

Quality  
and Quantity  
Assessment  
of Nucleic  
Acids and  
Proteins

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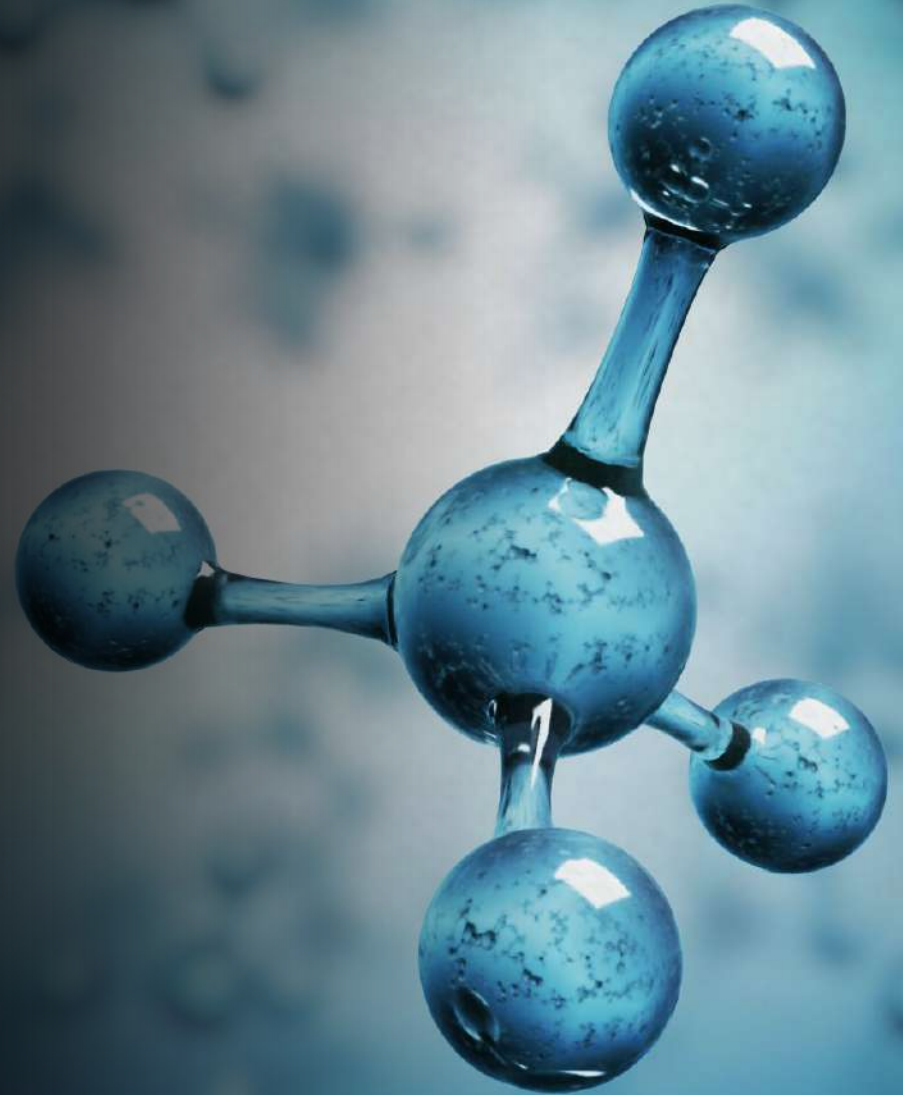
*Assoc. Prof. Dr. Ilker BUYUK*

Quantification of  
nucleic acids

Quality  
assessment of  
nucleic acids

Quantification of  
proteins

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The amount and quality of molecules (nucleic acids or proteins):

Reproducibility

Accuracy

Efficiency

# Quantification of Nucleic Acids

Three quantification methods in common use:

- Spectrophotometric measurement (UV spectrometry)
- Fluorescent dye (Fluorometry) based measurement
- Real-time amplification (Absolute quantification)

# Spectrophotometric Quantification

- Measurement of light intensity at different wavelengths
- *Transmittance*: the amount of light that passes completely through the sample
- *Absorbance*: measurement of light that is absorbed by the sample



# Spectrophotometric Quantification

Bases in RNA/DNA absorb UV at 250-265nm

Heterocyclic rings

Measurements at A260nm,  
A280nm, A230nm

Concentration estimation

# Spectrophotometric Quantification

- *A<sub>260nm</sub>*:
- Lambert-Beer Law:  $C_{\mu\text{g}/\mu\text{l}} = A \times \text{dilution factor} \times \epsilon$
- $\epsilon$ : molar extinction coefficient
  - physical constant
  - Unique
  - Amount of absorbance at 260nm of 1M nucleic acid solution measured in a 1cm path-length cuvette.

At a wavelength of 260 nm, the average **extinction coefficient** for double-stranded **DNA** is  $0.020 (\mu\text{g}/\text{ml})^{-1}\text{cm}^{-1}$ , for single-stranded **DNA** it is  $0.027 (\mu\text{g}/\text{ml})^{-1} \text{cm}^{-1}$ , for single-stranded RNA it is  $0.025 (\mu\text{g}/\text{ml})^{-1} \text{cm}^{-1}$  and for short single-stranded oligonucleotides it is dependent on the length and base composition.

# Spectrophotometric Quantification

- A230 and A280 readings
  - A260/A280
  - A260/A230
- A260: DNA/RNA, Guanidine isothiocyanate
- A270: Phenol, TRIzol
- A280: Proteins
- A230: Phenol, TRIzol, Guanidine HCL



# Spectrophotometric Quantification

A260/A280: ~1.8 for DNA, ~2.0 for RNA

## **Low A260/A280 ratio**

- Residual phenol or other reagent associated with the extraction protocol
- A very low concentration (> 10 ng/ul) of nucleic acid

## **High 260/280 ratio**

- RNA/DNA contamination

# Spectrophotometric Quantification

- $A_{260}/A_{230nm}$  ratio 2.0-2.2

## **Low $A_{260}/A_{230}$ ratio**

- Carbohydrate carryover (often a problem with plants).
- Residual phenol from nucleic acid extraction.
- Residual guanidine  
(often used in column based kits)
- Glycogen used for precipitation.

## **High $A_{260}/A_{230}$ ratio**

- Making a Blank measurement on a dirty pedestal
- Using an inappropriate solution for the Blank measurement.

# Factors Affecting Absorbance

- A260/A280 ratio:
  - pH
  - ionic strength
- Water often has an acidic pH
- Buffered solution (Tris-EDTA at pH 8.0)

# Conventional Spectrophotometers

- Conventional spectrophotometers:
  - Requires sample dilution
  - Low sensitivity (lower limit 0.5-1 $\mu$ g nucleic acid)



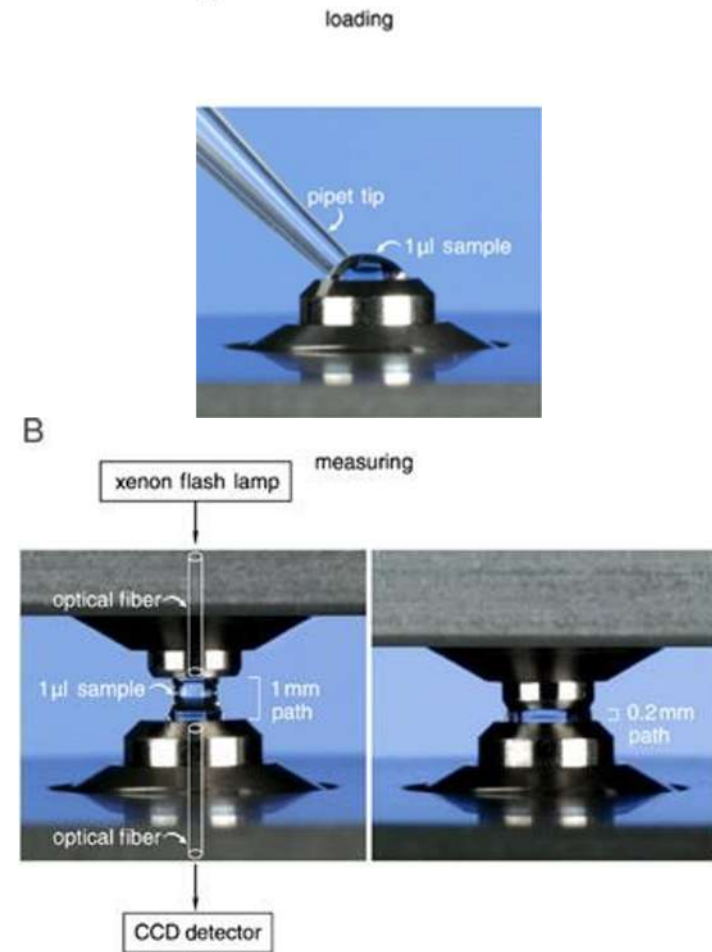
# NANOSPECTROPHOTOMETRY

- Miniaturization of UV spectrophotometers:
  - Rapid
  - Direct quantification of nucleic acids in microvolumes

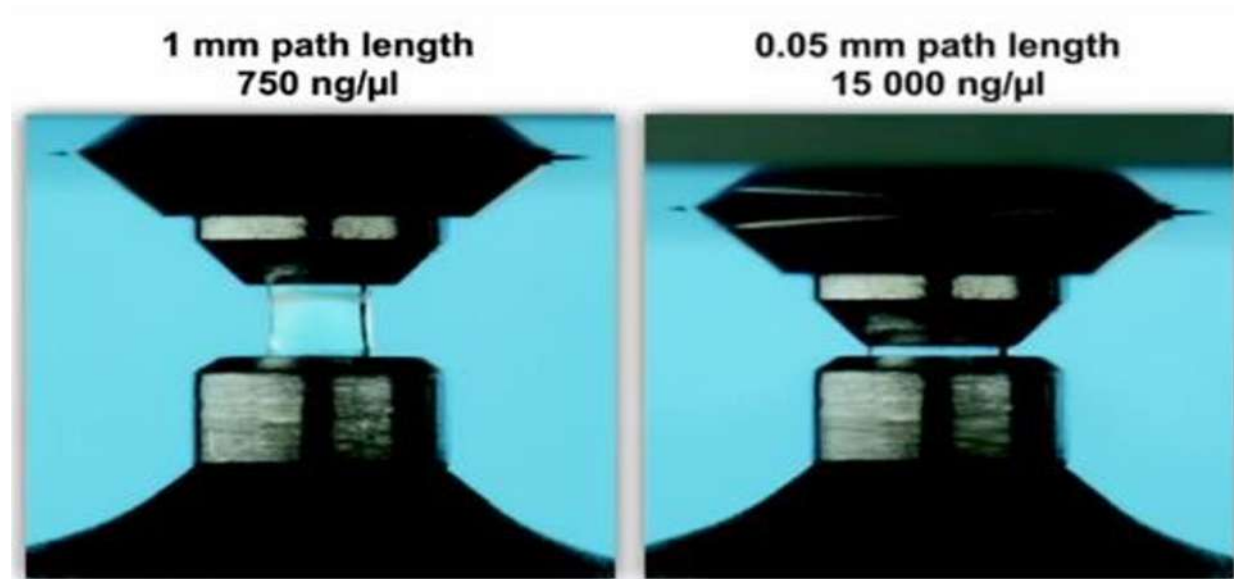


# NANOSPECTROPHOTOMETRY- NanoDrop

- Sample retention system
- Inherent surface tension of liquids
- Microvolume samples (0.5-2 $\mu$ l)
- Liquid column  $\rightarrow$  Vertical optical path



# NANOSPECTROPHOTOMETRY



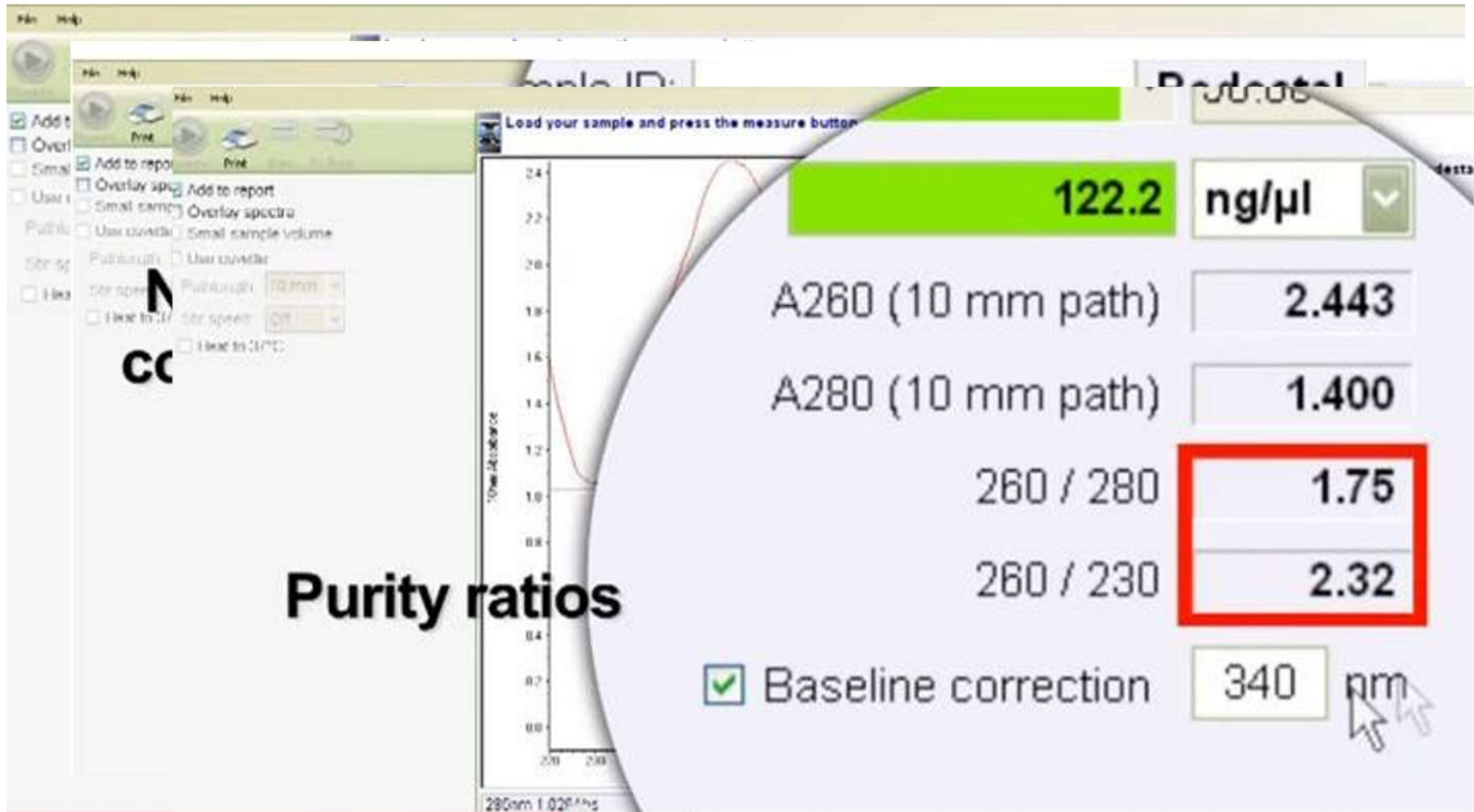
- Vertical path length
  - Automatically changed
  - Shorter path length → higher concentration of sample

# NANOSPECTROPHOTOMETRY

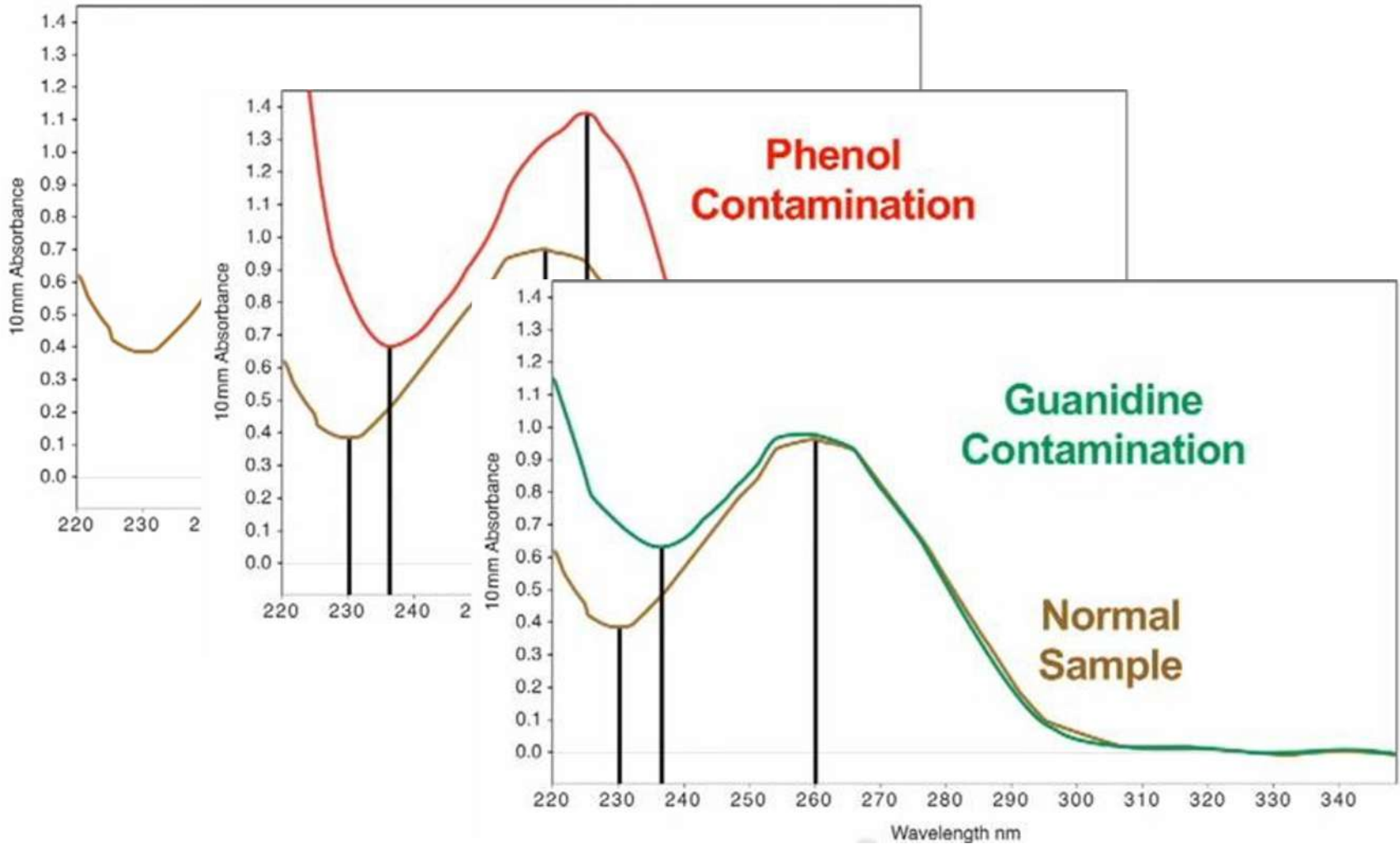
- Benefits:
  1. Small sample volume at 0.5-2 $\mu$ l
  2. Large dynamic range (2ng/ $\mu$ l-3700ng/ $\mu$ l)
  3. Cuvette free operation
  4. Short measurement time
  5. High accuracy and good reproducibility.



# NANOSPECTROPHOTOMETRY



# NANOSPECTROPHOTOMETRY



# Quantification with a Fluorescent Dye

- DNA/RNA intercalating dyes
- Measurement of fluorescence
- ~1000 times more sensitive than UV absorbance

# Quantification with a Fluorescent Dye

- Ethidium Bromide (EtBr)
- SYBR Green
- Hoechst 33258
- PicoGreen
- RiboGreen

# Quantification with a Fluorescent Dye

## EtBr:

- PCR products, gDNA
- Band intensity calculation
- Comparison to known reference
- Agarose and PAGE
- Not precise, relative

## SYBR Green I:

- Highly sensitive
  - 25-100 times more than EtBr
- ssDNA, dsDNA
- Agarose and PAGE
- Less mutagenic

# Quantification with a Fluorescent Dye

- Fluorometer

- Hoechst 33258

(DNA):

- Binds to A-T bp in dsDNA
- Emission Max. At 460nm

Emission max. at  
530nm

- PicoGreen

(DNA)

- RiboGreen

(RNA)

# Quantification with a Fluorescent Dye

TBS-380 Fluorometer  
3800: 2mL or 50 $\mu$ L with  
minicell adapter



Aquaflour:  
2mL

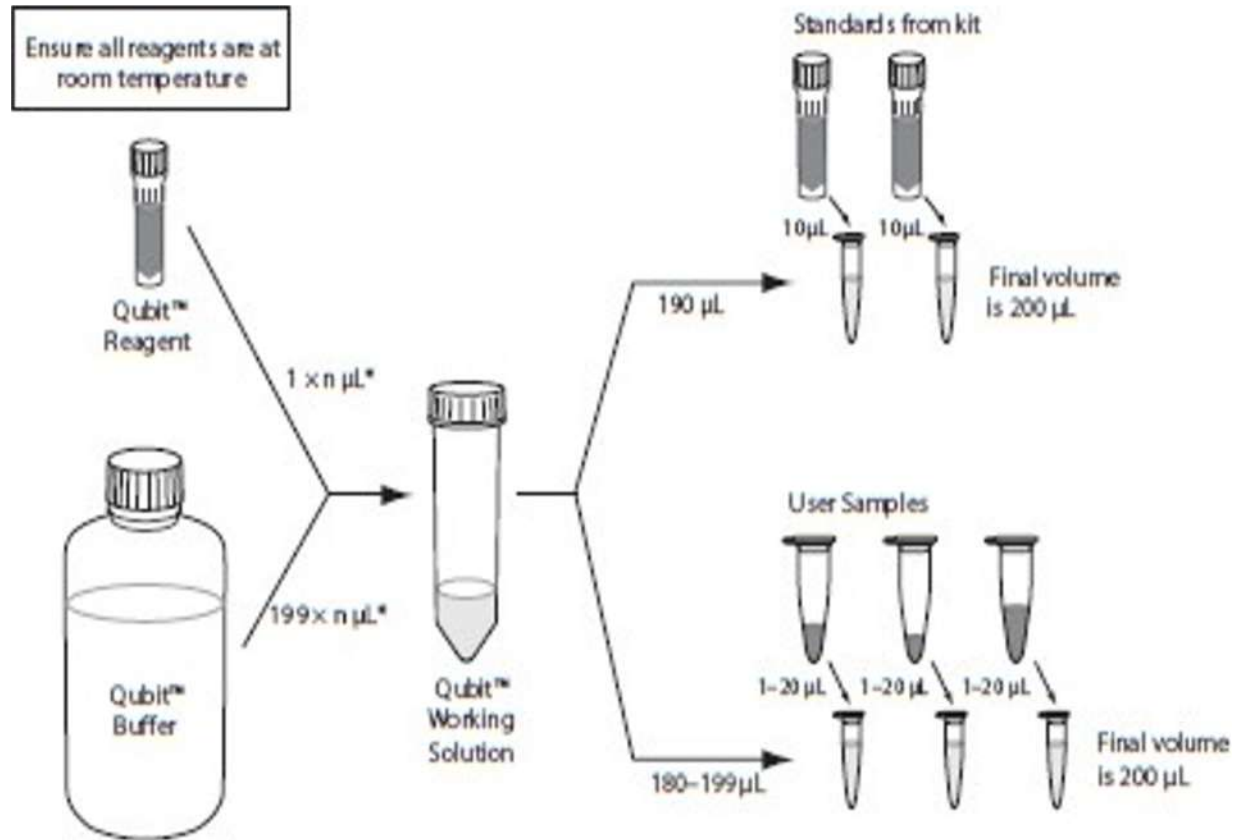


NanoDrop3300  
Fluorometer  
:



Qubit: 200 $\mu$ L

# Quantification with a Fluorescent Dye: Qubit



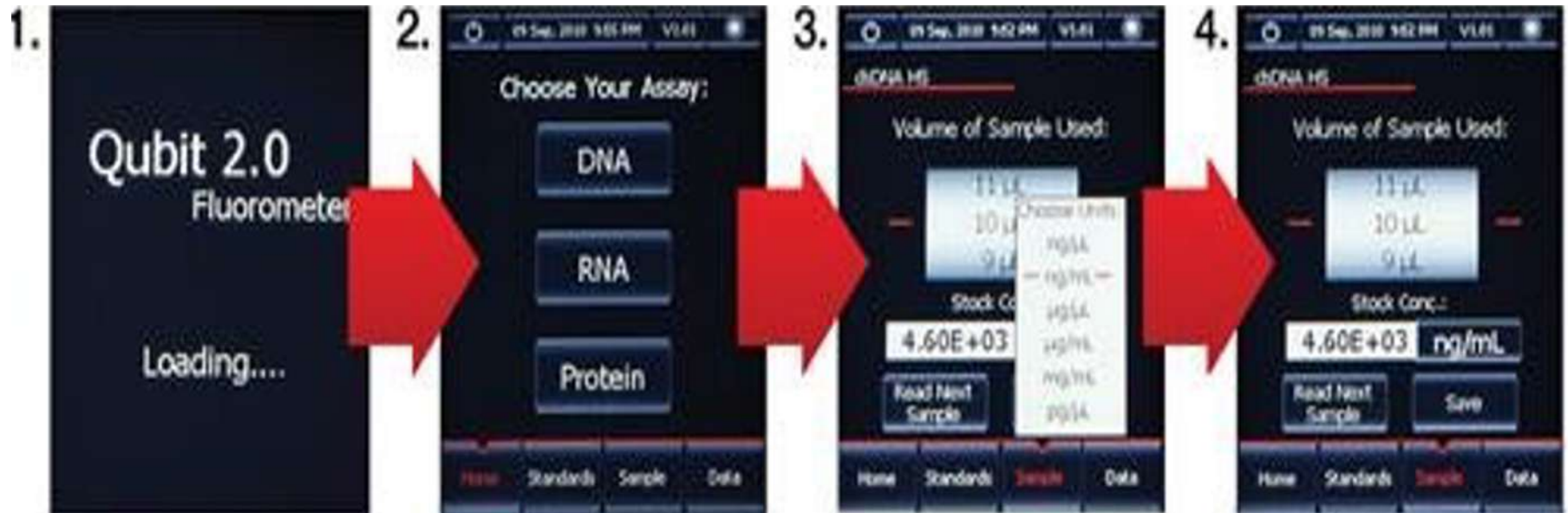


# Quantification with a Fluorescent Dye



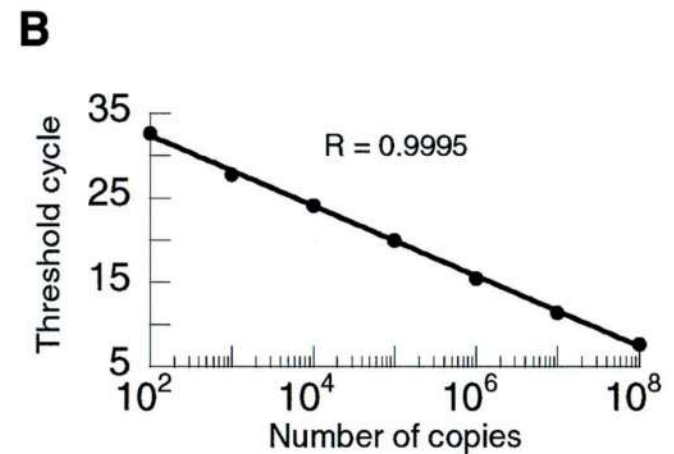
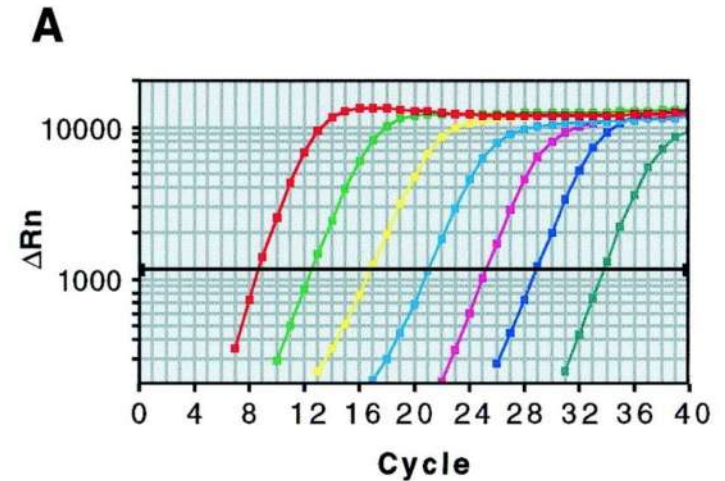
The Qubit® 2.0 Fluorometer displays the standard curve after completion of the calibration.

# Quantification with a Fluorescent Dye



# Quantification by Real-Time PCR

- DNA, RNA (cDNA)
- Absolute quantification
- Serially diluted standards  
→ Standard curve
- Determination of concentration of unknowns based on Ct (Threshold cycle) values



# Quality Assessment of Nucleic Acids

# Quality Assessment of Nucleic Acids

- Level of degradation
- Assay amenability (FFPE tissues)
- Method: nature of nucleic acid

# Methods of Quality Assessment of Nucleic Acids

## DNA

1. Agarose gel electrophoresis
2. PCR amplification of fragments with increasing length

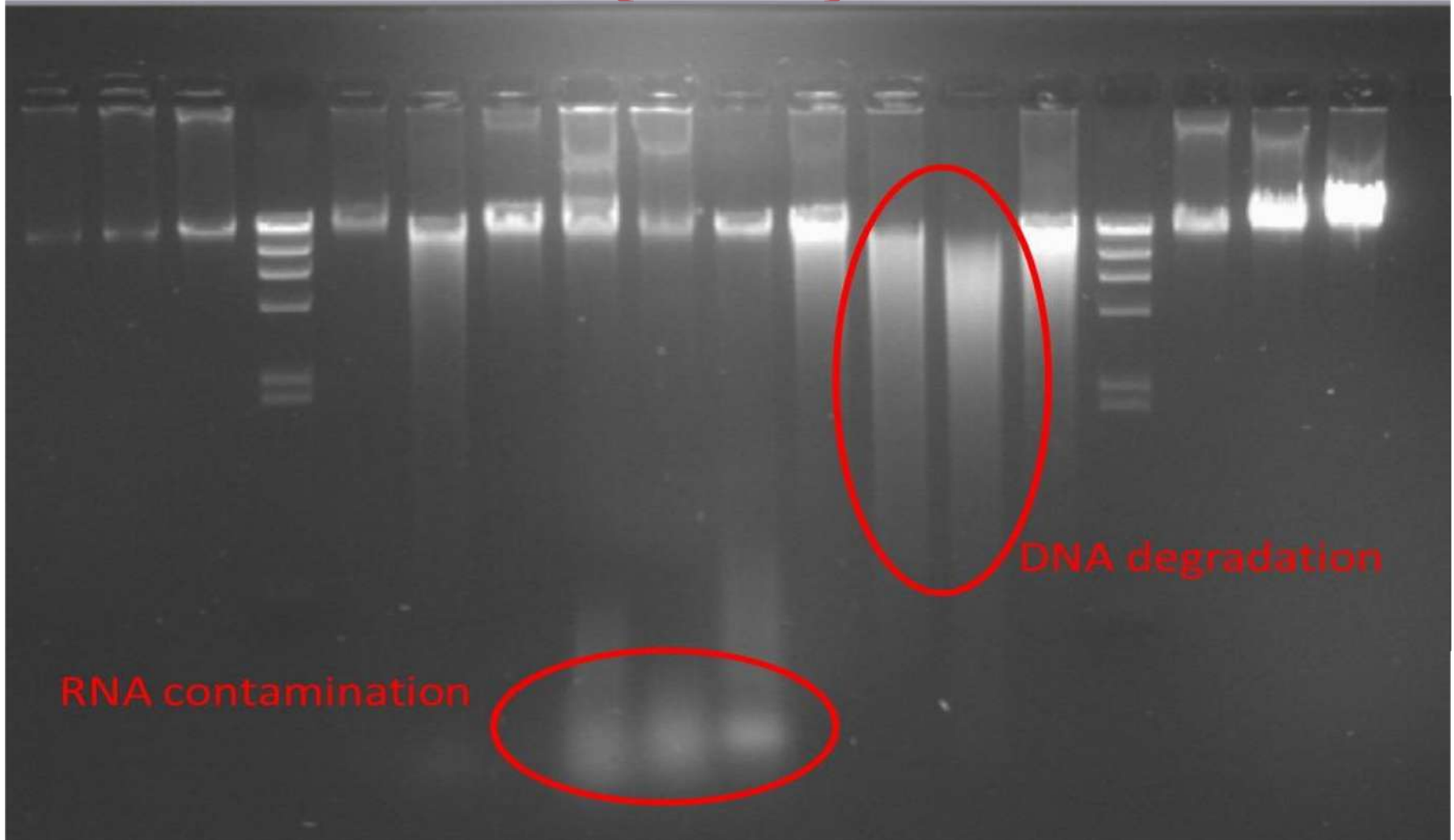
## DNA and RNA

1. Agilent 2100 Bioanalyzer

## RNA

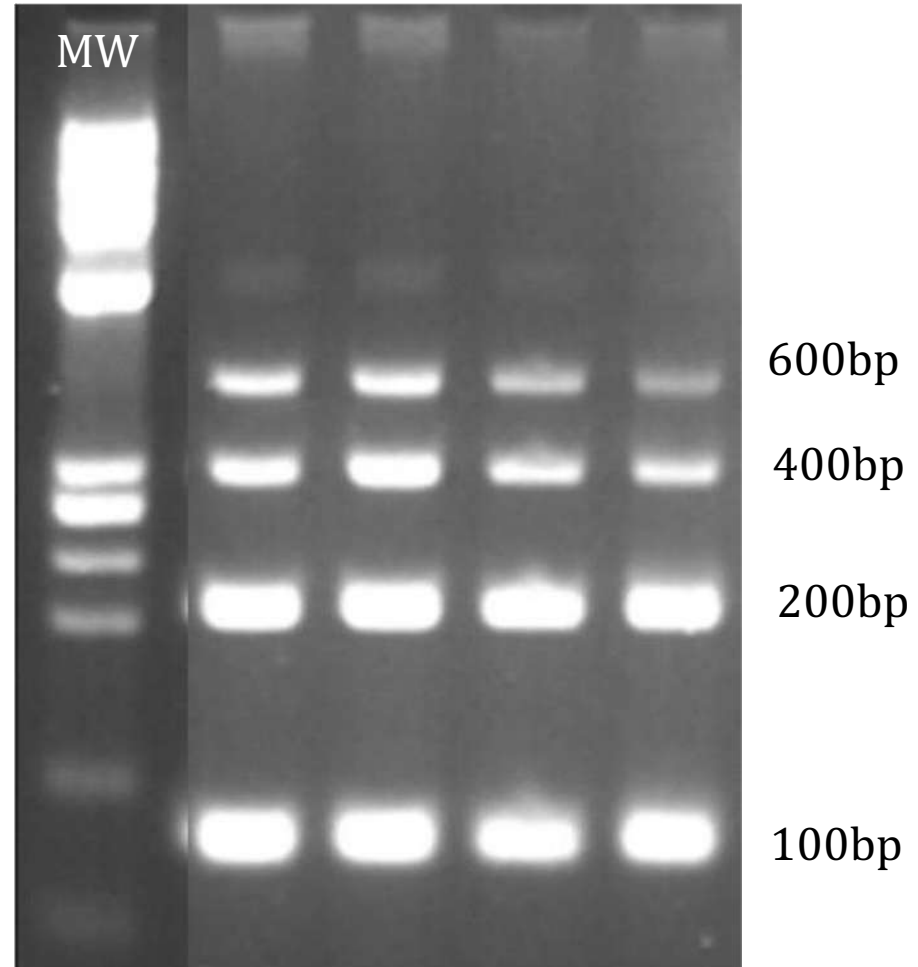
1. Denaturing gel electrophoresis
2. RT-PCR amplification of mRNA fragments of increasing length

# Agarose gel electrophoresis (DNA)



# PCR Amplification of Fragments with Increasing Length (DNA)

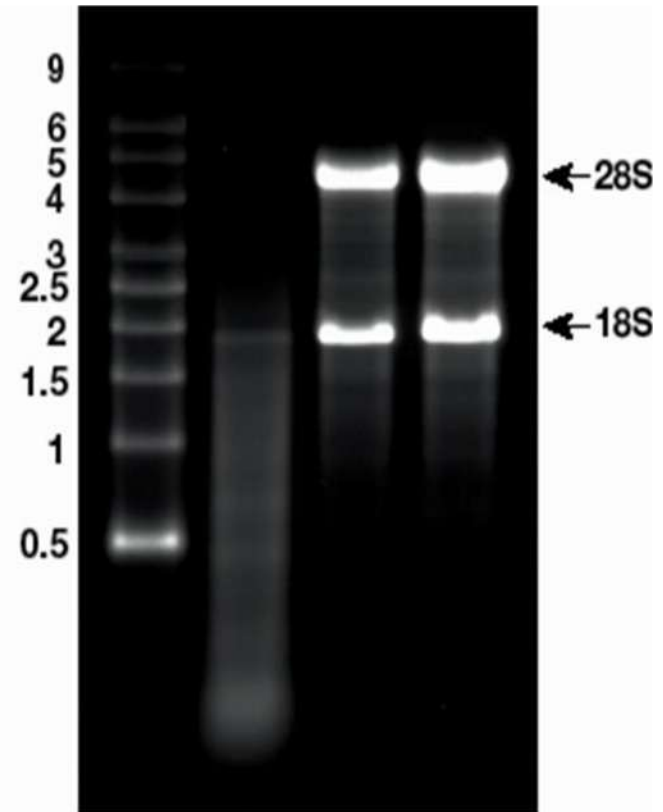
- Archival tissues
- Spesmen control size ladder
- Multiplex PCR





# Denaturing Agarose Gel Electrophoresis (RNA)

- Most common method of integrity assessment :
- Secondary structure of RNA → altered migration pattern
  - Electrophoresis buffer : Formaldehyde and MOPs (3-[N-Morpholino]-propanesulfonic acid)
  - Loading buffer: Glyoxal



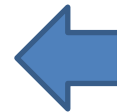
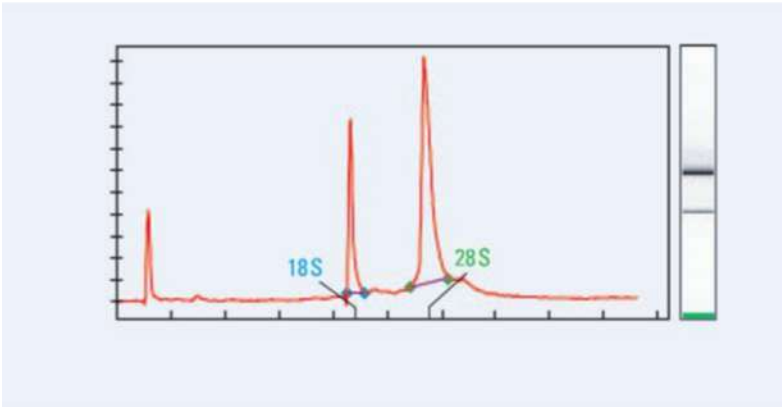
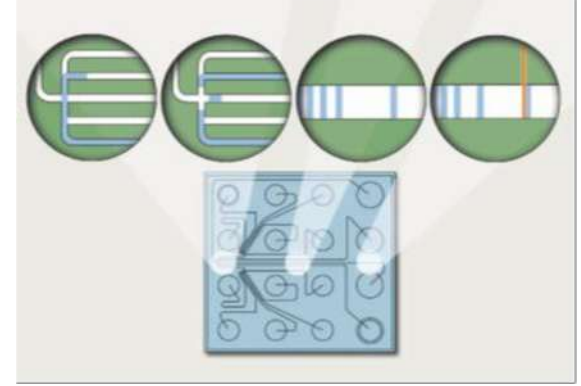
# RT-PCR Amplification of mRNA Fragments of Increasing Length

- mRNA integrity assessment
- Housekeeping gene
- cDNA subjected to amplification
- Fragments with increasing length
- Independent from rRNA integrity

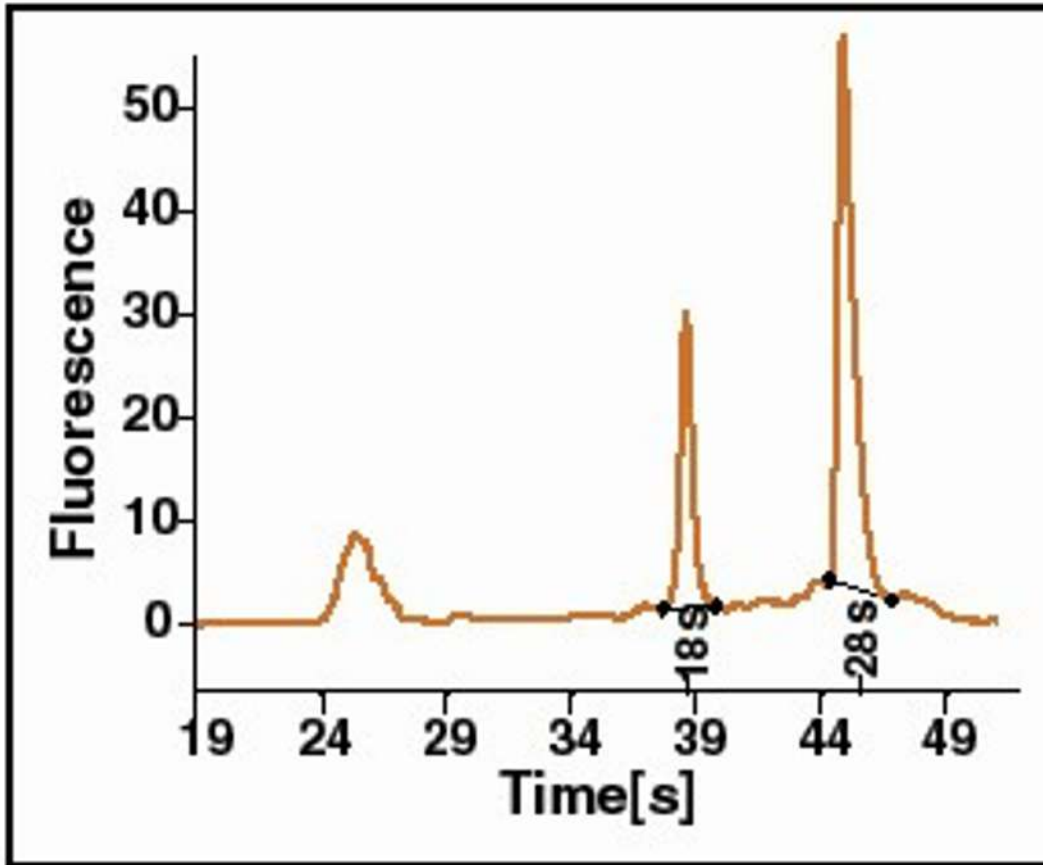
# Quality Assessment with Capillary Microchip Electrophoresis:

- LabChip systems (Caliper)
- MCE-202 MultiNA microchip  
electrophoresis system (Shimadzu)
- P/ACE MDQ (Beckman Coulter)
- 2100 BioAnalyzer (Agilent):  
microfluidics, capillary  
electrophoresis, fluorescent  
detection

# Agilent 2100 BioAnalyzer



# Agilent 2100 BioAnalyzer

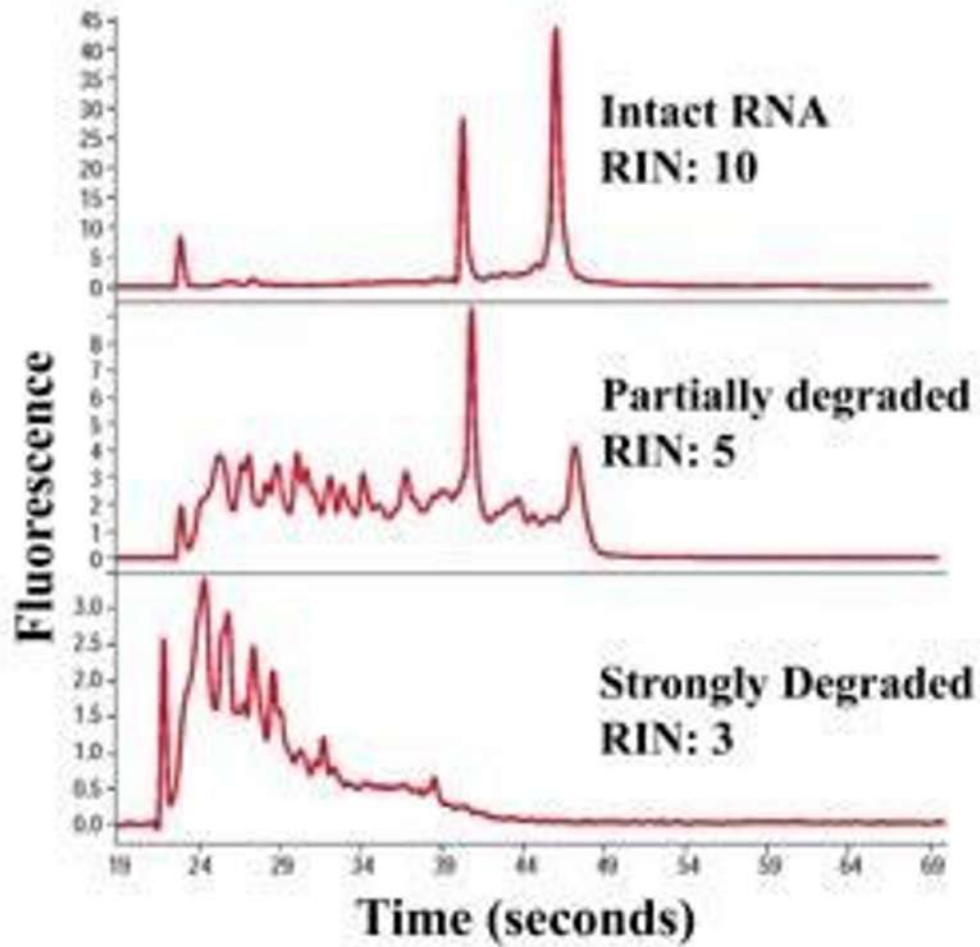


28S/18S ratios ~  
2

# The RNA Integrity Number (RIN)

- 28S/18S rRNA ratio is reasonable but not ideal!!!
- Nondenaturing conditions
- Software algorithm for the the entire electrophoretic trace
- Estimation of the integrity of total RNA samples.
- Numbering system 1-10

# RIN



RIN 1 : most  
degraded RIN 10:  
most intact

# RIN

- Downstream application
  - RT-PCR vs Microarray
- RINs  $> 7-8$  work well for most experiments.
- RINs  $< 7$  require extra validation studies



# Quantification of Proteins

- Different methods:
  - Accuracy required
  - Amount and purity of protein
- Spectrophotometric assays:
  - UV Absorbance methods
  - Colorimetric and fluorescent-based detection

# Quantification of Proteins

- Assay selection criteria:
  1. Sample volume (microplate assay vs cuvette-based)
  2. Sample recovery (UV spectroscopy)
  3. Throughput (microplate compatible rapid assay)
  4. Robustness (repeatability)
  5. Chemical modifications (Covalent modifications!)
  6. Protein aggregation (solubility of the protein)

# Quantification of Proteins

- UV absorbance: quantitation of purified protein
  - Proteins that contain Trp, Tyr residues
  - Cys-Cys disulphide bonds
- Colorimetric assays: uncharacterized protein solutions and cell lysate
  - Bradford
  - BCA
  - Lowry

# Quantification of Proteins: UV Absorption Spectroscopy

- UV Absorption at 280nm
  - Range 20-3000 $\mu$ g
  - Aromatic aa (tyrosine and tryptophan)
  - Molar extinction coefficient
    - Beer-Lambert Law:  $A = a_m \times C \times l$
  - Protein standard

# Quantification of Proteins: UV Absorption Spectroscopy

- UV Absorption at 205nm
  - Range 1-100 $\mu$ g
  - Absorption of photons by peptide bonds
    - Molar extinction coefficient at A205
    - Protein Standard

# UV Absorption Spectroscopy

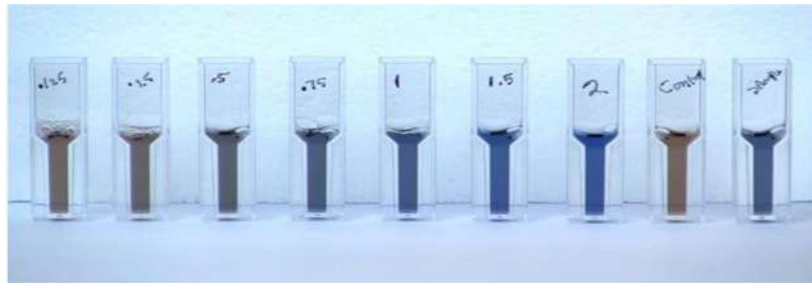
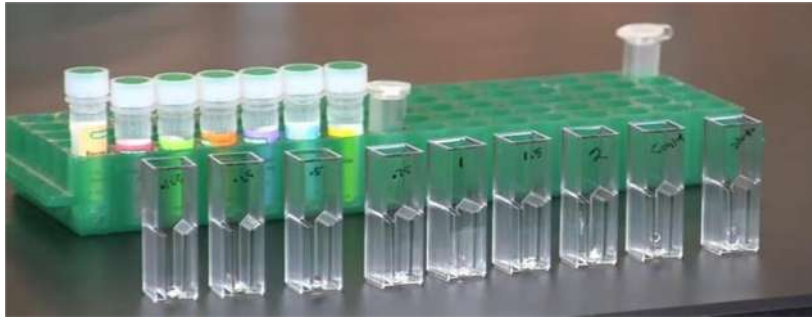
- NanoDrop 1000, NanoDrop 8000  
A280 modules
- Concentration of purified protein  
samples
- 1  $\mu$ l sample

# Dye-Based Assays: Bradford Assay

Bradford (Coomassie Blue) Assay (1-50 $\mu$ g):

- Binding of Coomassie Brilliant Blue mainly to Tryptophan and tyrosine residues at acidic pH
- Shift in the absorbance of acidic CB solution from 465nm to 595nm

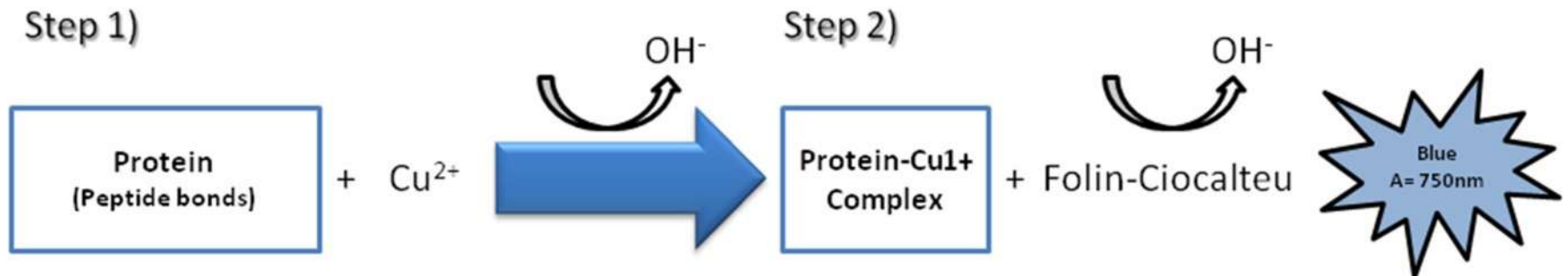
# Bradford Assay





# Dye-Based Assays: Lowry Assay

- Lowry (Alkaline Copper Reduction) Assay (5-100 $\mu$ g):
  - Two-step procedure
  - Reduction of Cu by proteins in alkaline solutions
  - Reduction of Folin reagent (a mixture of phosphotungstic acid and phosphomolybdic acid)
  - A blue color is formed with absorbance max. at 750nm



# Dye-Based Assays: Bicinchoninic Assay

Bicinchoninic (BCA) Assay (0.2-50 $\mu$ g)

- Bicinchoninic acid (replacement of Folin's reagent)
- Improved sensitivity
- Tolerance to interfering substances
- Intense purple complex (562nm)

# Protein analysis with the Agilent 2100 Bioanalyzer

- Microvolume analysis
- Different assays
  - For protein analysis in the low molecular weight range
  - General protein analysis up to 230 kDa
  - Picogram sensitivity

# Quality Assessment of Proteins

1. Composition-Based and activity-based analysis
2. Electrophoretic methods (SDS gel electrophoresis)
3. Chromatographic methods
  - I. Gel filtration Chromatography
  - II. Reversed phase HPLC
4. Sedimentation velocity methods
5. Mass spectrometry methods
6. Light scattering methods