



Association of Biomolecular Resource Facilities

Proteome Informatics Research Group (iPRG)

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**iPRG-2015 Proteome Informatics Research Group Study:
Differential Abundance Analysis in Label-Free Quantitative Proteomics**

Dear Potential Study Participant,

Label-free quantitation methods are commonly used in proteomics when isotopic or chemical labels are unavailable, not feasible, or prohibitively expensive. With rapid advancements in instrumentation, techniques such as spectral counting and intensity-based approaches are becoming increasingly utilized in everyday quantitative proteomics activities.

The Proteome Informatics Research Group (iPRG) of the Association of Biomolecular Resource Facilities (ABRF) invites you to participate in a collaborative data analysis study to evaluate software and statistical methods for label-free quantitation. Participants will be asked to detect proteins that exhibit significant differences in abundance in a yeast whole-cell lysate and report protein abundance ratios between pairs of four samples, each represented by three technical replicates, analysed by a quadrupole-orbitrap mass spectrometer. The study will primarily focus on post-identification processing steps, such as filtering false positives, computing the quantitative metrics, assembling peptide-level information to estimate protein abundance ratios, and statistical assessment. Accordingly, peptide identifications and associated peak areas will be provided as starting points of analyses. However, raw data files will also be made available, thereby affording options suitable for the preferences and level of experience of the participant. Guidance will be available for a number of the processing steps to assist those who are new to label-free quantitation. The overall goal of the study is to provide participants with a well-characterized dataset that can be used to test or explore methods for label-free quantitation. An added outcome will be identification of a number of "best practices" for label-free quantitation that can inform and guide the efforts of practitioners (new and experienced) in the fields of proteomics and bioinformatics.

To participate in this study, please go to:

<http://www.abrf.org/index.cfm/group.show/ProteomicsInformaticsResearchGroup.53.htm>

where detailed instructions will be provided on where to obtain the data and how to complete the analysis. Results must be returned by **January 31, 2015** in order to provide sufficient time for iPRG to evaluate the findings and prepare a presentation for the 2015 ABRF Meeting, March 28-31 in St. Louis, Missouri.

This study is open to both ABRF members and non-members. However, we do strongly encourage non-members to join and help support the ABRF. For more information, visit <http://www.abrf.org>.

We thank you for your support of the ABRF and look forward to your participation in this year's study.

Sincerely,

The ABRF Proteome Informatics Research Group (iPRG)

Eugene Kapp – Walter and Eliza Hall Institute of Medical Research (Co-chair)

Henry Lam – Hong Kong University of Science and Technology (Co-chair)

Brett Phinney – UC Davis (ABRF Executive Board Liaison)

John Cottrell – Matrix Science Ltd

Michael Hoopmann – Institute for Systems Biology

Sangtae Kim – Pacific Northwest National Laboratory

Thomas Neubert – New York University

Magnus Palmblad – Leiden University Medical Center

Olga Vitek – Northeastern University

Sue Weintraub – University of Texas Health Science Center at San Antonio