution of complex cases

Speakers: Magdalena Marcińska, Instytut Ekspertyz Sądowych, Krakow, Poland
Ten.Col. CC RT inv. sc. Andrea Berti, Reparto Carabinieri Investigazioni Scientifiche di Roma – Sezione di Biologia, Italy

During this symposium the speakers will present their validation work with the newest Applied Biosystems™ systems for forensic genetics: the SeqStudio™ HID Genetic Analyzer and the Rapid HiT™ Rapid DNA system.

QIAGEN

Date: Wednesday, 11th September 2019
Time: 13:30–14:20
Location: South Hall 1B, 1st floor

Identifying the missing

Speakers: Mrs. Ingrid Gudmundsson, Sweden
Dr. Thomas J. Parsons, Director of Science and Technology, ICMP, The Hague, Netherlands

How a new NGS workflow is enabling missing persons identification and bringing closure to families around the world.

Promega Corporation

Date: Thursday, 12th September, 2019
Time: 12:30–13:20
Location: Forum Hall, 2nd floor

Streamlined Workflows for Forensic DNA Extraction and Analysis

Speakers: Stefan Kutranov, Promega UK - Gro Bjørnstad, Oslo University Hospital, Norway – Dr. Richard Zehner, University of Frankfurt, Germany

During this symposium you will hear about the Latest advances in STR Analysis and the forensics workflow from Promega, an Evaluation of Promega’s Casework Direct Kit, Custom for DNA extraction from various casework samples, including a comparison of its performance to Chelex extraction, and Validation studies with the Maxwell® RSC 48 instrument.
# ISFG Working Groups Meetings

**Wednesday 11th September, 18:00 – 19:30**

<table>
<thead>
<tr>
<th>Working Group</th>
<th>Room</th>
</tr>
</thead>
<tbody>
<tr>
<td>Polish Speaking WG</td>
<td>Club D</td>
</tr>
<tr>
<td>French Speaking WG</td>
<td>ISFG Board meeting room (room number 2.3)</td>
</tr>
<tr>
<td>English Speaking WG</td>
<td>Forum Hall</td>
</tr>
<tr>
<td>Spanish/Portuguese (GHEP)</td>
<td>South Hall 1A (9th – 10th September)</td>
</tr>
<tr>
<td>German Speaking WG</td>
<td>Club C</td>
</tr>
<tr>
<td>Italian Speaking WG</td>
<td>Club A</td>
</tr>
<tr>
<td>Chinese Speaking WG</td>
<td>Club B</td>
</tr>
<tr>
<td>Korean Speaking WG</td>
<td>LOC meeting room (room number 241)</td>
</tr>
</tbody>
</table>
Social Programme

Opening Ceremony & Scientific Prize Lecture

Tuesday – 10th September 2019 (18:30 – 20:00)
Prague Congress Centre, 2nd floor, Forum Hall

Included in the registration fees for full delegates (all categories) and accompanying persons. NOT INCLUDED in the pre-congress workshop registrations.

The ISFG 2019 Congress will be officially opened on 10th September 2019 with the Opening Ceremony held in the Forum Hall where we will be welcome by our hosts and hosting institution representatives. We sincerely invite all our participants to take part and listen to Prof. Dr. Manfred Kayser (Scientific Prize Lecture) talking about Forensic appearance prediction from DNA: a journey through 10 years of scientific contributions as well as enjoy the Light Art show prepared especially for this purpose.

Welcome Cocktail

Tuesday – 10th September 2019 (20:00 – 22:00)
Prague Congress Centre, 2nd floor, exhibition foyer

Included in the registration fees for full delegates (all categories) and accompanying persons. NOT INCLUDED in the pre-congress workshop registrations.

The ISFG 2019 Congress will be officially opened with the Opening Ceremony & Scientific Prize Lecture starting at 18:30 in the Forum Hall. Afterward, all participants are kindly invited to take part in the Welcome Cocktail. It is the perfect opportunity to catch up with old acquaintances and network with your colleagues. This is an informal evening prior to the serious scientific discussions. Light cocktail refreshment will be served.

Dress code: smart casual.

Welcome Cocktail is kindly supported by the City of Prague.
Closing Ceremony & Congress Dinner

Friday – 13th September 2019 (19:30 – 23:30)
Municipal House – Smetana Hall, nam. Republiky
1090/5, 111 21 Prague 1
NOT INCLUDED in the delegate registration, pre-booking necessary

The Municipal House has been one of the most significant public buildings in Prague for over a hundred years. After the city administration had purchased the plots where the Royal Court, the medieval seat of the Bohemian kings, used to be located, they announced an architectural competition for the Municipal House in 1903. Unsatisfied with the results of the competition, the city administration awarded this project to architects Antonín Balšánek and Osvald Polívka.

Enjoy the last evening of the Congress, closing ceremony and an unforgettable cultural event in one. Experience the city of Prague while enjoying dinner and entertainment, showcasing Prague’s cuisine and arts.

Dress code: business attire.

Please note that transfers from and back to the venue won’t be provided. For transfers from and back to the hotels Holiday Inn and Corinthia Tower, please stop by at the registration to sign in.

How to get there:

Metro C+B (15 minutes):
- From the Prague Congress Centre take the Metro C (station Vyšehrad)
- to the station Florenc
- and change to Metro B (yellow line).
- Continue one stop to the station Náměstí Republiky.
- Walking distance to the Municipal House 150 m, 2 minutes.

Prague City Tours

Don’t forget to stop by the information kiosk of The Premiant City Tours located near the registration area. The staff will be happy to assist and inform you about the wide offer of guided tours that can be purchased separately at discounted prices.
Exhibition Floorplan

2nd Floor

List of Exhibitors

1. QIAGEN
2. Verogen
3. Carolina Biosystems
4. MENARINI SILICON BIOSYSTEMS
5. Promega
6. Thermo Fisher Scientific
7. GENETEK BIOPHARMA
8. Qualitype GmbH
9. Purdue University Northwest
10. HEALTH Gene Technologies
11. AXO Science
12. Miltenyi Biotec GmbH
13. NicheVision Forensics LLC
14. SERATEC GmbH
15. Forensic DNA Service
16. STRmix
17. MGI
18. GORDIZ
19. Independent Forensics
20. Spot On Sciences
21. GE Healthcare
22. CLIMS - VERISIS
23. HiMedia Laboratories GmbH
24. Xceltis
25. Bio-Port
Acknowledgment

PLATINUM SPONSOR

Thermo Fisher Scientific

GOLD SPONSORS

Promega

QIAGEN

SILVER SPONSOR

VEROGEN

BRONZE SPONSORS

MENARINI silicon biosystems

Carolina Biosystems

HIMEDIA

For Life is Precious

Spot On Sciences

MEDIA PARTNER

ELSEVIER

genes

CSSFG

PAR

HA

PRA

PRA

PRA

GAG
Company Profiles

Booth 1: QIAGEN

Contact Person: Inga Gerard
Telephone: +33 7 63 43 65 38
Email: inga.gerard@qiagen.com
Website: www.qiagen.com

QIAGEN is a global leader in Sample to Insight solutions in rapidly growing fields of molecular diagnostics and life sciences. We are at the forefront of human identity and forensic testing, and have actively supported the development of global forensic standards. Our product portfolio offers a full range of forensic DNA grade chemistries combined with high-quality instruments that address the diverse needs and challenges of crime scene investigation and human identification, covering every step in the workflow, from sample to result. QIAGEN quality, efficient solutions, innovative bioinformatics tools and comprehensive validation services help customers unlock valuable molecular insights. This is how we make improvements in life possible.

Booth 2: Verogen

Contact Person: Verogen
Telephone: +1 858 285 4101 (Global)
          +44 (20) 399 28411 (United Kingdom)
          +1 833 837 6436 toll-free (North America)
Email: info@verogen.com
Website: www.verogen.com

Verogen serves those who pursue the truth using genetic tools. Powered by Illumina’s gold standard technology and working in partnership with forensic laboratories, we are advancing massively parallel sequencing to help unlock the true potential of forensic genomics.

Booth 3: Carolina Biosystems

Contact Person: Marek Minarik
Telephone: +420 226 203 536
Email: info@carolinabiosystems.com
Website: www.carolinabiosystems.com

We supply original consumables for DNA sequencing and fragment analysis including polymers, kits, size standards, buffers etc. We also provide top-quality service and maintenance for ABI PRISM® line of capillary genetic analyzers. As an exclusive distributor for Softgenetics in Eastern Europe, we offer dedicated bioinformatics solutions for forensics (GeneMarker®HID).
Booth 4: MENARINI SILICON MENARINI

Contact Person: Massimo Scrobogna
Telephone: +39 3703344705
Email: mscrobogna@siliconbiosystems.com
Website: www.siliconbiosystems.com/forensics

Menarini Silicon Biosystems is a biotech company, which developed the DEPArray™ system. The instrument can work with low input and separates forensic samples composed of epithelial cells, white blood cells, and sperm cells into 100% pure cell type specific preparations, enabling clear-cut genetic profiles through Single Cell Forensics.

Booth 5: Promega Corporation

Contact Person: Nicole Siffling
Telephone: +49 621 8501283
Email: nicole.siffling@promega.com
Website: www.promega.com

Promega Corporation is a global leader in the development, distribution and sale of products for human identification. Promega offers flexible, reliable solutions for all stages in the DNA laboratory workflow, from pre-processing through STR analysis. Joining our workflow kit and reagent solutions are two CE instruments, as well as a new Maxwell instrument, our Maxwell RSC 48, which is capable of processing 48 samples in less than 30 minutes. Also available is the Maxprep Liquid Handler, which comes with all the methods preloaded and offers sample tracking and traceability through each step of the forensics workflow.

Booth 6: Thermo Fisher Scientific

Contact Person: Caroline Reddick
Telephone: +44 7738 312970
Email: caroline.reddick@thermofisher.com
Website: www.thermofisher.com/hid

Thermo Fisher Scientific is the world leader in serving science. Our mission is to enable our customers to make the world healthier, cleaner and safer. Through our Applied Biosystems brand, we offer an unmatched combination of innovative technologies, purchasing convenience and support. As a worldwide leader in forensics, we deliver some of the most comprehensively validated products, expertise, and application support available to the human identification community. From our trusted reagents, through high-performance genetic analyzers and software, to in-depth training and on-site technical assistance, our integrated systems work together to help maximize your productivity and enable your success.
Booth 7: GENETEK BIOPHARMA

Contact Person: Michael Onwuatuegwu
Telephone: +49 30 63927050
Email: onwuatuegwu@genetek.de
Website: www.genetek-biopharma.com

GENETEK Biopharma is located in the Science City of Adlershof in Berlin, Germany. The scope of the company includes Development, Production, Marketing and Distribution of in-vitro diagnostic kits for detection of genetic diseases and chromosomal anomalies, Human DNA profiling kits used in forensics and/or kinship issues and Horse identification kits.

Booth 8: Qualitype GmbH

Contact Person: Dr. Isabell Hilger
Telephone: +49 351 88382812
Email: i.hilger@qualitype.de
info@qualitype.de
Website: www.qualitype.de/de/start

As an internationally operating software company, we implement customised IT solutions – in use by customers in over 30 countries worldwide. These include classic off-the-shelf software, highly individualised software systems and central- or self-operated database solutions for laboratory and manufacturing applications.

Booth 9: Purdue University Northwest

Contact Person: George F. Kacenga
Telephone: +1-724-454-8734
Email: gkacenga@pnw.edu
Website: www.pnw.edu

As part of the Purdue University system, Purdue University Northwest (PNW) is a fully accredited comprehensive university proud to offer more than 70 areas of study. PNW offers one-of-a-kind proximity to active manufacturing, industry, the relaxing Lake Michigan shorefront, and the nearby opportunities of the third largest city in the United States – Chicago!

Booth 10: HEALTH Gene Technologies

Contact Person: Ausma Bernot
Telephone: +86 (0)574 2797 8799
Email: ausma.b@healthgenetech.com
Website: www.healthgenetech.net

Health Gene Technologies is a developer and manufacturer of proprietary molecular diagnostics products for forensic STR testing. Established in 2011, Health Gene Technologies has taken on the challenge to bring in further options of routine STR testing kits alongside innovative STR analysis reagents to forensic laboratories.
Booth 11: AXO Science

**Contact Person:** Samuel Serraz  
**Telephone:** +33 6 07 44 51 10  
**Email:** samuel.serraz@axoscience.com  
**Website:** www.axoscience.com

STK Sperm Tracker is the perfect solution for semen screening both in the lab and directly on the crime scene.  
STK Lab: specific, sensitive, STK Lab is NOT toxic and is ready to use.  
STK Spray: spray the scene directly with and reveal unsuspected semen stains on the field.

Booth 12: Miltenyi Biotec GmbH

**Contact Person:** Carola Kluefer  
**Telephone:** +49 2204 83066619  
**Email:** carolak@miltenyibiotec.de  
**Website:** www.miltenyibiotec.com

Miltenyi Biotec provides products that advance biomedical research and cellular therapy. Our innovative tools support research from basic research to translational research to clinical application. Our 30 years of expertise includes immunology, stem cell biology, neuroscience, and cancer. Miltenyi Biotec has 2,500 employees in 28 countries.

Booth 13: NicheVision Forensics, LLC

**Contact Person:** Victor Meles  
**Telephone:** +1-330-252-2711  
**Email:** vic@nichevision.com  
**Website:** www.nichevision.com

NicheVision develops and commercializes software solutions for forensic DNA human identity including tools like STRmix™, ArmedXpert™ and DNAXpress™, and most recent releases including PACE™ using artificial intelligence to automatically determine number of contributors in mixture and MixtureAce™ for typing and resolving MPS mixture data.

Booth 14: SERATEC GmbH

**Contact Person:** Alexander Griberman  
**Telephone:** +49 551 504800  
**Email:** contact@seratec.com  
**Website:** www.seratec.com

We manufacture tests for the detection of forensically relevant body fluids such as seminal fluid, saliva, blood and menstrual blood. They are rapid, easy in use and compatible with the subsequent DNA extraction and STR typing techniques.
Booth 15: Forensic DNA Service

**Contact Person:** Dr. Daniel Vanek  
**Telephone:** +420 603 979 915  
**Email:** daniel.vanek@fdnas.cz  
**Website:** www.fdnas.cz

Forensic DNA Service provides the services of paternity and genealogical testing, forensic DNA testing, specie identification of unknown biological material, individual identification of selected species and contracted research. Forensic DNA Service distributes products of the following companies: ZymoResearch, Eppendorf, Biomatrica, Seratec, COPAN, BIOO Scientific, and NZYTech.

Booth 16: STRmix™

**Contact Person:** Adam McCarthy  
**Telephone:** +44(0)7590 405 501  
**Email:** adam.mccarthy@esr.cri.nz  
**Website:** www.strmix.com

STRmix™ uses a world leading, fully continuous approach for the interpretation of DNA profiles and is now in over 150 laboratories globally. Recently we have released DBLR™ for the rapid calculation of likelihood ratios. Please come and see us for a demonstration of our latest release, STRmix™ v2.7, and DBLR™.

Booth 17: MGI

**Contact Person:** Xiaoxi Guo  
**Telephone:** +86 13428999426  
**Email:** shirley.guo@genomics.cn  
**Website:** www.en.mgitech.cn

MGI Tech Co., Ltd. (MGI), a subsidiary of BGI Group, is committed to enabling effective and affordable healthcare solutions for all. Based on its proprietary technology, MGI produces sequencing devices, equipment, consumables and reagents to support life science research, medicine and healthcare.

Booth 18: GORDIZ

**Contact Person:** Vladimir Orekhov  
**Telephone:** +7 903 799 38 72  
**Email:** orekhov@gordiz.ru  
**Website:** www.gordiz.com

GORDIZ Ltd. – biotechnology company that develops and manufactures the reagents for forensics and animal genetics. We developed a unique range of solutions in the field of DNA identification in close cooperation with forensic laboratories covering all the stages of analysis – from DNA extraction to fragment and sequencing.
Booth 19: Independent Forensics

Contact Person: Dina Mattes
Telephone: +1 708-234-1200
Email: info@ifi-test.com
Website: www.ifi-test.com

Solutions for your most difficult forensic DNA cases: touch and sexual assault evidence. Fully accredited ISO17025 facility develops products to increase sensitivity of DNA profiling & accurately identify body fluids to triage cases. Confirmatory tests for human blood, semen, and sperm. The most sensitive/scientifically justified tests for saliva, urine and feces. ONETOUCH kits for obtaining DNA profiles from fingerprints, tape lifts, and touched items designed to fully integrate your latent section. AMPLICON Rx for repairing data from partial profiles. On-site demonstrations/workshops/training/installations/validation/microscope systems for forensic laboratories world-wide.

Booth 20: Spot On Sciences

Contact Person: Nathalie Donche
Telephone: +415 347-3402
Email: nathalie.donche@spotonsciences.com
Website: www.spotonsciences.com

Spot On Sciences is a medical device company offering groundbreaking improvements in biospecimen sample collection, storage, and transport. Unmatched by any other products on the market, their signature devices are unique in offering innovative sample protection, increased safety, stability, longevity, and speed. With the assistance of industry leaders, Spot On Sciences is moving toward making its devices global standard of care.

Booth 21: GE Healthcare

Contact Person: Olga Bogonina / Inga Gerard
Email: olga.bogonina@ge.com
      inga.gerard@qiagen.com
Website: www.gehealthcare.com

GE Healthcare is excited for QIAGEN to take its Whatman FTA technology to the next level and advance the field of forensic science. Our forensic portfolio is now part of QIAGEN, and you can visit booth #1 to learn more from the experts.
Booth 22: CLIMS - VERIS

Contact Person: Murat Isik
Telephone: +90 5556044010
Email: misik@verisis.co
Website: www.verisis.co

VERISIS A.S. is a 30 years old company mainly focused on developing solutions, consultancy and training based on Forensic Laboratories. Our main solution CLIMS – Forensic Laboratory Solutions Platform is a Case and Workflow Management solution together with DNA Banking & Matching and Kinship & Paternity Analysis.

Booth 23: HIMEDIA LABORATORIES PVT LTD

Contact Person: Aseem Trehan
Telephone: +91 22 6147 1919
Email: info@himedialabs.com
atrehan@himedialabs.com
Website: www.himedialabs.com

HiMedia possesses excellent hi-tech expertise for manufacturing a complete range of standard microbiological, chromogenic, HiVeg™, animal & plant tissue culture media, Molecular biology, laboratory chemicals & biochemicals products. We are ISO, CE Mark, WHO-GMP certified, US-FDA registered company exporting to over 130 countries, specializing in Automated Instrumentation solutions in Molecular Biology.

Booth 24: Xceltis GmbH

Contact Person: Steffen Roth
Telephone: +49-621-872096-0
Email: info@xceltis.de
Website: www.xceltis.de

Xceltis GmbH is a privately held company founded in 2008 and headquartered in Mannheim, Germany, that markets pioneering products for life science research and routine diagnostics. This includes both laboratory equipment and reagents. One of these innovative products is the “Erase Sperm Isolation Kit”, that is used for forensic investigations.

Booth 25: Bio-Port Europe

Contact Person: Eva Mitášová, PhD.
Telephone: +420 602 251 901
Email: orders@bio-port.cz
Website: www.bio-port.cz

Bio-Port Europe is the Czech distributor company of premier brands like Thermo Fisher Scientific, Bio Molecular Systems, Jena Bioscience or Apogee. We provide advancing solutions for life sciences research, medical research and clinical laboratories.
ABSTRACTS
The ISFG 2019 Abstracts USB is given to each delegate upon registration; it contains all Abstracts that were accepted by the Scientific Programme Committee as well as those submitted by keynote speakers and presenters of invited sessions.

BADGES
Along with your registration, you will receive your name badge, which must be worn when attending all sessions and official congress programme. Participants without a badge will not be allowed to enter sessions.

CASH POINTS
A Komerční Banka cash point is located right between the venue entrances no. 5 and 6, and there is a Česká spořitelna cashpoint next to the underground station Vyšehrad.

CERTIFICATE OF ATTENDANCE
The certificates of attendance will be sent to all attending delegates by email after the congress.

CLOAKROOM
A cloakroom is located on the first floor near the registration area. The service is provided free of charge to all registered participants.

CURRENCY
The Czech currency is called the Czech crown (CZK). Exchange offices are located all around the city centre (exchange offices, banks, post offices).

CONFERENCE LANGUAGE
The congress language is English. No simultaneous translation is provided.

DISCLAIMER
The Congress Organizers have taken all reasonable care in making arrangements for the congress, including accommodation and social events. In the event of unforeseen disruptions, neither ISFG, CSSFG, and C-IN the Conference Organizer nor their agents can be held responsible for any losses or damages incurred by delegates. The programme is accurate at the time of printing, but organizers reserve the right to alter the programme if and when deemed necessary. The Congress Organizers act as agents only in securing hotels, transport and travel services and shall in no event be liable for acts or omissions in the event of injury, damage, loss, accident, delay or irregularity of any kind whatsoever during arrangements organized through contractors or by the employees of such contractors. Hotel and transportation services are subject to the terms and conditions under which they are offered to the general public. Delegates should make their own arrangements with respect to personal insurance. The Congress Organizers reserve the right to make changes as and when deemed necessary without prior notice to the parties concerned. All disputes are subject to resolution under Czech law.

DOCTOR / FIRST AID / PHARMACY
No first aid is available at the Prague Congress Centre. In case of emergency, please contact the Registration desk or dial 112 to get specialized help.
A Medical Centre (Poliklinika Budějovicka) is located at the station Budějovicka, three underground stations from the station Vyšehrad (the location of the venue).

**MEDICON A.S. – POLIKLINIKA BUDĚJOVICKA**  
Antala Staška 1670/80  
140 46 Praha 4  
Tel.: +420 261 006 111

**EMERGENCY PHONE NUMBERS**

<table>
<thead>
<tr>
<th>Service</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>General emergency</td>
<td>112</td>
</tr>
<tr>
<td>Police</td>
<td>158</td>
</tr>
<tr>
<td>Fire department</td>
<td>150</td>
</tr>
<tr>
<td>Emergency medical service</td>
<td>155</td>
</tr>
</tbody>
</table>

**EXHIBITION**

**OPENING HOURS**

- Tuesday, 10th September: 19:30 – 21:30
- Wednesday, 11th September: 09:30 – 18:00
- Thursday, 12th September: 09:30 – 18:00
- Friday, 13th September: 09:30 – 17:30

**FOOD AND BEVERAGES**

Coffee breaks and lunches are included in the pre-congress and congress registration fee and will be served at designated times within the coffee break and lunch stations.

**INSURANCE AND LIABILITY**

The Congress Organizers will accept no liability for personal injuries sustained by or for loss or damage to property belonging to conference participants, accompanying persons either during or as a result of the conference or during all tours and events. Upon registration participants accept this proviso. Participants are strongly advised to seek insurance coverage for health and accident, lost luggage and trip cancellation.

**INTERNET**

Free Wi-Fi internet connection is available throughout the congress premises.  
Network name: ISFG2019  
Password: ISFG2019

**LOST & FOUND**

A lost and found service is available at the information desk at the registration.

**MESSAGE BOARD / JOBS BOARD**

This is located on the ground floor, next to the Registration desk, and is available for all delegates to use.

**MOBILE APPLICATION**

**CONGRESS APP**

Stay updated and download the ISFG 2019 congress app via Apple app store or Google Play Store. Once logged in, you can make use of the app every day, any time...

**SEARCH THE CONGRESS PROGRAMME**

- View individual abstracts
- Create your own agenda
- Search by speaker name
- Search by keyword
- Rate oral presentations (scale 1 – 5 stars) and poster presentations
- See the venue floorplans
- Send messages to other congress participants
- Receive notifications from congress organizers

To use the full range of features, please note you will need to use the password/code upon the first login. The code and login procedure have been emailed to you by the congress secretariat. If you are unable to locate your login information, the registration desk staff will be happy to provide assistance.
INTERACTIVE SCIENTIFIC PROGRAMME AND INDIVIDUAL PLANNING
Full program details are available in the section: Scientific Program – Create your own personalized schedule for the ISFG 2019 Congress:
• Add session to My program
• Add the presentation to My program
To view your personalized program, use the My Program button at the bottom right corner of your screen within the Scientific Program section.

ATTENDEE PROFILES
Each pre-registered delegate is featured within the Attendee list. If you wish you can customize and update your own delegate profile by adding a website, a profile picture and short bio. To do so, click the blue “hamburger” button at the top left corner of your main screen and click the account email address (first item in the list). Speakers can also edit or delete biographies (submitted during abstract submission and published automatically from the database) as desired.

SEND MESSAGES TO OTHER PARTICIPANTS
Take advantage of networking with ISFG 2019 participants – search within the attendees and speakers list and send messages within the app to selected contacts. To send a message to selected attendee, click his name in the list and then click the blue envelope button () at the top right corner of the screen. Note: Attendees who are available and logged-in are highlighted with a blue dot beside their name in the Attendee List and are available for messaging. No contact information is visible to delegates and communications are all carried out in a closed environment only available to those with password access.

OFFLINE OPTIONS
The ISFG 2019 app is available offline except the following features:
• in-app messaging
• all external links (marked with a link icon)
• updating content
• receiving announcements

UPDATING THE APPLICATION CONTENT
The application updates the content automatically in the background upon each app restart (static meeting poster appears on the screen). Alternatively, you can force the application to update the content by pressing the last button in the list on the main screen – “Refresh event data”. Each menu item containing updated data will be labelled automatically.

MOBILE PHONES
Participants are kindly requested to keep their mobile phones turned off/muted in all meeting rooms while sessions are being held.

POSTERS
The Poster Area is placed on the second floor (South Hall). For more information about Poster Sessions please check respective pages in this Programme book (page number 9).

SPEAKERS’ PREVIEW ROOM – UPLOADING YOUR PRESENTATION ONSITE
Your presentation must be handed over to the technicians in the SPEAKERS’ PREVIEW ROOM (located on the first floor near the registration area) as much in advance as possible, but no later than TWO HOURS BEFORE the beginning of the corresponding session. The presentation for an early morning session must be handed over the day before.
SPEAKERS’ PREVIEW OPENING HOURS:
Monday 9th September  8:00 – 18:00
Tuesday 10th September  8:00 – 20:00
Wednesday 11th September  7:30 – 19:00
Thursday 12th September  7:30 – 19:00
Friday 13th September  7:30 – 17:00

PROGRAMME CHANGES
The Congress Organizers cannot assume liability for any changes in the programme due to external or unforeseen circumstances.

REGISTRATION OPENING HOURS
Monday 9th September  8:00 – 18:00
Tuesday 10th September  8:00 – 20:00
Wednesday 11th September  7:30 – 19:00
Thursday 12th September  7:30 – 19:00
Friday 13th September  7:30 – 18:00
Registration hotline: +420 724 566 445

REGISTRATION DESK
The Registration Desk is located on the first floor.

CONGRESS FEE INCLUDES:
• Admission to all scientific sessions, exhibition and poster area
• Congress bag with all materials incl. programme book, abstract book (USB)
• Admission to Welcome Cocktail
• Coffee breaks and lunches during main congress days
• Prague public transport ticket valid throughout the congress dates

WORKSHOP REGISTRATION FEE INCLUDES:
• Admission to pre-congress workshops
• Coffee breaks and lunches during pre-congress day(s)

SHOPPING HOURS
Most shops in Prague are open from 09:00 to 18:00, Monday through Saturday. Shops in the city centre are usually open from 09:00 – 20:00, Monday through Sunday.

SMOKING POLICY
Please note that smoking is not permitted in the venue.

TAXI
The most comfortable option is to use one of many taxi services mobile applications. Czech app “Liftago” connects several taxi providers in one application. Install and use it as it is safe and reliable. www.liftago.com.

Uber works in Prague properly as well. Other: AAA (+ 420 14 014),
City Taxi (+420 257 257 257) or Speed Cars (+420 224 234 234).
Boarding charge: approximately 40 CZK.

TRANSPORTATION
With your free ISFG transport ticket you can travel where ever you want around Prague using metro, tram, bus, train, funicular to Petrin or our nice little ferries. www.dpp.cz/en

VENUE
Prague Congress Centre
5. kvetna 65
140 21 Prague 4
Czech Republic
**List of Orals**

<table>
<thead>
<tr>
<th>Title</th>
<th>Presenter</th>
</tr>
</thead>
<tbody>
<tr>
<td>Forensic Appearance Prediction from DNA: A Journey Through 10 Years of Scientific Contributions</td>
<td>Kayser, Manfred</td>
</tr>
<tr>
<td>Development and Optimization of the Visage Prototype Tools for Bio-Geographic Ancestry and Appearance Traits Inference Using Targeted MPS</td>
<td>Xavier, Catarina</td>
</tr>
<tr>
<td>Approaches to Explain and Potentially Predict the Complex Architecture of the Human Face</td>
<td>Walsh, Susan</td>
</tr>
<tr>
<td>Introduction of a Predictive DNA Test for the Occurrence of Freckles</td>
<td>Branicki, Wojciech</td>
</tr>
<tr>
<td>Forensic DNA Phenotyping: A Service Provider Trial</td>
<td>Raymond, Jennifer</td>
</tr>
<tr>
<td>Comparison of CE- and MPS-Based Analyses of Forensic Markers with Single Cell After Whole Genome Amplification</td>
<td>Chen, Man</td>
</tr>
<tr>
<td>Presentation of the Human Pigmentation (HUPI) AmpliSeq Custom Panel</td>
<td>Meyer, Olivia Strunge</td>
</tr>
<tr>
<td>Predictive DNA Analysis of Human Head Hair Greying Using Whole-Exome and Targeted NGS Data Examined with Deep Learning Methods</td>
<td>Pośpiech, Ewelina</td>
</tr>
<tr>
<td>A Comparison of DNA Methylation Technologies and Performance of Age Prediction Models</td>
<td>Freire-Aradas, Ana</td>
</tr>
<tr>
<td>A Coming of Age Tale</td>
<td>Aliferi, Anastasia</td>
</tr>
<tr>
<td>In Search of Central- and Eastern European-Specific Ancestry Informative Markers</td>
<td>Woźniak, Marcin</td>
</tr>
<tr>
<td>Explaining Bayesian Inference Principles Nonverbally: How to Help Non-Mathematicians Understanding the Weight of Evidence</td>
<td>Šimková, Halina</td>
</tr>
<tr>
<td>How to Avoid Driving DNA Caseworkers Crazy: Casesolver, an Expert System to Investigate Complex Crime Scenes</td>
<td>Prieto, Lourdes</td>
</tr>
</tbody>
</table>
O015 COMPARISON OF CE AND MPS BASED ANALYSIS FOR THE PROBABILISTIC INTERPRETATION OF MIXED STR PROFILES
Benschop, Corina

O016 USING GENETIC COMPLEXITY TO SOLVE FORENSIC COMPLEXITY: A NEW CLASS OF COMPLEX HYPERVARIABLE STR MARKERS FOR DECONVOLUTION OF COMPLEX DNA MIXTURES
Ralf, Arwin

O017 THE FIRST MPS-STR BASED CONVICTION IN A CRIMINAL CASE?
De Knijff, Peter

O018 ENHANCING STR SEQUENCE ALLELE REPRESENTATION FOR PROBABILISTIC GENOTYPING
Just, Rebecca

O019 A MASSIVELY PARALLEL SEQUENCING ASSAY OF MICROTYPOTYPES FOR MIXTURE DECONVOLUTION
Oldoni, Fabio

O020 A TOP-DOWN APPROACH TO MIXTURE EVALUATION
Slooten, Klaas

O021 FROM REFERENCE TO MIXTURE TO MIXTURE TO MIXTURE AND BEYOND
Kruijver, Maarten

O022 EXPLORING DNA INTERPRETATION SOFTWARE USING THE PROVEDIT DATASET
Riman, Sarah

O023 ARE REPORTED LIKELIHOOD RATIOS WELL CALIBRATED?
Hannig, Jan

O024 FORENSIC GENETICS AND DTC GENOMICS: FRIEND OR FOE?
Erlich, Yaniv

O025 DEVELOPING PRIORITIES FOR DISCUSSION AND OVERSIGHT OF THE RAPIDLY EVOLVING FIELD OF GENETIC GENEALOGY
Phillips, Christopher

O026 THE EFFECTIVENESS OF FORENSIC GENEALOGY TECHNIQUES IN THE UNITED KINGDOM – AN EXPERIMENTAL ASSESSMENT
Thomson, Jim

O027 FORENSIC GENEALOGY – PERFORMANCE OF DENSE SNP DATA TO TRACE DISTANT RELATIVES
Kling, Daniel

O028 AN INTERNATIONAL CONSIDERATION OF A STANDARDS-BASED APPROACH TO FORENSIC GENETIC GENEALOGY
Scudder, Nathan

O029 WHOLE GENOME SEQUENCING OF HUMAN REMAINS TO ENABLE GENEALOGY DNA DATABASE SEARCHES – A CASE REPORT
Tillmar, Andreas

O030 ETHICAL, SOCIAL AND LEGAL ISSUES OF FAMILIAL SEARCHING: NEW AND OLD DEBATES
Granja, Rafaela
THE GENETIC IDENTIFICATION OF DEAD MIGRANTS IN THE MEDITERRANEAN SEA: THE LAMPEUSA 2013 SHIPWRECK
Bertoglio, Barbara

RE-EVALUATION OF DNA BASED IDENTIFICATION RESULTS OF VICTIMS OF A TERRORIST ATTACK 25 YEARS LATER
Corach, Daniel

NEW ISO STANDARDS FOR FORENSICS: DNA “FREE” CONSUMABLES AND THE FORENSIC PROCESS
Bastisch, Ingo

REFLECTIONS AND EXAMPLES OF PROBLEMATIC REPORTING IN DNA CASES: THE NEED FOR ACCREDITED FORMATS AND CERTIFIED REPORTING COMPETENCE
Hicks, Tacha

DNA TRANSFER: ASPECTS RELEVANT TO FORENSIC INVESTIGATIONS
van Oorschot, Roland

TRANSFER, PERSISTENCE AND RECOVERY OF EPITHELIAL CELLS ON THE SKIN IN DIRECT AND SECONDARY TRANSFER SCENARIOS
Fonneløp, Ane Elida

MODELLING DNA TRANSFERS IN COMPLEX SCENARIOS
Taylor, Duncan

ASSIGNING FORENSIC BODY FLUIDS TO DNA DONORS IN MIXED SAMPLES BY TARGETED RNA/DNA DEEP SEQUENCING OF CODING REGION SNPS USING ION TORRENT TECHNOLOGY
Ballantyne, John

VISUALISING DNA TRANSFER: LATENT DNA DETECTION USING DIAMOND DYE
Champion, Jessica

IN AND OUT OF TOUCH: RELATIVE ACCUMULATION OF CELLULAR AND ACELLULAR “TOUCH DNA” FROM ENDOGENOUS AND EXOGENOUS SOURCES ON HANDS OVER TIME
Burrill, Julie

CHARACTERIZATION OF TISSUE-SPECIFIC BIOMARKERS WITH THE EXPRESSION OF CIRCRNAS IN FORENSICALLY RELEVANT BODY FLUIDS
Yang, Qinrui

BODY FLUID IDENTIFICATION USING MRNA – BETTER, FASTER, CHEAPER – WHAT METHOD IS BEST OR SHOULD A COMBINATION OF TECHNIQUES BE USED?
Harbison, Sallyann

PREDICTING THE ORIGIN OF FORENSICALLY RELEVANT BIOLOGICAL MATERIAL USING A MACHINE LEARNING APPROACH
Iacob, Diana

DEVELOPMENT OF A MIRNA BODY FLUID PREDICTION SYSTEM USING PROBABILISTIC APPROACHES
Li, Zhilong

PROTEOMIC GENOTYPING: USING MASS SPECTROMETRY TO INFER SNP GENOTYPES IN A FORENSIC CONTEXT
Parker, Glendon
<table>
<thead>
<tr>
<th>Session</th>
<th>Title</th>
<th>Presenter</th>
</tr>
</thead>
<tbody>
<tr>
<td>O046</td>
<td>BACKGROUND SELECTION AND BIASED GENE CONVERSION AFFECT MORE THAN 95% OF THE HUMAN GENOME AND BIAS DEMOGRAPHIC INFERENCES</td>
<td>Pouyet, Fanny</td>
</tr>
<tr>
<td>O047</td>
<td>Y-PROFILE EVIDENCE: CLOSE PATERNAL RELATIVES AND MIXTURES</td>
<td>Andersen, Mikkel Meyer</td>
</tr>
<tr>
<td>O048</td>
<td>INFERENCE OF ADMixed ANCESTRY WITH ANCESTRY INFORMATIVE MARKERS</td>
<td>Tvedebrink, Torben</td>
</tr>
<tr>
<td>O049</td>
<td>THE IMPACT OF IGNORING INBREEDING IN KINSHIP EVALUATIONS</td>
<td>Kjelgaard Brustad, Hilde</td>
</tr>
<tr>
<td>O050</td>
<td>STR SEQUENCE NOMENCLATURE: PROGRESS REPORT FROM THE STRAND WORKING GROUP</td>
<td>Gettings, Katherine</td>
</tr>
<tr>
<td>O051</td>
<td>THE STRIDER REPORT ON QUALITY CONTROL OF AUTOSOMAL STR DATASETS – THE GOOD, THE NOT SO GOOD AND THE UGLY</td>
<td>Bodner, Martin</td>
</tr>
<tr>
<td>O052</td>
<td>ADVANCING MITOCHONDRIAL GENOME DATA INTERPRETATION IN MISSING PERSONS CASEWORK</td>
<td>Marshall, Charla</td>
</tr>
<tr>
<td>O053</td>
<td>CSY? A PANEL-BASED MPS APPROACH INCLUDING 12,523 Y-CHROMOSOME POLYMORPHISMS</td>
<td>Claerhout, Sofie</td>
</tr>
<tr>
<td>O054</td>
<td>ANALYSIS OF RECOMBINATION AND MUTATION EVENTS FOR 12 X-CHR STR LOCI: A COLLABORATIVE FAMILY STUDY OF THE ITALIAN SPEAKING WORKING GROUP GE.F.I.</td>
<td>Bini, Carla</td>
</tr>
<tr>
<td>O055</td>
<td>GENETIC PEOPLING OF PAKISTAN AND THE IMPACT OF HISTORICAL MIGRATIONS, ETHNIC CULTURES AND THE PRACTICE OF ENDOGAMY ON THE FORENSIC MATCH PROBABILITIES</td>
<td>Anwar, Ijaz</td>
</tr>
<tr>
<td>O056</td>
<td>THE SCOPE AND LIMITATIONS OF THE LIKELIHOOD RATIO METHOD APPLIED TO STR DATA FOR DETERMINING GENETIC KINSHIP IN ANCIENT OR ISOLATED HUMAN POPULATIONS</td>
<td>Zvenigorosky, Vincent</td>
</tr>
<tr>
<td>O057</td>
<td>USING MICROBIOME TOOLS TO ESTIMATE THE POSTMORTEM INTERVAL OF HUMAN REMAINS</td>
<td>Metcalf, Jessica</td>
</tr>
<tr>
<td>O058</td>
<td>ENVIRONMENTAL DNA TO ASSIST FORENSIC INVESTIGATIONS, COUNTER-TERROrISM, FRAUDULENT MEDICINES AND DRUG SEIZURES</td>
<td>Young, Jennifer</td>
</tr>
<tr>
<td>O059</td>
<td>TAXONOMY-INDEPENDENT DEEP LEARNING MICROBIOME APPROACH FOR ACCURATE CLASSIFICATION OF FORENSICALLY RELEVANT HUMAN BIOMATERIALS USING TARGETED MPS</td>
<td>Díez López, Celia</td>
</tr>
</tbody>
</table>
O060  PERFORMANCE OF ENVIRONMENTAL DNA METABARCODING IN SOIL TRACE MATCHING AND PROVENANCING
Frøslev, Tobias Guldberg

O061  COLLABORATION ACROSS BORDERS TO IMPLEMENT A EUROPEAN DATABASE FOR CANINE STR IDENTIFICATION MARKERS
Giangasparo, Federica

O062  MULTI-LOCUS DNA METABARCODING FOR AUTHENTICATION OF HIGHLY PROCESSED MEAT PRODUCTS COLLECTED IN SOUTH AFRICA
Pietroni, Carlotta

O063  SPECIES IDENTIFICATION USING MASSIVELY PARALLEL SEQUENCING – DETECTING MULTIPLE SPECIES IN MIXED SOURCES
Dellamico, Barbara

O064  SPECIES IDENTIFICATION IN ROUTINE CASEWORK SAMPLES USING THE SPINDEL KIT
Pereira, Filipe

O065  WHOLE-GENOME SEQUENCING OF NEISSERIA GONORRHOEAE IN A FORENSIC TRANSMISSION CASE
Gonzalez-Candelas, Fernando

O066  WHOLE TRANSCRIPTOME ANALYSIS OF AGED BIOLOGICAL CRIME SCENE TRACES
Salzmann, Andrea

O067  PREVALENCE OF DNA IN VEHICLES: OPTIMIZING SAMPLING STRATEGY AND ACTIVITY LEVEL EVALUATION OF DNA TYPING RESULTS
Kokshoorn, Bas
## List of Posters

<table>
<thead>
<tr>
<th>Poster</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>P001</td>
<td>Forensic genetics and genomics of human and non-human biological samples</td>
<td>Liu, Ying</td>
</tr>
<tr>
<td>P010</td>
<td>A CASE OF MOTHER-DAUGHTER RELATIONSHIP WITH 5 LOCI INCONSISTENT WITH HEREDITARY LAW IN 56 AUTOSOMAL STR MARKERS</td>
<td>Liu, Ying</td>
</tr>
<tr>
<td>P002</td>
<td>Population genetics and forensic DNA databases</td>
<td>Uerlings, Sonja</td>
</tr>
<tr>
<td>P003</td>
<td>DNA typing methodologies and strategies</td>
<td>Garrett-Rickman, Samara</td>
</tr>
<tr>
<td>P004</td>
<td>Forensic mathematics and statistics</td>
<td>Marino, Miguel</td>
</tr>
<tr>
<td>P005</td>
<td>A CONTINUOUS SAMPLING TECHNIQUE FOR THE STUDY OF SOFT TISSUE DECOMPOSITION</td>
<td>Garrett-Rickman, Samara</td>
</tr>
<tr>
<td>P006</td>
<td>Standards, quality control, accreditation, and ethics</td>
<td>Subhani, Zuhaib</td>
</tr>
<tr>
<td>P007</td>
<td>Standards, quality control, accreditation, and ethics</td>
<td>Ji, Anquan</td>
</tr>
<tr>
<td>P008</td>
<td>New polymorphisms of forensic interest</td>
<td>Almohammed, Eida</td>
</tr>
<tr>
<td>P009</td>
<td>Standards, quality control, accreditation, and ethics</td>
<td>Almohammed, Eida</td>
</tr>
<tr>
<td>Paper ID</td>
<td>Title</td>
<td>Authors</td>
</tr>
<tr>
<td>----------</td>
<td>----------------------------------------------------------------------</td>
<td>------------------</td>
</tr>
<tr>
<td>P011</td>
<td>A USEFUL SOLUTION IN CASES OF HUMAN IDENTIFICATION</td>
<td>Michalak, Eliza</td>
</tr>
<tr>
<td>P012</td>
<td>ALLELIC DIVERSITY AND FORENSIC ESTIMATIONS OF THE BEIJING HANS: COMPARATIVE DATA ON SEQUENCE-BASED AND LENGTH-BASED STRS</td>
<td>Kang, Kelai</td>
</tr>
<tr>
<td>P013</td>
<td>AN APPROACH TO EXTRACTING USEFUL SEQUENCE INFORMATION FROM COMPLEX MIXTURES OF HUMAN DNA</td>
<td>Burgoyne, Leigh</td>
</tr>
<tr>
<td>P014</td>
<td>AN ENHANCED DNA AMPLIFICATION METHOD TO DETECT THE SPECIES ORIGINS OF THE ROOTLESS HAIR SHAFTS</td>
<td>Zhang, Suhua</td>
</tr>
<tr>
<td>P015</td>
<td>AN UNUSUAL KINSHIP CASE FROM THE SPANISH CIVIL WAR (1936 – 1939): ANCIENT VERSUS CRITICAL SAMPLE’S INVESTIGATION</td>
<td>Gomes, Cláudia</td>
</tr>
<tr>
<td>P016</td>
<td>ANALYSIS AND INTERPRETATION OF MIXTURE DNA USING AS-PCR OF MTDNA</td>
<td>Wang, Bao-Jie</td>
</tr>
<tr>
<td>P017</td>
<td>ANALYSIS OF 16S RDNA IN SOIL BACTERIAL BY T-RFLP AND ITS APPLICATION IN LEGAL MEDICINE</td>
<td>Wang, Xudong</td>
</tr>
<tr>
<td>P018</td>
<td>ANALYSIS OF DNA TRANSFER TO FIREARMS UNDER REALISTIC CONDITIONS CONSIDERING RELEVANT ALTERNATIVE HANDLING SCENARIOS</td>
<td>Gosch, Annica</td>
</tr>
<tr>
<td>P019</td>
<td>ANALYSIS OF FULL AND HALF SIBLINGS USING A STR, INDEL AND SNP MARKERS COMBINED SYSTEM</td>
<td>Liu, Xiling</td>
</tr>
<tr>
<td>P020</td>
<td>ANALYSIS OF SKELETAL REMAINS EXUMED FROM A “DRY WATER WELL” USED AS A SECONDARY CLANDESTINE BURIAL IN ARGENTINA</td>
<td>Vullo, Carlos</td>
</tr>
<tr>
<td>P021</td>
<td>APPLICATION OF 13 LOCI STR MULTIPLEX FOR CANNABIS SATIVA GENOTYPING</td>
<td>Fabbri, Matteo</td>
</tr>
<tr>
<td>P022</td>
<td>APPLICATION OF DROPLET DIGITAL PCR TO SIMULTANEOUS QUANTIFICATION OF NUCLEAR DNA AND MITOCHONDRIAL DNA</td>
<td>Ohuchi, Tsukasa</td>
</tr>
<tr>
<td>P023</td>
<td>APPLICATION OF METAPOPULATION ANALYSIS OF THE 16S RNA REGION IN CASES OF SEXUAL CRIMES</td>
<td>Czarny, Jakub</td>
</tr>
<tr>
<td>P024</td>
<td>APPLICATION OF THE NGS FOR THE ANALYSIS OF SEA EPIBIONT CLUSTERS ACCORDING TO CHANGES IN WATER TEMPERATURE</td>
<td>Lee, Han Seong</td>
</tr>
<tr>
<td>P025</td>
<td>ASSESSMENT OF INDIVIDUAL SHEDDER STATUS AND BACKGROUND DNA ON OBJECTS: DIRECT OR INDIRECT TRANSFER?</td>
<td>Porto, Maria</td>
</tr>
<tr>
<td>P026</td>
<td>AUTOMATION OF HIGH VOLUME MPS MIXTURE INTERPRETATION USING CASESOLVER</td>
<td>Bleka, Øyvind</td>
</tr>
</tbody>
</table>
P027  BACKGROUND DNA ON FLOORING: THE EFFECTS OF CLEANING
Szkuta, Bianca

P028  BIRD OF PREY CE & MPS MULTIPLEXES: HIGH DISCRIMINATION FOR FORENSIC AND CONSERVATION APPLICATIONS
Beasley, Jordan

P029  BODE BIOSAFE SWAB: PREVENTING CRIME SCENE “CULTURE” FROM DEGRADING DNA EVIDENCE
Ahmed, Manzar

P030  BONE SAMPLING CRITERIA FOR DNA GENOTYPING: MACROSCOPIC SAMPLE CATEGORIZATION AND STR TYPING RESULTS ASSOCIATION
Rocha, Andrea

P031  BUSTING THE MYTHS: DNA TYPEABILITY AFTER 48 HOURS OF BOIL
Tikalova, Eva

P032  CANINE MITOCHONDRIAL INVESTIGATION: A CALL FOR ALL DOGS
Giangasparo, Federica

P033  CASEWORK EXPERIENCE USING mRNA ANALYSIS FOR HUMAN BODY FLUID AND TISSUE IDENTIFICATION
Neis, Maximilian

P034  CHARACTERIZATION OF MITOCHONDRIAL AND NUCLEAR DNA IN SINGLE SHED HAIRS
Irwin, Jodi

P035  CHARACTERIZATION OF NEW CHLOROPLAST POLYMORPHISMS TO DETERMINE BIOGEOGRAPHICAL ORIGIN AND CROP TYPE OF CANNABIS SATIVA SAMPLES
Di Nunzio, Michele

P036  CIRCRNA: A NOVEL BIOMARKER FOR FORENSIC AGE ESTIMATION?
Li, Shujin

P037  COMPARATIVE ANALYSIS OF AUTOMATED DNA EXTRACTION PROCEDURES FOR USE IN FORENSIC CASE WORK
Lee, Hye Jin

P038  COMPARISON OF DNA YIELD AFTER LONG-TERM STORAGE OF SECOND WORLD WAR BONE SAMPLES
Zupanič Pajnič, Irena

P039  COMPARISON OF FOUR SWAB TYPES FOR STAIN COLLECTION
Währer, Jonathan

P040  CREATING A METAGENOMIC ‘DNA MAP’ OF THE LONDON UNDERGROUND TRANSIT SYSTEM
Mason-Buck, Gabriella

P041  CUTANEOUS MIRNAS EXPRESSION IN HUMAN HANGING INJURIES
Fabbri, Matteo

P042  DEAD MIGRANTS IN THE MEDITERRANEAN: GENETIC ANALYSIS OF BONE SAMPLES EXPOSED TO SEAWATER
Previdere’, Carlo
P043  DETERMINATION OF AN EFFECTIVE INTERNAL REFERENCE GENE FOR THE QUANTIFICATION OF MRNA FOR BODY FLUIDS IDENTIFICATION
Zhao, Yixia

P044  DETERMINATION OF DNA YIELD RATES IN SIX DIFFERENT SKELETAL ELEMENTS IN ANCIENT BONES
Zupanič Pajnič, Irena

P045  DEVELOPMENT OF A BODY FLUID-SPECIFIC mRNA MULTIPLEX PANEL: A NEW APPROACH BASED ON WTA FOR GENOTYPING FORENSIC TRACE SAMPLES
Zhang, Ji

P046  DEVELOPMENT OF A MULTIPLEX REAL-TIME PCR SURVEILLANCE ASSAY FOR MONITORING THE HEALTH STATUS OF ECUADORIAN AMPHIBIANS AT RISK OF EXTINCTION
Burgos Figueroa, German

P047  DEVELOPMENT OF A MULTIPLEX RT-PCR ASSAY AND ITS STATISTICAL EVALUATION FOR THE FORENSIC IDENTIFICATION OF VAGINAL FLUID
Akutsu, Tomoko

P048  DEVELOPMENT OF AN INNOVATIVE APPROACH TO HUMAN DNA QUANTIFICATION ANALYSIS
Sabadra, Priti

P049  DEVELOPMENT OF HUMAN OR ANIMAL IDENTIFICATION KIT
Kim, Min-Hee

P050  DEVELOPMENT OF MULTIPLEX PCR SYSTEM FOR METABARCODING OF DIVERSE PLANT MIXTURE
Oh, Hyehyun

P051  DIFFERENT SKELETAL ELEMENTS AS A SOURCE OF DNA FOR GENETIC IDENTIFICATION OF SECOND WORLD WAR VICTIMS
Zupanič Pajnič, Irena

P052  DIFFERENTIATION OF BLOOD STAINS ORIGINATING FROM IDENTICAL TWINS BASED ON XENOBIOTIC ANALYSIS
Czarny, Jakub

P053  DISCRIMINATION OF THE POISONOUS UROBOTRYA SIAMENSIS FROM THE GREEN-LEAF VEGETABLE ‘PAK-WAN’
Bunakkharasawat, Wanasphon

P054  DNA EXTRACTED FROM SECOND CERVICAL VERTEBRA IS PREFERENTIAL FOR STR TYPING OF OLD HUMAN REMAINS
Kunin, Victor

P055  DNA PROFILING SUCCESS RATES OF COMMONLY SUBMITTED CRIME_SCENE ITEMS
Ng, Shilen

P056  DNA TRANSFER PROBABILITIES REFLECTING DIFFERENT CASEWORK-RELEVANT SCENARIOS
Banemann, Regine

P057  EFFECT OF THE ACTIVITY IN SECONDARY TRANSFER OF DNA PROFILES
López-Parra, Ana María
P058  ENHANCING THE SEXUAL ASSAULT WORKFLOW: DEVELOPMENT OF A RAPID MALE SCREENING ASSAY INCORPORATING MOLECULAR NON-MICROSCOPIC SPERM IDENTIFICATION
Ballantyne, John

P059  ENVIRONMENTAL INFLUENCES ON POST MORTEM BRAIN MRNA TRANSCRIPTION
Oliveira, Silviene

P060  EPIGENOME-WIDE ASSOCIATION STUDY FOR SUDDEN UNEXPECTED INFANT DEATH
Hashiyada, Masaki

P061  ESTIMATION OF GENOTYPING ERRORS OF SSR MARKERS IN DOGS AND WOLVES
Stikarová, Radka

P062  ESTIMATION OF THE NUMBER OF CONTRIBUTORS IN MIXTURE SAMPLES BY MITOCHONDRIAL DNA ANALYSES USING MASSIVELY PARALLEL SEQUENCING
Nakanishi, Hiroaki

P063  EUROPEAN VALIDATION OF A CANNABIS SATIVA 13-LOCUS STR MULTIPLEX KIT FOR GENETIC IDENTIFICATION: A PRELIMINARY STUDY
Di Nunzio, Michele

P064  EVALUATING THE POTENTIAL OF MIRNA PROFILING IN VITREOUS HUMOR TO DETERMINE THE TIME OF DEATH
Corradini, Beatrice

P065  EVALUATING THE VIABILITY OF OBTAINING DNA Profiles FROM DNA ENCAPSULATED BETWEEN THE LAYERS OF COMPOSITE COUNTERFEIT BANKNOTES
Kwok, Ross

P066  EVALUATION OF DNA LEVELS RECOVERED FROM FORENSIC BONE SAMPLES THROUGH THE OPTIMIZATION OF A SEMI-AUTOMATED EXTRACTION METHOD
Porto, Maria

P067  EVALUATION OF NEXT GENERATION MTGENOME SEQUENCING BASED ON DIFFERENT LIBRARY CONSTRUCTION PRINCIPLES
Zhang, Chi

P068  EVALUATION OF STR Profiles OF SINGLE TELOGEN HAIR USING PROBABILISTIC METHODS
Heß, Sarah Aurora

P069  EVALUATION OF THE FORENSEQ® DNA SIGNATURE PREP KIT WITH SKELETAL REMAINS FROM MISSING PERSONS CASES
Idrizbegović, Šejla

P070  EVALUATION OF VAGINAL MRNA MARKERS IN FERTILE AND POSTMENOPAUSAL WOMEN: A GEFI COLLABORATIVE STUDY
Robino, Carlo

P071  EVERYDAY CHALLENGES OF DATA INTERPRETATION IN CAPILLARY ELECTROPHORESIS RESOLVED USING APPLIED BIOSYSTEM DATA COLLECTION & GENEMAPPER ID-X ANALYSIS SW
Sabadra, Priti

P072  EXPANDING THE KNOWLEDGE OF TRI-ALLELIC PATTERN AT AUTOSOMAL STR LOCI IN CHINESE POPULATION
Yang, Qinrui
P073  EXPLORATION OF FTIR-ATR SPECTROSCOPY COMBINED WITH DATA MANIPULATION TO PREDICT DNA PRESERVATION IN SKELETAL REMAINS
Zupanič Pajnič, Irena

P074  EXPLORING OF RARE DIFFERENCES IN MTGENOMES BETWEEN MZ TWINS USING MASSIVELY PARALLEL SEQUENCING
Wang, Zheng

P075  FLANKLY, IS IT WORTH IT?
Devesse, Laurence

P076  FORENSIC IDENTIFICATION OF MATERIAL FROM HUMAN ANUS BASED ON METAPOPULATION STUDIES OF THE BACTERIAL 16S RNA GENE
Powierska-Czarny, Jolanta

P077  FORENSIC SCIENCE & HUMAN MIGRATION: THE ROLE OF FORENSIC GENETICS
Johnston, Emma

P078  GENDER TYPING OF HIGHLY FRAGMENTED HUMAN DNA SAMPLES
Kim, Kijeong

P079  GENETIC AND CHROMOSOMAL VARIATIONS CAUSED INCONSISTENCIES IN TWO PARENTAL TESTS
Li, Yifan

P080  GENETIC IDENTIFICATION OF A COMMUNISM REGIME VICTIM: THE STORY OF 70 YEARS OLD TENT TARPAULIN
Dalihodová, Simona

P081  GENETIC STRUCTURE AND CONSERVATION STATUS OF THE BLUE SHARK BASED ON THE MITOCHONDRIAL D-LOOP REGION
Martins, Silvia

P082  GENETIC TAPHONOMY: EVALUATION OF QUALITY AND QUANTITY OF DNA FROM SKELETAL REMAINS
Arciszewska, Joanna

P083  GIVING THEM BACK THEIR NAMES AND FACES. DNA ANALYSES AND MATERIAL CULTURE STUDIES OF UNDOCUMENTED MIGRANTS FROM CENTRAL AMERICA AND MEXICO TO TEXAS
Ossowski, Andrzej

P084  HIGH RESOLUTION MELTING ANALYSIS (HRM) BASED ON 16SRRNA AS A TOOL FOR PERSONAL IDENTIFICATION WITH THE HUMAN ORAL MICROBIOME
Luo, Haibo

P085  HOW LONG CAN DNA BE SUCCESSFULLY INVESTIGATED WHEN SAMPLED POSTMORTEM FROM ANIMALS SLAUGHTERED BY PREDATORS?
Schwark, Thorsten

P086  HOW MANY DNA ANALYSES ARE PERFORMED ON ADULT SEXUAL ASSAULT VICTIMS IN MILAN (ITALY)? A TEN-YEAR REVIEW
Piccinini, Andrea

P087  IDENTIFICATION OF CETACEAN SPECIES IN FORENSIC CASES
M. De Pancorbo, Marian
P088 IDENTIFICATION OF VAGINAL SECRETIONS BASED ON METAPOPULATION STUDIES OF THE BACTERIAL 16S RNA GENE
Powierska-Czarny, Jolanta

P089 IMPLEMENTATION OF THE PRECISION ID MTDNA WHOLE GENOME PANEL FOR FORENSIC CASE WORK: HOW TO HANDLE INCONSISTENT RESULTS
Buchard, Anders

P090 IMPROVED IDENTIFICATION OF HUMAN BONE REMAINS BY THE INTRODUCTION OF A SNP ANALYSIS SYSTEM
Cho, Sohee

P091 IMPROVING THE DETECTION OF SEMEN ON NYLON FLOCKED SWABS AND FABRICS USING STANDARD PRESUMPTIVE TESTS
Castella, Vincent

P092 IN-HOUSE VALIDATION OF FOUR COMMON PCR ASSAYS FOR AVIAN GENDER INVESTIGATION
Kitpipit, Thitika

P093 INTEGRATING MOLECULAR AND MORPHOLOGICAL DATA IN THE SECONDARY SEXUAL IDENTIFICATION OF MUSEUM SPECIMENS OF TAMANDUA TETRADACTYLA (XENARTHRA, PILOSA)
Martins, Silvia

P094 INTERNAL VALIDATION OF GLOBALFILERTM KIT USING HALF VOLUME
Al-Ali, Fatma

P095 INTERNAL VALIDATION STUDY OF THE NEXT GENERATION SEQUENCING OF GLOBALFILERTM PCR AMPLIFICATION KIT FOR THE ION TORRENT S5 SEQUENCER
Gentile, Fabiano

P096 INTERPRETATION OF SECONDARY BIOLOGICAL TRANSFER TRACES IN JUDICIAL GENETIC IDENTIFICATION
Streba, Irina

P097 INTERSEXUALITY AS A POTENTIAL SOURCE OF ERROR IN SEX DETERMINATION USING FORENSIC MULTIPLEX KITS
Dunkelman, Bettina

P098 INTRA - BONE NUCLEAR DNA VARIABILITY IN SECOND WORLD WAR METATARSAL AND METACARPAL BONES
Zupanič Pajnič, Irena

P099 INVESTIGATION INTO THE TRANSFER OF MICROBIOMES WITHIN A FORENSIC LABORATORY SETTING
Neckovic, Ana

P100 INVESTIGATION OF PARENTAGE OF MENDEL GRAPEVINE
Drábek, Jiří

P101 IS IT RELIABLE TO USE PARAFFIN EMBEDDED HISTOLOGICAL TISSUES AS BIOLOGICAL EVIDENCE IN PARENTAGE CASES?
Serin, Ayse

P102 ISOLATION OF PURE SPERM CELLS FROM SEXUAL ASSAULT MOCK ANAL SWABS USING DEPArray™ DIGITAL SORTER
Wang, Tzuming
P103  JANE DOE’S IDENTIFICATION FROM TEETH BY AUTOMATE DNA EXTRACTION
Dumache, Raluca

P104  KINSHIP ANALYSIS ON SKELETAL ANCIENT REMAINS: THE CASE OF “EL CERRO DE LA HORRA” (BURGOS, SPAIN)
Gomes, Cláudia

P105  ‘KITOME’: THE KRYPTONITE OF FORENSIC METAGENOMICS
Mason-Buck, Gabriella

P106  MASSIVE PARALLEL SEQUENCING AND OSTEOGENESIS IMPERFECTA: AN ESSENTIAL TOOL FOR FORENSIC INVESTIGATION OVER CHILD ABUSE
Onofri, Valerio

P107  MASSIVELY PARALLEL SEQUENCING OF AUTOSOMAL STRS AND IDENTITY-INFORMATIVE SNPS WITH THE FORENSEQ SYSTEM HIGHLIGHTS CONSANGUINITY IN SAUDI ARABIA
Khubrani, Yahya M.

P108  METAPOPULATION ANALYSIS OF THE BACTERIAL 16S RNA GENE AS A TOOL FOR IDENTIFYING THE PREPUTIAL SPECIMEN OF A MAN
Powierska-Czarny, Jolanta

P109  MITOCHONDRIAL DNA ANALYSIS IN THE UNITED ARAB EMIRATES POPULATIONS
Almheiri, Reem

P110  MITOGENOME SEQUENCE VARIATION IN HAIR SHAFTS: A PILOT-STUDY
Pereira, Vania

P111  MOLECULAR DISSECTION OF A CRIME SCENE - INTRODUCING STR SEQUENCING IN ROUTINE INVESTIGATION
Diepenbroek, Marta

P112  MOLECULAR IDENTIFICATION AND GENETIC DIVERGENCE OF NEW-WORLD CALLITHRICHNIAE MAMMALS BASED ON THE MITOCHONDRIAL COI GENE
Martins, Silvia

P113  MOLECULAR IDENTIFICATION OF POISONOUS PUFFERFISHES AND CROSS-ATLANTIC GENETIC DIVERGENCE PATTERNS BASED ON THE MITOCHONDRIAL COI GENE
Martins, Silvia

P114  MRNA MPS TISSUE IDENTIFICATION ASSAY TO AID IN THE INVESTIGATION OF TRAUMATIC INJURIES
Ballantyne, John

P115  MULTIPLEX DNA METHYLATION PROFILING BY ARMS-PCR FOR BODY FLUID IDENTIFICATION
Tian, Huan

P116  MUTATION RATES OF SIX Y-CHROMOSOMAL STR LOCI ESTIMATED FROM 210 PEDIGREES IN CHINESE HAN POPULATION
Liu, Jing

P117  MVC: AN INTEGRATED MITOCHONDRIAL VARIANT CALLER FOR FORENSICS
Roth, Chantal

P118  MYOCARDIAL TRANSCRIPTOME ANALYSIS IN SUDDEN UNEXPLAINED DEATH (SUD) IN THE YOUNG
Neubauer, Jacqueline
<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>P119</td>
<td>NAILS AS A SOURCE OF DNA FOR MOLECULAR GENETIC IDENTIFICATION OF DECOMPOSED HUMAN REMAINS</td>
<td>Inkret, Jezerka</td>
</tr>
<tr>
<td>P120</td>
<td>NAPOLEON’S SOLDIERS FROM 1813: DNA ANALYSIS OF LINEAGE MARKERS</td>
<td>Votrubova, Jitka</td>
</tr>
<tr>
<td>P121</td>
<td>NEW HOPE IN HUMAN IDENTIFICATION CASES: MPS STUDY ON DEGRADED BONE MATERIAL WITH USE OF VEROGEN’S FORENSEQ KIT</td>
<td>Szargut, Maria</td>
</tr>
<tr>
<td>P122</td>
<td>NON-DESTRUCTIVE MEANS OF SAMPLING PAPER DOCUMENTS FOR GENERATION OF STR PROFILES</td>
<td>Wood, Zoe</td>
</tr>
<tr>
<td>P123</td>
<td>NON-INVASIVE PRENATAL PATERNITY TESTING BY MATERNAL PLASMA DNA SEQUENCING IN TWIN PREGNANCIES</td>
<td>Wang, Yicong</td>
</tr>
<tr>
<td>P124</td>
<td>NOVEL INDEX OF BODY FLUID-RNA INTEGRITY BASED ON SMALL RNA ELECTROPHOREGRAM</td>
<td>Fujimoto, Shuntaro</td>
</tr>
<tr>
<td>P125</td>
<td>NOVEL TRI-ALLELIC PATTERN OF THE FGA MARKER</td>
<td>Poór, Viktor</td>
</tr>
<tr>
<td>P126</td>
<td>OPTIMIZATION AND COMPARISON OF MULTIPLEX MRNA-BASED BODY FLUID IDENTIFICATION BY CAPILLARY ELECTROPHORESIS (CE) AND MASSIVE PARALLEL SEQUENCING (MPS)</td>
<td>Bamberg, Malte</td>
</tr>
<tr>
<td>P127</td>
<td>OPTIMIZATION AND APPLICATION OF A LARGE SNP PANEL UTILIZING UNIQUE MOLECULE INDICES FOR MISSING PERSONS IDENTIFICATIONS</td>
<td>Bittner, Felix</td>
</tr>
<tr>
<td>P128</td>
<td>OPTIMIZING THE PROCESSING OF DATABASING SAMPLES USING THE HAMILTON EASYPUNCH® STARLET</td>
<td>Ahmed, Manzar</td>
</tr>
<tr>
<td>P129</td>
<td>PARALLEL SEQUENCING OF 48 Y-CHROMOSOME STR AND SNP MARKERS</td>
<td>Tao, Ruiyang</td>
</tr>
<tr>
<td>P130</td>
<td>PETROUS BONE: AN OPTIMAL SUBSTRATE IN LEGAL MEDICINE?</td>
<td>Gonzalez, Angéla</td>
</tr>
<tr>
<td>P131</td>
<td>PILOT IDENTITY PROJECT. MISSING BUT NOT FORGOTTEN – IDENTIFICATION OF THE POLISH AIR FORCE IN GREAT BRITAIN PILOT MIA IN 1943</td>
<td>Ossowski, Andrzej</td>
</tr>
<tr>
<td>P132</td>
<td>POPULATION GENETIC DATA FOR 27 AUTOSOMAL STR MARKERS IN THE KUWAITI POPULATION USING MASSIVELY PARALLEL SEQUENCING</td>
<td>Haidar, Mahdi</td>
</tr>
<tr>
<td>P133</td>
<td>POPULATION STRUCTURE AND THE CONSERVATION STATUS OF THE ROUGH-TOOTHED DOLPHINS BASED ON THE ANALYSIS OF THE MITOCHONDRIAL CONTROL REGION</td>
<td>Martins, Silvia</td>
</tr>
</tbody>
</table>
Senst, Alina

PRECISION ID GLOBALFILER MIXTURE STUDY
Tvedebrink, Torben

PRELIMINARY EVALUATION OF FORENSIC CASEWORK SAMPLES USING THE PRECISION ID ANCESTRY PANEL – MANUAL AND AUTOMATED AMPLISEQ WORKFLOW
Aldosari, Waad

PRESERVATION OF DNA INTEGRITY IN BIOLOGICAL MATERIAL
D’Amato, Maria Eugenia

PREVALENCE OF DNA IN VEHICLES: LINKING AN ITEM AWAY FROM A VEHICLE TO OCCUPANCY OF THE VEHICLE
Boyko, Toni

PREVALENCE OF DNA IN VEHICLES: PERSISTENCE OF DNA FROM A TEMPORARY DRIVER AFTER REUSE BY ITS REGULAR DRIVER ON ITEMS LESS COMMONLY TARGETED
Boyko, Toni

QUANTITATIVE EVALUATION OF DNA ISOLATED FROM BACKSPATTER RECOVERED FROM FIREARMS AND WOUND PROFILE CHARACTERISTICS AS EFFECTS OF SHOOTING DISTANCE
Euteneuer, Jan

RECOVERY OF HOMININ DNA FROM PLEISTOCENE SEDIMENTS AT DENISOVA CAVE
Zavala, Elena

ROOM TEMPERATURE STORAGE OF TISSUE SAMPLES (BOVINE) IN READILY AVAILABLE MEDIA DURING MASS FATALITY INCIDENTS
Chan, Xavier

SCREENING FOR CPG SITES ADJACENT TO COMMON SNPS FOR BLOOD-SPECIFIC GENOTYPING FROM MIXED BODY FLUID SAMPLES
Watanabe, Ken

SEMI-AUTOMATED AUDITING AND ANNOTATION OF REFERENCE DATABASES OF DNA BARCODES FOR SPECIES IDENTIFICATION
Amorim, Antonio

SEQUENCE VARIATION OBSERVED IN 27 Y-STR MARKERS WITH U.S. POPULATION SAMPLES
Steffen, Becky

SEQUENCING OF FULL MITOCHONDRIAL GENOMES FOR NIST POPULATION SAMPLES
Kiesler, Kevin

SHEDDER STATUS – FACT OR MYTH?
Ng, Shilen

SKETCHING MAN’S BEST FRIEND – CANINE DNA PHENOTYPING FOR FORENSIC PURPOSES
Heinrich, Josephin
<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Author(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>P149</td>
<td>SMRT SEQUENCING HELP DEEPLY DELVE MITOCHONDRIAL VARIATIONS</td>
<td>Li, Shujin</td>
</tr>
<tr>
<td></td>
<td>FOR MONOZYGOTIC TWINS DISCRIMINATION</td>
<td></td>
</tr>
<tr>
<td>P150</td>
<td>SPECIFIC M(I)RNA PROFILING FROM DNA ELUATES FOR BODY FLUID IDENTIFICATION</td>
<td>Grabmüller, Melanie</td>
</tr>
<tr>
<td>P151</td>
<td>SPONTANEOUS DETERMINATION OF THE TYPE AND THE TIME SINCE DEPOSITION</td>
<td>Su, Chih-Wen</td>
</tr>
<tr>
<td></td>
<td>OF A BIOLOGICAL STAIN</td>
<td></td>
</tr>
<tr>
<td>P152</td>
<td>STABILITY COMPARISON OF RNA MARKERS IN BLOOD STAIN SAMPLS UNDER</td>
<td>Wang, Yanyun</td>
</tr>
<tr>
<td></td>
<td>DIFFERENT CONDITIONS</td>
<td></td>
</tr>
<tr>
<td>P153</td>
<td>STORAGE OF SECOND WORLD WAR BONE SAMPLES: BONE FRAGMENTS VERSUS BONE</td>
<td>Zupanič Pajnič, Irena</td>
</tr>
<tr>
<td></td>
<td>POWDER</td>
<td></td>
</tr>
<tr>
<td>P154</td>
<td>STR PROFILE OF TOUCH DNA EXPOSED TO SEA WATER</td>
<td>Joo, Hyunjung</td>
</tr>
<tr>
<td>P155</td>
<td>STUDY OF BIOMARKERS RELATED TO SUDDEN ARRHYTHMIC DEATH SYNDROME</td>
<td>M. De Pancorbo, Marian</td>
</tr>
<tr>
<td>P156</td>
<td>STUDY OF Y CHROMOSOME MARKERS WITH FORENSIC RELEVANCE IN LISBON</td>
<td>Vieira Da Silva, Cláudia</td>
</tr>
<tr>
<td></td>
<td>IMMIGRANTS FROM AFRICAN COUNTRIES – ALLELIC VARIANTS STUDY</td>
<td></td>
</tr>
<tr>
<td>P157</td>
<td>SUDDEN UNEXPECTED DEATH IN INFANCY: NEXT GENERATION SEQUENCING ADDS</td>
<td>Heathfield, Laura</td>
</tr>
<tr>
<td></td>
<td>VALUE TO CASES FROM CAPE TOWN, SOUTH AFRICA</td>
<td></td>
</tr>
<tr>
<td>P158</td>
<td>SUITABILITY OF CEREBRAL MATTER FOR THE FORENSIC IDENTIFICATION OF</td>
<td>Helm, Katharina</td>
</tr>
<tr>
<td></td>
<td>HIGHLY DECOMPOSED BODIES</td>
<td></td>
</tr>
<tr>
<td>P159</td>
<td>TAPHONOMIC EFFECTS ON DNA DEGRADATION IN POST-MORTEM BODY TISSUES</td>
<td>Garrett-Rickman, Samara</td>
</tr>
<tr>
<td></td>
<td>IN AN AUSTRALIAN SETTING</td>
<td></td>
</tr>
<tr>
<td>P160</td>
<td>THE ANALYSIS OF ANCIENT DNA FOR FORENSIC APPLICATIONS</td>
<td>Park, Sun Hee</td>
</tr>
<tr>
<td>P161</td>
<td>THE BREED MAKES THE DIFFERENCE: PEDIGREE COMPOSITION, CANINE STR ALLELE</td>
<td>Berger, Burkhard</td>
</tr>
<tr>
<td></td>
<td>FREQUENCIES, AND RANDOM MATCH PROBABILITIES</td>
<td></td>
</tr>
<tr>
<td>P162</td>
<td>THE EFFECT OF CLIMATIC SIMULATIONS ON DNA PERSISTENCE ON GLASS, COTTON</td>
<td>Meakin, Georgina</td>
</tr>
<tr>
<td></td>
<td>AND POLYESTER</td>
<td></td>
</tr>
<tr>
<td>P163</td>
<td>THE EFFECT OF HYDROLYSIS ON DNA</td>
<td>Schulze Johann, Kristina</td>
</tr>
<tr>
<td>P164</td>
<td>THE EFFECT OF THE HIGH QUANTITY OF FEMALE DNA EXTRACTED FROM VAGINAL</td>
<td>Cho, Hyun Kuk</td>
</tr>
<tr>
<td></td>
<td>FLUID ON THE DETECTION OF Y-STR PROFILE AND THE QUANTITATIVE VALUE OF</td>
<td></td>
</tr>
<tr>
<td></td>
<td>MALE DNA</td>
<td></td>
</tr>
<tr>
<td>Page</td>
<td>Title</td>
<td>Author</td>
</tr>
<tr>
<td>------</td>
<td>----------------------------------------------------------------------</td>
<td>-------------------------</td>
</tr>
<tr>
<td>P165</td>
<td>THE EFFECTS OF VARIOUS HOUSEHOLD CLEANING METHODS ON DNA PERSISTENCE ON MUGS AND KNIVES</td>
<td>Meakin, Georgina</td>
</tr>
<tr>
<td>P166</td>
<td>THE INFLUENCE OF THE SHEDDER STATE ON DNA TRANSFER</td>
<td>Schmidt, Max</td>
</tr>
<tr>
<td>P167</td>
<td>THE PRESENCE OF BACKGROUND DNA ON COMMON ENTRY POINTS TO HOMES</td>
<td>Szkuta, Bianca</td>
</tr>
<tr>
<td>P168</td>
<td>THE SEQUENCE IDENTIFIER (SID): AN OPERATIONAL NOMENCLATURE FOR MIXED-DNA CASEWORK USING MPS</td>
<td>Young, Brian</td>
</tr>
<tr>
<td>P169</td>
<td>THE USING OF MASSIVELY PARALLEL SEQUENCING OF MITOCHONDRIAL DNA TO ASSIST THE MISSING PERSON IDENTIFICATION: HUMAN REMAINS IN THE WILD</td>
<td>Mienkerd, Sirirat</td>
</tr>
<tr>
<td>P170</td>
<td>THE VAMPIRE PROJECT</td>
<td>Ossowski, Andrzej</td>
</tr>
<tr>
<td>P171</td>
<td>TIGRIS ID: SCIENCE AGAINST AN ILLEGAL TRADE OF PANTHERA TIGRIS IN THE HEART OF EUROPE</td>
<td>Vaněk, Daniel</td>
</tr>
<tr>
<td>P172</td>
<td>TIME ESTIMATION OF FOUR DIFFERENT SURFACES EXPOSED IN MARINE ENVIRONMENTS USING MARINE BIOFOULING</td>
<td>Lee, Han Seong</td>
</tr>
<tr>
<td>P173</td>
<td>TIME SINCE DEPOSITION OF BIOLOGICAL FLUIDS USING RNA DEGRADATION</td>
<td>Bird, Thomas</td>
</tr>
<tr>
<td>P174</td>
<td>TOWARDS SUCCESSFUL IDENTIFICATION OF CHILD-VICTIMS FROM SEVERAL DECADES AGO</td>
<td>Cytacka, Sandra</td>
</tr>
<tr>
<td>P175</td>
<td>TWO LOCI ‘EXCLUSION’ OF TRUE PATERNITY IS DUE TO GENETIC DISORDER IN A CHILD</td>
<td>Borovko, Sergey</td>
</tr>
<tr>
<td>P176</td>
<td>UNDERSTANDING THE BEHAVIOR OF STUTTER THROUGH THE SEQUENCING OF STR ALLELES</td>
<td>Vallone, Peter</td>
</tr>
<tr>
<td>P177</td>
<td>UPDATE IN THE GENETIC IDENTIFICATION OF SKELETAL REMAINS FROM VICTIMS OF THE SPANISH CIVIL WAR AND POSTERIOR DICTATORSHIP</td>
<td>Baeta, Miriam</td>
</tr>
<tr>
<td>P178</td>
<td>USE OF FORENSEQTM DNA SIGNATURE PREP KIT ON IDENTIFICATION OF FORMALIN-FIXED TUMOR TISSUES</td>
<td>Li, Shujin</td>
</tr>
<tr>
<td>P179</td>
<td>VALIDATION AND ASSESSMENT OF AN OPTIMIZED MASSIVELY PARALLEL SEQUENCING WORKFLOW FOR WHOLE MITOCHONDRIAL GENOMES OF REFERENCE SAMPLES</td>
<td>Sukser, Viktorija</td>
</tr>
<tr>
<td>P180</td>
<td>VALIDATION AND IMPLEMENTATION OF MITOCHONDRIAL DNA WITH MASSIVELY PARALLEL SEQUENCING</td>
<td>Chang, Joseph</td>
</tr>
</tbody>
</table>
P181  VALIDATION OF A UNIVERSAL DNA EXTRACTION METHOD FOR HUMAN AND MICROBIAL DNA ANALYSIS
Alessandrini, Federica

P182  VALUE OF MASSIVE PARALLEL SEQUENCING IN POSTMORTEM GENETIC ANALYSES OF SUDDEN UNEXPECTED DEATH CASES
Scheiper, Stefanie

P183  VERIFICATION OF TRANSLOCATION BETWEEN X AND Y CHROMOSOME
Li, Yifan

P184  X-INDELS EFFICACY EVALUATION IN A CRITICAL SAMPLES’ PATERNITY CASE: A SPANISH CIVIL WAR CASE FROM THE MEMORIAL OF THE CAMPOSINES (TARRAGONA, SPAIN)
Gomes, Claudia

P185  Y-STR HAPLOTYPING USING DIRECT PCR ENRICHMENTS IN MASSIVELY PARALLEL SEQUENCING
Lee, James

P186  Y-STR PROFILES DETECTABLE IN FEMALE RECIPIENT’S PLASMA AFTER KIDNEY TRANSPLANTATIONS FROM MALE DONORS
Dauber, Eva-Maria

Population genetics and forensic DNA databases

P187  A COMPLICATED FULL SIBLING IDENTIFICATION CASE SOLVED BY THREE METHODS
Liu, Zhiyong

P188  A LOOK OF PATERNAL ANCESTRY IN A SAMPLE OF ECUADORIAN “MESTIZOS” POPULATION ANALYZED THROUGH POWERPLEX Y23
Burgos Figueroa, German

P189  A Y-CHROMOSOMAL STUDY OF SOUTHERN MANSI POPULATION GROUP IN THE URAL
Pamjav, Horolma

P190  ADMIXTURE AND POPULATION STRUCTURE IN MAYAS AND LADINOS FROM GUATEMALA BASED ON 15 STRS
Rangel Villalobos, Hector

P191  ALLELE FREQUENCIES OF 22 AUTOSOMAL STR LOCI IN POPULATION OF 1000 INDIVIDUALS FROM SOUTHEASTERN SERBIA
Takić Miladinov, Dijana

P192  ALLELE FREQUENCY DATA FOR 15 AUTOSOMAL STRS AND ANCESTRAL PROPORTIONS USING AIMS-INDELS IN THE SHUAR ETHNIC GROUP FROM ECUADOR
Zambrano, Ana Karina

P193  AN APPROACH TO MATERNAL ANCESTRY IN A SAMPLE OF ECUADORIAN “MESTIZOS” POPULATION BY SEQUENCING THE CONTROL REGION OF MTDNA
Burgos Figueroa, German

P194  AN OPTIMISED METHOD FOR THE DEVELOPMENT OF A MITOCHONDRIAL POPULATION DATABASE IN NEW ZEALAND
Forsythe, Bethany

P195  AN UPDATE OF STR MUTATION RATES OF PATERNITY TESTS STUDIED FOR 14 YEARS (2005 – 2018) AT IDENTIGEN LAB, UNIVERSIDAD DE ANTIOQUIA, COLOMBIA
Burgos Figueroa, German
P196 ANALYSIS OF MUTATION RATE OF 13 RAPIDLY MUTATING Y-CHROMOSOME SHORT TANDEM REPEATS IN TANZANIAN FATHER-SON PAIRED SAMPLES
Alghafri, Rashed

P197 ANALYSIS OF PATERNAL LINEAGES LEGACY IN SALTA PROVINCE, NORTHWEST ARGENTINA
Picornell, Antonia

P198 ANALYSIS OF THE COMPLETE MTDNA IN BRAZILIAN SAMPLES: HAPLOTYPES DIFFERENTIATION AND NEW VARIATIONS IDENTIFICATION IN NATIVE AMERICAN HAPLOGROUPS
Braganholi, Danilo

P199 ANALYSIS OF TWO X-STRS MARKERS PANELS IN SÃO PAULO STATE POPULATION (BRAZIL)
Alves De Jesus Silva, Flávia

P200 ANALYTICAL IMPROVEMENTS IN BIOGEOGRAPHIC ANCESTRY INFERENCE
Gabriel, Matt

P201 ANCESTRAL ANALYSIS OF A NATIVE AMERICAN ECUADORIAN FAMILY WITH CONGENITAL INSENSITIVITY TO PAIN WITH ANHIDROSIS
Zambrano, Ana Karina

P202 ANCESTRAL PROPORTIONS BASED ON 22 AUTOSOMAL STR OF AN ADMIXED POPULATION (MESTIZOS) FROM PENINSULA DE YUCATAN, MEXICO
Gonzalez-Herrera, Lizbeth

P203 ANCESTRY EVALUATION IN A POPULATION SAMPLE OF THE TUNJA CITY, DEPARTMENT OF BOYACÁ – COLOMBIA
Builes Gomez, Juan Jose

P204 ASSESSMENT OF AUTOSOMAL, Y-STRs AND MITOCHONDRIAL DNA PROFILES IN THE ZAMBIAN POPULATION (R.I.P)
Makasa, Innocent

P205 AUSTRIAN STR POPULATION DATA USING THE POWERSEQ GY46 SYSTEM AND MASSIVELY PARALLEL SEQUENCING
Müller, Petra

P206 AUTOSOMAL STR LENGTH, REPEAT AND FLANKING REGION SEQUENCE VARIATION IN THE NORWEGIAN POPULATION USING THE MISEQ FGX FORENSIC GENOMICS SYSTEM
Janssen, Kirstin

P207 CAN THE ANALYSIS OF THE Y CHROMOSOME HAPLOTYPES BE HELPFUL IN EXPLAINING THE MYSTERY OF THE FIRST SLAV MIGRATION?
Czarny, Jakub

P208 CHARACTERIZATION FROM NORTHERN SOUTH AMERICA POPULATIONS REVEALS THE NEED FOR THE SUBSTRUCTURE ESTIMATORS USE IN FORENSIC STATISTICS
Usaquén Martinez, William

P209 CHUETA POPULATION: DIVERSITY AND FORENSIC PARAMETERS OF AN SMALL, ISOLATED AND ENDOGAMIC POPULATION
Ferragut, Joana Francesca
P210 CODIS-LIKE CLOUD EXPERT SYSTEM FOR HANDLING AND EXCHANGE OF THE NON-HUMAN DNA STR ANALYSIS RESULTS
Vanek, Daniel

P211 COMPARISON OF GLOBALFILERTM PCR AMPLIFICATION KIT AND PRECISION ID GLOBALFILERTM NGS STR PANEL – IMPLICATIONS ON FORENSIC CASEWORK
Keckarevic Markovic, Milica

P212 COMPARISON OF MINIDOGFILER AND “ASCH” STR MULTIPLEX SYSTEMS FOR PRELIMINARY ESTIMATION OF VARIABILITY WITHIN WOLF’ S LIKE DOG BREEDS
Štikarová, Radka

P213 COMPARISON OF Y-STR HAPLOTYPES IN IRANIAN, AFGHAN, AND MONGOLIAN POPULATIONS
Joudaki, Atefeh

P214 COMPLETE MITOCHONDRIAL GENOME VARIATION IN SWISS POPULATIONS USING THE ION S5
Gysi, Mario

P215 CONCURRENT SEQUENCE VARIANT AT D21S11 AND PENTA D LOCI IN A PATERNITY TESTING CASE
Liu, Zhiyong

P216 DEEPENING IN THE Y-CHROMOSOME GENETIC LANDSCAPE OF A MICRONESIAN POPULATION
M. De Pancorbo, Marian

P217 DEVELOPMENT OF A NEW 17 Y-STRS SYSTEM USING FLUORESCENT-LABELLED UNIVERSAL PRIMERS AND ITS APPLICATION IN SHANXI POPULATION IN CHINA
Liu, Jinding

P218 DEVELOPMENTAL VALIDATION OF THE MICROREADER™ 20A ID SYSTEM
Liang, Weibo

P219 DEVELOPMENTAL VALIDATION OF THE MICROREADER™ 40Y ID SYSTEM PCR AMPLIFICATION KIT
Liang, Weibo

P220 DIACHRONIC STUDY OF THE LONG TIME OCCUPIED ARCHAEOLOGICAL SITE OF SEGÓBRIGA (SPAIN) AND COMPARISON WITH NOWADAYS POPULATION
Gomes, Cláudia

P221 DNA IDENTIFICATION OF SKELETAL REMAINS BY INVESTIGATOR’S INTUITION
Ricci, Ugo

P222 ESTIMATES ANCESTRY PROPORTIONS OF THE MIDWEST REGION (BRAZIL)
Ambrosio, Isabela

P223 ESTIMATING THE INFORMATIVENESS OF FORENSIC ANCESTRY MARKERS
Cheung, Elaine YY

P224 EVALUATING THE IMPACT OF THE Y CHROMOSOME HAPLOGROUP R1B-DF27 IN HISPANIC ADMIXED POPULATIONS FROM LATIN AMERICA
M. De Pancorbo, Marian

P225 EVALUATION OF 30 INSERTION/DELETION POLYMORPHISMS AS FORENSIC MARKERS IN THE KUWAITI POPULATION
Haidar, Mahdi
<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>P226</td>
<td>EVALUATION OF HOMOPLASY IN Y23 LOCI: A PILOT STUDY ON SAMPLES WITH KNOWN 400-YEARS-LONG GENEALOGICAL HISTORY IN EASTERN CZECHIA</td>
<td>Stenzl, Vlastimil</td>
</tr>
<tr>
<td>P227</td>
<td>EVALUATION OF RAPIDLY MUTATING Y-STRS IN PAKISTANI POPULATION</td>
<td>Alghafri, Rashed</td>
</tr>
<tr>
<td>P228</td>
<td>FALSE POSITIVE RESULTS IN PATERNITY TESTINGS BASED ON NUMBER OF ANALYZED LOCI</td>
<td>Stefanovic, Aleksandra</td>
</tr>
<tr>
<td>P229</td>
<td>FIRST-DEGREE FAMILIAL RELATIONSHIPS COINCIDENCES IN A POPULATION DATABASE OF JUJUY (ARGENTINA) COMPARED WITH SIMULATED POPULATIONS</td>
<td>Miozzo, María Cecilia</td>
</tr>
<tr>
<td>P230</td>
<td>FORENSIC AND POPULATION GENETIC ANALYSIS OF SERBIAN POPULATION USING 21 STR LOCI OF GLOBALFILER™ PCR AMPLIFICATION KIT</td>
<td>Zgonjanin, Dragana</td>
</tr>
<tr>
<td>P231</td>
<td>FORENSIC CHARACTERISTICS OF TIBETO-BURMAN-SPEAKING TIBETANS REVEALED BY 50 INDELS</td>
<td>Wang, Mengge</td>
</tr>
<tr>
<td>P232</td>
<td>FORENSIC FEATURES OF CHINESE HAN AND GENETIC STRUCTURE AT INSERTION/DELETION POLYMORPHISMS WITH OTHER 31 CHINESE ETHNIC GROUPS</td>
<td>Zou, Xing</td>
</tr>
<tr>
<td>P233</td>
<td>FORENSIC GENETIC ANALYSIS OF SOUTH PORTUGUESE POPULATION WITH THE SIX DYE POWERPLEX® FUSION 6C</td>
<td>Vieira Da Silva, Cláudia</td>
</tr>
<tr>
<td>P234</td>
<td>FORENSIC GENETIC ANALYSIS OF THE POPULATION OF GUJARAT WITH POWERPLEX 21 MULTIPLEX SYSTEM</td>
<td>Mishra, Aditi</td>
</tr>
<tr>
<td>P235</td>
<td>FORENSIC PARAMETERS AND GENETIC STRUCTURE BASED ON Y-CHROMOSOME SHORT TANDEM REPEATS IN LESOTHO POPULATION</td>
<td>D'Amato, Maria Eugenia</td>
</tr>
<tr>
<td>P236</td>
<td>FORENSIC STATISTICAL PARAMETERS OF 22 AUTOSOMAL STRS IN MESTIZOS FROM THE PENÍNSULA DE YUCATÁN, MEXICO</td>
<td>Sosa-Escalante, Javier Enrique</td>
</tr>
<tr>
<td>P237</td>
<td>FREQUENCY OF NULL ALLELES IN PATERNITY CASES FROM MEXICO FOR THE LOCUS PENTA E</td>
<td>Rangel Villalobos, Hector</td>
</tr>
<tr>
<td>P238</td>
<td>GENES INVOLVED IN DAMAGE RESPONSE CAUSED BY UV RADIATION IN ECUADORIAN POPULATION OF DIFFERENT ALTITUDE REGIONS</td>
<td>Zambrano, Ana Karina</td>
</tr>
<tr>
<td>P239</td>
<td>GENETIC ANALYSIS OF 12 X-CHROMOSOMAL STRs AN AUTOCHTHONOUS POPULATION OF SOUTHEAST SPAIN</td>
<td>Jiménez, Susana</td>
</tr>
<tr>
<td>P240</td>
<td>GENETIC CHARACTERIZATION AND ANCESTRY OF THE ADMIXED POPULATION OF MARAJÓ ISLAND, NORTHERN OF BRAZIL, WITH AUTOSOMAL AND LINEAGE MARKERS</td>
<td>Martins, Silvia</td>
</tr>
<tr>
<td>Abstract Number</td>
<td>Title</td>
<td>Authors</td>
</tr>
<tr>
<td>-----------------</td>
<td>----------------------------------------------------------------------</td>
<td>---------</td>
</tr>
<tr>
<td>P241</td>
<td>GENETIC CHARACTERIZATION OF 12 STRS (INVESTIGATOR HDPLEX) IN ECUADORIAN POPULATION</td>
<td>Gaviria, Anibal</td>
</tr>
<tr>
<td>P242</td>
<td>GENETIC CHARACTERIZATION OF MTDNA CONTROL REGION FROM GYPSIES OF PAKISTAN</td>
<td>Ali, Babar</td>
</tr>
<tr>
<td>P243</td>
<td>GENETIC CHARACTERIZATION OF SOUTHEAST POPULATIONS FROM BRAZIL: 32 INSERTION AND DELETION POLYMORPHISMS ANALYSIS OF THE X CHROMOSOME</td>
<td>Alves De Jesus Silva, Flávia</td>
</tr>
<tr>
<td>P244</td>
<td>GENETIC DATA AND MUTATION RATES OF 23-YSTRS IN THE SÃO PAULO STATE POPULATION, BRAZIL</td>
<td>Ambrosio, Isabela</td>
</tr>
<tr>
<td>P245</td>
<td>GENETIC IDENTIFICATION OF SPANISH CIVIL WAR VICTIMS. THE STATE OF THE ART IN CATALONIA (NORTH-EAST SPAIN)</td>
<td>Gomes, Cláudia</td>
</tr>
<tr>
<td>P246</td>
<td>GENETIC INSIGHT INTO NIGERIAN POPULATION GROUPS USING AN X-CHROMOSOME DECAPLEX SYSTEM</td>
<td>Gomes, Iva</td>
</tr>
<tr>
<td>P247</td>
<td>GENETIC INVESTIGATION OF CHINESE SHE ETHNIC BASED ON AUTOSOMAL STRS AND X-STRS</td>
<td>Zhang, Suhua</td>
</tr>
<tr>
<td>P248</td>
<td>GENETIC POLYMORPHISM AND PHYLOGENETIC ANALYSIS OF 21 NON-CODIS STR LOCI IN A SHANGHAI HAN POPULATION</td>
<td>Sun, Kuan</td>
</tr>
<tr>
<td>P249</td>
<td>GENETIC POLYMORPHISM AND POPULATION STRUCTURE OF TORGHUT MONGOLS AND COMPARISON WITH A MONGOLIAN POPULATION 3,000 KILOMETERS AWAY</td>
<td>Sun, Hongyu</td>
</tr>
<tr>
<td>P250</td>
<td>GENETIC POLYMORPHISM OF 125 Y-SNPS IN HAN POPULATION FROM EASTERN CHINA</td>
<td>Bian, Yingnan</td>
</tr>
<tr>
<td>P251</td>
<td>GENETIC POLYMORPHISM OF 125 Y-SNPS IN HAN POPULATION FROM SHANDONG PROVINCE, CHINA</td>
<td>Li, Min</td>
</tr>
<tr>
<td>P252</td>
<td>GENETIC POLYMORPHISM OF 30 AUTOSOMAL INDEL LOCI IN CHINESE LI POPULATION FORM HAINAN</td>
<td>Hou, Yiping</td>
</tr>
<tr>
<td>P253</td>
<td>GENETIC POLYMORPHISMS OF 12 X-STRS OF INVESTIGATOR ARGUS KIT IN ECUADORIAN POPULATION</td>
<td>Gaviria, Anibal</td>
</tr>
<tr>
<td>P254</td>
<td>GENETIC POLYMORPHISMS OF 30 INSERTION/DELETION MARKERS IN JAPANESE, BANGLADESHI, AND INDONESIAN POPULATIONS</td>
<td>Nagai, Atsushi</td>
</tr>
<tr>
<td>P255</td>
<td>GENETIC PORTRAIT OF THE PUNJABI POPULATION FROM PAKISTAN USING THE PRECISION ID ANCESTRY PANEL</td>
<td>Shan, Muhammad Adnan</td>
</tr>
</tbody>
</table>
P256 GENETIC VARIATION OF 23 STR LOCI IN A NORTHEAST COLOMBIAN POPULATION (DEPARTMENT OF SANTANDER)
Castillo, Adriana

P257 GENETIC VARIATION OF 25 Y-CHROMOSOMAL AND 15 AUTOSOMAL STR LOCI IN THE HAN CHINESE POPULATION OF LIAONING PROVINCE, NORTHEAST CHINA
Yao, Jun

P258 GENETIC VARIATION OF HIGH-ALTITUDE ECUADORIAN POPULATION USING AUTOSOMAL STR MARKERS
Zambrano, Ana Karina

P259 GENOMIC PORTRAIT OF POPULATION OF UTTAR PRADESH, INDIA, DRAWN WITH AUTOSOMAL STRS AND Y-STRS
Srivastava, Ankit

P260 GEOLOCATION OF THE BRAZILIAN NATIONAL DNA DATABASE MATCHES AS A TOOL FOR IMPROVING PUBLIC SAFETY AND THE PROMOTION OF JUSTICE
Carneiro da Silva Junior, Ronaldo

P261 HAPLOTYPE DATA FOR THE 12 RM Y-STR LOCI IN A SYRIAN POPULATION
Serin, Ayse

P262 HUMAN TRAFFICKING – MULTINATIONAL CHALLENGE FOR FORENSIC SCIENCE
Buś, Magdalena

P263 IMPROVED DNA-DATABASE SEARCH WITH MIXED PROFILES USING SMARTRANK (1)
Eckert, Martin

P264 INCREASING CONVICTED OFFENDER GENETIC PROFILES IN THE BRAZILIAN NATIONAL DNA DATABASE – LEGISLATION, PROJECTS AND PERSPECTIVES
Carneiro da Silva Junior, Ronaldo

P265 INFERRING THE GENETIC STRUCTURE OF NORTHWESTERN ARGENTINA BY UNIPARENTAL SNP TYPING
Corach, Daniel

P266 INTRODUCING A FORENSIC VERSION OF PHYLOTREE FOR IMPROVED HAPLOGROUPING
Huber, Nicole

P267 LISBON POPULATION MTDNA ANALYSIS: STUDY OF A GENETIC MARKER WITH POPULATION, EVOLUTION AND FORENSIC INTEREST
Vieira Da Silva, Cláudia

P268 LOW DISCRIMINATION POWER OF THE YFILERTM PLUS PCR AMPLIFICATION KIT IN AFRICAN POPULATIONS. DO WE NEED MORE RM Y-STRS?
Della Rocca, Chiara

P269 MASSIVELY PARALLEL SEQUENCING OF FORENSIC MARKERS IN THE PEOPLE OF THE BRITISH ISLES
Huszar, Tunde Ildiko

P270 MATERNAL GENETIC ANCESTRY OF CROATS: POPULATION GENETICS AND FORENSIC PERSPECTIVE
Barbarić, Lucija

P271 MATERNAL GENETIC CHARACTERIZATION OF A COLOMBIAN ANDEAN POPULATION
Castillo, Adriana
P272  MITOCHONDRIAL CONTROL REGION VARIATION IN THE SOUTHERN AFRICAN POPULATION SAMPLE SET  
D'Amato, Maria Eugenia  
P273  MITOCHONDRIAL DNA SEQUENCING FOR FORENSIC HUMAN IDENTIFICATION ON A SAMPLE OF SAUDI POPULATION  
Aloraer, Dinah  
P274  MITOCHONDRIAL DNA STUDY IN THE SHUAR ETHNIC GROUP FROM ECUADOR  
Zambrano, Ana Karina  
P275  MITOCHONDRIAL GENETIC PROFILE OF THE YORUBA POPULATION FROM NIGERIA  
Martinez, Beatriz  
P276  MOLECULAR VARIANTS ASSOCIATED WITH FLAVOR PERCEPTIONS AND ANCESTRAL PROPORTIONS OF ECUADORIAN POPULATION  
Zambrano, Ana Karina  
P277  MUTATION RATE ANALYSIS OF 24 AUTOSOMAL STR’S MEASURED ALONG A 10 YEARS PERIOD IN ARGENTINA  
Sala, Andrea  
P278  MUTATION RATES INVESTIGATION OF 27 Y-STRS IN 101 FATHER-SON PAIRS  
Li, Chengtao  
P279  NGS-BASED MICROHAPLOTYPE GENOTYPING: 124-PLEX ASSAY, ALLELE-CALLING SOFTWARE AND PROPOSED ALLELE NOMENCLATURE  
Zhang, Chi  
P280  NOVEL APPROACHES TO POPULATION GENETIC ANALYSES OF X-CHROMOSOMAL DATA – EXEMPLIFIED USING A NORWEGIAN POPULATION SAMPLE  
Kling, Daniel  
P281  ON THE STATE GENOME REGISTRATION IN THE RUSSIAN FEDERATION  
Perepechina, Irina  
P282  OPTIMIZATION OF THE GENOGEOGRAPHER’S REFERENCE POPULATION FOR GREENLAND  
Mogensen, Helle Smidt  
P283  POLYMORPHISM ANALYSES FOR CHINESE HAN POPULATION USING FORENSEQTM DNA SIGNATURE PREP KIT  
Li, Shujin  
P284  POPULATION DATA FOR 29 BIALLELIC MARKERS ON Y CHROMOSOME FROM THREE GROUPS OF CHINESE HAN INDIVIDUALS  
Li, Li  
P285  POPULATION DATA OF 12 X-STRS IN TURKEY  
Serin, Ayse  
P286  POPULATION DATA OF D6S1043, PENTA D AND PENTA E LOCI IN SOUTH OF ITALY (CALABRIA)  
La Marca, Angelo  
P287  POPULATION GENETIC DATA AND FORENSIC STATISTICAL PARAMETERS OF 23 STR AUTOSOMAL MARKERS IN ARGENTINA  
Herrera Piñero, Mariana
P288  POPULATION GENETICS DATA OF 23 AUTOSOMAL STR LOCI FOR THREE POPULATIONS IN UNITED ARAB EMIRATES
Naji, Mohammed

P289  POPULATION GENETICS OF 30 INSERTION–DELETION POLYMORPHISMS IN POLISH POPULATIONS USING INVESTIGATOR® DIPPLEX KIT (QIAGEN)
Michalak, Eliza

P290  POPULATION GENOMICS OF THE MITOCHONDRIAL GENOME SEGMENTS AND THE PREDICTION OF NEUTRAL AND SELECTIVE TRENDS FOR IDENTIFICATION AND ASSOCIATION STUDIES
Iannacone De La Flor, Gian Carlo

P291  POPULATION SUB-STRUCTURE WITHIN THE BRITISH ISLES DETECTED WITH Y-STR AND Y-SNP MARKERS
Wetton, Jon

P292  PRELIMINARY ASSESSMENT OF THE DNASEQEX 29 Y-STR PANEL DESIGNED FOR THE MISEQ FGX®
Qian, Xiaoqin

P293  RAPIDLY MUTATING Y-STRS FOR QATARI POPULATION
Almohammed, Eida

P294  RARE GENETIC STRUCTURE OBSERVED IN POPULATION GENETIC ANALYSIS OF THE GLOBALFILER STR LOCI IN THE GHANAIAN POPULATION
Wepeba, Pet-Paul

P295  RELATED ANALYSIS OF SURNAME AND Y CHROMOSOME HAPLOTYPE IN THE JAPANESE POPULATION
Ochiai, Eriko

P296  REVISITING THE MATRILINEAL LINEAGES AND HYPOXIC ADAPTATION OF HIGHLAND TIBETANS
Wang, Zheng

P297  SEQUENCE ANALYSIS OF 25 AUTOSOMAL STRS INCLUDING SE33 USING AN IN-HOUSE MPS PANEL IN FOUR POPULATIONS
Kwon, Ye-Lim

P298  SEQUENCE DATA OF 31 AUTOSOMAL STR LOCI FROM 498 SPANISH INDIVIDUALS
Barrio, Pedro

P299  SEQUENCE POLYMORPHISMS OF 58 STR LOCI IN A TIBETAN POPULATION USING MASSIVELY PARALLEL SEQUENCING
Peng, Dan

P300  SEQUENCE VARIATION AND POPULATION CHARACTERISTICS OF THE NEW ZEALAND POPULATION USING THE FORENSEQ™ DNA SIGNATURE PREP KIT
Harbison, Sallyann

P301  SEQUENCE-BASED SAUDI POPULATION DATA FOR THE SE33 LOCUS
Alsafiah, Hussain

P302  SOCIAL, ETHICAL, AND SCIENTIFIC IMPLICATIONS FOR IDENTIFYING SUSPECTS BY USING FAMILIAL SEARCHES IN DNA DATABASES
Janevski, Robert
P303 START-UP OF THE CRIMINAL GENETIC DATABASE IN MENDOZA, ARGENTINA
Marino, Miguel

P304 STUDY OF GENETIC MARKERS WITH MEDICO-LEGAL AND FORENSIC INTEREST IN LISBON’S POPULATION (PRELIMINARY RESULTS)
Vieira Da Silva, Cláudia

P305 STUDY OF INSERTION-DELETION POLYMORPHISMS (INDELS) IN THE UAE POPULATION
Almheiri, Maryam

P306 THE EUROFORGEN NAME AMPLISEQ CUSTOM PANEL: A SECOND TIER PANEL DEVELOPED FOR DIFFERENTIATION OF INDIVIDUALS FROM THE MIDDLE EAST/NORTH AFRICA
Truelsen, Ditte

P307 WITHDRAWN

P308 THE IMPACT OF THE PRÜM TREATY ON THE PORTUGUESE FORENSIC DNA DATABASE – A BRIEF REVIEW
Porto, Maria

P309 THE MATERNAL INHERITANCE OF THE ASHANINKA NATIVE GROUP FROM PERU
Simão, Filipa

P310 THE MOST FREQUENT AUTOSOMAL STRS (POWERPLEX FUSION) INVOLVED IN EXCLUSION OF PATERNITY CASES IN A POPULATION FROM SOUTHEAST, MEXICO
Lopez Gonzalez, Paola Nicte

P311 THE PHYLOGENETIC ANALYSIS OF TWO ETHNIC GROUPS LIVING IN THE LÂM ĐÔNG PROVINCE, VIETNAM, BASED ON Y CHROMOSOMAL STR LOCI
Zielinska, Grażyna

P312 THE SPECIFIC HAPLOTYPE OBSERVED IN MONGOLIAN POPULATION
Ganbold, Uyanga

P313 TRACING THE GENETIC ORIGINS OF THE MALTESE POPULATION
Vella, Joanna

P314 TRI-ALLELIC PATTERN AT THE DYS385A/B LOCUS
Turrina, Stefania

P315 UTILIZATION OF THE CIFS DNA DATABASE TO MONITOR RECIDIVISM
Boonderm, Nongnuch

P316 VALIDATION OF A POPULATION SIMULATION MODEL FOR THE ESTIMATION OF Y-HAPLOTYPE FREQUENCIES IN FORENSIC CASES USING A LARGE FRENCH-CANADIAN DATASET
Landry, Roxane

P317 VALIDATION OF THE MICROREADERTM 28A ID KIT: A 28 LOCI SYSTEM FOR FORENSIC APPLICATION
Liang, Weibo

P318 VALIDATION OF Y-ANCESTOR TIME CALCULATORS FOR FORENSIC FAMILIAL SEARCHING
Claerhout, Sofie

P319 WEIGHING SUBSTRUCTURE IN ARGENTINA CONSIDERING DIFFERENT POPULATION CLUSTERS
Pinto, Nadia
P320  X-CHROMOSOME ANALYSIS IN AN UNUSUAL DEFICIENCY MATERNITY CASE
   Di Nunzio, Ciro

P321  X-STR DECAPLEX STUDY ON THE POPULATION OF IMBABURA-ECUADOR
   Gaviria, Anibal

P322  Y CHROMOSOME SEQUENCE VARIATION OF COMMON FORENSIC STR MARKERS AND THEIR FLANKING REGIONS AMONG POLISH POPULATION
   Wróbel, Maria

P323  Y-CHROMOSOMAL HAPLOTYPE DIVERSITY FOR 27 STR LOCI IN THE TIGRAY POPULATION (NORTHERN ETHIOPIA)
   Robino, Carlo

P324  Y-CHROMOSOME STR HAPLOTYPES STUDY IN A POPULATION SAMPLE FROM ARGENTINA
   Herrera Piñero, Mariana

---

DNA typing methodologies and strategies

P325  “UNUSUAL” TISSUES AND SAMPLE COLLECTION STRATEGIES ON EXHUMED BODIES
   Agostini, Vincenzo

P326  A MODIFIED DIRECT PCR AMPLIFICATION USING THE GLOBALFILER™ PCR AMPLIFICATION KIT ON BLOODSTAINS COLLECTED USING MICROFLOQ™ DIRECT SWABS
   Chan, Xavier

P327  A NEW SET OF DIP-SNP MARKERS FOR DETECTION OF UNBALANCED AND DEGRADED DNA MIXTURES
   Liu, Jinding

P328  A PILOT STUDY COMPARING EFFICIENCY OF CONVENTIONAL STR TYPING AND MASSIVELY PARALLEL SEQUENCING IN SPANISH CIVIL WAR SKELETAL SAMPLES
   Baeta, Miriam

P329  A RARE GENETIC GENDER ANOMALY IDENTIFIED IN A PATERNITY CASE PRESENTING AMEL-Y DROPOUT
   Barbarii, Ligia Elena

P330  A STUDY ON DIRECT PCR AMPLIFICATION USING THE GLOBALFILER™ PCR AMPLIFICATION KIT ON TOUCH AND SALIVA ARTICLES COLLECTED USING MICROFLOQ™ DIRECT SWABS
   Syn, Kiu Choong Christopher

P331  A VERY RAPID EXTRACTION METHOD FOR DNA-PROFILING OF BONE POWDER
   Duijs, Francisca Elisabeth

P332  ACHIEVING GREATER UNIFORMITY IN THRESHOLD DETERMINATIONS: RECOMMENDATIONS FOR STATISTICAL CONSIDERATIONS AND VALIDATION DESIGN
   Westring, Christian

P333  ADVANCED MITOCHONDRIAL CAPTURE ANALYSIS WITH MPS
   Ballard, David

P334  AN INNOVATIVE DNA EXTRACTION METHOD: WATER VERSUS COMMERCIAL BUFFERS
   Gomes, Claudia
P335  ANALYSIS OF 124 SNP LOCI INCLUDED IN HID AMPLISEQ IDENTITITY PANEL IN A SMALL POPULATION OF RIO DE JANEIRO, BRAZIL
Bottino, Carolina

P336  ANALYSIS OF CASE WORK SAMPLE MIXTURES, LAST STEPS IN FORENSIC VALIDATION OF THE FORENSEQ™ DNA SIGNATURE PREP KIT
Harbison, Sallyann

P337  ANALYSIS OF FORENSIC SAMPLES BY INVESTIGATOR ESSPLEX QS (QIAGEN) USING HALF PCR REACTION VOLUMES
La Marca, Angelo

P338  APPLICATION OF HRM-PCR (HIGH RESOLUTION MELTING PCR) FOR IDENTIFICATION OF FORENSSICALLY IMPORTANT COLEOPTERA SPECIES
Soltyszewski, Ireneusz

P339  APPLICATION OF MHANALYSER SOFTWARE IN THE STUDY OF MICROHAPLOTYPES IN FORENSICS
Chen, Peng

P340  APPLICATION OF NGM DETECT™ PCR AMPLIFICATION KIT IN CRITICAL FORENSIC EVIDENCE
Brescia, Gloria

P341  APPLICATION OF PARTIAL STR PROFILES GOTTEN BY ARTIFICIAL DNA MIXTURE DECONVOLUTION
Chen, Jing

P342  APPLICATION OF THE GNANO 31-PLEX ANCESTRY PREDICTION ASSAY IN AN AUSTRALIAN CONTEXT
Henry, Julianne

P343  APPLIED BIOSYSTEMS™ VERIFILER™ PLUS KIT WITH INTERNAL QUALITY CONTROL SYSTEM PROVIDES CONFIDENT ANSWERS IN CHALLENGING FORENSIC SAMPLES
Lackey, Angie

P344  ASSESSMENT AND PREVENTION OF FORENSIC DNA CONTAMINATION IN DNA PROFILING FROM LATENT FINGERPRINT
Bunakkharasawat, Wanasphon

P345  ASSESSING DNA RECOVERY FROM HIGHLY DEGRADED SKELETAL REMAINS BY USING SILICA-BASED EXTRACTION METHODS
Vinueza Espinosa, Diana Carolina

P346  ASSESSMENT MIXTURE ANALYSIS UTILIZING SNP PROBE CAPTURE ENRICHMENT AND MASSIVELY PARALLEL SEQUENCING
Shih, Shelly

P347  ASSESSMENT OF DNA QUANTITY AND QUALITY IN A WIDE RANGE OF FORENSIC SAMPLES USING THE INVESTIGATOR QUANTIPLEX PRO RGQ KIT (QIAGEN)
La Marca, Angelo

P348  ASSESSMENT OF THE DNA REPAIR FOR RESTORATION OF STR PROFILES FROM DAMAGED MIXTURES WITH VARIOUS RATIOS
Kim, Eun Hye
P349 AUTOMATED ESTIMATION OF THE NUMBER OF CONTRIBUTORS IN AUTOSOMAL STR PROFILES
Benschop, Corina

P350 BACKGROUND NOISE ASSESSMENT OF ILLUMINA MITOGENOME DATA FOR HETEROPLASMY DETECTION
Andreaggi, Kimberly

P351 BIOLOGICAL STAIN COLLECTION – ABSORBING PAPER IS SUPERIOR TO COTTON SWABS
Janssen, Kirstin

P352 BRINGING FORENSIC Y-CHROMOSOME HAPLOGROUPING TO THE NEXT RESOLUTION LEVEL BY USING TARGETED MASSIVELY PARALLEL SEQUENCING
Ralf, Arwin

P353 CAPTURING SPERMATOZOA FOR STR ANALYSIS OF SEXUAL ASSAULT CASES USING ANTI-SPERM ANTIBODIES
Alsalafi, Dina

P354 CHARACTERISATION OF THE IMPACT OF INHIBITION ON STR PROFILES: CAUSES, MECHANISMS AND CONSEQUENCES
Moore, David

P355 CHARACTERIZATION OF A 41-PLEX PCR AMPLIFICATION ASSAY FOR MALE-SPECIFIC DATABASING APPLICATIONS
Ludeman, Matthew

P356 CHARACTERIZING STUTTERS IN FORENSIC STRS WITH MASSIVELY PARALLEL SEQUENCING
Li, Ran

P357 CHIMERICISM ANALYSIS USING NEXT GENERATION SEQUENCING
Ricci, Ugo

P358 COMPARATIVE ANALYSIS OF DIFFERENT DNA RECOVERY METHODS FROM TOUCH DNA DEPOSITED ON PLASTIC BAGS AND ALUMINIUM FOIL
Kecmanovic, Miljana

P359 COMPARATIVE STUDY ON THE EFFECTS OF REDUCED PCR REACTION VOLUMES OF THE FORENSEQ® DNA SIGNATURE PREP KIT
Turrina, Stefania

P360 COMPARING FORENSEQ AND GENOME-WIDE SNP DATA FOR KINSHIP DEDUCTION
Colucci, Margherita

P361 COMPARISON OF SILICA FIBRES COATED WITH CHITOSAN FOR THE EFFECTIVE CAPTURE AND RELEASE OF DNA
Rennie, Jarrad

P362 COMPARISON OF TWO DNA EXTRACTION METHODS: PREPFILER® BTA AND MODIFIED PCI-SILICA BASED FOR DNA ANALYSIS FROM BONE
Hasap, Laila

P363 COMPARISONS OF ALLELE SIZING BETWEEN GENOTYPING SOFTWARE
Conte, Jillian

P364 COMPLETELY AUTOMATED INTERPRETATION OF REFERENCE SAMPLES
Weirich, Volker
P365  CONSIDERING THE DNA TRANSFER ISSUES UNDER A RETROSPECTIVE ANALYSIS OF FORENSIC EXAMINATION
Perepechina, Irina

P366  CRITICAL EVALUATION OF TOUCH DNA RECOVERY METHODS FOR FORENSIC PURPOSES
Hartless, Sophie

P367  DEALING WITH LOW AMOUNTS OF DEGRADED DNA: EVALUATION OF SNP TYPING OF CHALLENGING FORENSIC SAMPLES BY USING MASSIVE PARALLEL SEQUENCING
Turchi, Chiara

P368  DEGRADED DNA TYPING HIGHLY IMPROVED BY A CODIS CORE + ESS MEGAPLEX BASED ON SUPERPRIMERS
Mautner, Martin E.

P369  DETECTION OF CELLULAR MATERIAL WITHIN HANDPRINTS
Kanokwongnuwut, Piyamas

P638  DEVELOPING A DNA METHYLATION-BASED MULTIPLEX SNP ASSAY FOR THE IDENTIFICATION OF SEMEN IN MIXED STAINS
Haibo Luo

P370  DEVELOPMENT AND VALIDATION OF 21-PLEX STR PANEL
Khodeneva, Natalya

P371  DEVELOPMENT AND VALIDATION STUDY OF THE MONSTR FORENSIC IDENTITY PANEL, A MULTIPLEX STR KIT FOR MASSIVELY PARALLEL SEQUENCING
Silvery, Janine

P372  DEVELOPMENT OF A 40 LINKED AUTOSOMAL STRS PANEL USING MASSIVELY PARALLEL SEQUENCING
Fan, Qingwei

P373  DEVELOPMENT OF A MODIFIED PROTOCOL FOR EZ1 (QIAGEN) AUTOMATED DNA EXTRACTION FROM HUMAN REMAINS
La Marca, Angelo

P374  DEVELOPMENT OF INVESTIGATOR 26PLEX QS, A NEW MULTIPLEX PCR KIT FOR GLOBAL STR ANALYSIS
Vranes, Miroslav

P375  DEVELOPMENTAL VALIDATION OF A PROBE CAPTURE NGS SYSTEM FOR ANALYSIS OF WHOLE MITOCHONDRIAL GENOME OF FORENSICALLY CHALLENGING SAMPLES
Shih, Shelly

P376  DEVELOPMENTAL VALIDATION OF THE CASEWORK DIRECT KIT FOR EFFICIENT SCREENING OF SEXUAL ASSAULT AND TOUCH DNA SAMPLES
Thompson, Jonelle

P377  DIAMOND™ NUCLEIC ACID DYE AND MICRO FLOQ® DIRECT SWABS FOR FORENSIC CASEWORK
Proff, Carsten

P378  DIFFERENTIAL EXTRACTION METHOD AS A GOLDEN STANDARD IN ANALYZING OF SEMEN STAINS IN SEXUAL-ASSAULT CASES
Jankova, Renata
P379  DIRECT PCR OF BLOODSTAINS COLLECTED FROM DECEASED INDIVIDUALS FOR IDENTIFICATION PURPOSES
Bowman, Zoe

P380  DIRECT PCR USING MICROFLOQ™ DIRECT SWABS WITH A MODIFIED QIAGEN INVESTIGATOR 24PLEX GO! PROTOCOL FROM DECOMPOSING HUMAN REMAINS FOR DVI APPLICATIONS
Hughes, Sheree

P381  DNA EXTRACTION FROM DIFFERENT SKELETAL HUMAN REMAINS WITH DEMINERALIZATION PROTOCOLS, ORGANIC EXTRACTION AND USING SILICA Carrasco Ramirez, Jose Andres

P382  DNA POLYMERASE PERFORMANCE ON THE DEGRADED HUMAN DNA SAMPLES
Kim, Kyungyong

P383  DNA PROFILES OBTAINED FROM URINE IN SNOW
Dufva, Charlotte

P384  DNA RECOVERY FROM SERATEC IMMUNOCHROMATOGRAPHIC TESTS
Conte, Jillian

P385  DNA TESTING OF TOUCH EVIDENCE ON A HAND TOWEL
Honda, Katsuya

P386  DNA TYPING FROM SKELETAL REMAINS USING GLOBALFILER® PCR AMPLIFICATION AND INVESTIGATOR® 24PLEX QS KITS
Zgonjanin, Dragana

P387  EFFECT OF PHI29 POLYMERASE-BASED MULTIPLE STRAND DISPLACEMENT WHOLE GENOME AMPLIFICATION ON THE PROPORTION IN DNA MIXTURE
Zhang, Ji

P388  EFFICIENCY OF CASEWORK DIRECT KIT FOR EXTRACTION OF TOUCH DNA SAMPLES OBTAINED FROM CARS STEERING WHEELS
Fridman, Cintia

P389  EFFICIENT PRESERVATION OF DNA EXTRACTED FROM BLOOD IN FTA CARDS BY CHELEX METHOD
Burgos Figueroa, German

P390  ESTABLISHING STR AND IDENTITY SNP ANALYSIS_THRESHOLDS THAT ENABLE RELIABLE INTERPRETATION AND PRACTICAL IMPLEMENTATION FOR MPS GENOMIC DNA CASEWORK
Didier, Meghan

P391  ESTIMATION OF EXTRACTION EFFICIENCY BY DROPLET DIGITAL PCR
Romsos, Erica

P392  EVALUATING THE AMPLIFICATION EFFICIENCY OF MALBAC® SINGLE CELL DNA KIT FOR TRACE DNA
Liu, Xiling

P393  EVALUATING THE USE OF HYPOXIA SENSITIVE MARKERS FOR BODY FLUID STAIN AGE PREDICTION
Williams, Graham

P394  EVALUATION OF FIVE PRESERVATION METHODS FOR RECOVERY OF DNA FROM BONE
Iyavoo, Sasitarian
P395  EVALUATION OF RAPIDLY MUTATING Y-STRS ON SOUTH INDIAN PEDIGREE SAMPLES
   Iyavoo, Sasitaran

P396  EVALUATION OF SOLVENTS USED TO RECOVER DNA AND RNA FROM CRIME SCENE STAINS
   Williams, Graham

P397  EVALUATION OF STANDARD SEXUAL ASSAULT EVIDENCE COLLECTION KIT: COMPARISON OF THE SUCCESS RATE OF STR ANALYSIS FROM PSA POSITIVE SWABS VERSUS RINSES
   Jehaes, Els

P398  EVALUATION OF THE PERFORMANCE OF THE BETA VERSION OF THE FORENSEQ DNA SIGNATURE PREP KIT ON THE MISEQ FGX FORENSIC GENOMICS SYSTEM
   Marcińska, Magdalena

P399  EVALUATION OF THE POWERQUANT® SYSTEM ON THE QUANTSTUDIO™ 5 REAL-TIME PCR SYSTEM
   Hopwood, Andy

P400  EVALUATION OF TWO DNA FORENSIC EXTRACTION METHODS WITH WATER: STERILE VERSUS DISTILLED WATER
   Gomes, Cláudia

P401  EVALUATION OF USEFULNESS OF FURTHER Y-STR ANALYSIS IN SEXUAL ASSAULT CASES ON PSA POSITIVE Samples RESULTING IN FEMALE AUTOSOMAL STR PROFILING
   Nelis, Eva

P402  EVOLUTION OF RAPIDHIT ID SYSTEM
   Ludeman, Matthew

P403  EXPLORING OF NEW AGE-RELATED CPGS USING METHBANK DATABASE AND THE PYROSEQUENCING
   Song, Feng

P404  EXTRACTION OF DNA FROM SKELETAL REMAINS BURIED IN ACIDIC SOILS
   Edson, Suni

P405  FACS BASED METHOD FOR EVALUATION OF EFFICIENCY OF THE DNA EXTRACTION METHODS
   Sadam, Maarja

P406  FORENSIC ANALYSIS OF MPS MTDNA DATA USING QIAGEN BIOMEDICAL GENOMICS WORKBENCH AND AQME TOOL – PRELIMINARY RESULTS
   Porto, Maria

P407  FORENSIC APPLICATION OF A MTDNA MINISEQUENCING 52PLEX: TRACING MATERNAL LINEAGES IN SPANISH CIVIL WAR REMAINS
   Baeta, Miriam

P408  FORENSIC EVALUATION OF 6-DYE CHEMISTRY KIT COMPOSED OF 23 LOCI WITH CASEWORK SAMPLES
   Aljanaahi, Naeeema

P409  FORENSIC IDENTIFICATION AND INTELLIGENCE SNP DATA FROM LATENT DNA USING MASSIVE PARALLEL SEQUENCING
   Young, Jennifer

P410  GO! DIRECT – FOR FASTER INSIGHTS INTO YOUR FORENSIC CASEWORK SAMPLES
   Prochnow, Anke
HIGH THROUGHPUT SEQUENCING DATA ANALYSIS WORKFLOW: MTDNA VARIANT DETECTION AND IDENTIFICATION OF STR/YSTR ALLELES AND ISOALLELES
Snyder-Leiby, Teresa

HISTOLOGICAL SPECIMENS IN GENETIC IDENTIFICATION OF NN CADAVERS AND PATERNITY TESTING
Soltsyewski, Ireneusz

HOW MANY STR MARKERS ARE ENOUGH?
Penacino, Antonella Belen

IDEAL STR KIT FOR DIRECT PCR ON TOUCH DNA SAMPLES
Martin, Belinda

IDENTIPLEX: A NEW STR KIT FOR HUMAN IDENTIFICATION DEVELOPED AND VALIDATED AT IDENTIGEN LAB (COLOMBIA)
Burgos Figueroa, German

IDENTITY SNP TYPING VIA THE FORENSEQ ASSAY: IMPLICATIONS FOR PRACTICAL USE
Just, Rebecca

IMPACT OF DNA DEGRADATION ON MASSIVELY PARALLEL SEQUENCING-BASED AUTOSOMAL STR AND IISNP NUCLEAR DNA TYPING SYSTEMS
Zavala, Elena

IMPACT OF MUTATION IN A LOCUS D2S441 ON ELECTROPHORETIC MOBILITY
Sadam, Maarja

IMPLEMENTATION OF PREP-N-GO™ BUFFER FOR DNA EXTRACTION FROM BUCCAL SWABS
Iyavoo, Sasitaran

IMPLEMENTING AN OPTIMIZED DNA EXTRACTION PROTOCOL FOR ANCIENT AND HIGHLY DEGRATED SAMPLES
Xavier, Catarina

IMPORTANCE OF DNA ANALYSIS FOR IDENTIFICATION AND CONFIRMATION OF HUMAN REMAINS, FOLLOWING A FORENSIC AUTOPSY
Zgonjanin, Dragana

INITIAL ASSESSMENT OF NGS AS A TOOL TO AUGMENT ROUTINE CE ANALYSIS OF STRS
Revoir, Andrew

INTERNAL VALIDATION OF LATEST GENERATION STR KITS FOR DIRECT STR TYPING FROM REFERENCE SAMPLES
Thanakiatkrai, Phuvadol

INTERNAL VALIDATION OF SUREID 21G HUMAN STR IDENTIFICATION KIT (HEALTH GENE TECHNOLOGIES)
La Marca, Angelo

INVESTIGATING THE RESOLUTION OF ANCESTRY TESTING IN GEOGRAPHIC REGIONS CHARACTERIZED BY A HIGH POPULATION ADMIXTURE
Alshamali, Farida

INVESTIGATION OF THE EFFICIENCY OF WHOLE GENOME AMPLIFICATION PRIOR TO SHORT TANDEM REPEAT ANALYSIS USING DEGRATED DNA
Machida, Mitsuyo
IS GENOMIC DNA EXTRACTED AND STORED AT -20 °C FOR LONG TIME USEFUL IN FORENSIC FIELD?
Sguazzi, Giulia

LARGE-SCALE CONCORDANCE STUDY FOR 16 AUTOSOMAL STRS ANALYSED WITH POWERPLEX ESI 17 PRO AND NGMSELECT
Haas, Alexandra

LOST AT SEA: A PILOT STUDY INVESTIGATING DNA RECOVERY FROM TEETH IN A SOUTH AFRICAN NATURAL MARINE ENVIRONMENT
Finaughty, Chandra

MASSIVELY PARALLEL SEQUENCING (MPS) TECHNOLOGIES APPLIED TO IMPROVE THE RESOLUTION OF FORENSIC CASEWORK
Mosquera-Miguel, Ana

MASSIVELY PARALLEL SEQUENCING OF STRS HAS GAINED NUMBER OF TYPED MARKERS IN THE ANALYSIS OF DEGRADED DNA
Shin, Kyoung-Jin

MAXIMIZE INFORMATION FROM YOUR MIXTURE SAMPLES USING A COMBINED AUTOSOMAL STR AND Y-STR MULTIplex SYSTEM
Macphetridge, Ann

MITOCHONDRIAL DNA DATA ANALYSIS STRATEGIES THAT INFORM MPS-BASED FORENSIC CASEWORK IMPLEMENTATION
Holt, Cydne

MPS REVEALS ISOMETRIC PCR ARTEFACTS IN DEGRADED SAMPLES
Fattorini, Paolo

NAKED EYE AMELOGENIN Y DETECTION USING DNAZYMES ON A MICROPAD TOWARDS RAPID GENDER DISCRIMINATION
M. De Pancorbo, Marian

NEW APPROACH TO SIMULTANEOUSLY IDENTIFY MITOCHONDRIAL DNA HAPLOGROUPS BY MULTIPLEX PCR-RFLPS AND CAPILLARY ELECTROPHORESIS
Burgos Figueroa, German

NEW INSIGHT: WHOLE GENOME SEQUENCING DATA IN FORENSIC STR ANALYSIS
Wang, Yicong

NEW STRATEGIES IN THE FIELD OF MIXTURE DECONVOLUTION
Anslinger, Katja

NEXT GENERATION SEQUENCING TECHNOLOGY IN SECOND WORLD WAR VICTIM IDENTIFICATION
Zupanič Pajnič, Irena

NON-DESTRUCTIVE DNA COLLECTION FACILITATING A REVISED FORENSIC WORKFLOW FOR HANDWRITTEN DOCUMENTS
Prinz, Mechthild

NONINVASIVE PRENATAL PATERNITY TESTING (NIPAT) THROUGH MATERNAL PLASMA DNA SEQUENCING WITH A TWO-STEP MULTIPLEX PCR STRATEGY
Wang, Yicong

OPTIMISING DNA RECOVERY
Rennie, Jarrad
P443  OPTIMIZATION OF SINGLE CELL AMPLIFICATION AFTER DEPARRAYTM ISOLATION  
Barni, Filippo

P444  OPTIMIZATION OF THE COLLECTION AND ANALYSIS OF TOUCH DNA TRACES  
Pereira, Vania

P445  OPTIMIZED STRATEGIES FOR COLLECTION AND ANALYSIS OF MICRO TRACES  
Dierig, Lisa

P446  PATERNITY INCONSISTENCY AT CHROMOSOME 2 – AS AN EXAMPLE OF UNIPARENTAL DISOMY  
Doniec, Andrzej

P447  PERFORMANCE AND CONCORDANCE OF THE FORENSEQ™ SYSTEM FOR THE ANALYSIS OF CHALLENGING SAMPLE TYPES  
Mckiernan, Heather

P448  PERFORMANCE COMPARISON OF TWO MOST RECENT Y-STR MULTIPLEX SYSTEMS FOR REAL FORENSIC CASEWORK ANALYSIS  
Shrivastava, Pankaj

P449  PERFORMANCE EVALUATION OF THE PRECISION ID GLOBALFILER™ NGS STR PANEL V2 AND CONVERGE SOFTWARE V2.1  
Gross, Theresa E.

P450  PERUS WORKING GROUP: A DNA-LED MULTIDISCIPLINARY PROJECT FOR THE IDENTIFICATION OF POLITICAL MISSING PERSONS FROM THE 1970’S IN BRAZIL  
Ferreira, Samuel

P451  PRELIMINARY EXPLORATION OF A NOVEL METHOD FOR THE DECONVOLUTION OF DNA MIXTURES BY PYROSEQUENCING  
Zhang, Ji

P452  PREVALENCE AND IMPACT OF PCR ARTIFACTS FROM SOIL SAMPLES USING THE APPLIED BIOSYSTEMS™ GLOBALFILER™ PCR AMPLIFICATION KIT  
Diegoli, Toni

P453  Q1a3a NATIVE-AMERICAN Y-HAPLOGROUP DETECTION IN DNA QUANTIFICATION STEP  
Ginart, Santiago

P454  QUANTITATIVE DETECTION OF SIGNATURE PEPTIDE IN BODY FLUIDS BY LIQUID CHROMATOGRAPHY TANDEM MASS SPECTROMETRY (LC-MS/MS)  
Browne, Tebah

P455  RECOMMENDATION OF GE.F.I. (ITALIAN SPEAKING GROUP OF ISFG)  
Buscemi, Loredana

P456  RESOLUTION OF MTDNA MIXTURES USING A PROBE CAPTURE NEXT GENERATION SEQUENCING SYSTEM AND CUSTOM ANALYSIS SOFTWARE  
Shih, Shelly

P457  SALTY OR SWEETY? ALTERNATIVES FOR BONE PRESERVATION ALONG EXTENDED PERIODS OF TIME  
Corach, Daniel

P458  SEQFORSTRS (SEQUENCING OF FORENSIC STRS) – PROJECT UPDATE  
Schultheiss, Eva
<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>P459</td>
<td>SERS-ACTIVE FORENSIC EVIDENCE SWABS FOR CONFIRMATORY IDENTIFICATION AND GENOTYPING OF HUMAN BODILY FLUIDS</td>
<td>Evanoff, David</td>
</tr>
<tr>
<td>P460</td>
<td>SIMPLIFIED, RAPID DNA EXTRACTION PROTOCOL FOR STR TYPING FROM BONES</td>
<td>Phua, Cheng Ho</td>
</tr>
<tr>
<td>P461</td>
<td>SINGLE STEP STRATEGY FOR ESTIMATING UNKNOWN STR ALLELE FREQUENCIES IN A POPULATION</td>
<td>Corach, Daniel</td>
</tr>
<tr>
<td>P462</td>
<td>SLIMDNA – AN IN-HOUSE EXPERT SYSTEM FOR STR PROFILING</td>
<td>Sanga, Malin</td>
</tr>
<tr>
<td>P463</td>
<td>STUDY BY NEXT GENERATION SEQUENCING OF SUDDEN CARDIAC DEATH (SCD)</td>
<td>Ricci, Ugo</td>
</tr>
<tr>
<td>P464</td>
<td>THE APPLIED BIOSYSTEMS™ GLOBALFILER™ IQC PCR AMPLIFICATION KIT: A 24-PLEX STR CASEWORK KIT WITH AN INTERNAL QUALITY CONTROL SYSTEM ENHANCEMENT</td>
<td>Ludeman, Matthew</td>
</tr>
<tr>
<td>P465</td>
<td>THE BEST POSSIBLE RESULT FROM THE MINIMUM AVAILABLE</td>
<td>Ricci, Ugo</td>
</tr>
<tr>
<td>P466</td>
<td>THE DEVELOPMENT AND EVALUATION OF AN NGS PANEL INCLUDING 42 AUTOSOMAL STRS</td>
<td>Li, Shujin</td>
</tr>
<tr>
<td>P467</td>
<td>THE EFFECT OF SURFACE TYPE, COLLECTION AND EXTRACTION METHODS ON TOUCH DNA</td>
<td>Alketbi, Salem</td>
</tr>
<tr>
<td>P468</td>
<td>THE EFFECT OF TIME AND ENVIRONMENTAL CONDITIONS ON TOUCH DNA</td>
<td>Alketbi, Salem</td>
</tr>
<tr>
<td>P469</td>
<td>THE IMPACT OF FDSTOOLS NOISE CORRECTION ON THE ANALYSIS OF DATA FROM THE FORENSEQ DNA SIGNATURE PREP KIT</td>
<td>Van Der Gaag, Kristiaan</td>
</tr>
<tr>
<td>P470</td>
<td>THE MODIFICATION OF CHELEX-100 DNA EXTRACTION METHOD</td>
<td>Wang, Hui</td>
</tr>
<tr>
<td>P471</td>
<td>THE NEED FOR AUTOMATION IS LIMITED WHEN USING A QUICK AND INEXPENSIVE ONE-TUBE DNA EXTRACTION PROTOCOL FOR CRIME SCENE SAMPLES</td>
<td>Forsberg, Christina</td>
</tr>
<tr>
<td>P472</td>
<td>THE SUCCESSFUL USE OF CARTILAGE AND MUSCLE, AFTER 23 DAYS OF INHUMATION, FOR DNA TYPING. AND IDENTIFICATION OF TWO STILLBORN EXchanged AT A HOSPITAL</td>
<td>Ferreira, Samuel</td>
</tr>
<tr>
<td>P473</td>
<td>THE VALIDATION OF DNA/RNA COEXTRACTION USING STR LOCI AND MRNA MARKERS WITH FORENSIC PURPOSE</td>
<td>Bai, Peng</td>
</tr>
<tr>
<td>P474</td>
<td>THE YARA GAMBIRASIO CASE: COLLECTION STRATEGY AND DNA MASS SCREENING USED TO FIND THE PERPETRATOR DNA IN A CHALLENGING SCENARIO</td>
<td>Gentile, Fabiano</td>
</tr>
<tr>
<td>Page</td>
<td>Title</td>
<td>Author</td>
</tr>
<tr>
<td>------</td>
<td>----------------------------------------------------------------------</td>
<td>-------------------------------------------</td>
</tr>
<tr>
<td>P475</td>
<td>TILED AMPLICON MTDNA SEQUENCING USING PID NGS SYSTEM AND CONVERGE™</td>
<td>Lim, Jessica</td>
</tr>
<tr>
<td></td>
<td>ANALYSIS SOFTWARE: A ROBUST AND SENSITIVE ASSAY FOR FORENSIC CASEWORK</td>
<td></td>
</tr>
<tr>
<td></td>
<td>APPLICATIONS</td>
<td></td>
</tr>
<tr>
<td>P476</td>
<td>TISSUE STORAGE SOLUTION FOR PRESERVATION AND TRANSFER OF FORENSIC</td>
<td>Panvisavas, Nathinee</td>
</tr>
<tr>
<td></td>
<td>SPECIMEN IN HIGH AMBIENT-TEMPERATURE</td>
<td></td>
</tr>
<tr>
<td>P477</td>
<td>TOWARDS INCREASING THE EFFECTIVENESS OF RECOVERING, IDENTIFYING</td>
<td>Clayton, Tim</td>
</tr>
<tr>
<td></td>
<td>AND SEPARATING SPERMATOZOA PRESENT ON VAGINAL SWABS TAKEN IN SEXUAL</td>
<td></td>
</tr>
<tr>
<td></td>
<td>ASSAULT CASES</td>
<td></td>
</tr>
<tr>
<td>P478</td>
<td>USING REAL TIME PCR AS STRATEGY TO EVALUATE PERFORMANCE OF PCR AND</td>
<td>Burgos Figueroa, German</td>
</tr>
<tr>
<td></td>
<td>SANGER SEQUENCING REACTIONS</td>
<td></td>
</tr>
<tr>
<td>P479</td>
<td>VALIDATION OF A NOVEL MASSIVELY PARALLEL SEQUENCING PLATFORM FOR</td>
<td>Wang, Yicong</td>
</tr>
<tr>
<td></td>
<td>FORENSIC GENETICS</td>
<td></td>
</tr>
<tr>
<td>P480</td>
<td>VALIDATION OF A STREAMLINED RT-qPCR METHOD FOR BODY FLUID IDENTIFICATION</td>
<td>Moore, David</td>
</tr>
<tr>
<td>P481</td>
<td>VALIDATION OF THE PRECISION ID WHOLE MTDNA GENOME PANEL IN A WORLDWIDE</td>
<td>Strobl, Christina</td>
</tr>
<tr>
<td></td>
<td>LINEAGE STUDY</td>
<td></td>
</tr>
<tr>
<td>P482</td>
<td>VALIDATION OF THE QUANTipLEX PRO RGQ DNA KIT</td>
<td>Kupiec, Tomasz</td>
</tr>
<tr>
<td>P483</td>
<td>VALIDATION STUDY AND FORENSIC APPLICATION OF INVESTIGATOR 24PLEX QS KIT</td>
<td>Brescia, Gloria</td>
</tr>
<tr>
<td>P484</td>
<td>VERIFICATION OF THE GNANO 31-PLEX ANCESTRY PREDICTION ASSAY FOR</td>
<td>Henry, Julianne</td>
</tr>
<tr>
<td></td>
<td>FORENSIC CASEWORK</td>
<td></td>
</tr>
<tr>
<td>P485</td>
<td>VISUALISING LATENT DNA ON TAPES</td>
<td>Kanokwongnuwut, Piyamas</td>
</tr>
<tr>
<td>P486</td>
<td>WHEN AUTOMATION IS AN ISSUE: DEVELOPMENT OF DNAXS, A SOFTWARE EXPERT</td>
<td>Nagel, Jord</td>
</tr>
<tr>
<td></td>
<td>SYSTEM FOR DNA PROFILE INTERPRETATION AND MIXTURE ANALYSIS</td>
<td></td>
</tr>
<tr>
<td>P487</td>
<td>WHO DO YOU THINK YOU ARE? LONG RANGE FAMILIAL SEARCHES USING THE 23ANDME</td>
<td>Phillips, Christopher</td>
</tr>
<tr>
<td></td>
<td>AND GEDMATCH RELATIVE MATCHING TOOLS</td>
<td></td>
</tr>
<tr>
<td>P488</td>
<td>WHOLE GENOME AMPLIFICATION VERSUS LOW-TEMPLATE DNA PROFILING: A</td>
<td>Lim, Hong Han</td>
</tr>
<tr>
<td></td>
<td>COMPARATIVE STUDY</td>
<td></td>
</tr>
<tr>
<td>P489</td>
<td>WHOLE GENOME MITOCHONDRIAL DNA ANALYSIS USING MASSIVELY PARALLEL</td>
<td>Downey, Lotte</td>
</tr>
<tr>
<td></td>
<td>SEQUENCING SYSTEMS</td>
<td></td>
</tr>
</tbody>
</table>
YFILER™ PLUS AMPLIFICATION KIT: RAPIDLY MUTATING Y-STR MARKERS AND THEIR PRACTICAL USE IN FORENSICS
Pacholíková, Petra

Forensic mathematics and statistics

A DEEP LEARNING APPROACH FOR PAIRWISE KINSHIP INFERENCE
Liang, Weibo

A FORENSIC MARKER SELECTION METHOD FOR POPULATION STRUCTURE EVALUATION
Zhou, Yuxiang

A MULTIVARIATE STATISTICAL TOOL FOR THE EVALUATION OF THE BIOGEOGRAPHICAL ANCESTRY INFORMATION FROM TRADITIONAL STR DATA
Alladio, Eugenio

A NEW STRATEGY TO IDENTIFY FOUR KINDS OF BODY FLUIDS USING 6 MIRNAS
Zhao, Yixia

APPLICATION OF A METHODOLOGY TO EVALUATE DNA RESULTS WITH PROPOSITIONS AT THE ACTIVITY LEVEL USING BAYESIAN NETWORK
Samie, Lydie

APPLYING Autosomal STR PROBABILISTIC GENOTYPING MODELS TO SNP DATA USING HIERARCHICAL BAYESIAN MODELLING
Taylor, Duncan

BAYESIAN NETWORKS FOR EVALUATING SNP-STR PROFILING RESULTS FROM UNBALANCED DNA MIXTURES
Lyu, Meili

BAYESIAN NETWORKS FOR SOURCE LEVEL ATTRIBUTION OF SALIVA: DEVELOPMENT AND APPLICATION IN CASEWORK
Harbison, Sallyann

COMPARISON OF WEIGHT OF EVIDENCE RESULTS GENERATED FROM TWO MCMC BASED PROBABILISTIC GENOTYPING SOFTWARE
Foley, Megan

COMPLETION OF THE MIX 13 CASE STUDY BY EVALUATION OF MOCK MIXTURES WITH THE PROBABILISTIC GENOTYPING SOFTWARE GENOPROOF® MIXTURE 3
Harthun, Maria

DEVELOPMENT OF A NEW SOFTWARE FOR ESTIMATING CONFIDENCE INTERVAL OF STATISTICAL INDEXES USED FOR DNA EVIDENCE INTERPRETATION
Manabe, Sho

ESTIMATES OF MUTATION RATES FROM INCOMPATIBILITIES ARE MISLEADING – GUIDELINES FOR PUBLICATION AND RETRIEVAL OF MUTATION DATA URGENTLY NEEDED
Pinto, Nadia

EVALUATION OF MACHINE LEARNING ALGORITHMS FOR IDENTIFICATION OF HUMAN REMAINS IN DVI INCIDENTS
Luque, Juan

EVALUATION OF SENSITIVITY AND SPECIFICITY OF SIBSHIP DETERMINATION IN THE CAUCASIAN POPULATION OF THE RUSSIAN FEDERATION USING 23 STR LOCI
Zavarin, Vladislav
<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>P505</td>
<td>Evolutionary Operator for Calculating the Frequency of Occurrences of Many Allelic Variants of the Genes HLA, STR, and Y-STR Loci</td>
<td>Kurganov, Sardarxodja</td>
</tr>
<tr>
<td>P506</td>
<td>Famlink2 – a Comprehensive Tool to Accommodate Great Numbers of Linked Markers Accounting for Mutations and Subpopulation Effects</td>
<td>Kling, Daniel</td>
</tr>
<tr>
<td>P507</td>
<td>Forensic Computations in Pedigrees with Inbred Founders</td>
<td>Vigeland, Magnus Dehli</td>
</tr>
<tr>
<td>P508</td>
<td>Hybridmark: Eliminating the PCR Hybrid Artefacts in Forensic MPS DNA Profiles</td>
<td>Hoogenboom, Jerry</td>
</tr>
<tr>
<td>P509</td>
<td>Integrating Concept for Genetic Identity Assessment</td>
<td>Perepechina, Irina</td>
</tr>
<tr>
<td>P510</td>
<td>Interpreting Multiple LR Values from Different Probabilistic Software: A Joined Approach Involving Logistic Regression</td>
<td>Alladio, Eugenio</td>
</tr>
<tr>
<td>P511</td>
<td>Is Linkage Significant in Complex Kinship Testing? A Preliminary Simulating Study Based on the Goldeneye™ 20A Kit</td>
<td>Zhang, Yinming</td>
</tr>
<tr>
<td>P512</td>
<td>Isoallelic Frequency Estimation for STR Markers from Massive Parallel Sequencing Data</td>
<td>Andersen, Mikkel Meyer</td>
</tr>
<tr>
<td>P513</td>
<td>Kinship Statistics: Massive Parallel Sequencing vs. Capillary Electrophoresis</td>
<td>Navarro-Vera, Isabel</td>
</tr>
<tr>
<td>P514</td>
<td>Lumping of Alleles in Mutation Models Vastly Improves Computational Efficiency</td>
<td>Kling, Daniel</td>
</tr>
<tr>
<td>P515</td>
<td>Machine Learning Algorithms for a Case to Predict Y-SNP Haplogroup Based on Y-STR Haplotypes</td>
<td>Song, Mengyuan</td>
</tr>
<tr>
<td>P516</td>
<td>Massively Parallel Sequencing for Kinship Analysis: How Important are Genetic Linkage Corrections?</td>
<td>Davenport, Lucinda</td>
</tr>
<tr>
<td>P517</td>
<td>Moving From a Consensus Approach to Probabilistic Genotyping: Impact on the Value of DNA Profile Comparisons</td>
<td>Gehrig, Christian</td>
</tr>
<tr>
<td>P518</td>
<td>Moving From a Consensus Approach to Probabilistic Genotyping: Integration in a Laboratory Workflow</td>
<td>Grosjean, Frederic</td>
</tr>
<tr>
<td>P519</td>
<td>Mutation in Y-STRs: Repeat Motif Gains vs. Losses</td>
<td>Antão Sousa, Sofia</td>
</tr>
<tr>
<td>P520</td>
<td>Outlier Detection in Forensic Science Using Graphical Models</td>
<td>Tvedebrink, Torben</td>
</tr>
</tbody>
</table>
P521 PERFORMANCE OF EUROFORMIX DECONVOLUTION ON POWERPLEX® FUSION 6C PROFILES
Benschop, Corina

P522 RELATION BETWEEN STUTTER RATIO AND THE DNA SEQUENCE: FURTHER IMPROVEMENT OF EXPLAINING DISTRIBUTION OF STUTTER RATIO AT COMPLEX REPEAT LOCI
Inokuchi, Shota

P523 RELMIX: AN OPEN SOURCE SOFTWARE FOR DNA MIXTURES WITH RELATED CONTRIBUTORS
Egeland, Thore

P524 THE NUMBER OF CONTRIBUTORS IS A NUISANCE (PARAMETER) FOR DNA MIXTURE EVIDENCE EVALUATION
Caliebe, Amke

P525 THE ROLE OF DNA CONCENTRATIONS IN FORENSIC CASEWORK RESULTS- REGRESSION MODELS APPLICATION
Vieira Da Silva, Cláudia

P526 TRISOMY 21 IN PATERNITY TESTING AND FORENSIC CASEWORK
Schulze Johann, Kristina

P527 UNDERESTIMATION AND MISCLASSIFICATION OF MUTATIONS AT X CHROMOSOME STRS DEPEND ON POPULATION ALLELIC PROFILE
Antão Sousa, Sofia

P528 VALIDATING THE OUTPUT OF DNA INTERPRETATION SOFTWARE USING THE CONCEPT OF CALIBRATION
Mcgovern, Catherine

P529 VALIDATION OF MASTR™ SOFTWARE: EXTENSIVE STUDY OF FULLY-CONTINUOUS PROBABILISTIC MIXTURE ANALYSIS USING POWERPLEX® FUSION 2 – 5 CONTRIBUTOR MIXTURES
Snyder-Leiby, Teresa

DNA phenotyping, pharmacogenetics, and epigenetics

P530 A SYNTHETIC REAL-TIME PCR SENSOR FOR ESTIMATING THE RELATIVE LOSS OF TEMPLATE DNA DURING BISULFITE CONVERSION
Niederstätter, Harald

P531 AGE PREDICTION METHOD BASED ON DNA METHYLATION FOR USE IN FORENSIC ANALYSIS
Franken, Benjamin

P532 AN ENHANCED SNP MULTIPLEX FOR THE PREDICTION OF HUMAN PIGMENTATION BY COMBINING ESTABLISHED GENOTYPING ASSAYS
Fondevila Alvarez, Manuel

P533 AN EXTENDED AGE PREDICTION MODEL FROM CHILDHOOD TO THE ELDERLY
Freire-Aradas, Ana

P534 APPLICATION OF THE ION AMPLISEQ™ HIRISPLEX-S METHOD FOR PREDICTING PIGMENTATION TRAITS IN DEGRADED BONE SAMPLES
Ossowski, Andrzej
BIOGEOGRAPHICAL ANCESTRY PREDICTION ACCURACY – A SWEDISH PERSPECTIVE
Tillmar, Andreas

BMI PREDICTION THROUGH DETECTION OF DNA METHYLATION
Kotková, Lucie

BUILDING THE BRIDGE BETWEEN SCIENCE AND INVESTIGATION
Daniel, Runa

DEVELOPMENT AND VALIDATION OF THE VISAGE TOOLS TO ESTIMATE AGE BY MASSIVELY PARALLEL SEQUENCING
Heidegger, Antonia

DEVELOPMENT OF A DNA METHYLATION BASED AGE ESTIMATION MODEL INCLUDING 4 CPG SITES
Schwender, Kristina

DEVELOPMENT OF A FORENSIC AGE PREDICTOR FOR SALIVA/BUCCAL SWABS BASED ON DNA METHYLATION
Ambroa-Conde, Adrián

DEVELOPMENT OF A FORENSIC DNA PHENOTYPING PANEL USING MASSIVE PARALLEL SEQUENCING
Turchi, Chiara

DEVELOPMENT OF ANCESTRY INFORMATIVE MARKER SETS FOR THE VISAGE BASIC AND ENHANCED MPS TOOLS
Phillips, Christopher

DEVELOPMENT OF BMI-ASSOCIATED PREDICTION MODELS FOR A KOREAN POPULATION: A COMPARISON WITH EWAS STUDY
Lee, Jeong Min

DNA METHYLATION-BASED AGE PREDICTION FROM SKELETAL REMAINS
Lee, Hwan Young

EARLY EVALUATION OF FIVE AGE-CORRELATED DNA METHYLATION MARKERS IN AN ITALIAN POPULATION SAMPLE
Gentile, Fabiano

EFFICIENCY OF EYE COLOUR PREDICTION ALGORITHMS IN CASE OF HIGH FREQUENCY OF INTERMEDIATE COLOUR: AN ITALIAN STUDY
Gentile, Fabiano

ENHANCED CELL-TYPE INFERENCE BY QUANTITATIVE “ON/OFF” CPG METHYLATION PROFILING
Gausterer, Christian

EPIGENETIC AGE ESTIMATION IN SEMEN SAMPLES – ON THE WAY TO GOOD MARKERS AND METHODS
Pisarek, Aleksandra

EPIGENETIC AGE ESTIMATION OF HEALTHY CZECH POPULATION BY AGEPLEX
Drábek, Jiří

EPIGENETICS MEETS STR AND MTDNA IN FORENSIC GENETICS
Naue, Jana
P551 EVALUATION OF HIRISPLEX-S SYSTEM MARKERS FOR EYE, SKIN AND HAIR COLOR PREDICTION IN AN ADMIXED BRAZILIAN POPULATION
Fridman, Cintia

P552 EVALUATION OF SKIN-RELATED VARIANTS IN AFRICAN ANCESTRY POPULATIONS AND THEIR ROLE IN PERSONAL IDENTIFICATION
Veltre, Virginia

P553 EVALUATION OF THE HIRISPLEX-S SYSTEM IN A BRAZILIAN POPULATION SAMPLE
Telles Carratto, Thássia Mayra

P554 EXAMINATION OF AGE-ESTIMATION MODEL FOR THE JAPANESE USING DNA METHYLATION SITES
Guan, Xueling

P555 FORENSIC AGE PREDICTION WITH 25 NG OF INITIAL INPUT DNA USING BISULFITE PYROSEQUENCING
Thong, Zhonghui

P556 FORENSIC COGINFOCOM CHALLENGES OF DNA-PHENOTYPING
Nogel, Monika

P557 GENETIC INVESTIGATIONS OF BROWN EYED INDIVIDUALS WITH THE RS12913832:GG GENOTYPE
Meyer, Olivia Strunge

P558 GLOBAL VARIABILITY AND PATTERNS OF LINKAGE DISEQUILIBRIUM IN THE OCA2-HERC2 REGION ASSOCIATED WITH HUMAN PIGMENTATION
Hall, Diana

P559 HERC2 (RS12913832) AND OCA2 (RS1800407) GENES POLYMORPHISMS IN RELATION TO IRIS COLOR VARIATION IN BELARUSIAN POPULATION
Borovko, Sergey

P560 IDENTIFICATION OF BLOOD-SPECIFIC AGE-RELATED DNA METHYLATION MARKERS ON THE ILLUMINA METHYLATIONEPIC BEADCHIP
Alsaleh, Hussain

P561 IDENTIFICATION OF MRNA- AND DNA METHYLATION MARKERS FOR HUMAN AGE ESTIMATION BY MPS TECHNIQUES
Hartmann, Katharina

P562 IDENTIFICATION OF NOVEL SPERM-CELL SPECIFIC EPIGENETIC AGE PREDICTORS USING AGILENT’S HUMAN DNA METHYLATION MICROARRAY
Pisarek, Aleksandra

P563 IDENTIFICATION OF Y-CHROMOSOME METHYLATION MARKERS FOR MALE AGE ESTIMATION OF FORENSIC SAMPLES
Richards, Rebecca

P564 IMPLEMENTATION OF MASSIVELY PARALLEL SEQUENCING FOR FORENSIC DNA PHENOTYPING – RESULTS OF A WORLD-WIDE SURVEY
Gross, Theresa E.

P565 IMPROVING ACCURACY OF AGE PREDICTION MODEL THROUGH MACHINE LEARNING ALGORITHM
Thong, Zhonghui
P566 INCORPORATING AND VALIDATING THE IMPACT OF PRIORS ON DNA PREDICTION OF EXTERNAL VISIBLE CHARACTERISTICS
Katsara, Maria-Alexandra

P567 IS IT POSSIBLE TO DISTINGUISH BREAST-FEEDING FROM BOTTLE-FED INFANTS WITH MICRORNA PROFILING OF GASTRIC CONTENT?
Kakimoto, Yu

P568 MAPLEX – AN ANCESTRY-INFORMATIVE ASSAY FOR THE ASIA PACIFIC REGION
Phillips, Christopher

P569 NEW MULTIPLEX STRATEGY FOR DNA METHYLATION-BASED AGE PREDICTIONS FROM LOW AMOUNTS OF DNA VIA PYROSEQUENCING
Fleckhaus, Jan

P570 OXFORD NANOPORE SEQUENCING AS A GOOD STRATEGY TO STUDY DNA VARIATION OF THE ENTIRE MC1R GENE
Pospiech, Ewelina

P571 PERCEPTION OF BLUE AND BROWN EYE COLOURS
Meyer, Olivia Strunge

P572 PHENOTYPE PREDICTION ACCURACY – A SWEDISH PERSPECTIVE
Hedman, Johannes

P573 PREDICTION AND VALIDATION OF EYE COLOR ACROSS IRANIAN POPULATION WITH A SINGLE BASE EXTENSION GENOTYPING ASSAY
Hosseini, Sayed Mostafa

P574 QBICO: A NOVEL LAB TOOL FOR THE COMBINED ACCURATE ASSESSMENT OF BISULFITE-CONVERTED DNA QUALITY AND QUANTITY IN FORENSIC EPIGENETIC APPLICATIONS
Vidaki, Athina

P575 SCHIZOPHRENIA AND EPIGENETICS IN FORENSIC SCIENCES
Cevik, Filiz Ekim

P576 STABILITY OF DNA METHYLATION STATUS OVER THREE DIFFERENT DAYS
Holländer, Olivia

P577 THE DEVELOPMENT OF EPIGENETIC METHYLATION FOR APPLICATIONS IN BODY FLUID IDENTIFICATION AND PHENOTYPING
Mccord, Bruce

P578 THE EYELID TRAIT ASSOCIATED SNPS INVESTIGATION IN CHINESE HAN ADULTS
Wang, Qian

P579 TIME FRAME PREDICTION FOR THE DEPOSITION OF A BIOLOGICAL SAMPLE USING CLOCK GENE EXPRESSION PATTERNS
Mosquera-Miguel, Ana

P580 VALIDATED INFERENCE OF SMOKING HABITS FROM BLOOD WITH A FINITE DNA METHYLATION MARKER SET
Vidaki, Athina

P581 VICTORIA’S UNIDENTIFIED HUMAN REMAINS – WHAT MORE CAN WE DO TO IMPROVE MISSING PERSON’S INVESTIGATIONS?
Stock, April
WHAT MAKES YOUR “EYES” LOOK DIFFERENT?
Wang, Yanyun

Y-CHROMOSOME BASED EPIGENETIC AGE ESTIMATION IN BLOOD: A NOVEL APPROACH FOR ESTIMATING AGE OF MALES FROM MALE-FEMALE DNA MIXTURES
Vidaki, Athina

New polymorphisms of forensic interest

38 INSERTION-DELETION (INDEL) MARKERS ANALYSIS AND ITS APPLICATION IN FORENSIC CASES
Simoes Dutra Correa, Heitor

A COMMON INDEL POLYMORPHISM OF THE DESMOGLEIN-2 (DSG2) IS ASSOCIATED WITH SUDDEN CARDIAC DEATH IN CHINESE POPULATIONS
Gao, Yuzhen

A NEW APPROACH TO DETECT A SET OF SNP-SNP MARKERS: COMBINING ARMS-PCR WITH SNAPSHOT TECHNOLOGY
Liang, Weiibo

A STUDY OF QATARI POPULATION USING FORENSEQ™ DNA KIT
Almohammed, Eida

ANALYSIS OF 55 KIDD ANCESTRY SNP OF QATARI POPULATION COMPARED TO 139 WORLD WIDE POPULATION
Almohammed, Eida

APPLICATION OF A SNP-STR MULTIPLEX ASSAY FOR FORENSIC DNA MIXTURE INTERPRETATION
Zhang, Lin

ASSOCIATING DONOR AND CELL TYPE USING RNA SNPs
Van Den Berge, Margreet

CONFIRMATION OF PHASED-INFERRED SNP HAPLOTYPE DATA OF 74 MICROHAPLOTYPE LOCI AND ANCESTRY PREDICTION BY MASSIVELY PARALLEL SEQUENCING
Yoon, Leena

DEVELOPMENT OF A MULTIALLELIC INDEL FORENSIC ASSAY: INSERTION-DELETION SHORT MICROHAPLOTYPES
Fondevila Alvarez, Manuel

ESTABLISHING MASS SPECTROMETRY-BASED IDENTIFICATION OF BODY FLUIDS FOR CASEWORK
Kuhlmann, Stephan

EURASIAPLEX II: A NOVEL SELECTION OF SNPS FOR REFINED DIFFERENTIATION OF EURASIAN ANCESTRIES
Fondevila Alvarez, Manuel

EVALUATION OF A COSTUMIZED PANEL OF 117 NOVEL MICROHAPLOTYPES SELECTED FOR FORENSIC IDENTIFICATION IN TWO MPS PLATFORMS
Phillips, Christopher

EVALUATION OF ALU INSERTION POSITIONS OBSERVED IN SILICO IN JAPANESE WHOLE GENOME SEQUENCINGS
Yamamoto, Toshimichi
P597 EVALUATION OF MICROHAPLOTYPES – A PROMISING NEW TYPE OF FORENSIC MARKER
Staadig, Adam

P598 EVALUATION OF TWO DNA/RNA CO-EXTRACTION METHODS FOR BODY FLUID IDENTIFICATION IN FORENSICS
Gomes, Iva

P599 FORENSIC EVALUATION OF SE33 MARKER IN INDIAN POPULATION USING GLOBAL FILER, FUSION 6C AND PANGLOBAL AUTOSOMAL STR MULTIPLEX
Shrivastava, Pankaj

P600 GENOME-WIDE CNV ANALYSIS IN THE CZECH POPULATION AND A NEW CONCEPT FOR DISTANT RELATEDNESS DETERMINATION
Korabecna, Marie

P601 GENOME-WIDE SEARCH OF DIP-STRs CANDIDATES BY USING THE 1000 GENOME PROJECT DATASET
Hall, Diana

P602 INVESTIGATION ON RAPIDLY MUTATING Y-STRS MULTIPLEX IN INDIAN POPULATION: A PILOT STUDY
Shrivastava, Pankaj

P603 MPS-BASED COMPARISON OF MTDNA HETEROPLASMY IN HAIRS AND CORRESPONDING BUCkALS TO INFORM MPS INTERPRETATION GUIDELINES
van der Gaag, Kris

P604 PERFORMANCE OF A MASSIVE PARALLEL SEQUENCING MICROHAPLOTYPES ASSAY ON DEGRADED DNA
Turchi, Chiara

P605 PROBABLILISTIC GENOTYPING OF MICROHAPLOTYPES
Podini, Daniele

P606 PROPOSED A NEW NOMENCLATURE FOR MICROHAPLOTYPES
Chen, Dan

P607 SEQUENCE CHARACTERIZATION OF MICROVARIANT ALLELES AT DYS627 AND DYS458
Hou, Yiping

P608 THE APPROPRIATENESS OF THE ANALYSIS OF SOME KNOWN MICRO-RNAS TO DETECT THE PRESENCE OF SEMEN IN OLD STAINS
Lancia, Massimo

P609 THE POTENTIAL FOR ANCESTRY INFERENCE OF DIP-SNP
Zhang, Lin

P610 THE STUDY OF 95 IDENTITY SNPS FOR QATARI POPULATION
Almohammed, Eida

P611 THE UNIQ-TYPER™ Y-10 GENOTYPING IN SOUTH AFRICAN POPULATIONS: NOVEL ALLELES, SEQUENCE VARIATION AND ALLELIC LADDER UPDATES
Kasu, Mohaimin

P612 TRIAL TO SEARCH FOR MITOCHONDRIAL DNA MUTATION ASSOCIATED WITH CANCER DETECTED BY MASSIVE PARALLEL SEQUENCING
Honda, Katsuya
VALIDATION OF THE CONSISTENCY OF CSNP ANALYSIS BETWEEN DNA AND RNA USING SNAPSHOT METHOD
Wang, Shouyu

VARIANT ALLELE 6.2 AT LOCUS D19S433 IN SYRIAN FAMILY SAMPLES
Iyavoo, Sasitaran

WHOLE MIRNAOME ANALYSIS IN SALIVA STAIN BASED ON MASSIVE PARALLEL SEQUENCING: A PILOT STUDY
Yan, Jiangwei

Standards, quality control, accreditation, and ethics

BRAZIL’S DNA PROFILE DATABASE – ESTABLISHMENT, LEGISLATION AND ACCREDITATION
Iwamura, Edna

COMPARISON OF THREE DIFFERENT PRETREATMENT METHODS AND STORAGE TEMPERATURE FOR BLOOD RNA EXTRACTION
Li, Chengtao

CONTAMINATION ON THE OUTSIDE OF ALLELIC LADDER CONTAINERS
Senst, Alina

DEVELOPING LEGAL REGULATION OF FORENSIC DNA-PHENOTYPING IN HUNGARY
Nogel, Monika

DEVELOPMENT OF A COMPUTER TOOL TO BETTER DETECT LOW-LEVEL DNA CONTAMINATIONS
Houde, Josée

DNA TRANSFER BETWEEN EVIDENCE BAGS DURING CASEWORK
Mercer, Claire

EVALUATION OF THE GEDNAP PROFICIENCY TESTS 2016 – 2018
Meyer, Miriam

FIVE-YEAR EVALUATION OF FORENSIC BODY FLUID IDENTIFICATION AND DNA MIXTURE ANALYSIS FROM THE ACCREDITED GHEP-ISFG PROFICIENCY TEST
Fernández Oliva, Coro

FORENSIC DNA PHENOTYPING AND GENETIC GENEALOGY AS PART OF A FORENSIC IDENTIFICATION TOOLKIT
Scudder, Nathan

FORENSIC GENETICS IN SEXUAL ASSAULT: A RETROSPECTIVE STUDY ON THE COLLECTION OF EVIDENCE AT THE EMERGENCY DEPARTMENT
Tozzo, Pamela

IN-HOUSE VALIDATION OF MPS-BASED METHODS IN A FORENSIC LABORATORY
Sidstedt, Maja

METHOD DESIGN TO CREATE AND CHARACTERIZE SIMULATED SEXUAL-ASSAULT SAMPLES AND ESTABLISH ITS USEFULNESS TO VALIDATE FORENSIC ANALYSIS TECHNIQUES
Reyes, Patricio
<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Author(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>P628</td>
<td>MINIMIZING HAND-TO-GLOVE DNA CONTAMINATION</td>
<td>Van Den Berge, Margreet</td>
</tr>
<tr>
<td>P629</td>
<td>NIST SCIENTIFIC FOUNDATION REVIEW ON DNA MIXTURE INTERPRETATION</td>
<td>Butler, John</td>
</tr>
<tr>
<td>P630</td>
<td>ON THE ROAD – ACCREDITATION OF FOREnsic DNA LABORATORIES AS A PART OF THE “EFSA 2020” CONCEPT</td>
<td>Nogel, Monika</td>
</tr>
<tr>
<td>P631</td>
<td>PAST, RECENT AND FUTURE HUNGARIAN LEGISLATION OF FORENSIC DNA ANALYSIS</td>
<td>Nogel, Monika</td>
</tr>
<tr>
<td>P632</td>
<td>STANDARDIZATION IN FORENSIC GENETICS AS A MULTI-FACETED CHALLENGE IN POLAND</td>
<td>Iyavoo, Sasitaram</td>
</tr>
<tr>
<td>P633</td>
<td>STANDARDIZING DNA-REPORTING ON ACTIVITY LEVEL: A CHALLENGING OPPORTUNITY</td>
<td>Laan, Nick</td>
</tr>
<tr>
<td>P634</td>
<td>STRNAMING: STANDARDIZED STR SEQUENCE ALLELE NAMING TO SIMPLIFY MPS DATA ANALYSIS AND INTERPRETATION</td>
<td>Hoogenboom, Jerry</td>
</tr>
<tr>
<td>P635</td>
<td>THE IMPACT OF FORENSIC GENETICS ON THE MANAGEMENT OF SEXUAL ASSAULT VICTIMS: A MULTICENTRE GE.F.I PROJECT</td>
<td>Fattorini, Paolo</td>
</tr>
<tr>
<td>P636</td>
<td>UNLEASHING NOVEL STR LOCI VIA CHARACTERIZATION OF GENOME IN A BOTTLE REFERENCE SAMPLES</td>
<td>Gettings, Katherine</td>
</tr>
<tr>
<td>P637</td>
<td>VALIDATION OF MISEQ FGX™ FORENSIC GENOMICS SYSTEM TO ACHIEVE ISO17025 ACCREDITATION</td>
<td>Navarro-Vera, Isabel</td>
</tr>
</tbody>
</table>
Congress Secretariat

C-IN
Prague Congress Centre
5. kvetna 65, 140 21 Prague 4, Czech Republic
Tel.: +420 261 174 301
Fax: +420 261 174 307
E-mail: info@isfg2019.org
Website: www.c-in.eu
Identifying the missing

Join our symposium at the 2019 ISFG Congress, Prague:

Date: Wednesday, September 11, 2019
Time: 13:30–14:20
Location: South Hall 1B, 1st floor, Prague Congress Centre

Agenda

13:30 – 13:35 Welcome
13:35 – 13:45 How missing persons identification enables the families of the missing to move on. A personal story.
   Speaker: Mrs. Ingrid Gudmundsson, Sweden
13:45 – 14:15 Development of a large, massively parallel sequencing SNP panel for missing persons identification
   Speaker: Dr. Thomas J. Parsons, Director of Science and Technology, International Commission on Missing Persons (ICMP), The Hague, Netherlands
14:15 – 14:20 Wrap up

Visit https://go.qiagen.com/isfg-symposium to register.
Visit us at Booth #1 to find out what’s new.

Trademarks: QIAGEN®, Sample to Insight® (QIAGEN Group). Registered names, trademarks, etc. used in this document, even when not specifically marked as such, are not to be considered unprotected by law.

PROM-14691-001 07/2019 © 2019 QIAGEN, all rights reserved.
Join us at booth #6 to learn how the Applied Biosystems™ RapidHIT™ ID and the Applied Biosystems™ SeqStudio™ HID Genetic Analyzer can help expand your capabilities.

Traditional CE remains the platform of choice for STR analysis in forensic labs. Rapid DNA helps central labs and law enforcement agencies partner to solve crimes and can become an ideal tool when time to results is critical, or to help process less critical samples, so analysts can focus on more challenging samples.

Find out more at thermofisher.com/ce-ngs