Project: ELISA paper project

Date: 20.05.2020 Test No.: 2

Performed by: Dorothy Smith on: 22.05.2020 18:07

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	empty	empty	empty	empty	empty	empty	sam2	sam2	sam2	empty	empty	empty
C	empty	empty	empty	std1	std1	std1	std4	std4	std4	empty	empty	empty
D	sam4	sam4	sam4	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	sam5	sam5	sam5
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	1.307609	1.308786	1.213975	1.200574	1.185898	1.916499	2.001106	1.898378	3.525774	3.477452	3.21106
B	1.04875	1.050746	1.052007	1.276472	1.285824	1.276472	2.040102	2.058752	1.967178	3.701729	3.534246	3.09504
C	1.05369	1.052218	1.052428	1.333357	1.336027	1.337765	2.415243	2.479111	2.497025	3.250146	3.479192	3.11273
D	1.06279	1.059079	1.059079	1.425325	1.399759	1.428750	2.879740	2.888103	2.796867	3.529302	3.905165	3.62734
E	1.07412	1.071543	1.073903	1.461700	1.410297	1.450923	2.847382	2.737376	2.847667	3.593404	3.694333	3.76181
F	1.09111	1.086868	1.090024	1.583124	1.536950	1.547437	3.099683	3.091635	2.999663	3.650996	3.946780	3.78483
G	1.10484	1.108270	1.096146	1.598395	1.664126	1.624013	3.254049	3.224571	3.018923	3.638240	3.746043	3.8787
H	1.12389	1.124007	1.123333	1.722712	1.802546	1.758041	3.424995	3.195680	3.138673	3.460801	3.717681	BLQ

Calibration standards

Std. name	Number	Absorbance	Conc.	Variation
std1	3	1.3357	0.02	0.00136
std2	3	1.5557	0.04	0.01266
std3	3	1.9381	0.08	0.02293
std4	3	2.4635	0.20	0.01431
std5	3	3.0633	0.50	0.01489
std6	3	3.6839	2.00	0.04274

Model: Logarithmic fitting in ln_lin system

Absorbance = A*ln(Conc) + B

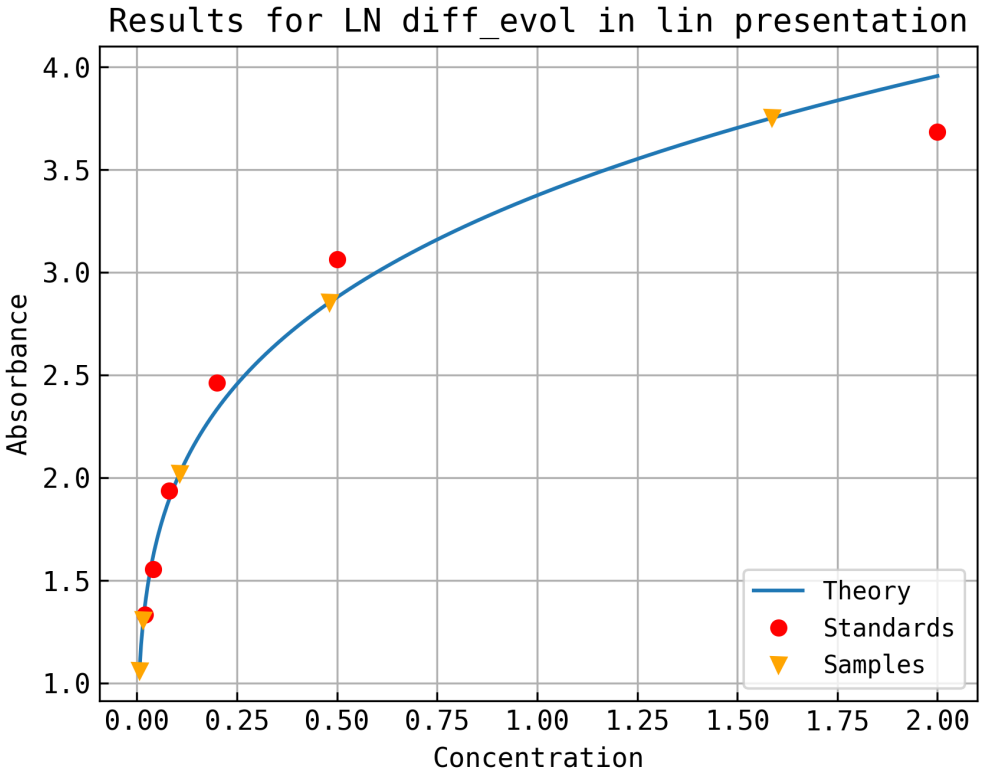
Model parameters

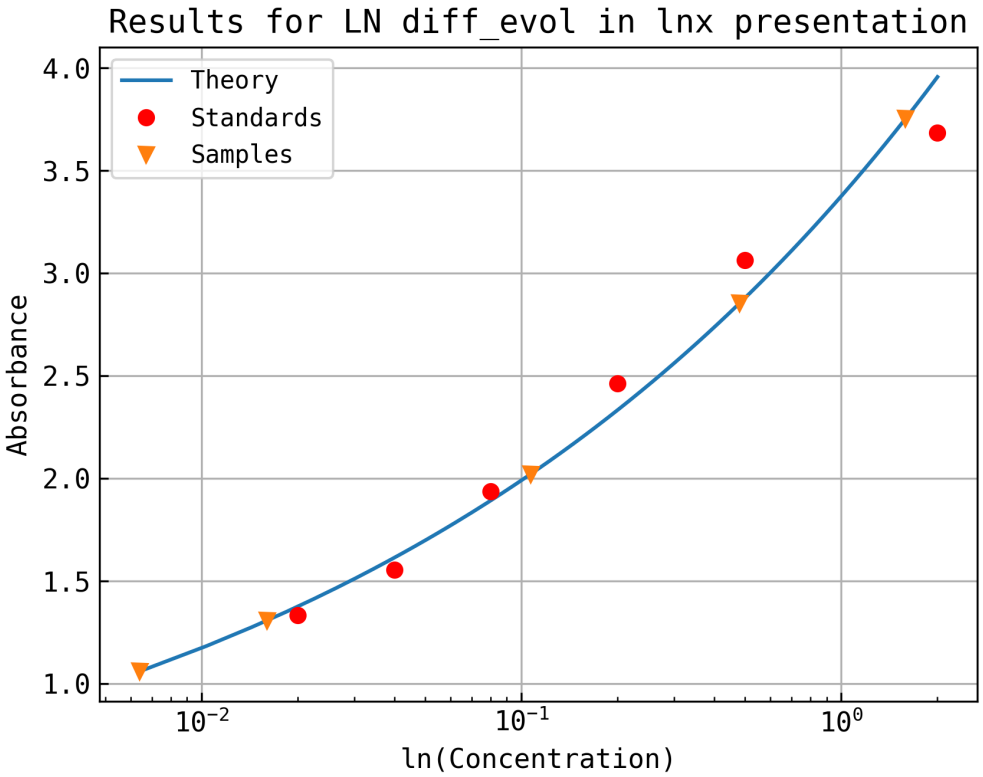
A= 0.229183, B= 1.216699

Model diagnostics

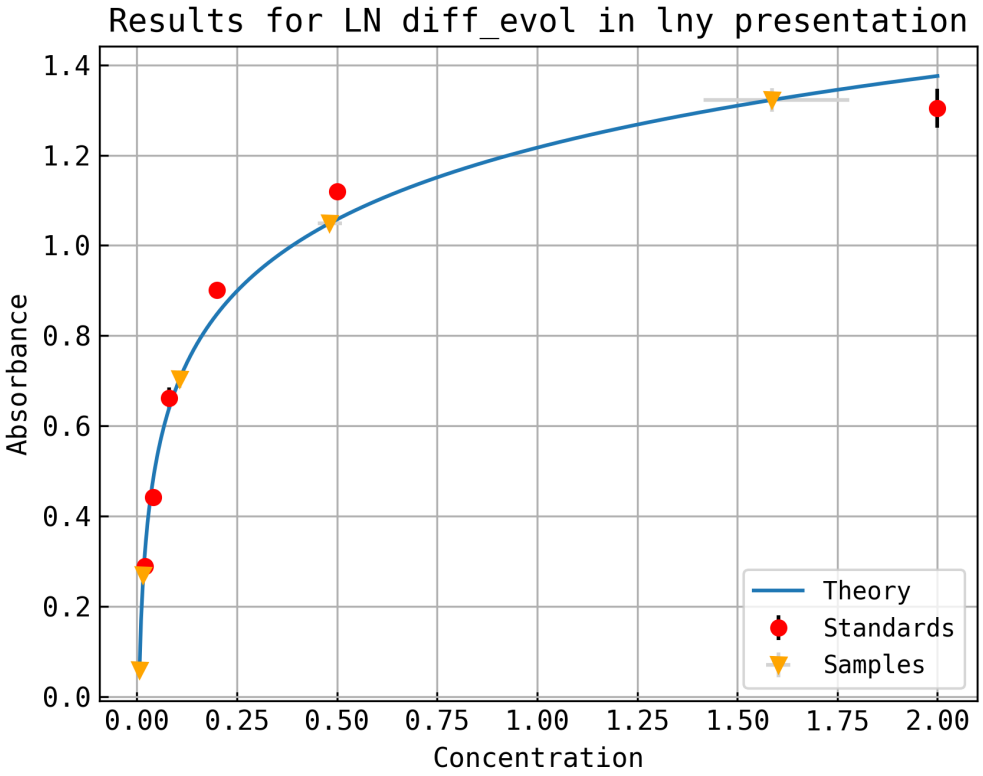
The Residual Sum of Squares **RSS** = 0.00245
Coefficient of Determination $\mathbf{R^2}$ = 0.980988
Akaike Information Criterion **AIC** = -32.069772
Bayesian Information Criterion **BIC** = -32.486253
Coefficient of Correlation **r** = 0.990449
Time of calculatin = 0.171 [s]

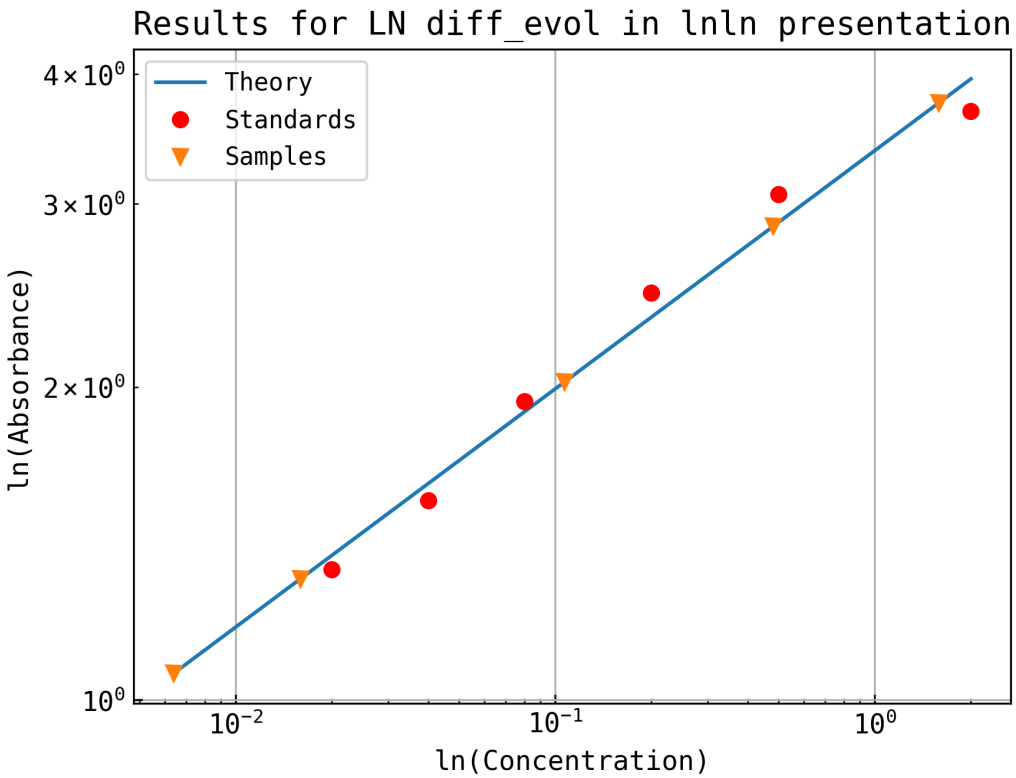
Plots





Plots





Calculation results

Good Samples	Conc.	SD down Conc.	SD up Conc.	Absorbance	SD Abs.
sam1	0.016	0.00003	0.00003	1.30820	0.00045
sam2	0.107	0.00956	0.00877	2.02162	0.01966
sam3	0.481	0.03140	0.02948	2.85460	0.01450
sam4	0.006	0.00005	0.00005	1.06032	0.00165
sam5	1.587	0.19192	0.17121	3.75304	0.02616

BLQ samples

	Bad Sample	Comment
1	sam1	blq_1_1
2	empty	blq_8_12