

<i>Title of module</i>	Modular Advanced Practical in the Focal Point Programme "Molecular Medicine VZ185780, 185781": "HLA-D Typing and LightCycler Applications"		
<i>Credit points</i>	4	<i>Available in semester(s)</i>	1
<i>Hours per week</i>	5.25	<i>Compact course</i>	<input type="checkbox"/>
<i>Lecturer(s)</i>	HP Rihs, T. Brüning		
<i>Teaching methods</i>	A two-week all-day practical course with an integrated seminar.		
<i>Evaluation of learning progress</i>	Active participation in the practical course, feedback during the experiments		
<i>Mode of examination</i>	Assessment of active and successful participation in the practical (50%) and a written project report (50%)		
<i>Learning objectives</i>	During the first part students will get theoretically introduced to and learn to practically carry out molecular biological techniques designed to determine the <i>DRB1</i> and <i>DQB1</i> alleles in the genomic DNA of the students own blood samples and buccal swabs. In the second part the DNA from both sources will be used to analyze certain SNPs with two different techniques. Finally, students will perform a deduction of the <i>NAT2</i> acetylation status by analyzing seven SNPs using a combination of sequencing and real-time PCR on a LightCycler system.		
<i>Soft skills</i>	Planning and performing a project that requires to conduct a series of connected, consecutive experiments that build on each other. Teamwork capabilities; writing of a comprehensive project report.		

Contents of module

- Genomic DNA isolation of own buccal swabs
- Genomic DNA isolation of own white blood cells
- Agarose gel electrophoresis
- HLA-D typing for *DRB1* and *DQB1* genes by PCR with sequence-specific primers (SSP-PCR) and other methods (i.e. non-radioactive sequencing)
- SNP analyses of certain genes like *GSTM1*, *GSTT1* and *GSTP1* using two different techniques (PCR-RFLP and Real-time PCR) and two different DNA sources (buccal swabs and EDTA blood)
- Deduction of the acetylation status by analysis of seven SNPs in the *NAT2* gene by a combination of sequencing and LightCycler analyses.