

Project: ELISA paper project

Date: 20.05.2020

Test No.: 2

Performed by: Dorothy Smith

on: 22.05.2020 18:00

Approved by:

on:

**Sample pipetting scheme**

|    | Abbr  | Description              | Position         |
|----|-------|--------------------------|------------------|
| 1  | std1  | Standard1 (0.0005 mg/mL) | C-4, C-5, C-6    |
| 2  | std2  | Standard2 (0.001 mg/mL)  | F-4, F-5, F-6    |
| 3  | std3  | Standard3 (0.002 mg/mL)  | A-7, A-8, A-9    |
| 4  | std4  | Standard4 (0.003 mg/mL)  | C-7, C-8, C-9    |
| 5  | std5  | Standard5 (0.004 mg/mL)  | F-7, F-8, F-9    |
| 6  | std6  | Standard6 (0.005 mg/mL)  | D-10, D-11, D-12 |
| 7  | std7  | Standard7 (0.01 mg/mL)   |                  |
| 8  | std8  | Standard8 (0.015 mg/mL)  |                  |
| 9  | std9  | Standard9 (0.02 mg/mL)   |                  |
| 10 | std10 | Standard10 (0.025 mg/mL) |                  |
| 11 | std11 | Standard11 (0.03 mg/mL)  |                  |
| 12 | std12 | Standard12 (0.04 mg/mL)  |                  |
| 13 | std13 | Standard13 (0.05 mg/mL)  |                  |
| 14 | std14 | Standard14 (0.06 mg/mL)  |                  |
| 15 | std15 | Standard15 (0.08 mg/mL)  |                  |
| 16 | std16 | Standard16 (0.1 mg/mL)   |                  |
| 17 | std17 | Standard17 (0.2 mg/mL)   |                  |
| 18 | std18 | Standard18 (0.3 mg/mL)   |                  |
| 19 | std19 | Standard19 (0.4 mg/mL)   |                  |
| 20 | std20 | Standard20 (0.5 mg/mL)   |                  |
| 21 | std21 | -                        |                  |
| 22 | std22 | -                        |                  |
| 23 | std23 | -                        |                  |
| 24 | std24 | -                        |                  |
| 25 | std25 | -                        |                  |
| 26 | std26 | -                        |                  |
| 27 | std27 | -                        |                  |
| 28 | std28 | -                        |                  |
| 29 | std29 | -                        |                  |
| 30 | std30 | -                        |                  |
| 31 | sam1  | -                        | A-1, A-2, A-3    |
| 32 | sam2  | -                        | B-7, B-8, B-9    |
| 33 | sam25 | -                        |                  |
| 34 | sam26 | -                        |                  |
| 35 | sam27 | -                        |                  |
| 36 | sam28 | -                        |                  |
| 37 | sam29 | -                        |                  |
| 38 | sam30 | -                        |                  |
| 39 | sam31 | -                        |                  |
| 40 | sam32 | -                        |                  |
| 41 | sam33 | -                        |                  |
| 42 | sam34 | -                        |                  |
| 43 | sam35 | -                        |                  |
| 44 | sam36 | -                        |                  |
| 45 | sam37 | -                        |                  |
| 46 | sam38 | -                        |                  |
| 47 | sam39 | -                        |                  |
| 48 | sam40 | -                        |                  |

### Multiwell plate map

|   | 1     | 2     | 3     | 4     | 5     | 6     | 7     | 8     | 9     | 10    | 11    | 12    |
|---|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| A | BLQ   | sam1  | sam1  | empty | empty | empty | std3  | std3  | std3  | empty | empty | empty |
| B | sam4  | sam4  | sam4  | empty | empty | empty | sam2  | sam2  | sam2  | empty | empty | empty |
| C | empty | empty | empty | std1  | std1  | std1  | std4  | std4  | std4  | empty | empty | empty |
| D | empty | empty | empty | empty | empty | empty | sam3  | sam3  | sam3  | std6  | std6  | std6  |
| E | empty | empty | empty | empty | empty | empty | empty | empty | empty | empty | empty | empty |
| F | empty | empty | empty | std2  | std2  | std2  | std5  | std5  | std5  | empty | empty | empty |
| G | empty | empty | empty | empty | empty | empty | empty | empty | empty | empty | empty | empty |
| H | empty | empty | empty | empty | empty | empty | empty | empty | empty | empty | empty | BLQ   |

### Initial measurement results

|   | 1      | 2      | 3      | 4      | 5      | 6      | 7      | 8      | 9      | 10     | 11     | 12     |
|---|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| A | BLQ    | 0.2682 | 0.2691 | 0.1939 | 0.1828 | 0.1705 | 0.6505 | 0.6937 | 0.6410 | 1.2601 | 1.2463 | 1.1666 |
| B | 0.0476 | 0.0495 | 0.0507 | 0.2441 | 0.2514 | 0.2441 | 0.7130 | 0.7221 | 0.6766 | 1.3088 | 1.2625 | 1.1298 |
| C | 0.0523 | 0.0509 | 0.0511 | 0.2877 | 0.2897 | 0.2910 | 0.8818 | 0.9079 | 0.9151 | 1.1787 | 1.2468 | 1.1355 |
| D | 0.0609 | 0.0574 | 0.0574 | 0.3544 | 0.3363 | 0.3568 | 1.0577 | 1.0606 | 1.0285 | 1.2611 | 1.3623 | 1.2885 |
| E | 0.0715 | 0.0691 | 0.0713 | 0.3796 | 0.3438 | 0.3722 | 1.0464 | 1.0070 | 1.0465 | 1.2791 | 1.3068 | 1.3249 |
| F | 0.0872 | 0.0833 | 0.0862 | 0.4594 | 0.4298 | 0.4366 | 1.1313 | 1.1287 | 1.0985 | 1.2950 | 1.3729 | 1.331  |
| G | 0.0997 | 0.1028 | 0.0918 | 0.4690 | 0.5093 | 0.4849 | 1.1799 | 1.1708 | 1.1049 | 1.2915 | 1.3207 | 1.3555 |
| H | 0.1168 | 0.1169 | 0.1163 | 0.5439 | 0.5892 | 0.5642 | 1.2311 | 1.1618 | 1.1438 | 1.2415 | 1.3131 | BLQ    |

### Calibration standards

| Std. name | Number | Absorbance | Conc. | Variation |
|-----------|--------|------------|-------|-----------|
| std1      | 3      | 0.2895     | 1.02  | 0.00136   |
| std2      | 3      | 0.4419     | 1.04  | 0.01266   |
| std3      | 3      | 0.6617     | 1.08  | 0.02293   |
| std4      | 3      | 0.9016     | 1.22  | 0.01431   |
| std5      | 3      | 1.1195     | 1.65  | 0.01489   |
| std6      | 3      | 1.3040     | 7.39  | 0.04274   |

### Model: Logarithmic fitting in lin\_ln system

Absorbance =  $A \cdot \ln(\text{Conc}) + B$

### Model parameters

A= 0.229183, B= 1.216699

### Model diagnostics

The Residual Sum of Squares **RSS** = 0.00245

Coefficient of Determination **R<sup>2</sup>** = 0.980988

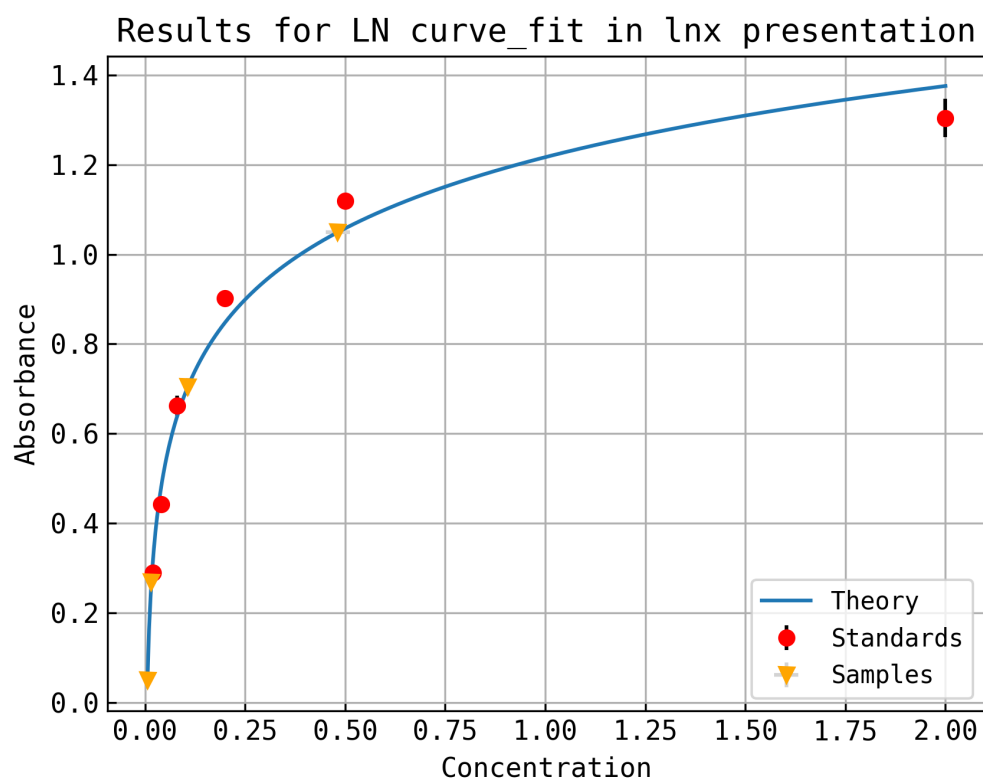
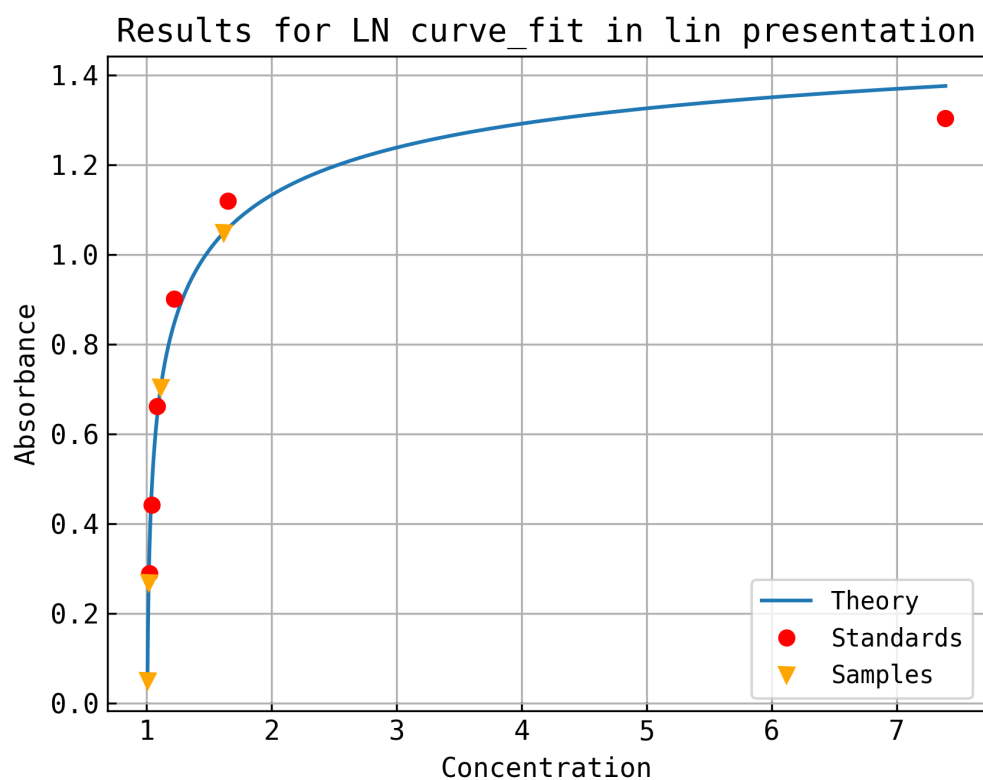
Akaike Information Criterion **AIC** = -32.069772

Bayesian Information Criterion **BIC** = -32.486253

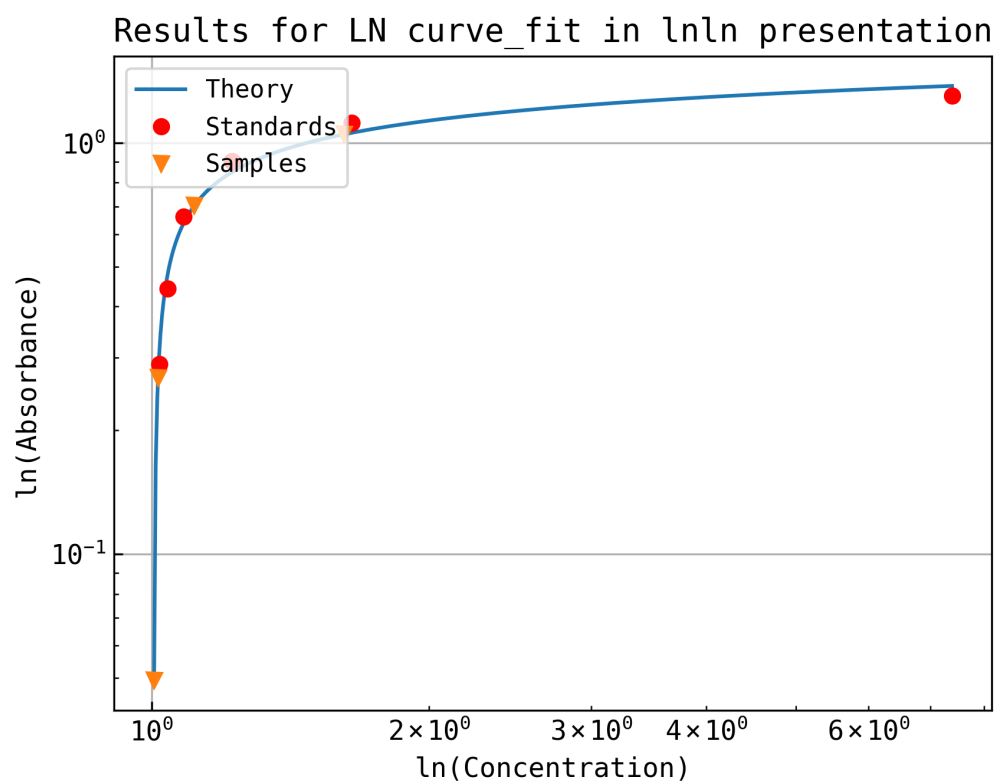
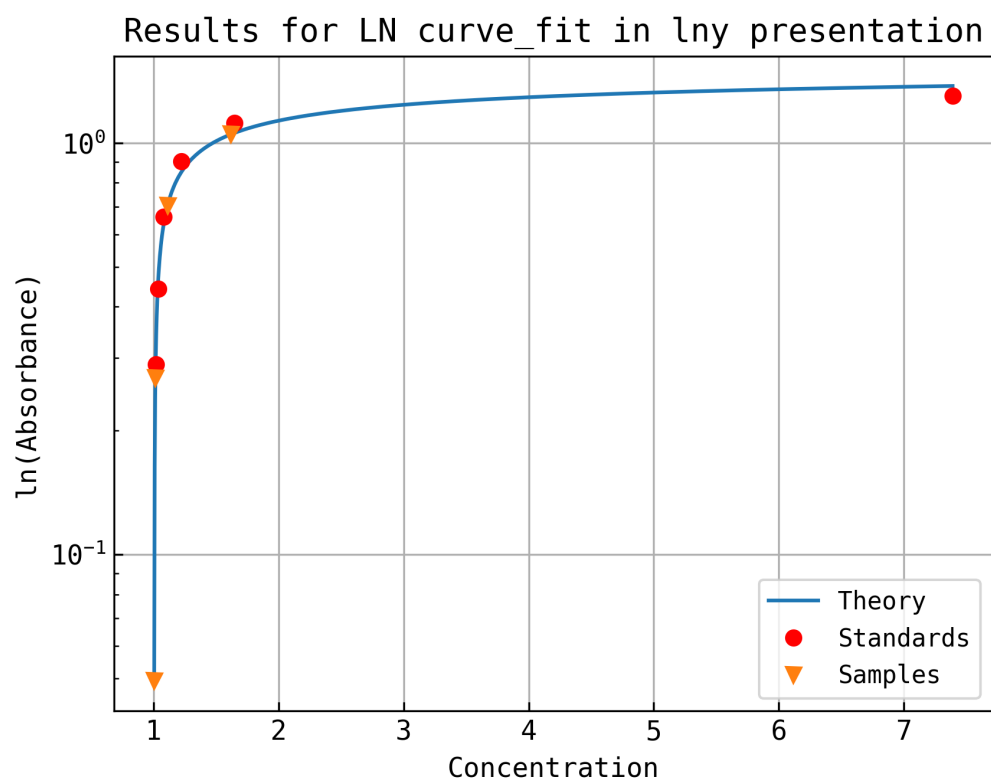
Coefficient of Correlation **r** = 0.990449

Time of calculatin = 0.004 [s]

## Plots



## Plots



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**Calculation results**

| Good Samples | Conc. | SD down Conc. | SD up Conc. | Absorbance | SD Abs. |
|--------------|-------|---------------|-------------|------------|---------|
| sam1         | 1.016 | 0.00003       | 0.00003     | 0.26865    | 0.00045 |
| sam2         | 1.113 | 0.00956       | 0.00877     | 0.70390    | 0.01966 |
| sam3         | 1.618 | 0.03140       | 0.02948     | 1.04893    | 0.01450 |
| sam4         | 1.006 | 0.00003       | 0.00003     | 0.04927    | 0.00128 |

**BLQ samples**

|   | Bad Sample | Comment  |
|---|------------|----------|
| 1 | sam1       | blq_1_1  |
| 2 | empty      | blq_8_12 |