

PrimExtend - A software for Multiplex Genotyping Primer Design for mass spectrometry based assays

Kirsten, H¹, Dienst, S², Ahnert, P¹

¹*Biotechnologisches Biomedizinisches Zentrum / IKIT, Universität Leipzig, Deutschland*

²*Institut für Informatik, Universität Leipzig, Deutschland*

ahnert@uni-leipzig.de

Genotyping by Matrix Assisted Laser Desorption and Ionisation Time Of Flight (MALDI-TOF) mass spectrometry is now one of the most automated and efficient single nucleotide polymorphism (SNP) detection methods. It delivers highly accurate results with exceptional reliability. Such genotyping assays are preferentially performed in multiplex format to save costs and increase throughput. For each assay, specific PCR primer and specific genotyping primer are necessary. PCR or genotyping primers belonging to the same multiplex assay should be designed as compatible as possible. Although freely available tools for multiplex PCR primer design exist, there is no accordant integrated tool for the design of compatible multiplex genotyping primers. Especially for a higher multiplex level, it is extremely tedious to design them manually. Here we present a software for such automatic compatible multiplex genotyping primer design. It is called "PrimExtend" and is applicable for the most common MALDI-TOF mass spectrometry based assay formats (Probe assay, Pinpoint assay, VSET assay, assays with cleavable primers of different cleavage chemistry, and combinations). The software comprises an intuitive graphical user interface and accounts for the resolution of the mass spectrometry device, cationic adducts, matrix effects, formation of secondary structures, GC contents, melting temperatures, single base repeats, and the preferred multiplex level. The software is based on Java (TM) technology and is freely available upon request from the authors.