



**Lunedì 12 Novembre**

**Incontro annuale del Gruppo di Biologia Computazionale e di Sistema  
della Società Italiana di Biochimica e Biologia Molecolare (SIB)**

**CNR, Aula Bisogno  
Piazzale Aldo Moro 7 – 00185 Roma**

**10:15-10:30 – Welcome**

**10:30-12:30 – Session 1: Genome analysis, mutations and disease**

10:30-11:30 – Marco Punta (The Institute for Cancer Research, London - Centre for Evolution and Cancer)  
*Cancer genomics, cancer vaccines and cancer resistance mutations*

11:30-11:50 – Giovanni Minervini (Università di Padova)  
*Genotype-phenotype relations of the von Hippel-Lindau tumor suppressor inferred from a large-scale analysis of disease mutations and interactors*

11:50-12:10 – Valerio Marino (Università di Verona)  
*Evolutionary-conserved structural communication in two Neuronal Calcium Sensor proteins investigated by SNP analysis*

12:10-12:30 – David Sasah Staid (Università "Sapienza" di Roma)  
*Identification of point mutations related to drug resistance in bacteria*

**12:30-14:00 – Pranzo**

**14:00-17:00 – Session 2: Protein structure, function and dynamics**

14:00-14:20 – Castrense Savojardo (Università di Bologna)  
*Computing protein-protein interaction sites from structure and sequence*

14:20-14:40 – Marco Necci (Università di Padova)  
*Integrated resources for the study of protein intrinsic disorder*

14:40-15:00 – Fabio Polticelli (Università di Roma Tre)  
*A comprehensive in silico analysis of huntingtin and its interactome*

**15:00-15:30 – Coffee-break**

15:30-15:50 – Giacomo Janson (Università "Sapienza" di Roma)  
*How to improve protein homology modelling within MODELLER*

15:50-16:10 – Leonardo Guidoni (Università dell'Aquila)  
*Atomistic simulations in Biochemistry*

16:10-16:30 – Veronica Morea, Allegra Via (CNR-IBPM)  
*Activities of the Bioinformatics group @IBPM-CNR*

**16:30-17:00 – Conclusions**