Project: ELISA paper project

Date: 20.05.2020 Test No.: 2

Performed by: Dorothy Smith on: 25.05.2020 17:46

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	0.1082	0.2991	0.1939	0.1828	0.17050	0.6505	0.7637	0.5210	1.2601	1.2463	1.1666
B	0.0476	0.0495	0.0507	0.2441	0.2514	0.24410	0.7130	0.8221	0.5766	1.3088	1.2625	1.1298
C	0.0823	0.0209	0.0511	0.1877	0.2897	0.39100	0.8218	0.9079	0.9711	1.1787	1.2468	1.1355
D	0.0809	0.0374	0.0574	0.3544	0.3363	0.35680	1.0577	1.1606	0.9585	1.2011	1.4123	1.2885
E	0.0715	0.0691	0.0713	0.3796	0.3438	0.37220	1.0464	1.0070	1.0465	1.2791	1.3068	1.3249
F	0.0872	0.0833	0.0862	0.5694	0.4298	0.32366	1.2113	1.1287	1.0285	1.2950	1.3729	1.331
G	0.0997	0.1028	0.0918	0.4690	0.5093	0.48490	1.1799	1.1708	1.1049	1.2815	1.2907	1.3055
H	0.1168	0.1169	0.1163	0.5439	0.5892	0.56420	1.2311	1.1618	1.1438	1.2415	1.3131	BLQ

Calibration standards

Std. name	Number	Absorbance	Conc.	Variation
std1	3	0.2895	0.02	0.08300
std2	3	0.4410	0.04	0.10063
std3	3	0.6451	0.08	0.09916
std4	3	0.9003	0.20	0.06119
std5	3	1.1228	0.50	0.07474
std6	3	1.3006	2.00	0.08665

Model: Linear fitting in lin_lin system

Absorbance = B*Conc + A

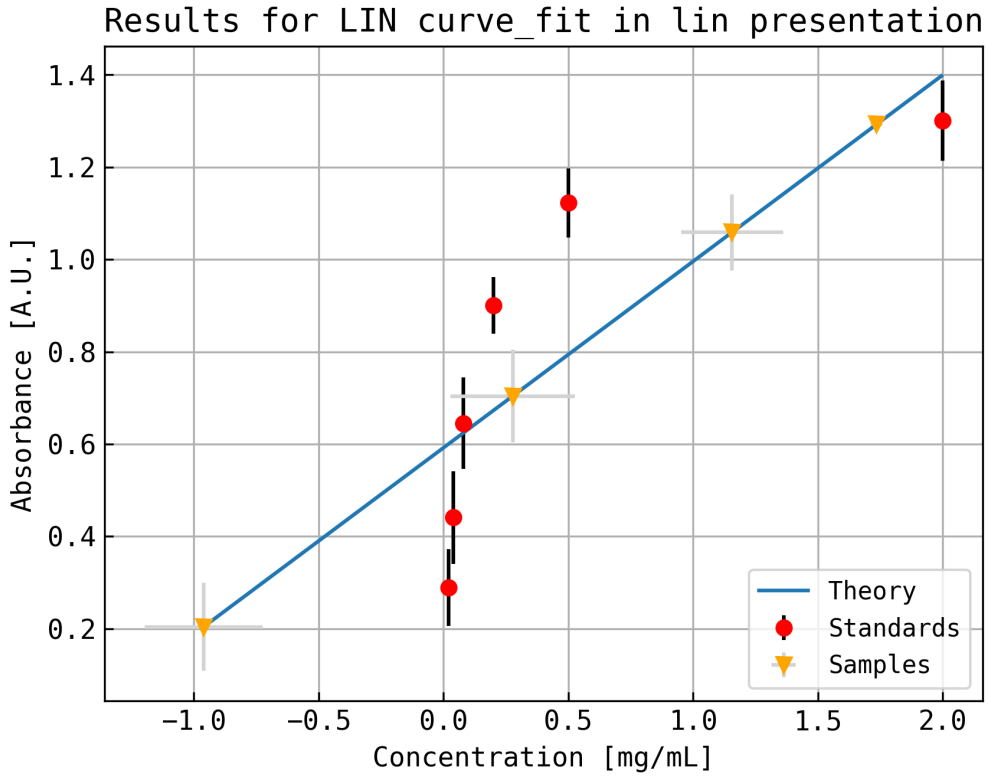
Model parameters

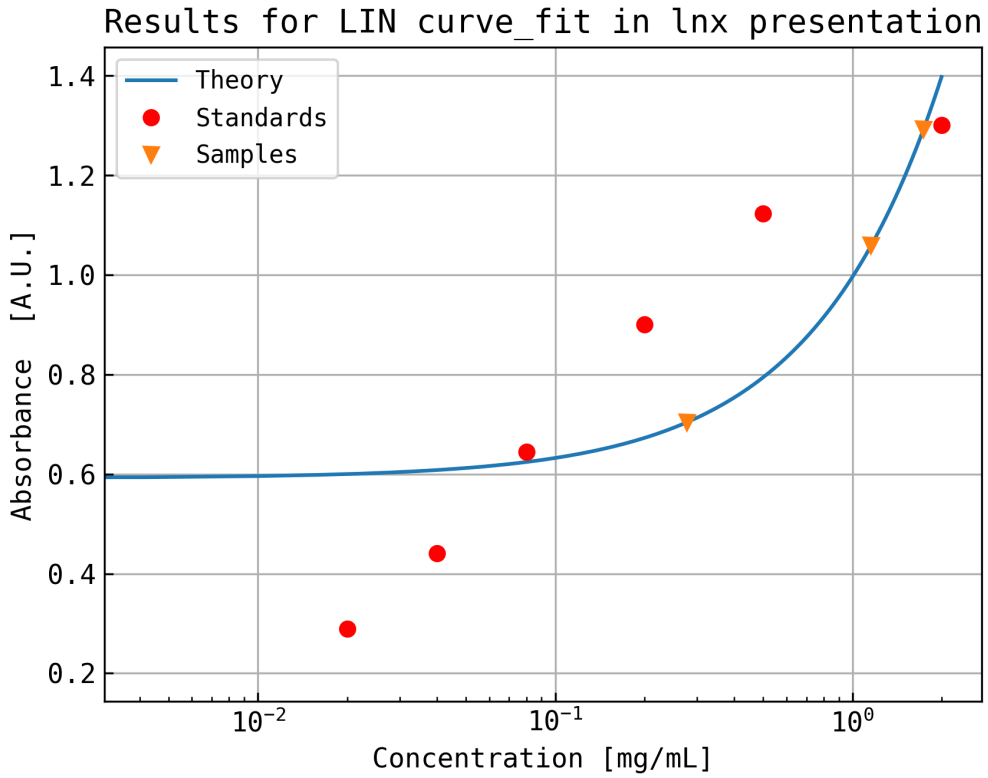
A= 0.591976, B= 0.404001

Model diagnostics

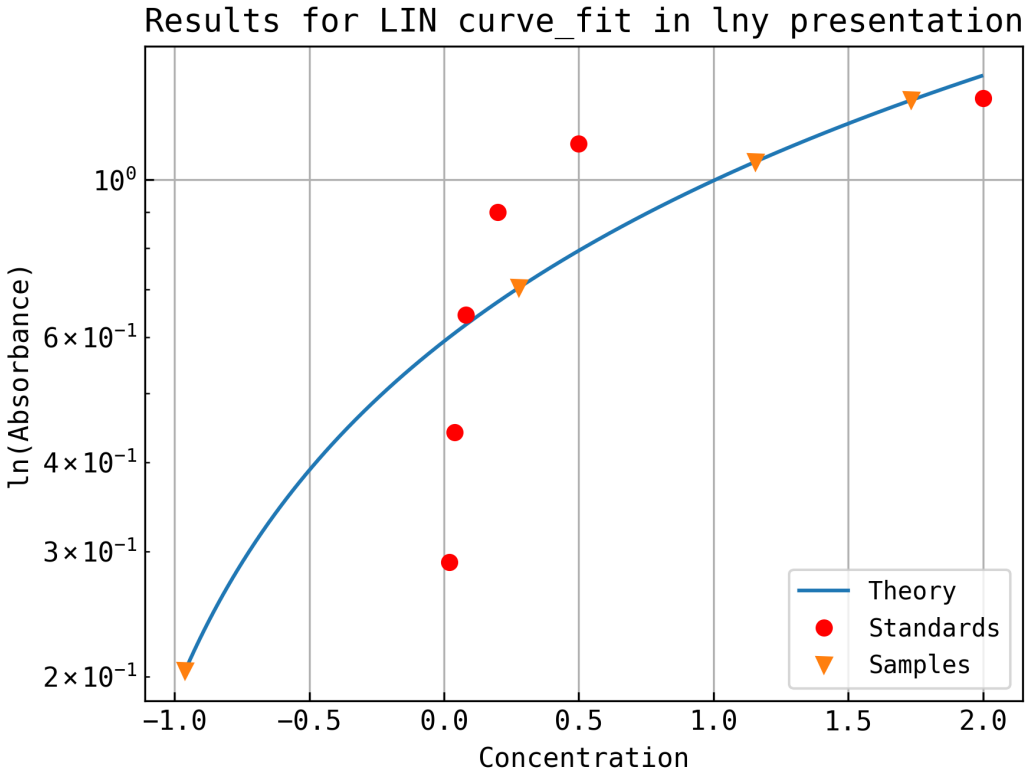
The Residual Sum of Squares **RSS** = 0.049103
Coefficient of Determination $\mathbf{R^2}$ = 0.620722
Akaike Information Criterion **AIC** = -14.083066
Bayesian Information Criterion **BIC** = -14.499547
Coefficient of Correlation **r** = 0.787859
Time of calculatin = 0.013 [s]

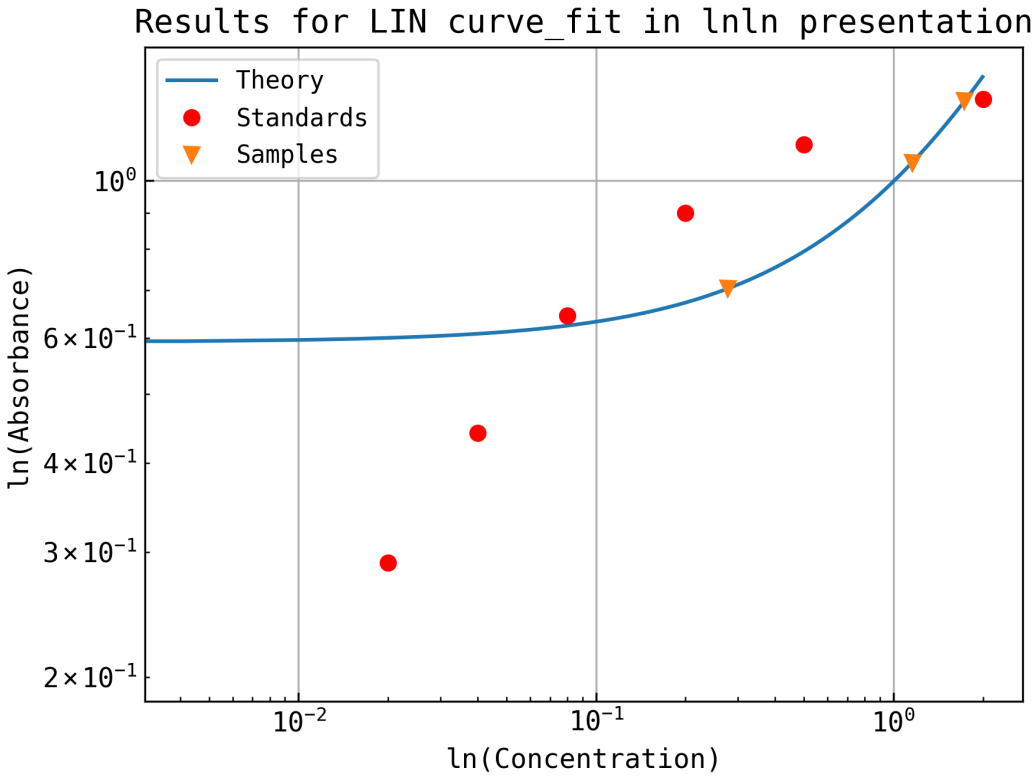
Plots





Plots





Calculation results

Good Samples	Conc.	SD down Conc.	SD up Conc.	Absorbance	SD Abs.
sam1	-0.961	0.23626	0.23626	0.20365	0.09545
sam2	0.277	0.24859	0.24859	0.70390	0.10043
sam3	1.156	0.20424	0.20424	1.05893	0.08251
sam5	1.734	0.02447	0.02447	1.29257	0.00989

BLQ samples

	Bad Sample	Comment
1	sam1	blq_1_1
2	empty	blq_8_12
3	sam4	err1