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

**Session 4. Practical exercises: 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**

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**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. Hadzidimitriou  
12:45 – 13:00 Wrap up – P. Ghia, A. Wiestner

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