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Development of forensic genomics research toolkits by the use of Massively Parallel Sequencing

Gaag, K.J. van der

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Stellingen behorend bij het proefschrift

Development of forensic genomics research toolkits by the use of Massively Parallel Sequencing

Kristiaan J. van der Gaag

1. The quality of Sanger sequencing as golden standard is overrated.
2. The lack of MPS analysis standards delays the implementation of MPS in forensic casework.
3. Well discussed STR sequencing nomenclature is essential for worldwide exchange of sequencing data.
4. Fragment length is the only relevant detail for comparing CE and sequence data. (this thesis)
5. It would be beneficial for the scientific community if respected journals demand wet lab validation for selection of new loci. (this thesis)
6. It is surprising that PCR hybrids are hardly mentioned in forensic literature.
7. PCR hybrids are likely to be the next limiting factor for mixture analysis. (this thesis)
8. The level of implementation of MPS as routine forensic tool will depend mostly on the cost of commercially available assays. (this thesis)
9. Bioinformatic support is a prerequisite for pioneers in Massively Parallel Sequencing.
10. For routine implementation of MPS, software should be available that can be operated by technicians without extensive bioinformatic experience.
11. Microhaplotypes have limited potential when the fragment size exceeds 150 base pairs.
12. Making music while doing a PhD can help to keep a well-balanced stress level.