March 28

Session 1. Setting the tone
Chair: Gerald Marti
09:00 – 09:10 Welcome - A. Wiestner, P. Ghia
09:10 – 09:40 On the road to CLL - P. Ghia
09:40 – 10:05 CLL clonal dynamics - N. Chiorazzi
10:05 – 10:30 IG genes in CLL: biological aspects - K. Stamatopoulos

Session 2. Immunoglobulin gene sequence analysis
Chair: Marie-Paule Lefranc
10:50 – 11:10 Mechanisms of immunoglobulin diversity - F. Davi
11:10 – 11:40 From the patient to the sequence: Primers, PCR, Detection of clonality, Sanger sequencing - L. Sutton
11:40 – 12:00 IMGT tools for interpretation of IG gene sequence data - V. Giudicelli
12:00 – 12:20 Specific challenges in IG gene interpretation and tailored bioinformatics solutions - A. Hadzidimitriou

Session 3. Practicalexercises: basic
Chair: Laura Rassenti
13:00 – 13:45 Hands-on exercises I
- K. Stamatopoulos
13:45 – 14:30 Sequence interpretation
- K. Stamatopoulos

Session 4. Practicalexercises: advanced
Chair: Diane Jelinek
15:00 – 16:00 Hands-on exercises II
- A. Agathangelidis
16:00 – 17:00 Sequence interpretation
- F. Davi

Social Program and Reception

March 29

Session 5. The IG as a biomarker and a therapeutic target in CLL
Chair: Paolo Ghia
09:00 – 09:45 Targeting signaling pathways to treat CLL - A. Wiestner
10:45 – 10:30 Prognostic considerations - R. Rosenquist

Session 6. New directions - standards
Chair: R. Rosenquist
11:00 – 11:30 NGS IG analysis - basic principles - A. Langerak
11:30 – 12:00 NGS IG analysis in CLL - prognostication - F. Davi
12:00 – 12:30 How to report IG gene sequence data in clinical diagnostics - L. Sutton
12:30 – 12:45 The ERIC IG Network - A. Chatzidimitriou
12:45 – 13:00 Wrap up – P. Ghia, A. Wiestner

Meeting Location
Clinical Center of the National Institutes of Health, Bethesda, MD