



Sep 08, 2020

## DNA Quantification -- CHEM 584

Forked from [DNA Concentration Measurement \(Protocol for Thermo Scientific NanoDrop™ 1000 Spectrophotometer\)](#)

Alba Balletbó<sup>1</sup>, Ken Christensen<sup>2</sup>

<sup>1</sup>Wageningen University; <sup>2</sup>Brigham Young University

*In Development*

[dx.doi.org/10.17504/protocols.io.bk4xkyxn](https://dx.doi.org/10.17504/protocols.io.bk4xkyxn)



Ken Christensen  
Brigham Young University

### ABSTRACT

Protocol adapted from the NanoDrop Spectrophotometer User's Manual.

### DOI

[dx.doi.org/10.17504/protocols.io.bk4xkyxn](https://dx.doi.org/10.17504/protocols.io.bk4xkyxn)

### PROTOCOL CITATION

Alba Balletbó, Ken Christensen 2020. DNA Quantification – CHEM 584. **protocols.io**  
<https://dx.doi.org/10.17504/protocols.io.bk4xkyxn>

### FORK FROM

Forked from [DNA Concentration Measurement \(Protocol for Thermo Scientific NanoDrop™ 1000 Spectrophotometer\)](#), Alba Balletbó

### LICENSE

————— This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

### CREATED

Sep 08, 2020

### LAST MODIFIED

Sep 08, 2020

### PROTOCOL INTEGER ID


41847

### MATERIALS TEXT

TE Buffer or MQ Water  
DNA Sample

- 1 Start a new experiment using the Nanodrop touchscreen.
- 2 Click on the corresponding application module (e.g., dsDNA).
- 3 Open the sampling arm and load a blank sample (e.g., TE Buffer, MQ Water, etc.).

2 µl

- 4 Close the sampling arm on the machine to cover the blank sample.
- 5 Click "OK" to read the blank if the Nanodrop is not already in automatic mode.
- 6 Open the sampling arm and clean the blank off the upper and lower pedestals using a Kim Wipe.
- 7 Load your DNA sample and close the sampling arm.  
 2 µl
- 8 Click "Measure sample" if the Nanodrop is not in automatic mode.
- 9 Take a picture of the screen that shows your results and the corresponding spectra for your records.
- 10 Clean the nucleic acid sample off of the upper and lower pedestals using a Kim Wipe.
- 11 Repeat for all samples.
- 12 Close program.