

Welcome



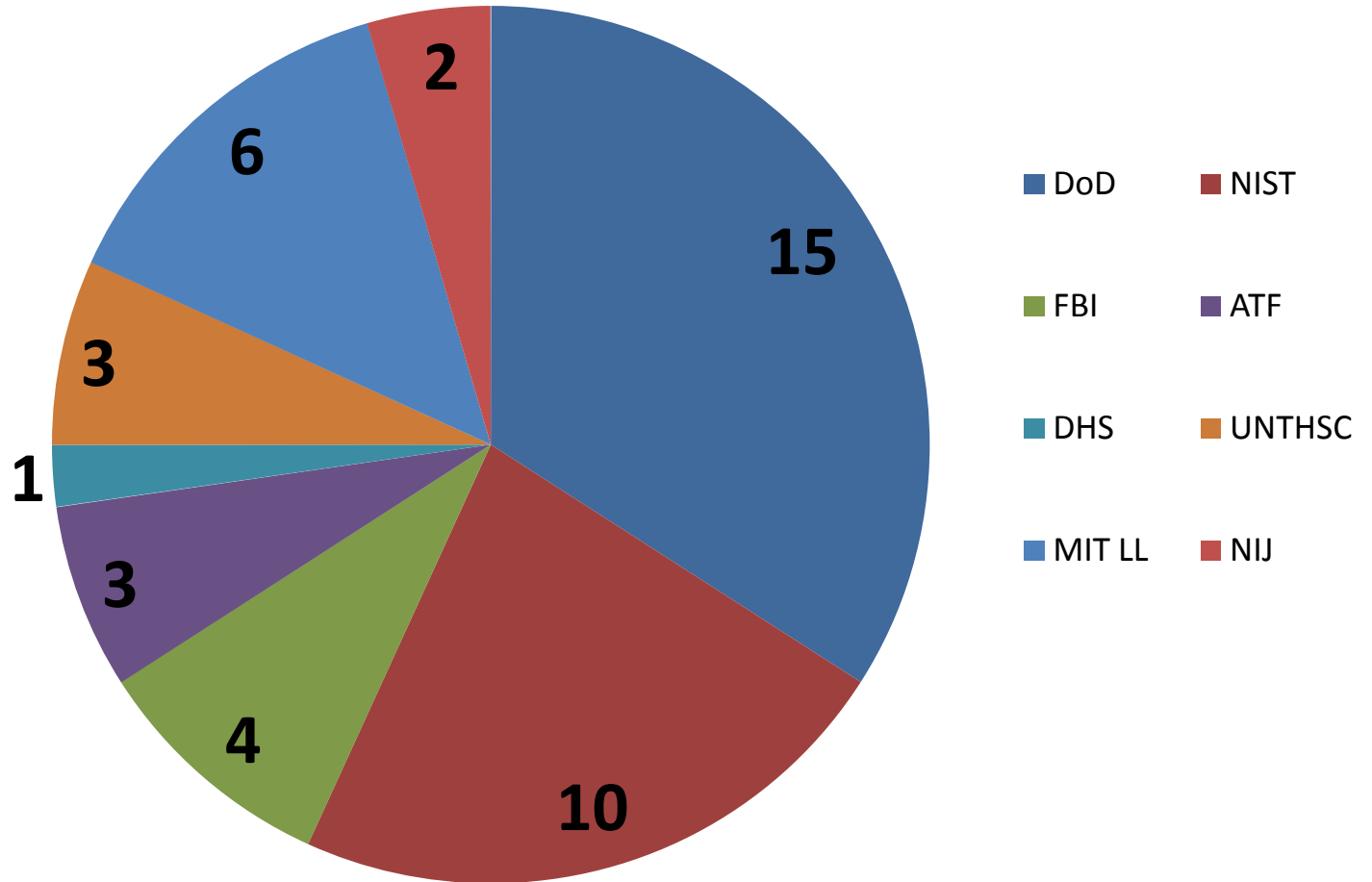
**Interagency Workshop on the use of  
Next-Generation DNA Sequencing for  
Human Identification and Characterization**

**January 31, 2012**

# Agenda

<b>8:30 am</b>	<b>Arrival and Coffee</b>	<b>Room B208</b>
<b>9:00 am</b>	<b>Welcome, Workshop Objectives</b>	<b>Mr. Kroupa</b>
<b>9:15 am</b>	<b>DNA Sequencing Technologies and their Application to Human ID and Forensics</b>	<b>NIST/MIT-Lincoln Lab</b>
<b>10:45 am</b>	<b>Break</b>	
<b>11:00 am</b>	<b>DNA Sequencing Technologies and their Application to Human ID and Forensics</b>	<b>NIST/MIT-Lincoln Lab</b>
<b>12:00 pm</b>	<b>Lunch</b>	<b>Room B208</b>
<b>1:00 pm</b>	<b>Presentations from Additional Agencies</b>	<b>AFDIL (R. Just), ATF (T. Bille), others</b>
<b>1:30 pm</b>	<b>Discussion</b>	
<b>3:00 pm</b>	<b>Adjourn</b>	

# Attendees



## Points of discussion

- The **range of applications** that are envisioned for human DNA sequencing within your organization
- **Technical considerations/limitations** for application of Next-Generations sequencing to your problems that may be unique to your organization
- Your **programmatic plans** for developing and implementing this technology including **past and current investments** as well as timelines for making future investments
- **Policy implications** that you anticipate from the expansion of human DNA analysis for your intended applications
- Plans and/or issues associated with human genomic **data archiving, analysis, and curation.**
- Your organization's position on the **privacy and security issues** related to your envisioned use of human genomic sequence information and your vision and approach for addressing these issues

# Sequencing, Finishing, and Analysis in the Future (SFAF)

La Fonda on the Plaza, Santa Fe, NM — May 30<sup>th</sup> - June 1<sup>st</sup>, 2012

## Call for Abstracts (both talks and posters) Deadline March 30<sup>th</sup>, 2012

Please join us for the 7<sup>th</sup> annual "Sequencing, Finishing and Analysis in the Future" Meeting on Wednesday, May 30<sup>th</sup> through June 1<sup>st</sup> in beautiful, historic Santa Fe, New Mexico. The three day SFAF conference will focus on Next Generation Sequencing technologies, applications, and their effect on the rapidly advancing field of Genomics.

### Keynote Speakers:

- Rita Colwell, Ph.D., Distinguished Professor, University of Maryland & Johns Hopkins University
- Paul Keim, Ph.D., Regents' Professor of Biology, Northern Arizona University
- Pavel Pevzner, Ph.D., Ronald R. Taylor Chair Professor of Computer Science, UC San Diego

### Areas to be emphasized include, but are not limited to the following:

#### Genome Sequencing:

- New sequencing technologies (454, illumina, SOLiD, Ion Torrent, MiSeq, PacBio, etc.)
- Draft sequencing strategies (prokaryotes, eukaryotes, metagenomics, single cell, etc.)
- *De novo* sequencing, re-sequencing, Human seq., RNA seq., metagenomics, etc.



#### Genome Assembly:

- Whole genome assemblers and integration of next generation data
- *De novo* assemblers for short reads, hybrid assemblers
- Recalling and calibrating genome assemblies
- Single cell and metagenomic assemblies



#### Genome Finishing:

- Finishing systems and pipelines (automated, manual, etc.)
- Next generation finishing tools and technologies
- Human Genomics and genome improvement
- Quality standards for new technologies and mixed data sets
- Single cell / cell sorting and metagenomic finishing

#### Genome Analysis:

- Genome annotation and pathway identification tools and pipelines
- Comparative genomics, re-sequencing, SNPs, structural variation
- Large scale data management, cloud computing
- Metagenomic analysis

The conference is being sponsored and hosted by the DOE's Los Alamos National Laboratory and NO registration fee is required. Participants need to cover travel costs, hotel and dinner charges. Breakfast, lunch and snacks will be provided. A block of rooms are reserved at the La Fonda at a special conference rate of \$83 per night. A limited number of extra rooms are available before & after the conference for those that want to stay in the area a little longer (contact Chris Detter for more details).

Registration is limited to 150; please register soon if you plan to attend. **To register, submit an abstract, or obtain more information as it becomes available please visit our web site, <http://www.lanl.gov/finishinginthefuture/>. Registration will follow the same guidelines as in 2011 (see website for meeting information updates).**

**If you have any questions, or would like further information, please contact Chris Detter at (505)667-1326 or [cdetter@lanl.gov](mailto:cdetter@lanl.gov).**

We look forward to seeing you there!!!

The 2012 "Sequencing, Finishing and Analysis in the Future" Organizing Committee:



- \* Chris Detter, Ph.D., JGI- LANL, Genomics Center Director, LANL
- \* Johar Ali, Ph.D., Cancer Genomics Team Leader, OICR
- \* Patrick Chain, Metagenomics Team Leader, LANL
- \* Michael FitzGerald, Finishing Manager, Broad Institute
- \* Bob Fulton, M.S., Sequence Improvement Group Leader, WashU
- \* Darren Grafham, Team Leader Illumina Bespoke Team, Sanger Institute
- \* Alla Lapidus, Ph.D., Director Bioinformatics, IPM, FCCC
- \* Donna Muzny, M.S., Director of Operations, BCM
- \* Yu-Hui Rogers, VP Core Technology Development, JCVI

