



## Exploring the Functional Consequences of Genomic Variation

"Constitution AB"  
Grand Hyatt, Washington DC

2<sup>nd</sup> November 2010

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**7.45 – 8.30** Speakers arrive and hand in presentations  
Poster Mounting  
Registration

**8.35 – 8.40** **President's Welcome**  
Graham R. Taylor

**Session 1** **Interpreting Functions of Large Sequenced Regions**  
**Chair: William Oetting**

**8.40 – 8.45** **Introduction to the Meeting**  
William Oetting

**8.45 – 9.15** **INVITED SPEAKER**  
**Whole genome sequencing and analysis: minimizing false positives and characterizing non-coding variants**  
Elliot Margulies

**9.15 – 9.45** **INVITED SPEAKER**  
**Fine mapping QTL and functional context**  
Daniel Gaffney

**9.45 – 10.00** **Disease gene identification by exome sequencing**  
Alexander Hoischen

**10.00 – 10.15** **A Reference-Free Approach to the Analysis of Rearrangements In Sequenced Exomes**  
Jeffrey Rosenfeld





## Poster Presentations

**Evaluation of Targeted Enrichment Strategies for Next Generation Sequencing of Cardiomyopathy Associated Genes**

Shale Dames

**Performance Comparison of Three Commercial Softwares for Analysis of Illumina Genome Analyzer Next Generation Resequencing Data**

Jacob Durtschi

**Microattribution expands the community engaged in LSDBs**

Belinda Giardine

**Multi-sample pooling and Illumina Genome Analyzer sequencing to determine gene sequence variation for database development**

Rebecca Margraf

**Developing Ethnic-Based Reference Sequences: CFTR as a Model**

Perry G. Ridge

**Functional consequences of nullisomy**

Ahn Joo Wook