

# **ABRF Microarray Research Group**

## **Introduction: MARG activities and microRNA profiling**

Chris Harrington

Oregon Health & Science University

# MARG activities 2009/10

- Expansion of technology focus areas
- Mission review: genomic profiling
- New name to reflect changes
- New website for technology/application updates from member labs & community discussion
- Recruitment of new members

# MARG 2009 & 2010

## Research Projects

- miRNA profiling on microarray & next-gen sequencing platforms
- miRNA standards for validating methods and platforms

# MARG members - 2010

- Herbert Auer – IRB Barcelona, Spain
- Don Baldwin – University of Pennsylvania
- Chris Harrington – Oregon Health & Science University
- Nadereh Jafari – Northwestern University
- Nalini Raghavachari – NHLBI Genomics Core Facility, NIH
- Natalia Reyero – Jackson State University
- Wei Wang – Cornell University

Contact any MARG member if you are interested in joining MARG or email Chris Harrington at [harringc@ohsu.edu](mailto:harringc@ohsu.edu)

# MARG Session Outline

- MARG-sponsored online technology forum
  - Natalia Reyero
- Technology forum example
  - Nalini Raghavachari
- microRNA profiling: platform comparison
  - Don Baldwin
- microRNA synthetic reference project
  - Don Baldwin

# ABRF Microarray Research Group

## *MARG discussion forum: Wiki Page*

Natàlia G. Reyero Vinas  
Jackson State University

Nalini Raghavachari  
NHLBI Genomics Core-NIH



## Purpose of the Wiki Page

The idea was to create a forum moderated by MARG that everybody can use to post/ask about tips and troubleshooting.

The Wiki page allows this type of discussion.

It is free and anybody can join.

The users need to create a user account, but it is free and common for all wikis.



## How to Access:

### 1. Direct Link:

<http://abrf-marg.wikispaces.com/>

### 2. Wikipedia:

[http://en.wikipedia.org/wiki/Association\\_of\\_Biomolecular\\_Resource\\_Facilities](http://en.wikipedia.org/wiki/Association_of_Biomolecular_Resource_Facilities)

### 3. ABRF Site:

Under 'Activities': MARG wiki – technology discussion forum  
(also under links)



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# Association of Biomolecular Resource Facilities

From Wikipedia, the free encyclopedia

The **Association of Biomolecular Resource Facilities** (**ABRF**) is dedicated to advancing core and research biotechnology laboratories through research, communication, and education. ABRF members include over 700 scientists representing 267 different core laboratories, including those in industry, government, academic and research institutions.<sup>[1]</sup>

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- 5 ABRF Award
- 6 Journal of Biomolecular Techniques
- 7 ABRF Executive Board
- 8 ABRF Office
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- 10 External links



## History

[edit]

In 1986 a Research Resource Facility Satellite Meeting was held in conjunction with the Sixth International Conference on Methods in Protein Sequence Analysis. The next year protein sequencing and amino acid samples were sent to survey 103 core facilities. By 1989 the ABRF was formally organized and incorporated. Each year an annual meeting was held as a satellite meeting of the Protein Society until 1996 when separate meetings began.<sup>[2]</sup>

## ABRF Research Groups

[edit]

Research Groups are established to fulfill two of the purposes of the Association of Biomolecular Resource Facilities. First, to provide mechanisms for the self-evaluation and improvement of procedural and operational accuracy, precision and efficiency in resource facilities and research laboratories. Second, to contribute to the education of resource facility and research laboratory staff, users, administrators, and interested members of the scientific community.<sup>[3]</sup>

- DNA Sequencing Research Group (DSRG)
- Genomic Variation Research Group (GVRG)
- Glycoprotein Research Group (gPRG)
- Light Microscopy Research Group (LMRG)
- Metabolomics Research Group (MRG)
- Microarray Research Group (MARG): MARG discussion forum [1]
- Molecular Interactions Research Group (MIRG)
- Nucleic Acids Research Group (NARG)
- Protein Expression Research Group (PERG)
- Protein Sequencing Research Group (PSRG)
- Proteomics Research Group (PRG)
- Proteomic Informatics Research Group (iPRG)
- Proteomic Standards Research Group (sPRG)

## Resource Technologies

[edit]

Members of ABRF are involved in a broad spectrum of genomic and proteomic technologies such as:

- Automation: high throughput screening, LIMS, robotics.
- Biophysics: calorimetry, CD, fluorescence, light scattering, SPR, ultracentrifugation.
- Gene Expression and Profiling: gene arrays, real-time PCR.
- Mass Spectrometry: qualitative, quantitative, and structural analysis of proteins, carbohydrates, oligonucleotides, and lipids.
- Nucleic Acid Chemistry: DNA sequencing, DNA synthesis, RNA synthesis, genotyping.
- Protein Expression, Identification, and Profiling: differential fluorescence, conventional 2-D gel electrophoresis, disease biomarker discovery.
- Protein-DNA Chemistry: gene acid analysis, Mass Spectrometry, peptide synthesis, peptide libraries.

# ABRF Research Groups

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- [Glycoprotein Research Group \(gPRG\)](#)
- [Light Microscopy Research Group \(LMRG\)](#)
- [Metabolomics Research Group \(MRG\)](#)
- [Microarray Research Group \(MARG\)](#); [MARG discussion forum \[1\]](#) 
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### MicroArray Research Group (MARG)

#### Background

The goal of the Microarray Research Group is to provide both academic and industrial scientists useful information and guidance in the use of various microarray platforms and applications in their research. The main focus of the MARG is to promote communication and cooperation among core laboratories providing microarray and data analysis services. In addition, the MARG is charged with conducting studies to help assess technological advancements and provide information about these technologies to all interested parties. Information developed and communicated by the MARG should be used to help laboratories evaluate their performance and achieve the highest quality results possible from the use of microarray technologies. In order to accomplish these goals the MARG will also strive to provide ways for sharing information relevant to the administration of facility laboratories that provide microarray technologies as a shared resource.

#### Current Membership

- Herbert Auer - IRB Barcelona.
- [Dr Don A. Baldwin](#) (Co-chair) - University of Pennsylvania.
- [Dr Christina A. Harrington](#) (Co-chair) - Oregon Health & Science University.
- Nadereh Jafari - Northwestern University
- Nalini Raghavachari - NIH
- [Jack Simpson](#) - SA/C - Frederick.
- [Dr Wei Wang](#) - Cornell University.
- Natália Vinas - Jackson State University.

#### Studies

- MARG 2009 study.
- [MARG 2008 study](#)
- MARG 2007 study.
  - View document: [FinalCGHtalk.ppt](#)

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## Welcome message



**natalia\_vinas** Dec 10, 2009 10:46 am

Welcome to the new MARG wiki site. Please feel free to post your comments/questions.

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re: Welcome message

**natalia\_vinas** just now

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Illustration:  
Example from MARG  
member array projects

# Technical Challenges



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# Sample type

- Which is the best sample type for a clinical trial project of blood expression profiles
- Whole blood vs fractionated cell types
- Lymphoblastoid Cell lines

# PROS & CONS of different sample types for GEP

<b>Sample type</b>	<b>PROS</b>	<b>CONS</b>
<b>PAXgene</b>	easily accessible standardization of sample collection Multicenter clinical trials No complex procedure in sample collection No artificial activation of cells during cell fractionation cost effective	heterogeneous cell population interference of globins
<b>PBMC</b>	Homogenous cell population	labor intensive, expensive impractical at clinical sites Sample handling artifacts artificial induction of genes
<b>Buffy Coat</b>	easier to process than fractionating PBMCs	Sample handling artifacts artificial induction of genes impractical at clinical sites
<b>Cell Lines</b>	Homogenous cell population	Sample handling artifacts artificial induction of genes expensive Cell transformation effects on expressed genes

# Preparation of labeled targets

- Interference of Globins in whole blood samples
- Input RNA
- cDNA vs cRNA amplification

# QC samples

- Use of MAQC A and B
  - for data normalization
  - to correct for batch to batch variation
  - correct for reagent lot to lot variation

# Feedback

- Specifics from researchers can be posted
- Follow up discussions
- Possible conclusions