TABLE OF CONTENTS

PROTEOMICS WORKFLOW OVERVIEW .................................................................2
PROTEOMICS LIMS WORKFLOW .................................................................4
PROTEOMICS WORKFLOW OVERVIEW

Figure 1.0 illustrates proteomic workflow in Dr. Yeung’s laboratory in Fox Chase Cancer Center.

Figure 1.0 – Proteomic workflow: FCCC
Figure 2.0 illustrates proteomic workflow in Dr. Androlewicz’s laboratory in H. Lee Moffitt Cancer Center and Research Institute.

**Figure 2.0 – Proteomic workflow: Moffitt CC&RI**
**PROTEOMICS LIMS WORKFLOW**

The ProtLIMS workflow, Figure 3.0, illustrates sample and data flow for FCCC proteomic workflow.

*Figure 3.0 – Protlims workflow for FCCC*

**Raw sample – Generic sample:** Each raw sample can be processed into several different samples. Several samples can be mixed into one.

**Generic sample – 2D gel:** Several gels can be run from one sample.

**2D gel – Gel image:** Several images can be taken for each gel.

**Gel image – Reference gel image:** Several images can be combined into one reference gel image. Each gel image can be used in more than one reference image.

**Reference gel image – Gel spot:** Gel spots store coordinates and other properties of gel spots on gel image. In our workflow reference gel image is used to measure spot properties, but it’s also possible to use simple gel image as source of gel spots. These properties are obtained by gel analysis software. In FCCC workflow it’s Progenesis software.

**Gel spot – Gel plug:** Gel spot stores coordinates of a spot on gel image (and it means coordinates on gel as well). Gel plug is cut from gel; coordinates for the cut are determined by assigned gel spot(s). A pick list file can be associated with this step to link the physical spots with their upstream analysis information. Several gel spots can be cut into one gel plug; one gel spot can be cut as several gel plugs. Many-to-many relationships between gel spots and gel plugs are demanded by manual adjustments laboratory personnel make before actual plug cut.
The ProtLIMS workflow, Figure 4.0, illustrates sample and data flow for Moffitt center proteomic workflow.

**Figure 4.0 – Protlims workflow for Moffitt**

**Raw sample – Generic sample:** Each raw sample can be processed into several different samples. Several samples can be mixed into one.

**Generic sample – 2D gel:** Differently labeled samples are used to run one gel.

**2D gel – stained 2D gel:** Gel is stained with SYPRO Ruby dye

**2D gel – Gel image:** One image is taken for each dye (Cy2, Cy3, Cy5, SYPRO Ruby).

**Gel image – Reference map:** Reference map is analogue of reference gel image form FCCC workflow. Several images can be combined into one reference map.

**Reference gel image – Gel spot:** Gel spots store coordinates and other properties of gel spots on gel image. These properties are obtained by gel analysis software. In Moffitt workflow it’s DeCyder software.

**Gel spot – Gel plug:** Gel spot stores coordinates of a spot on gel image (and it means coordinates on gel as well). Gel plug is cut from gel; coordinates for the cut are determined by assigned gel spot(s). A pick list file can be associated with this step to link the physical spots with their upstream analysis information. Each gel plug is linked with only one gel spot.