

# Advancing analysis beyond the scope of traditional Western Blot at the University of Lausanne

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Séverine Lorrain, PhD

# Unil.

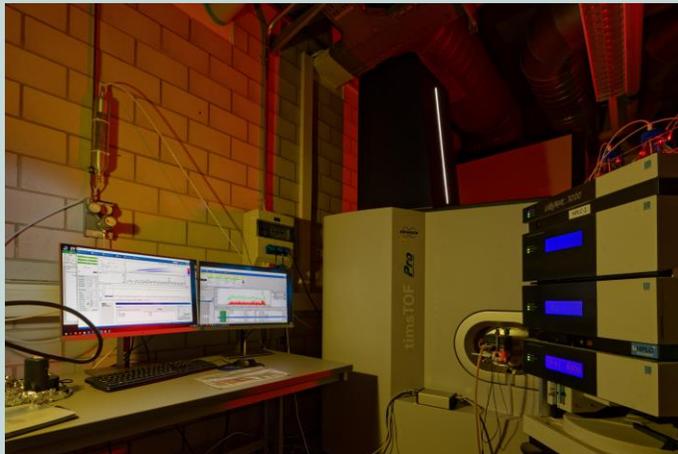
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and medicine**  
Protein Analysis  
Facility

# The Protein Analysis Facility

A core facility supporting the local community in the analysis of single proteins and complex proteomes

## MASS SPECTROMETRY

- Protein identification
- Protein quantification (label-free, isobaric/metabolic labelling)
- Analysis of post-translational modifications



## ANTIBODY-BASED PLATFORMS

Targeted quantification of proteins using antibodies



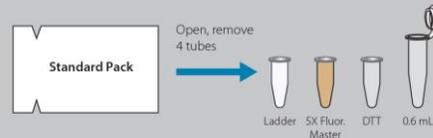
# Simple Western

An automated western blot in capillaries  
Courtesy of Helen Hall, 2023 Bio-Techne®

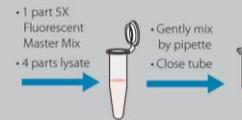
30-45 min

## 1. Prepare your reagents

### A PREPARE STANDARD PACK REAGENTS



### B PREPARE YOUR SAMPLES



### C DENATURE YOUR SAMPLES AND BIOTINYLATED LADDER



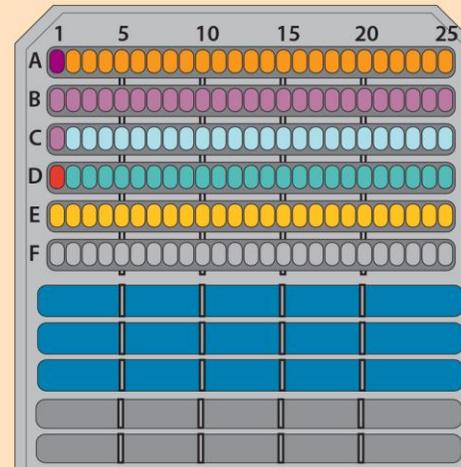
### D PREPARE REAGENTS FROM DETECTION MODULE



## Things you already do

- Pipette
- Mix
- Heat

## 2. Pipette your plate



Evaporation sensitive

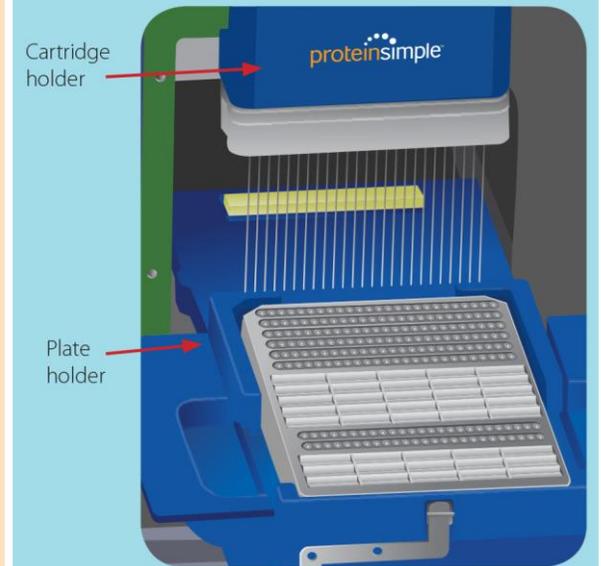
Peel off immediately before placing in instrument

## Things you already use

- Ladder
- Samples
- Ab diluent
- Primary Ab
- Secondary Ab
- Substrate

## 3. Start Abby / Jess

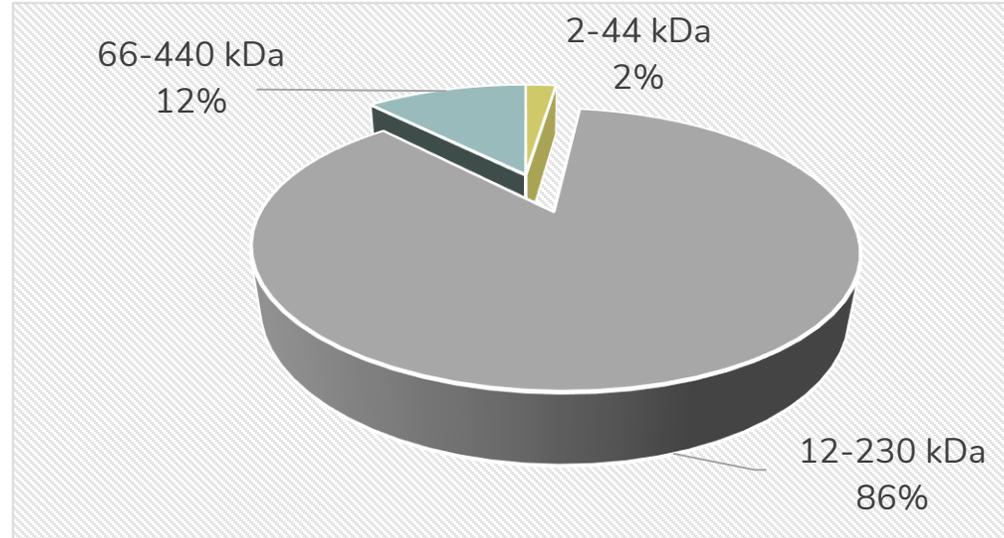
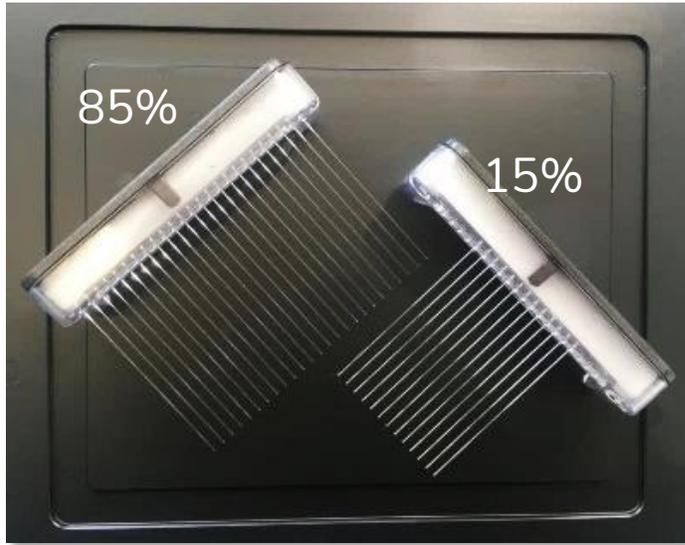
3h



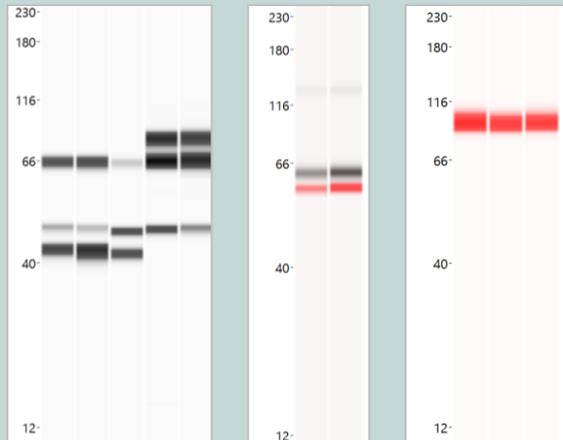
## Magic happens in the capillary

- Separate
- Immobilize
- Probe
- Detect

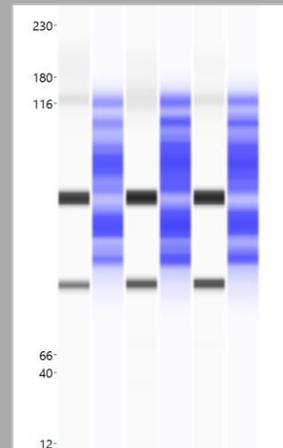




Chemiluminescence (1-4 antibodies)  
Fluorescence (mostly Near Infra Red)



RePlex 20 %  
Total protein Normalisation 15%

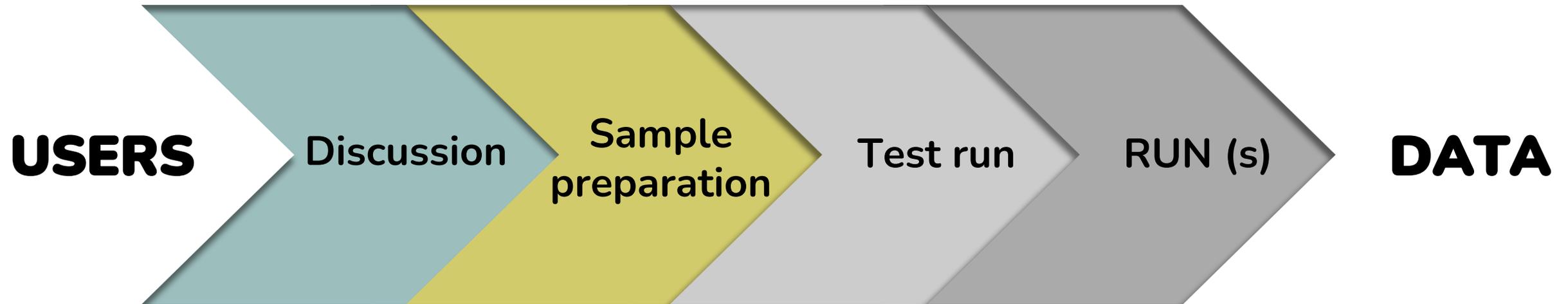


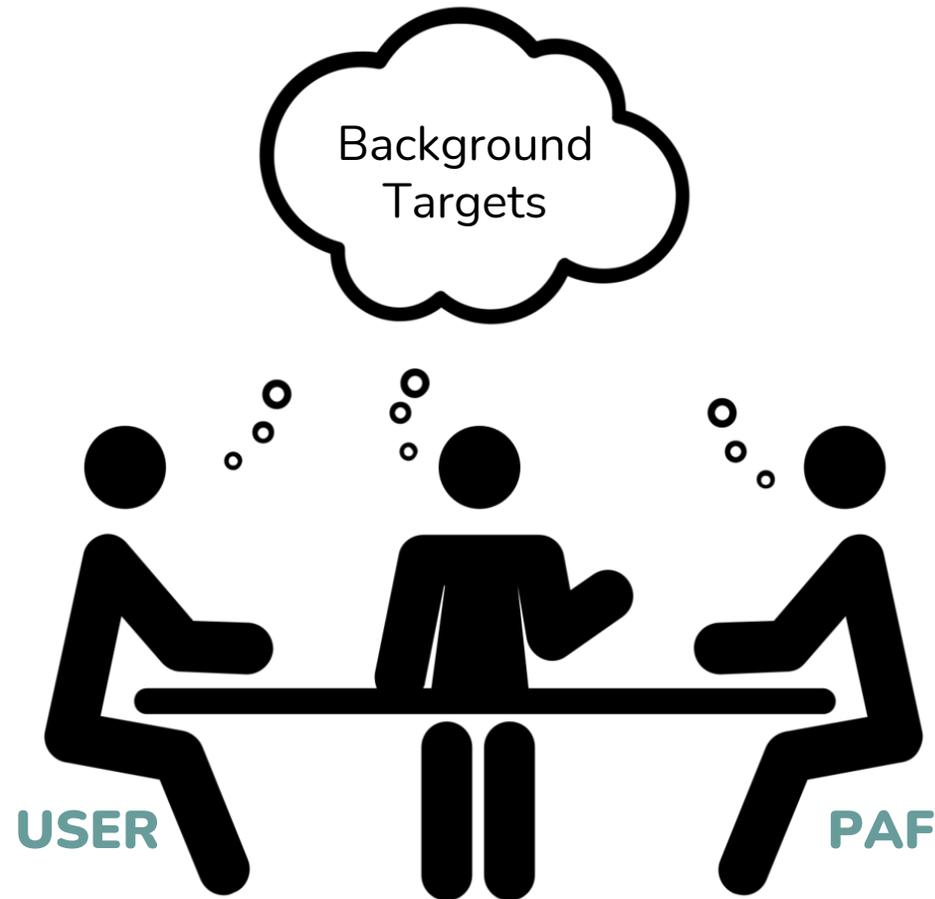
# Unil.

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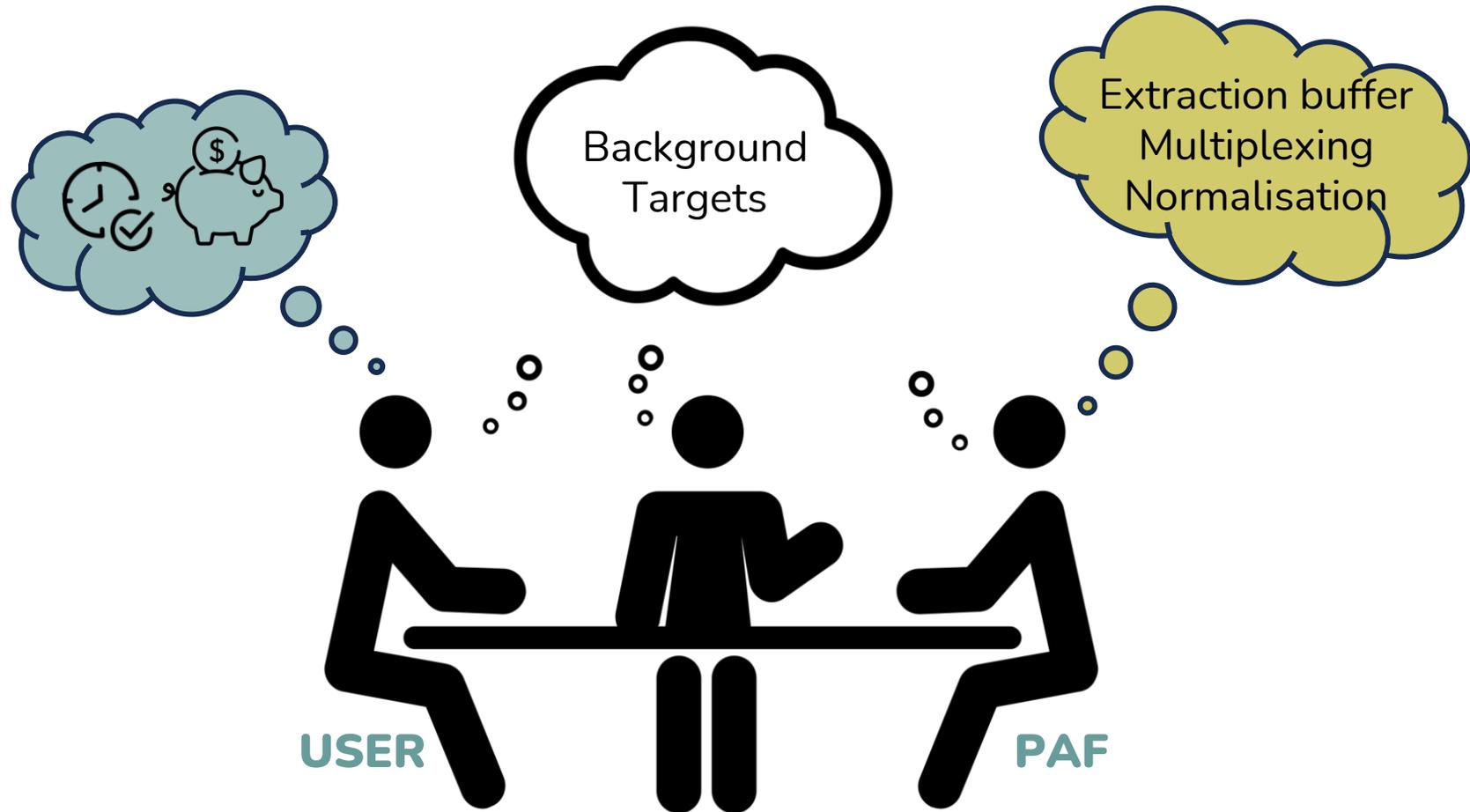
# How do we proceed

To avoid common pitfalls





- No experience in western blot
- Need quantitative data
- Many samples
- Low protein amount



Sample  
prep.

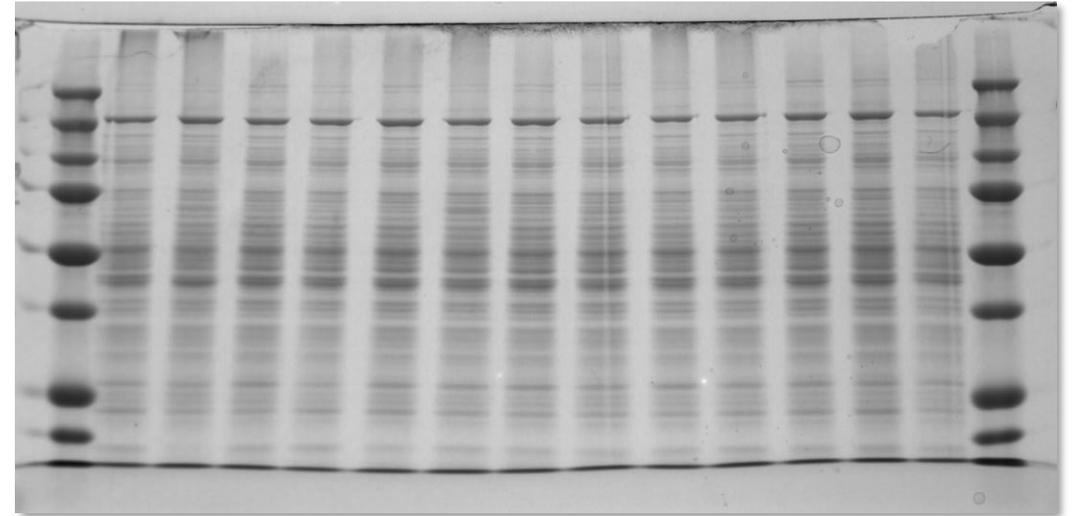
Protein extracts



Extraction



- ∅ Quantification (tryptophan fluorescence)
- ∅ Normalisation of loading amount
- ∅ Quality control (Coomasie staining)

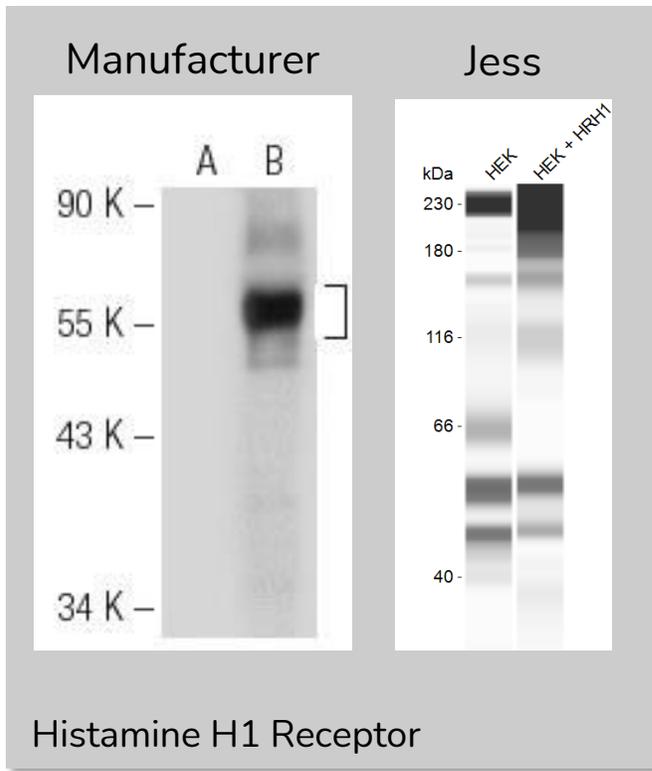


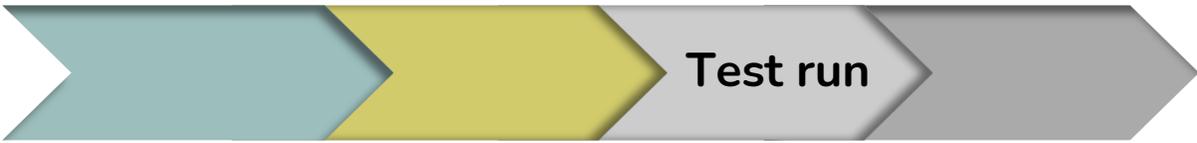
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# Test run

## 1. Antibody validation



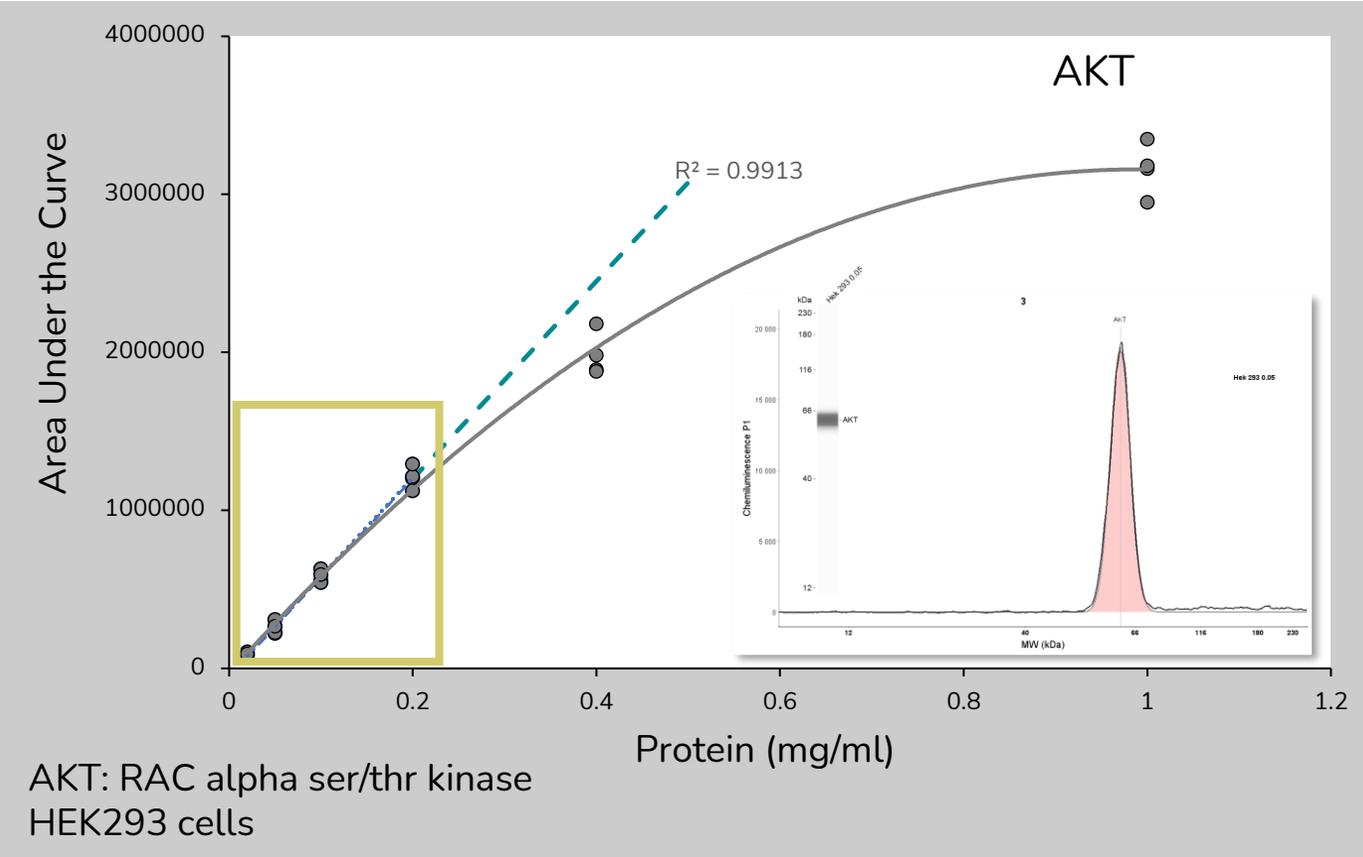


- Quick
- Flexible
- Reproductive
- Quantitative

### 1. Antibody validation



### 2. Antibody linear range





- Quick
- Flexible
- Reproductive
- Quantitative

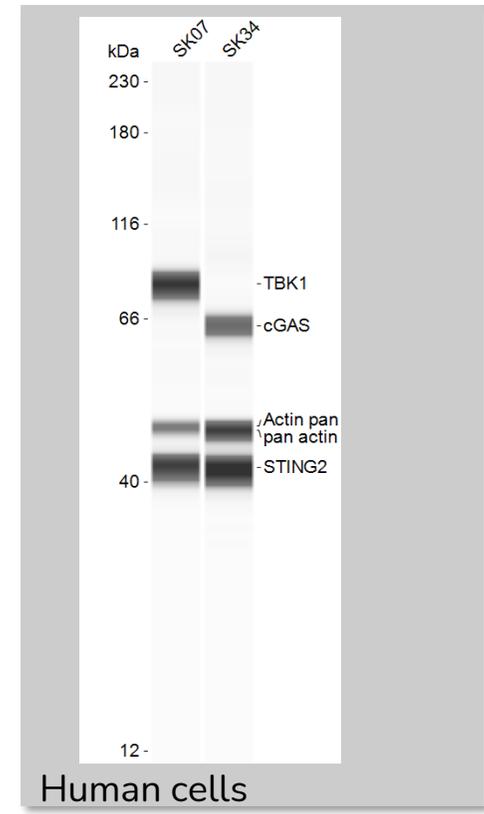
### 1. Antibody validation

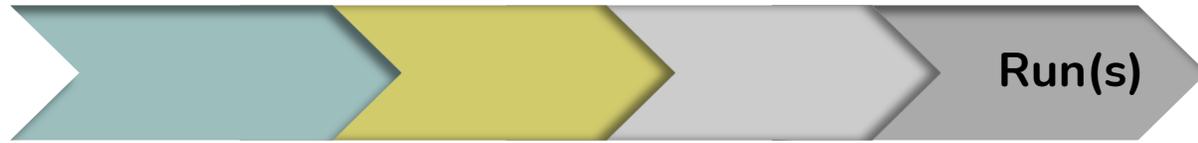


### 2. Antibody linear range

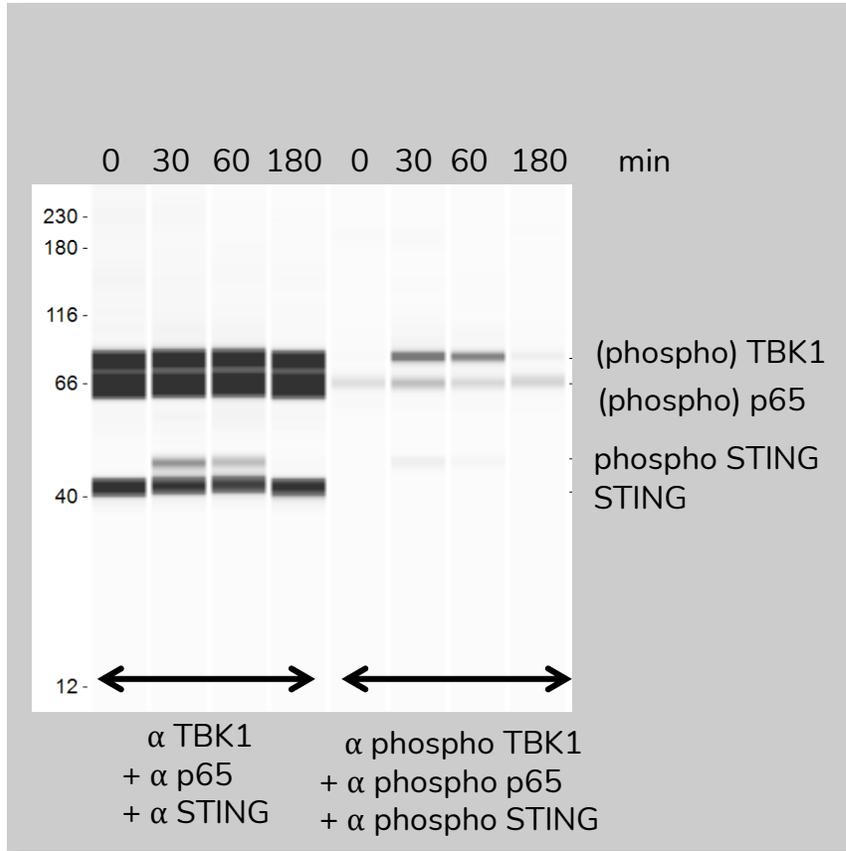


### 3. Multiplexing 3-4 antibodies

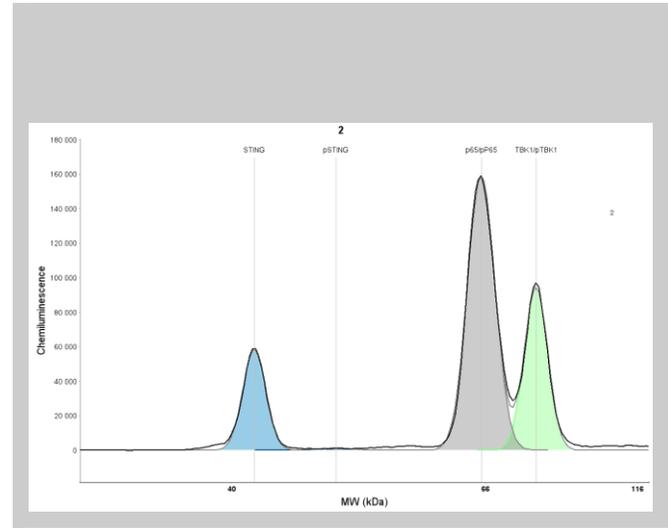




### Run

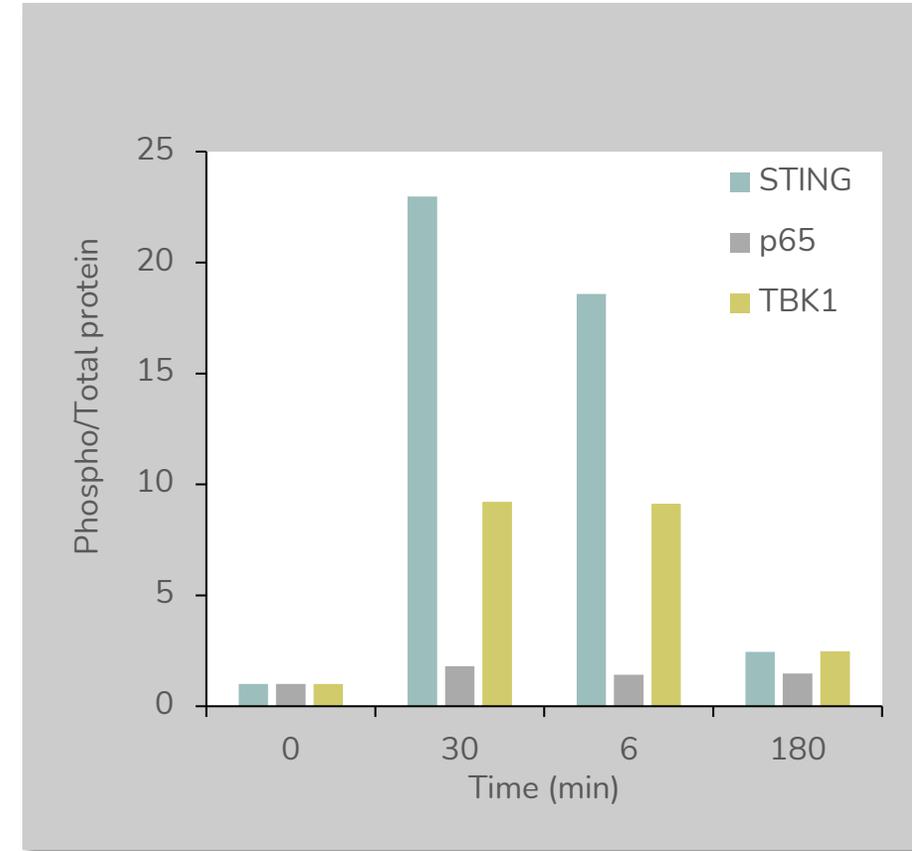


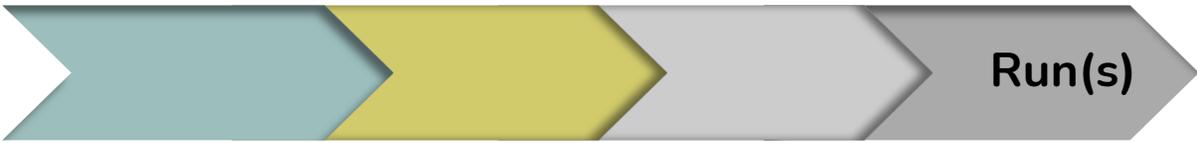
### Area Under the Curve



STING: Stimulator of Interferon Gene  
 p65: transcription factor  
 TBK1: serine/threonine protein kinase  
 Human cells

### Quantification

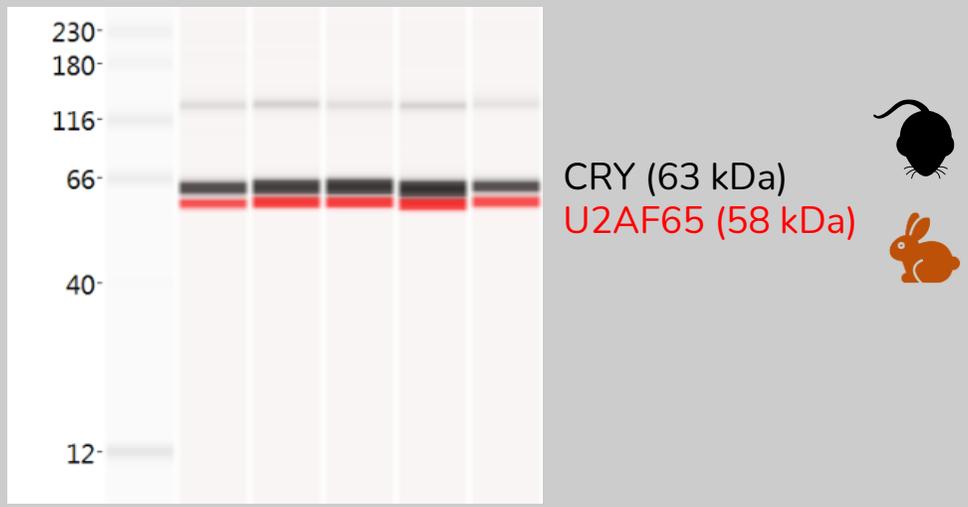




# Dealing with proteins of different intensity

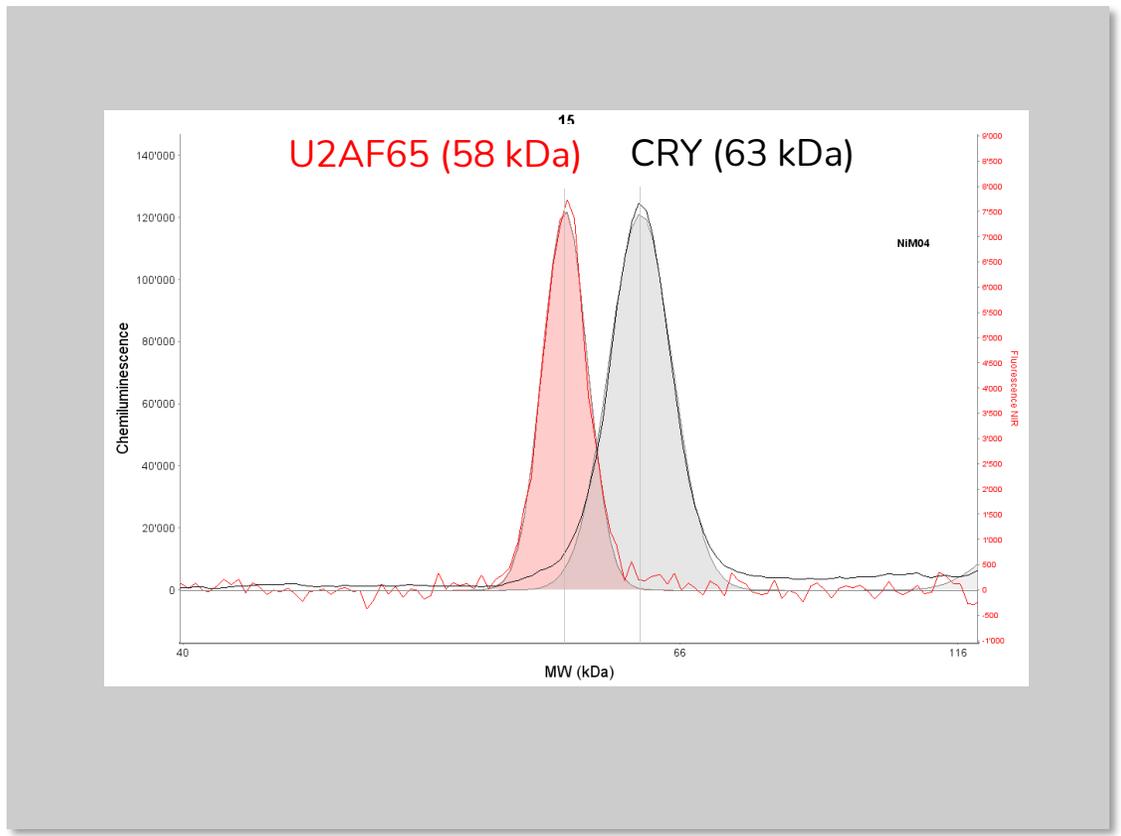
## Combining detection mode

Chemiluminescence for high sensitivity  
Near Infra Red for abundant proteins

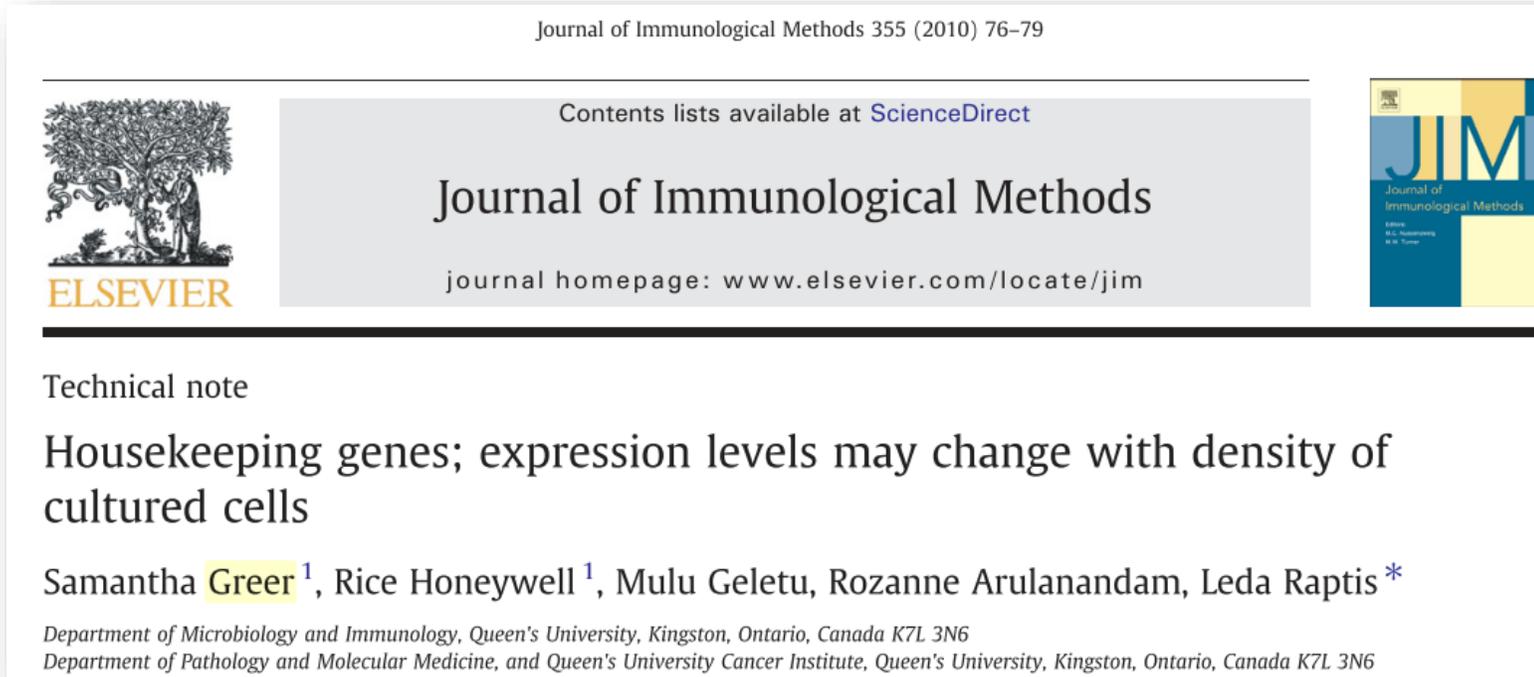


CRY: cryptochrome  
U2AF65: splicing factor, nuclear marker  
Mouse cells

## Area Under the Curve







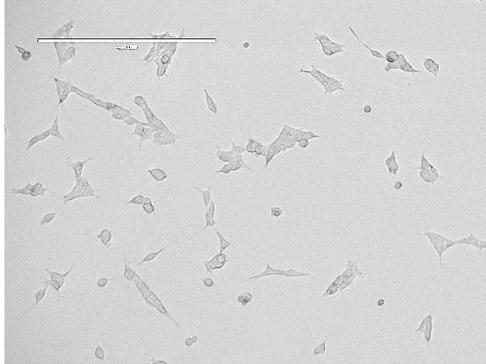
«Cell confluence significantly affects the levels of  $\alpha$ -tubulin and Glyceraldehyde-3-Phosphate Dehydrogenase (...)

Levels of **heat-shock protein-90** ( $\alpha$  and  $\beta$ ) and  **$\beta$ -actin** remained unchanged at a wide range of cell densities»

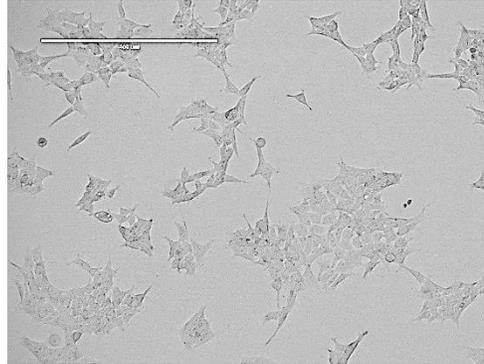
# Total *versus* house-keeping proteins

Sample selection

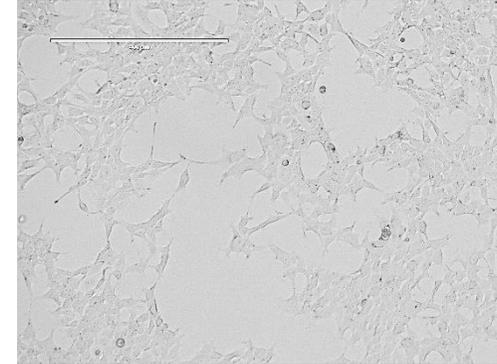
CONF1



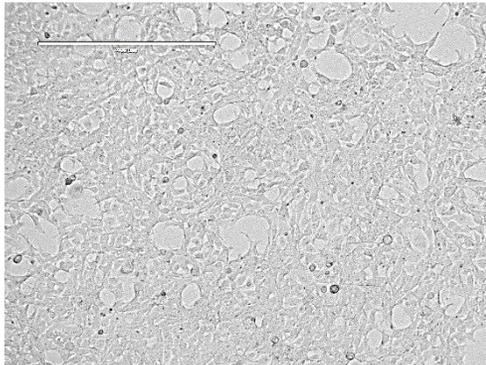
CONF3



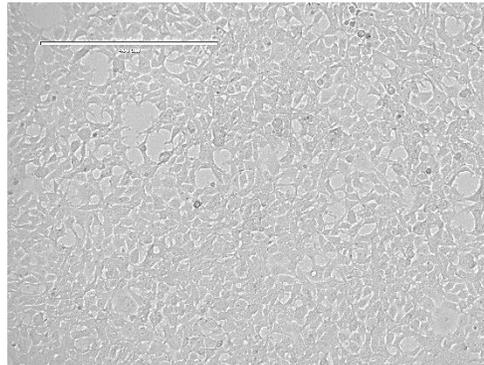
CONF5



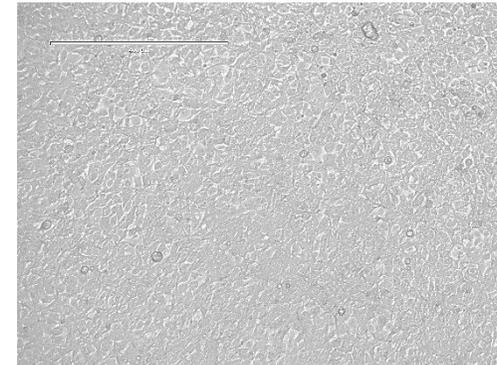
CONF6



CONF7



CONF8



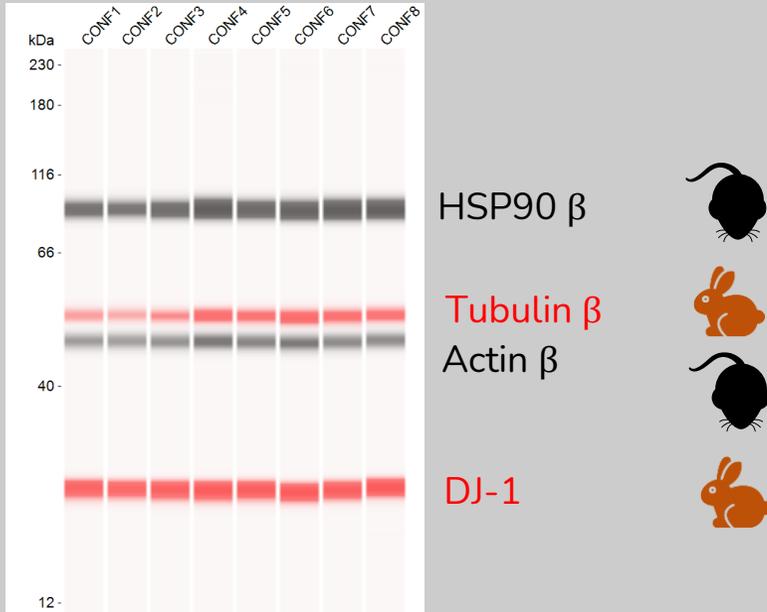
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# Total *versus* house-keeping proteins

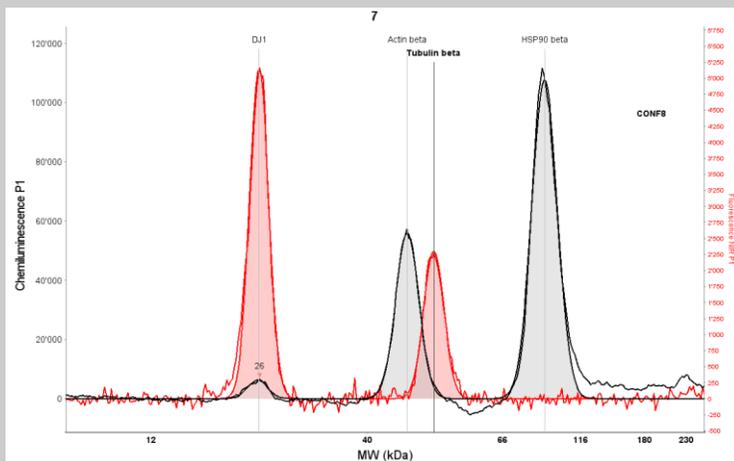
Multiplex and strip and reprobe with RePlex

## Probe 1 : antibodies



## Procedure

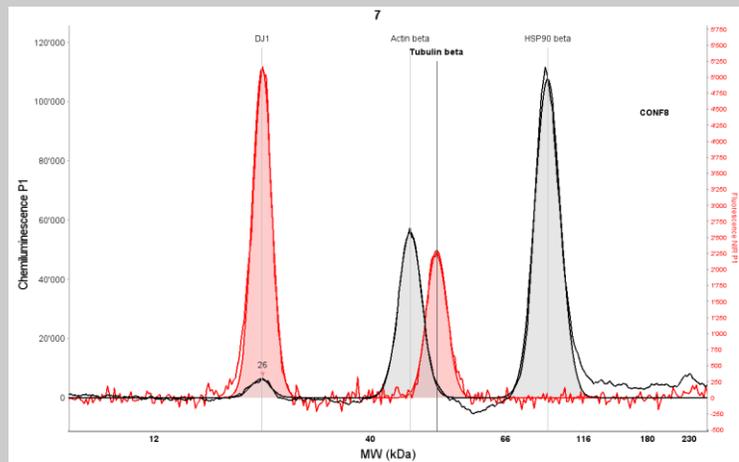
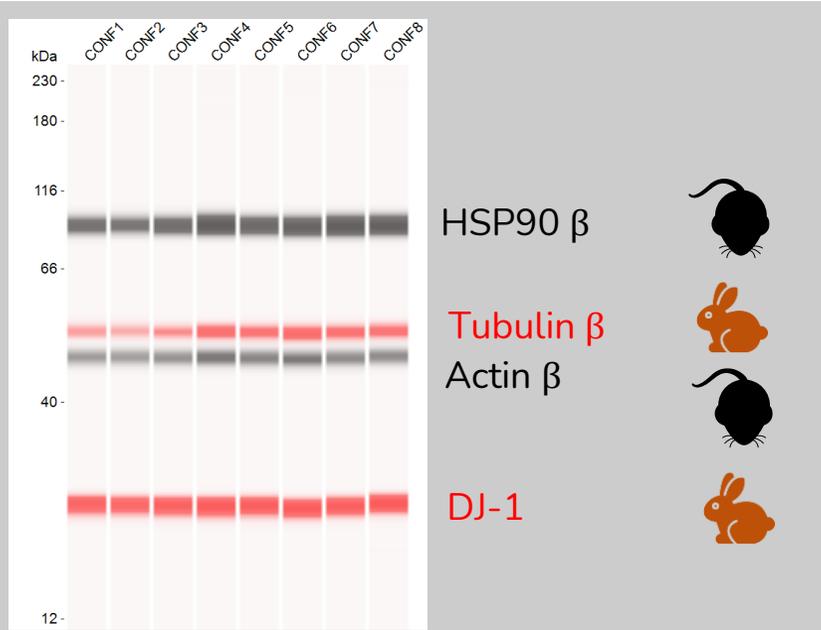
- ✓ Antibodies specificity
- ✓ Linear range for each antibody
- ✓ Choice of detection mode (chemi *versus* Near Infra Red)
- ✓ Multiplexing



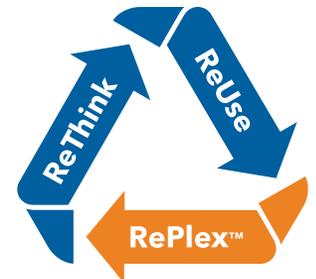
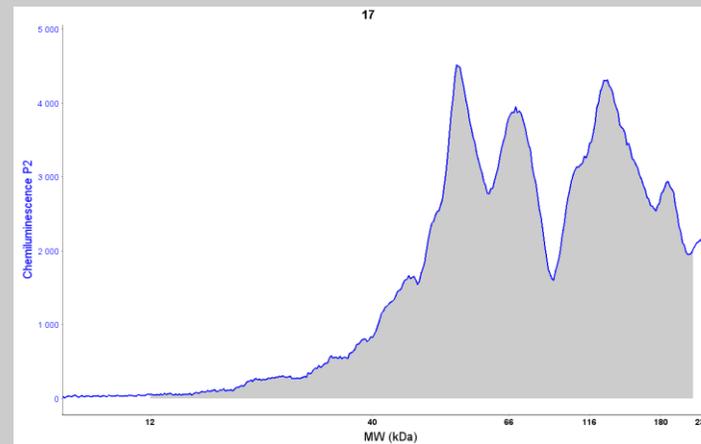
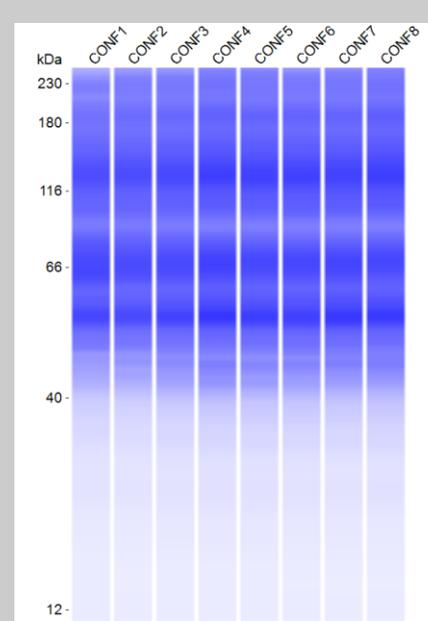
# Total *versus* house-keeping proteins

Multiplex and strip and reprobe with RePlex

## Probe 1 : antibodies

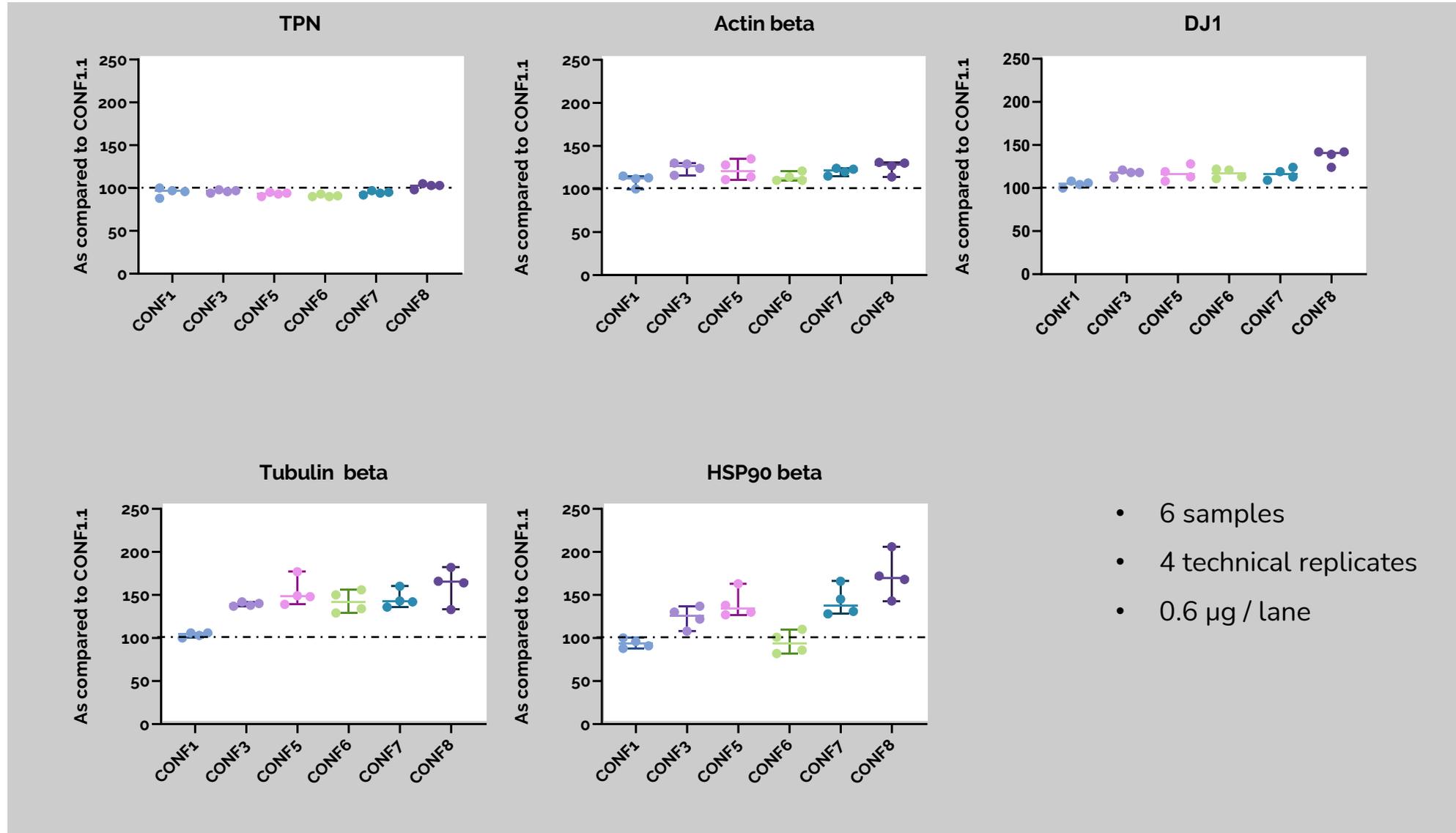


## Probe 2 : total protein detection



# Total *versus* house-keeping proteins

«House-keeping» protein signal depends on cell density



- 6 samples
- 4 technical replicates
- 0.6  $\mu\text{g}$  / lane

**USER**

Discussion

Sample prep.

Test run

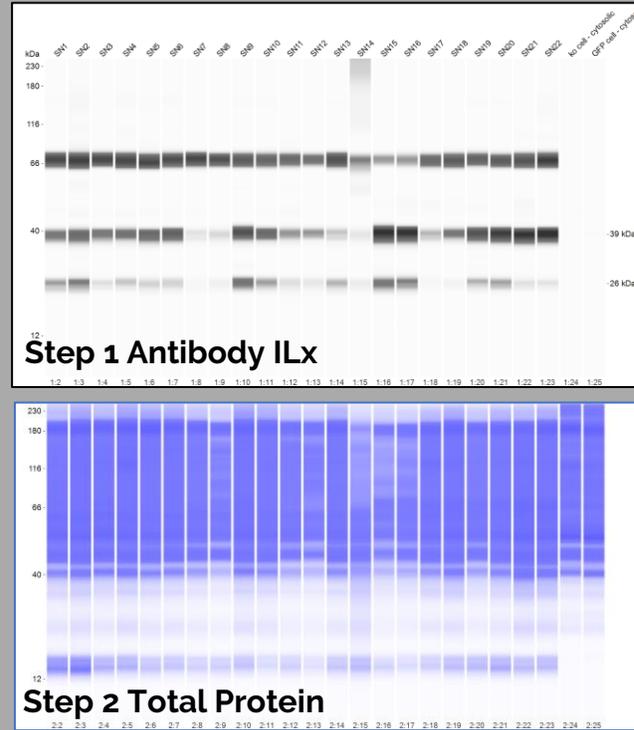
Run(s)

**DATA**

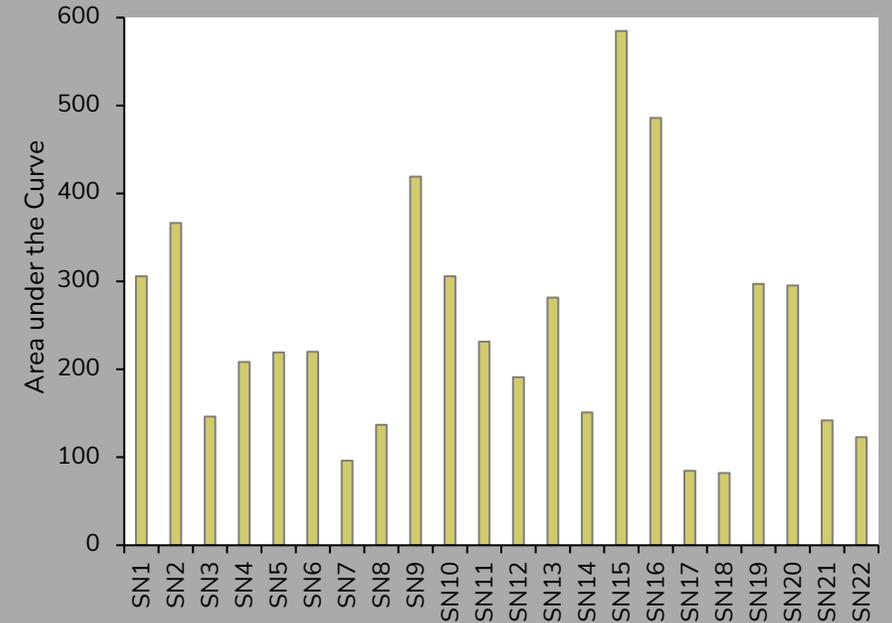
A representative run

- 24 samples
- 3  $\mu$ l sample
- 0.6  $\mu$ g / lane (often less)

- 30-45 min plate preparation
- 3h / 6 h (Replex) fully-automated run
- 3 runs / 24 hours
- Reproducible



ILx normalised to Total Proteins



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# Challenging Jess with low cell numbers

FAC sorted cells

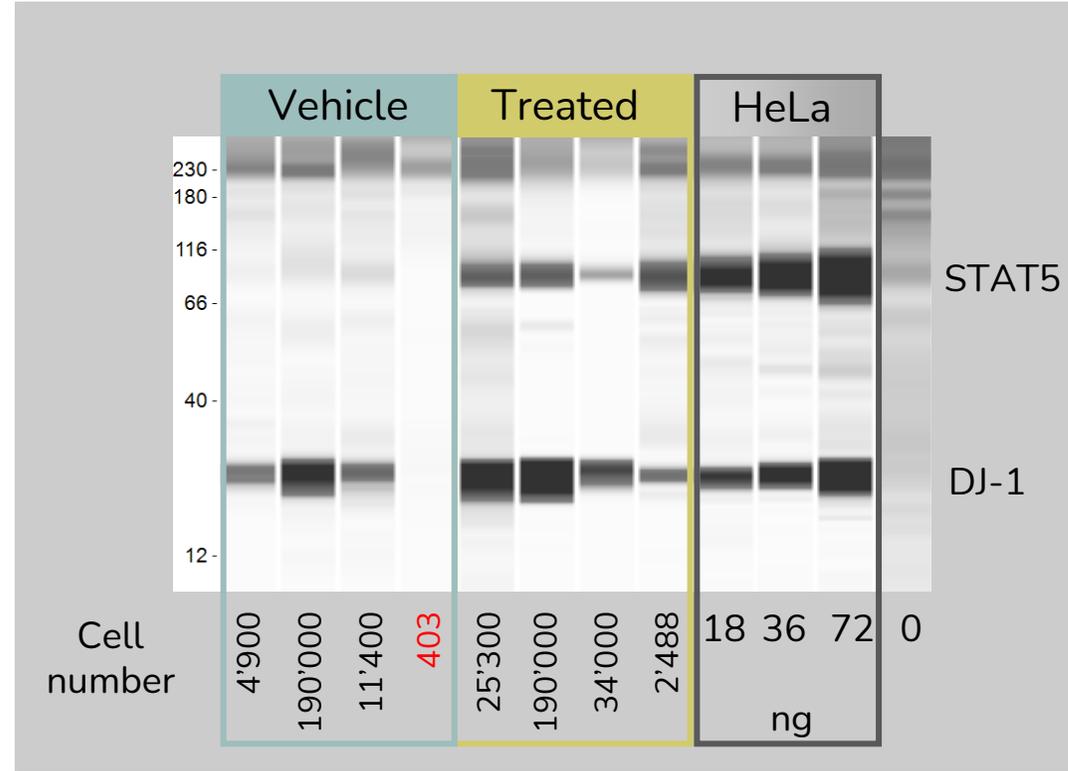


- Few cells: 400 – 200'000
- <15 µl protein sample
- Low protein /unknown concentration

**One shot experiment !**



- 3 µl protein
- Multiplex



Strongly dependant on target proteins **AND** antibody quality

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# Thank you for your attention!

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