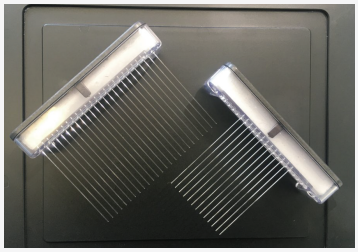
Jess™ : high troughput capillary western

UNIL | Université de Lausanne

PROTEIN ANALYSIS FACILITY

All steps of traditional western blotting are fully automated inside capillaries



- 12 or 24 independant samples/run
- Different antibodies in the same run
- 72 samples in 24h on one or more targets
- Separation 2-44 kDa
  12-230 kDa
  66-440 kDa

Regular run

3h

Load matrix and samples

Separate and immobilize

Antibody 1 immunoprobe

Detect and quantify target 1

RePlex run

5h30

If desired, a second run could be performed within the same capillary.

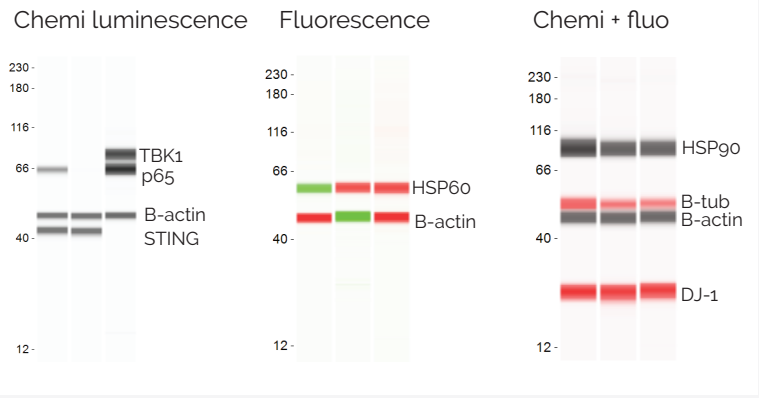
Remove antibody from 1st immunoprobe

Antibody 2 immunoprobe (or Total Protein Assay)

Detect and quantify target 2

Adapted from ProteinSimple

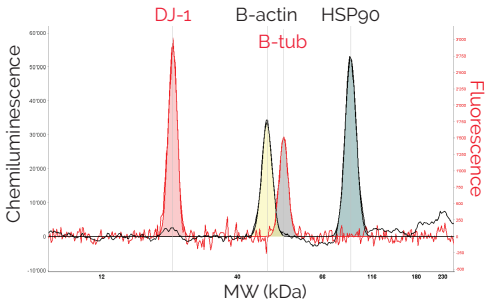
3 detection modes for multiplexing



Accurate quantification

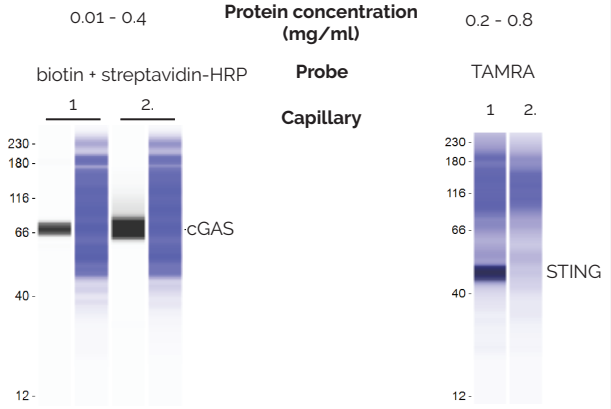
Area under the curve for precise and relative quantification.

Intra-run CV <10%
Inter-run CV < 20%



Total protein normalisation

More reliably than housekeeping proteins, data can be normalized to total proteins loaded into the capillary.



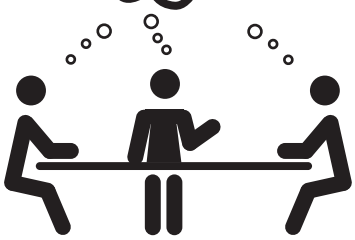
For low protein concentrations, target proteins are detected in step 1 and total proteins in step 2 of a RePlex run.

For more concentrated samples, total proteins are detected by TAMRA together with target proteins.

How to proceed

1 Discussion

Background, samples, antibodies



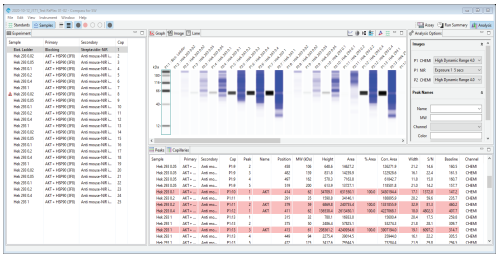
2 Test run

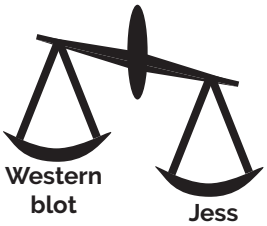
- 15 µg protein
- 5 µl antibody

→ Linear range
Antibodies saturating conditions
Multiplexing
Normalisation

3 Run (s)

Raw file
Analysis





- Fast
- Flexible
- Accurate
- Quantitative
- Reproducible
- Less material and antibodies