Appendix I

Media, buffer, solutions

Basal medium (BM)

Tryptone (Bacto, BD; USA)	7.5 g
Trypticase Peptone (Bacto, BD; USA)	7.5 g
Yeast Extract (Fluca, EU)	3 g
Beef extract (Acumedia, Michigan, USA)	5 g
NaCl (Sigma, USA)	5 g
K_2HPO_4 (BDH, USA)	2.3 g
KH_2PO_4 (UniVar, USA)	0.5 g
$MgSO_4 \cdot 7\ H_2O$ (Sigma, USA)	0.5 g
Resazurin –Anaerobic indicator	0.002 g
Distilled water added to make	1 L
Well mixed and sterilised by autoclave at 121°C for 15 min	
Filter-sterilised *L*-cysteine-HCl (add after autoclaving)	0.5 g
The final pH adjusted to 7.2 ± 0.2	

Brain Heart Infusion (BHI) broth

BHI powder (CM225, Oxoid, Hampshire, UK)	37 g
Distilled water added to make	1 L
Well mixed and sterilised by autoclave at 121°C for 15 min	

Dulbecco's modified Eagle's medium (DMEM) high glucose 1x

(Cat No. 11995, Invitrogen, Auckland, New Zealand)

6x gel loading dye

Bromophenol blue	0.25 g
Xylene cyanol FF	0.25 g
Ficoll Type 4000	15 g
0.5 M EDTA	24 mL

Distilled water added to make	100 mL

Minimum Essential Medium (MEM) 1x

(Cat No. 11095, Invitrogen, Auckland, New Zealand)

MRS Agar

MRS broth	1 L
Agar (Sigma, St. Louis, MO, USA)	15 g

Well mixed and sterilised by autoclave at 121°C for 15 min.

After cooled to 50 °C, the agar is poured into petri dishes 15-18 mL/each

MRS broth

De Man, Rogosa, Sharp (MRS) power (Difco$^{\text{TM}}$, Becton Dickinson, MD, USA)	55 g
Distilled water added to make	1 L

Well mixed and sterilised by autoclave at 121°C for 15 min

10x Phosphate buffered saline (10x PBS, pH 7.2)

(Cat No. 70013-032, Invitrogen, Auckland, New Zealand)

1x Phosphate buffered saline (1x PBS, pH 7.4)

10x Phosphate buffered saline	100 mL
Distilled water added to make	1 L

Mixed and sterilised by autoclave at 121°C for 15 min before use.

RPMI medium 1640 1x

(Cat. No. 22400, Invitrogen, Auckland, New Zealand)

50x TAE buffer

Tris base (Sigma, St. Louis, MO, USA)	242 g
Glacial acetic acid	57.1 mL
0.5 M EDTA (pH 8.0)	100 mL
Distilled water added to make	1 L

0.5x TAE buffer

50x TAE buffer	10 mL
Distilled water added to make	1 L

Appendix II

Data and analysis

Chapter 2

2.3.2 Antibacterial activities of *L. reuteri* DPC16 against pathogens

Agar diffusion assay:

Sample	Diameter of zone	Diameter of zone	Diameter of zone	Mean	SD
A.	8.8	8.3	11.0	9.4	1.5
B.	19.3	15.4	17.1	17.2	1.9
NC	8.3	7.7	8.3	8.1	0.3

```
Parameter           Value
Table Analyzed
Agar diffusion-D
One-way analysis of variance
  P value   0.0004
  P value summary     ***
  Are means signif. different? (P < 0.05)        Yes
  Number of groups    3
  F         36.64
  R squared           0.9243

ANOVA Table         SS          df          MS
  Treatment (between columns)   145.3       2           72.67
  Residual (within columns)     11.90       6           1.983
  Total     157.2       8

Tukey's Multiple Comparison Test            Mean Diff. q            P value      95% CI of diff
  NC vs A   -1.300      1.599       P > 0.05    -4.828 to 2.228
  NC vs B   -9.100      11.19       P < 0.001   -12.63 to -5.572
  A vs B    -7.800      9.593       P < 0.01    -11.33 to -4.272
```

Bacterial turbidity bioassays:

Expt-1:

DS	LM			SA		
Conc.	Growth(% of control)			Growth(% of control)		
0	102.24	97.01	100.87	96.93	107.33	95.86
0.8	113.59	111.10	109.35	74.23	69.39	76.24
1.6	118.58	101.25	102.00	77.54	82.39	83.45
3.1	121.32	114.21	120.20	64.66	66.55	58.98
6.3	138.15	136.28	137.66	78.25	74.35	68.68
12.5	153.62	146.01	138.15	64.07	56.15	41.61
25	135.66	168.20	65.96	53.07	54.96	28.49
50	55.24	58.98	57.48	39.24	34.04	30.97
PC	9.60	8.98	11.47	26.60	13.24	27.42

DS	ST			EC		
Conc.	Growth(% of control)			Growth(% of control)		
0	96.81	99.89	103.19	96.84	103.54	99.49
0.8	95.10	100.46	101.94	108.34	111.38	107.59
1.6	100.46	96.70	94.53	139.57	114.41	114.79
3.1	68.56	70.05	68.22	120.73	116.56	118.46
6.3	53.08	54.78	56.95	109.86	118.84	128.45
12.5	52.73	54.78	55.13	51.71	59.54	55.37
25	50.11	52.28	51.37	51.58	57.14	54.61
50	42.03	43.39	45.22	41.21	46.65	44.37
PC	7.06	8.77	8.77	12.90	13.27	12.52

Expt-2:

DS	LM			SA		
Conc.	Growth(% of control)			Growth(% of control)		
0	99.48	98.43	102.10	100.11	100.78	99.22
1.6	115.63	108.08	105.04	122.73	117.69	123.74
3.1	115.63	111.44	116.05	125.53	129.23	127.32
6.3	109.02	101.26	106.09	124.52	125.87	129.45
12.5	34.73	48.58	42.39	93.51	82.31	85.11
25	18.05	22.77	21.72	38.19	38.63	43.23
50	19.31	20.25	22.98	31.02	31.24	28.22
PC	42.29	35.99	40.92	34.27	37.18	37.74

DS	ST			EC		
Conc.	Growth(% of control)			Growth(% of control)		
0	98.32	99.91	101.86	98.94	103.83	97.13
1.6	122.73	117.69	123.74	105.32	95.32	101.17
3.1	125.53	129.23	127.32	106.28	98.10	100.06
6.3	124.52	125.87	129.45	78.94	76.49	78.30
12.5	93.51	82.31	85.11	66.91	69.68	67.34
25	38.19	38.63	43.23	40.74	34.15	35.64
50	31.02	31.24	28.22	38.40	40.53	31.06
PC	22.34	19.41	17.46	22.34	19.41	17.46

Expt-3:

DSg	LM			SA		
Conc.	Growth(% of control)			Growth(% of control)		
0	99.69	103.43	96.88	100.45	100.45	99.09
0.8	102.85	107.06	108.81	96.18	92.54	94.09
1.6	109.87	104.84	108.23	90.81	92.63	94.63
3.1	110.69	108.00	109.40	73.61	76.07	81.44
6.3	103.20	99.34	103.08	89.72	88.17	88.44
12.5	57.22	73.71	71.14	19.20	59.96	54.32
25	7.81	21.65	13.69	30.85	22.66	26.57
50	6.67	6.67	6.90	5.46	5.46	5.55

DSg	ST			EC		
Conc.	Growth(% of control)			Growth(% of control)		
0	103.24	99.97	96.79	101.12	100.05	98.83
0.8	108.83	105.36	103.05	100.40	101.05	98.98
1.6	110.95	108.44	105.07	99.90	98.98	97.69
3.1	114.51	113.84	109.12	103.19	102.26	101.47
6.3	108.15	104.98	107.77	105.04	105.11	103.19
12.5	68.28	74.54	65.10	56.02	57.37	62.58
25	29.35	21.38	19.45	23.57	18.48	17.98
50	6.07	6.26	6.16	5.42	5.49	5.21

Expt-4:

LM	DS			DSg		
Conc.	Growth(% of control)			Growth(% of control)		
0	95.79	100.84	103.23	95.79	100.84	103.23
1.6	109.83	121.77	125.00	121.49	103.93	131.74
3.1	140.03	120.93	120.51	116.29	118.40	113.06
6.3	125.14	120.22	113.90	101.83	118.26	112.64
12.5	99.72	115.31	110.11	69.80	71.91	70.65
25	88.06	111.94	116.57	43.26	45.22	45.22
50	50.00	33.29	43.96	-1.26	-1.12	-1.69
PC	-0.84	0.42	0.14	-0.84	0.42	0.14

SA	DS			DSg		
Conc.	Growth(% of control)			Growth(% of control)		
0	99.80	103.18	97.01	99.80	103.18	97.01
1.6	99.70	96.02	99.60	96.62	96.32	100.70
3.1	97.81	95.52	101.69	88.06	96.52	96.52
6.3	91.14	86.77	92.34	92.34	86.97	92.34
12.5	97.51	93.83	100.60	90.45	85.97	102.39
25	58.71	71.64	86.67	65.67	66.57	75.42
50	17.81	17.01	17.31	1.79	1.29	1.29
PC	-0.20	-0.70	-0.10	-0.20	-0.70	-0.10

ST	DS			DSg		
Conc.	Growth(% of control)			Growth(% of control)		
0	99.14	99.51	101.22	99.14	99.51	101.22
1.6	102.57	102.08	100.49	92.90	94.49	93.76
3.1	108.32	105.26	106.24	91.31	98.04	95.72
6.3	108.69	116.16	116.28	77.48	79.93	82.25
12.5	81.64	85.80	92.53	46.39	51.04	50.80
25	57.65	55.94	36.84	35.99	36.84	35.86
50	0.00	-0.37	0.12	-0.37	-0.12	-0.12
PC	-2.20	-2.20	-0.49	-2.20	-2.20	-0.49

EC	DS			DSg		
Conc.	Growth(% of control)			Growth(% of control)		
0	97.91	98.26	103.83	97.91	98.26	103.83
1.6	97.79	104.07	110.10	103.60	95.82	99.30
3.1	111.85	101.97	102.56	101.51	107.78	104.76
6.3	113.82	116.03	118.23	92.22	93.15	90.94
12.5	77.35	90.24	91.06	66.20	65.97	64.34
25	73.29	72.24	72.24	61.67	59.70	58.77
50	70.03	74.56	76.42	38.33	41.93	39.72
PC	-1.28	-0.70	-1.63	-1.28	-0.70	-1.63

Expt-5:

24h	NC			PC		
Strain	Growth(% of control)			Growth(% of control)		
LM	113.95	97.17	88.88	10.41	10.99	11.18
SA	102.79	103.05	94.16	27.16	27.16	28.68
ST	100.63	97.60	101.77	24.59	25.91	23.27
EC	97.23	85.45	117.32	21.02	19.86	23.79

24h	12.5% DS			12.5% DSg		
Strain	Growth(% of control)			Growth(% of control)		
LM	126.29	121.85	128.79	82.13	73.84	74.42
SA	103.81	109.14	120.30	32.23	32.23	31.98
ST	86.07	83.80	82.28	63.37	58.26	49.75
EC	78.29	76.21	93.30	55.66	44.34	90.07

Expt-6:

24h	NC			PC		
Strain	Growth(% of control)			Growth(% of control)		
LM	91.45	105.39	103.16	11.72	14.01	15.58
SA	97.56	101.36	101.07	22.29	23.70	20.52
ST	100.97	100.68	98.35	23.87	23.34	24.05
EC	97.02	97.45	105.53	11.49	11.99	11.23

24h	6.3% DS			6.3% DSg			6.3% Dg		
Strain	Growth(% of control)			Growth(% of control)			Growth(% of control)		
LM	145.82	150.84	129.93	75.69	83.14	87.06	159.81	169.38	172.97
SA	123.68	120.96	117.74	41.55	57.93	64.31	87.93	77.88	84.83
ST	117.64	120.93	118.02	66.52	64.32	63.02	87.55	52.48	72.41
EC	146.81	146.24	130.07	105.20	101.48	83.57	81.29	80.56	85.24

Expt-7:

Nonlinear regression (curve fit) analysis for *L. reuteri* DPC16 supernatants:

Supernatants against *Listeria monocytogenes:*

Sup	DS					
Conc.	Growth(% of control)					
0	99.26	99.00	98.57	100.20	101.31	101.65
0.8	102.51	102.51	104.65			
1.6	97.63	101.74	104.39			
3.1	103.71	103.96	108.84			
6.3	106.62	103.54	112.61			
12.5	105.59	103.19	97.12			
25	22.42	21.99	17.46			
50	10.52	15.06	16.26			
PC	0.68	0.86	0.34	0.26	0.09	1.20

Sup	DSg					
Conc.	Growth(% of control)					
0	99.26	99.00	98.57	100.20	101.31	101.65
0.8	105.93	106.62	106.19			
1.6	107.39	97.72	103.88			
3.1	107.56	103.37	101.48			
6.3	42.53	37.82	38.25			
12.5	14.03	13.26	12.41			
25	9.84	10.10	9.16			
50	2.57	2.65	2.40			
PC	0.68	0.86	0.34	0.26	0.09	1.20

Sup	Dg					
Conc.	Growth(% of control)					
0	99.26	99.00	98.57	100.20	101.31	101.65
0.8	107.73	88.65	103.96			
1.6	98.92	99.00	102.51			
3.1	106.02	105.85	97.80			
6.3	30.21	35.42	24.81			
12.5	5.22	9.33	8.64			
25	-0.09	0.17	7.02			
50	0.09	0.51	0.26			
PC	0.68	0.86	0.34	0.26	0.09	1.20

```
                                    DS          DSg        Dg        Global (shared)
Comparison of Fits
    Null hypothesis                                        2 parameters same for all data sets
    Alternative hypothesis                                           2 parameters different for each data set
    P value                                     P<0.0001
    Conclusion (alpha = 0.05)                                        Reject null hypothesis
    Preferred model                                        2 parameters different for each data set
    F (DFn, DFd)                                           316.4 (4,55)

2 parameters different for each data set
Best-fit values
```

```
   BOTTOM           7.011     7.011     7.011     7.011
   TOP    103.6     103.6     103.6     103.6
   LOGEC50          1.304     0.7578    0.7438
   HILLSLOPE        -8.295    -6.995    -9.030
   EC50   20.12     5.726     5.543
Std. Error
   BOTTOM           1.077     1.077     1.077     1.077
   TOP    0.9929    0.9929    0.9929    0.9929
   LOGEC50          0.02871   0.01991   0.05100
   HILLSLOPE        2.410     3.085     8.166
95% Confidence Intervals
   BOTTOM           4.851 to 9.171      4.851 to 9.171      4.851 to 9.171      4.851 to 9.171
   TOP    101.6 to 105.6      101.6 to 105.6      101.6 to 105.6      101.6 to 105.6
   LOGEC50          1.246 to 1.361      0.7179 to 0.7978    0.6415 to 0.8460
   HILLSLOPE        -13.13 to -3.463    -13.18 to -0.8083   -25.40 to 7.345
   EC50   17.62 to 22.97      5.223 to 6.277      4.380 to 7.015
Goodness of Fit
   Degrees of Freedom                                       55
   R²     0.9885    0.9930    0.9859    0.9900
   Absolute Sum of Squares    374.4     297.5     630.7     1303
   Sy.x                                 4.867
Normality of Residuals
   Kolmogorov-Smirnov distance0.1367    0.1840    0.1402
   P value  P > 0.10  0.0616    P > 0.10
   D'Agostino & Pearson omnibus K2      0.6132    1.865     1.267
   P value  0.7359    0.3937    0.5308
   Shapiro-Wilk W   0.9608    0.9342    0.9384
   P value  0.5326    0.1671    0.2022
Constraints
   BOTTOM           BOTTOM is shared    BOTTOM is shared    BOTTOM is shared
   TOP    TOP is shared       TOP is shared       TOP is shared
```

Supernatants against *Staphylococcus aureus*

Sup	DS					
Conc.	Growth(% of control)					
0	102.79	104.61	103.40	97.92	96.00	95.29
0.8	113.23	111.30	109.68			
1.6	107.15	105.93	113.63			
3.1	105.63	111.40	94.58			
6.3	95.18	93.06	87.28			
12.5	71.77	71.26	56.66			
25	16.73	20.88	17.64			
50	8.82	12.67	5.17			
PC	0.41	0.01	0.61	0.41	0.61	0.61

Sup	DSg					
Conc.	Growth(% of control)					
0	102.79	104.61	103.40	97.92	96.00	95.29
0.8	103.19	98.33	97.62			
1.6	64.77	58.08	58.69			
3.1	41.76	41.76	30.11			
6.3	16.52	18.45	14.60			
12.5	15.00	14.70	14.09			
25	9.83	8.51	8.92			
50	1.93	1.93	2.33			
PC	0.41	0.01	0.61	0.41	0.61	0.61

Sup	DS					
Conc.	Growth(% of control)					
0	102.79	104.61	103.40	97.92	96.00	95.29
0.8	94.68	98.12	96.71			
1.6	31.12	63.46	58.59			
3.1	8.11	35.07	22.61			
6.3	0.61	0.61	0.61			
12.5	0.71	0.91	0.41			
25	0.10	0.20	0.30			
50	0.41	0.61	0.61			
PC	0.41	0.01	0.61	0.41	0.61	0.61

```
                            DS          DSg         Dg          Global (shared)
Comparison of Fits
    Null hypothesis                                 2 parameters same for all data sets
    Alternative hypothesis                                      2 parameters different for each data set
    P value                             P<0.0001
    Conclusion (alpha = 0.05)                                   Reject null hypothesis
    Preferred model                                 2 parameters different for each data set
    F (DFn, DFd)                                    209.9 (4,54)

2 parameters different for each data set
Best-fit values
    BOTTOM              2.743       2.743       2.743       2.743
    TOP     110.6       110.6       110.6       110.6
    LOGEC50             1.131       0.3031      0.1786
    HILLSLOPE           -2.356      -1.684      -2.667
    EC50    13.53       2.010       1.509
Std. Error
    BOTTOM              1.632       1.632       1.632       1.632
    TOP     2.505       2.505       2.505       2.505
    LOGEC50             0.02504     0.03037     0.02534
    HILLSLOPE           0.2857      0.1805      0.3361
95% Confidence Intervals
    BOTTOM              -0.5314 to 6.016        -0.5314 to 6.016        -0.5314 to 6.016        -0.5314 to 6.016
    TOP     105.6 to 115.6          105.6 to 115.6          105.6 to 115.6          105.6 to 115.6
    LOGEC50             1.081 to 1.181          0.2422 to 0.3641        0.1278 to 0.2294
    HILLSLOPE           -2.929 to -1.783        -2.046 to -1.322        -3.341 to -1.992
    EC50    12.05 to 15.19          1.747 to 2.312          1.342 to 1.696
Goodness of Fit
    Degrees of Freedom                                          54
    R²      0.9814      0.9692      0.9520      0.9772
    Absolute Sum of Squares         631.0       684.1       1169        2484
    Sy.x                                        6.782
Normality of Residuals
    Kolmogorov-Smirnov distance 0.08923         0.1754      0.2555
    P value  P > 0.10   0.0911      0.0014
    D'Agostino & Pearson omnibus K2             0.3289      1.175       5.340
    P value  0.8483     0.5557      0.0692
    Shapiro-Wilk W      0.9815      0.9374      0.8645
    P value  0.9450     0.1932      0.0094
Constraints
    BOTTOM              BOTTOM is shared        BOTTOM is shared        BOTTOM is shared
    TOP     TOP is shared           TOP is shared           TOP is shared
```

Supernatants against *Salmonella typhimurium*

Sup	DS					
Conc.	Growth(% of control)					
0	91.39	95.54	99.94	101.07	104.46	107.61
0.8	104.46	112.51	116.91			
1.6	106.85	116.91	114.27			
3.1	103.96	114.52	109.87			
6.3	111.88	117.54	124.32			
12.5	118.42	123.95	119.92			
25	23.13	27.40	23.00			
50	18.98	22.25	10.31			
PC	0.00	0.01	0.50	0.13	0.00	0.13

Sup	DSg					
Conc.	Growth(% of control)					
0	91.39	95.54	99.94	101.07	104.46	107.61
0.8	117.28	117.28	119.30			
1.6	109.24	112.76	113.26			
3.1	117.54	119.92	117.16			
6.3	104.84	99.31	97.17			
12.5	21.37	17.98	17.35			
25	12.70	11.69	7.54			
50	2.51	2.26	2.14			
PC	0.00	0.01	0.50	0.13	0.00	0.13

Sup	DS					
Conc.	Growth(% of control)					
0	91.39	95.54	99.94	101.07	104.46	107.61
0.8	118.67	120.30	119.17			
1.6	107.86	110.50	113.64			
3.1	114.39	114.77	113.39			
6.3	62.48	32.56	42.11			
12.5	0.75	1.63	3.52			
25	-0.25	0.50	-0.13			
50	0.38	1.26	0.63			
PC	0.00	0.01	0.50	0.13	0.00	0.13

```
                             DS          DSg         Dg           Global (shared)
Comparison of Fits
    Null hypothesis                                  2 parameters same for all data sets
    Alternative hypothesis                                        2 parameters different for each data set
    P value                              P<0.0001
    Conclusion (alpha = 0.05)                                     Reject null hypothesis
    Preferred model                                  2 parameters different for each data set
    F (DFn, DFd)                                     266.3 (4,54)

2 parameters different for each data set
Best-fit values
    BOTTOM              5.401      5.401      5.401      5.401
    TOP       115.0     115.0      115.0      115.0
    LOGEC50             1.359      0.9456     0.7723
    HILLSLOPE           -17.44     -5.592     -14.25
    EC50      22.87     8.823      5.919
Std. Error
    BOTTOM              1.342      1.342      1.342      1.342
    TOP       1.085     1.085      1.085      1.085
```

```
    LOGEC50            3.106        0.01554    0.8185
    HILLSLOPE          1348         0.5719     430.3
95% Confidence Intervals
    BOTTOM             2.708 to 8.094          2.708 to 8.094          2.708 to 8.094          2.708 to 8.094
    TOP      112.8 to 117.1         112.8 to 117.1          112.8 to 117.1          112.8 to 117.1
    LOGEC50            -4.871 to 7.590         0.9144 to 0.9768        -0.8698 to 2.414
    HILLSLOPE          -2721 to 2686           -6.739 to -4.445        -877.5 to 849.0
    EC50     1.344e-005 to 3.890e+007          8.211 to 9.479          0.1350 to 259.6
Goodness of Fit
    Degrees of Freedom                                                 54
    R²       0.9722    0.9950       0.9937     0.9895
    Absolute Sum of Squares         1063       269.8       371.6       1705
    Sy.x                                       5.619
Normality of Residuals
    Kolmogorov-Smirnov distance     0.1137     0.1676      0.2165
    P value  P > 0.10  P > 0.10     0.0148
    D'Agostino & Pearson omnibus K2            0.4990      2.600       3.140
    P value  0.7792    0.2725       0.2080
    Shapiro-Wilk W     0.9738       0.9453     0.8618
    P value  0.8150    0.2772       0.0084
Constraints
    BOTTOM             BOTTOM is shared        BOTTOM is shared        BOTTOM is shared
    TOP      TOP is shared          TOP is shared           TOP is shared
```

Supernatants against *Escherichia coli*

Sup	DS					
Conc.	Growth(% of control)					
0	86.48	95.93	103.41	105.67	102.14	106.37
0.8	105.24	109.90	108.21			
1.6	99.32	116.67	119.07			
3.1	121.33	121.75	118.50			
6.3	129.09	125.14	113.85			
12.5	123.44	132.75	77.31			
25	0.42	29.06	2.40			
50	0.99	1.13	1.27			
PC	0.00	0.00	1.13	3.67	0.42	0.56

Sup	DSg					
Conc.	Growth(% of control)					
0	86.48	95.93	103.41	105.67	102.14	106.37
0.8	113.85	118.65	118.50			
1.6	123.02	125.98	124.01			
3.1	123.72	126.26	127.82			
6.3	75.05	57.70	107.22			
12.5	29.20	35.83	2.96			
25	13.26	25.82	9.17			
50	0.85	1.13	0.71			
PC	0.00	0.00	1.13	3.67	0.42	0.56

Sup	DS					
Conc.	Growth(% of control)					
0	86.48	95.93	103.41	105.67	102.14	106.37
0.8	122.17	97.77	102.00			
1.6	119.35	120.20	111.17			
3.1	119.63	116.81	99.74			
6.3	11.99	14.53	41.48			
12.5	1.55	1.55	1.69			
25	0.56	0.85	0.99			
50	0.00	0.14	0.42			
PC	0.00	0.00	1.13	3.67	0.42	0.56

```
                              DS        DSg       Dg        Global (shared)
Comparison of Fits
   Null hypothesis                                2 parameters same for all data sets
   Alternative hypothesis                                   2 parameters different for each data set
   P value                              P<0.0001
   Conclusion (alpha = 0.05)                                Reject null hypothesis
   Preferred model                                2 parameters different for each data set
   F (DFn, DFd)                                   66.29 (4,55)

2 parameters different for each data set
Best-fit values
   BOTTOM           3.054     3.054     3.054     3.054
   TOP    117.3     117.3     117.3     117.3
   LOGEC50          1.241     0.9023    0.6943
   HILLSLOPE        -7.371    -3.604    -6.524
   EC50   17.44     7.985     4.947
Std. Error
   BOTTOM           2.853     2.853     2.853     2.853
   TOP    2.315     2.315     2.315     2.315
   LOGEC50          0.03921   0.03059   0.03798
   HILLSLOPE        1.910     0.7262    2.100
95% Confidence Intervals
   BOTTOM           -2.666 to 8.774     -2.666 to 8.774     -2.666 to 8.774     -2.666 to 8.774
   TOP    112.7 to 122.0      112.7 to 122.0      112.7 to 122.0      112.7 to 122.0
   LOGEC50          1.163 to 1.320      0.8409 to 0.9636    0.6182 to 0.7705
   HILLSLOPE        -11.20 to -3.541    -5.060 to -2.148    -10.73 to -2.313
   EC50   14.55 to 20.90      6.933 to 9.196      4.151 to 5.895
Goodness of Fit
   Degrees of Freedom                                       55
   R²     0.9472    0.9459    0.9749    0.9590
   Absolute Sum of Squares    2814      3085      1505      7403
   Sy.x                                 11.60
Normality of Residuals
   Kolmogorov-Smirnov distance 0.09312  0.1313    0.1857
   P value  P > 0.10  P > 0.10  0.0570
   D'Agostino & Pearson omnibus K2      1.891     3.507     2.452
   P value  0.3886  0.1731    0.2934
   Shapiro-Wilk W   0.9680    0.9537    0.9497
   P value  0.6884  0.3985    0.3366
Constraints
   BOTTOM           BOTTOM is shared    BOTTOM is shared    BOTTOM is shared
   TOP    TOP is shared       TOP is shared       TOP is shared
```

Antibacterial activities of *L. reuteri* DPC16 supernatants and the effects of pH-neutralization

Sup	DS			DS7.0		
Conc.	Growth(% of control)			Growth(% of control)		
0	86.48	95.93	103.41	105.67	102.14	106.37
0.8	105.24	109.90	108.21	118.22	119.35	106.94
1.6	99.32	116.67	119.07	126.55	125.14	111.87
3.1	121.33	121.75	118.50	119.35	109.90	136.42
6.3	129.09	125.14	113.85	127.53	116.67	104.96
12.5	123.44	132.75	77.31	121.33	121.75	132.61
25	0.42	29.06	2.40	129.09	125.14	113.85
50	0.99	1.13	1.27	109.33	90.43	105.53
PC	0.00	0.14	1.13	3.67	0.42	0.56

```
                                    DS          DS7.0       Global (shared)
Comparison of Fits
    Null hypothesis                             3 parameters same for all data sets
    Alternative hypothesis                                  3 parameters different for each data set
    P value                         P<0.0001
    Conclusion (alpha = 0.05)                               Reject null hypothesis
    Preferred model                             3 parameters different for each data set
    F (DFn, DFd)                                83.81 (3,35)

3 parameters different for each data set
Best-fit values
    BOTTOM              1.088       -26.60
    TOP     118.5       118.5       118.5
    LOGEC50             1.256       1.745
    HILLSLOPE           -7.426      -19.27
    EC50    18.03       55.58
Std. Error
    BOTTOM              6.810       5.313e+009
    TOP     2.244       2.244       2.244
    LOGEC50             0.04428     979397
    HILLSLOPE           2.093       7.097e+006
95% Confidence Intervals
    BOTTOM              -12.75 to 14.92         -10790000000 to 1.079e+010
    TOP     113.9 to 123.0          113.9 to 123.0          113.9 to 123.0
    LOGEC50             1.166 to 1.346          -1990000 to 1.990e+006
    HILLSLOPE           -11.68 to -3.173        -14420000 to 1.442e+007
    EC50    14.66 to 22.18
Goodness of Fit
    Degrees of Freedom                                      35
    R²      0.9409      0.3482      0.9309
    Absolute Sum of Squares         3199        1547        4746
    Sy.x                            11.64
Normality of Residuals
    Kolmogorov-Smirnov distance 0.1175      0.1009
    P value  P > 0.10     P > 0.10
    D'Agostino & Pearson omnibus K2         2.628       0.4745
    P value  0.2688      0.7888
    Shapiro-Wilk W   0.9647      0.9730
    P value  0.6149      0.7973
Constraints
    TOP     TOP is shared           TOP is shared
```

Sup	DSg			DSg7.0		
Conc.	Growth(% of control)			Growth(% of control)		
0	86.48	95.93	103.41	105.67	102.14	106.37
0.8	113.85	118.65	118.50	118.22	119.35	121.04
1.6	123.02	125.98	124.01	126.55	125.14	125.98
3.1	123.72	126.26	127.82	133.88	136.84	136.00
6.3	75.05	57.70	107.22	128.10	127.25	117.23
12.5	29.20	35.83	2.96	94.80	94.24	79.99
25	13.26	25.82	9.17	0.85	1.98	1.13
50	0.85	1.13	0.71	0.85	0.99	1.69
PC	0.00	0.14	1.13	3.67	0.42	0.56

```
                        DSg         DSg7.0      Global (shared)
Comparison of Fits
    Null hypothesis                             2 parameters same for all data sets
    Alternative hypothesis                                  2 parameters different for each data set
    P value                         P<0.0001
    Conclusion (alpha = 0.05)                               Reject null hypothesis
    Preferred model                             2 parameters different for each data set
    F (DFn, DFd)                                51.99 (2,36)

2 parameters different for each data set
Best-fit values
    BOTTOM              4.102       4.102       4.102
    TOP     125.4       125.4       125.4
    LOGEC50             0.8753      1.113
    HILLSLOPE           -3.332      -23.38
    EC50    7.504       12.98
Std. Error
    BOTTOM              3.500       3.500       3.500
    TOP     2.272       2.272       2.272
    LOGEC50             0.02609     199.8
    HILLSLOPE           0.5870      279999
95% Confidence Intervals
    BOTTOM              -3.000 to 11.20         -3.000 to 11.20         -3.000 to 11.20
    TOP     120.8 to 130.0          120.8 to 130.0          120.8 to 130.0
    LOGEC50             0.8223 to 0.9282        -404.4 to 406.6
    HILLSLOPE           -4.523 to -2.141        -568300 to 568207
    EC50    6.643 to 8.477
Goodness of Fit
    Degrees of Freedom                                      36
    R²      0.9523      0.9891      0.9722
    Absolute Sum of Squares         2721        692.2       3413
    Sy.x                            9.737
Normality of Residuals
    Kolmogorov-Smirnov distance 0.1256          0.1452
    P value P > 0.10    P > 0.10
    D'Agostino & Pearson omnibus K2             0.6422      1.184
    P value 0.7253      0.5532
    Shapiro-Wilk W      0.9784      0.9574
    P value 0.9006      0.4657
Constraints
    BOTTOM              BOTTOM is shared        BOTTOM is shared
    TOP     TOP is shared           TOP is shared
```

Sup	Dg			Glycerol		
Conc.	Growth(% of control)			Growth(% of control)		
0	92.16	98.16	99.56	100.81	104.58	104.72
0.8	120.92	96.77	100.95	117.43	118.41	112.54
1.6	118.13	118.97	110.03	104.44	116.87	121.62
3.1	118.41	115.62	98.72	121.48	117.99	107.94
6.3	11.87	14.38	41.05	124.55	124.41	118.27
12.5	1.54	1.54	1.68	138.79	138.79	122.74
25	0.56	0.84	0.98	138.93	126.09	118.55
50	0.00	0.14	0.42	152.06	148.29	143.96
PC	0.00	0.00	0.14	0.00	0.00	0.56

```
                                        Dg            Glycerol      Global (shared)
Comparison of Fits
    Null hypothesis                                   3 parameters same for all data sets
    Alternative hypothesis                                          3 parameters different for each data set
    P value                             P<0.0001
    Conclusion (alpha = 0.05)                                       Reject null hypothesis
    Preferred model                                   3 parameters different for each data set
    F (DFn, DFd)                                      225.5 (3,35)

3 parameters different for each data set
Best-fit values
    BOTTOM                0.3796        115.4
    TOP       126.6       126.6         126.6
    LOGEC50               0.6607        0.7880
    HILLSLOPE             -4.774        15.60
    EC50      4.578       6.137
Std. Error
    BOTTOM                4.098         4.713
    TOP       3.204       3.204         3.204
    LOGEC50               0.03029       2.130
    HILLSLOPE             0.9029        1004
95% Confidence Intervals
    BOTTOM                -7.946 to 8.705             105.8 to 125.0
    TOP       120.1 to 133.2            120.1 to 133.2              120.1 to 133.2
    LOGEC50               0.5991 to 0.7222            -3.539 to 5.115
    HILLSLOPE             -6.608 to -2.940            -2023 to 2054
    EC50      3.973 to 5.275            0.0002890 to 130335
Goodness of Fit
    Degrees of Freedom                                              35
    R²        0.9541      0.3398        0.9588
    Absolute Sum of Squares             2693          2250          4943
    Sy.x                                11.88
Normality of Residuals
    Kolmogorov-Smirnov distance         0.2100        0.1705
    P value   0.0164      P > 0.10
    D'Agostino & Pearson omnibus K2                   3.380         1.559
    P value   0.1845      0.4587
    Shapiro-Wilk W        0.9223        0.9537
    P value   0.0966      0.3999
Constraints
    TOP       TOP is shared             TOP is shared
```

2.3.4 The effect of DSg on the growth kinetics of some pathogens and probiotics

Listeria monocytogenes:

LM	NC			DSg			PC		
Time(h)	OD			OD			OD		
0	0.056	0.057	0.056	0.058	0.058	0.058	0.058	0.060	0.059
8	0.340	0.350	0.339	0.056	0.055	0.057	0.055	0.056	0.055
10	0.508	0.518	0.485	0.075	0.065	0.066	0.054	0.058	0.055
12	0.750	0.748	0.715	0.226	0.171	0.133	0.054	0.058	0.055
14	0.933	0.948	0.901	0.425	0.375	0.349	0.058	0.056	0.057
16	1.070	1.095	1.053	0.552	0.538	0.511	0.059	0.057	0.054
18	1.116	1.297	1.267	0.652	0.679	0.687	0.055	0.055	0.055
20	1.239	1.273	1.291	0.768	0.798	0.832	0.058	0.056	0.058
22	1.340	1.307	1.273	0.848	0.896	0.827	0.058	0.057	0.056
24	1.390	1.232	1.245	0.901	0.837	0.812	0.059	0.054	0.054

```
                                                NC          DSg         Global (shared)
Comparison of Fits
    Null hypothesis                             3 parameters same for all data sets
    Alternative hypothesis                                  3 parameters different for each data set
    P value                         P<0.0001
    Conclusion (alpha = 0.05)                               Reject null hypothesis
    Preferred model                             3 parameters different for each data set
    F (DFn, DFd)                                678.6 (3,53)

3 parameters different for each data set
Best-fit values
    OD      0.05601     0.05601     0.05601
    C       1.325       0.8490
    MUE     0.1131      0.09800
    LAG     5.832       10.88
Std. Error
    OD      0.01256     0.01256     0.01256
    C       0.02884     0.03252
    MUE     0.005362    0.007002
    LAG     0.2894      0.3411
95% Confidence Intervals
    OD      0.03080 to 0.08123      0.03080 to 0.08123      0.03080 to 0.08123
    C       1.267 to 1.383          0.7837 to 0.9143
    MUE     0.1023 to 0.1238        0.08394 to 0.1121
    LAG     5.251 to 6.413          10.20 to 11.57
Goodness of Fit
    Degrees of Freedom                                      53
    R²      0.9893      0.9923      0.9927
    Absolute Sum of Squares         0.05784     0.02408     0.08192
    Sy.x                            0.03932
Normality of Residuals
    Kolmogorov-Smirnov distance 0.08588     0.1684
    P value P > 0.10    0.0296
    D'Agostino & Pearson omnibus K2             1.648       1.888
    P value 0.4387      0.3891
    Shapiro-Wilk W      0.9757      0.9412
    P value 0.7036      0.0978
Constraints
    OD      OD is shared            OD is shared
```

Staphylococcus aureus:

SA	NC			DSg			PC		
Time(h)	OD			OD			OD		
0	0.056	0.056	0.056	0.057	0.057	0.058	0.059	0.059	0.059
8	0.321	0.294	0.284	0.053	0.055	0.055	0.057	0.056	0.060
10	0.574	0.530	0.313	0.054	0.058	0.055	0.057	0.061	0.059
12	0.752	0.675	0.472	0.056	0.061	0.054	0.057	0.060	0.058
14	0.822	0.832	0.761	0.055	0.059	0.053	0.055	0.055	0.055
16	0.818	0.811	0.807	0.056	0.056	0.063	0.059	0.057	0.059
18	0.865	0.809	0.859	0.072	0.065	0.070	0.059	0.056	0.058
20	0.889	0.831	0.762	0.154	0.111	0.094	0.058	0.058	0.062
22	0.807	0.880	0.851	0.477	0.338	0.208	0.065	0.058	0.056
24	0.801	0.853	0.849	0.489	0.415	0.302	0.068	0.056	0.054

```
                                          NC          DSg          Global (shared)
Comparison of Fits
    Null hypothesis                       3 parameters same for all data sets
    Alternative hypothesis                            3 parameters different for each data set
    P value                         P<0.0001
    Conclusion (alpha = 0.05)                         Reject null hypothesis
    Preferred model                       3 parameters different for each data set
    F (DFn, DFd)                          519.1 (3,54)

3 parameters different for each data set
Best-fit values
    OD        0.0570      0.0570
    C         0.7967      0.3551
    MUE       0.1109      0.1339
    LAG       5.993       19.56
Std. Error
    C         0.02157     0.03764
    MUE       0.01553     0.03738
    LAG       0.5461      0.3085
95% Confidence Intervals
    C         0.7525 to 0.8410      0.2778 to 0.4323
    MUE       0.07900 to 0.1427     0.05718 to 0.2106
    LAG       4.873 to 7.114        18.93 to 20.19
Goodness of Fit
    Degrees of Freedom              27          27
    R²        0.9484      0.8915
    Absolute Sum of Squares         0.1134      0.05643
    Sy.x      0.06480     0.04572
Normality of Residuals
    Kolmogorov-Smirnov distance 0.2498      0.3230
    P value  P<0.0001   P<0.0001
    D'Agostino & Pearson omnibus K2         18.71       10.82
    P value  P<0.0001   0.0045
    Shapiro-Wilk W        0.8262      0.6994
    P value  0.0002       P<0.0001
Constraints
    OD        OD = 0.0570           OD = 0.0570
```

Salmonella typhimurium:

ST	NC			DSg			PC		
Time(h)	OD			OD			OD		
0	0.058	0.061	0.058	0.059	0.059	0.059	0.062	0.066	0.062
8	0.552	0.509	0.497	0.104	0.068	0.070	0.061	0.065	0.063
10	0.671	0.649	0.635	0.165	0.180	0.200	0.061	0.063	0.064
12	0.751	0.757	0.746	0.414	0.429	0.441	0.06	0.063	0.063
14	0.872	0.858	0.845	0.510	0.555	0.563	0.056	0.059	0.067
16	0.947	0.949	0.922	0.593	0.618	0.619	0.056	0.059	0.067
18	0.986	0.945	0.916	0.674	0.701	0.602	0.060	0.060	0.060
20	1.023	1.007	0.974	0.691	0.767	0.677	0.059	0.063	0.066
22	1.091	1.013	0.981	0.797	0.838	0.745	0.055	0.058	0.057
24	1.022	1.001	1.074	0.828	0.802	0.839	0.059	0.058	0.065

```
          NC        DSg       Global (shared)
Comparison of Fits
   Null hypothesis                    3 parameters same for all data sets
   Alternative hypothesis                       3 parameters different for each data set
   P value                  P<0.0001
   Conclusion (alpha = 0.05)                    Reject null hypothesis
   Preferred model                    3 parameters different for each data set
   F (DFn, DFd)                       377.8 (3,53)

3 parameters different for each data set
Best-fit values
   OD     0.04053   0.04053   0.04053
   C      1.028     0.7657
   MUE    0.07569   0.08106
   LAG    1.735     7.861
Std. Error
   OD     0.01688   0.01688   0.01688
   C      0.03172   0.02792
   MUE    0.005882  0.005420
   LAG    0.7365    0.3989
95% Confidence Intervals
   OD     0.006643 to 0.07442  0.006643 to 0.07442  0.006643 to 0.07442
   C      0.9648 to 1.092      0.7097 to 0.8217
   MUE    0.06388 to 0.08749   0.07018 to 0.09195
   LAG    0.2563 to 3.213      7.061 to 8.662
Goodness of Fit
   Degrees of Freedom                           53
   R²     0.9924    0.9782    0.9887
   Absolute Sum of Squares  0.01927   0.04941   0.06868
   Sy.x                     0.03600
Normality of Residuals
   Kolmogorov-Smirnov distance 0.1193  0.1110
   P value  P > 0.10  P > 0.10
   D'Agostino & Pearson omnibus K2     2.456     0.8219
   P value  0.2928    0.6630
   Shapiro-Wilk W   0.9731    0.9736
   P value  0.6271    0.6411
Constraints
   OD     OD is shared        OD is shared
```

Escherichia coli:

EC	NC			DSg			PC		
Time(h)	OD			OD			OD		
0	0.058	0.058	0.062	0.058	0.059	0.061	0.061	0.063	0.068
8	0.510	0.659	0.672	0.071	0.099	0.102	0.062	0.064	0.067
10	0.758	0.876	0.813	0.209	0.415	0.370	0.068	0.071	0.067
12	0.966	0.962	0.891	0.454	0.627	0.570	0.062	0.061	0.065
14	0.966	1.075	1.007	0.564	0.710	0.644	0.056	0.058	0.062
16	0.956	1.009	1.080	0.629	0.792	0.720	0.061	0.058	0.062
18	0.956	1.072	1.107	0.712	0.694	0.935	0.060	0.063	0.062
20	1.109	1.045	0.981	0.787	0.896	0.821	0.066	0.064	0.066
22	1.019	1.099	1.012	0.861	0.950	0.866	0.055	0.061	0.057
24	1.021	1.027	1.110	0.883	0.890	0.852	0.056	0.068	0.067

```
          NC        DSg       Global (shared)
Comparison of Fits
  Null hypothesis                       3 parameters same for all data sets
  Alternative hypothesis                          3 parameters different for each data set
  P value                     P<0.0001
  Conclusion (alpha = 0.05)                       Reject null hypothesis
  Preferred model                       3 parameters different for each data set
  F (DFn, DFd)                          131.4 (3,53)

3 parameters different for each data set
Best-fit values
  OD      0.04894   0.04894   0.04894
  C       1.002     0.8234
  MUE     0.1475    0.1001
  LAG     4.129     7.377
Std. Error
  OD      0.02536   0.02536   0.02536
  C       0.03196   0.03857
  MUE     0.02787   0.01106
  LAG     0.8986    0.5403
95% Confidence Intervals
  OD      -0.001974 to 0.09985 -0.001974 to 0.09985 -0.001974 to 0.09985
  C       0.9377 to 1.066     0.7460 to 0.9009
  MUE     0.09154 to 0.2034   0.07786 to 0.1223
  LAG     2.325 to 5.933      6.292 to 8.461
Goodness of Fit
  Degrees of Freedom                              53
  R²      0.9737    0.9498    0.9688
  Absolute Sum of Squares     0.07277   0.1387    0.2114
  Sy.x                        0.06316
Normality of Residuals
  Kolmogorov-Smirnov distance 0.1244    0.07572
  P value  P > 0.10  P > 0.10
  D'Agostino & Pearson omnibus K2       2.877     0.7623
  P value  0.2373    0.6831
  Shapiro-Wilk W    0.9535    0.9746
  P value  0.2101    0.6704
Constraints
  OD      OD is shared        OD is shared
```

L. acidophilus **DPC201:**

DPC201	NC			DSg			PC		
Time(h)	OD			OD			OD		
0	0.108	0.109	0.109	0.113	0.140	0.111	0.107	0.107	0.107
8	0.147	0.160	0.146	0.132	0.134	0.131	0.116	0.118	0.116
10	0.306	0.337	0.367	0.271	0.268	0.214	0.186	0.181	0.186
12	0.456	0.443	0.430	0.312	0.382	0.331	0.211	0.262	0.192
14	0.526	0.628	0.523	0.481	0.473	0.470	0.257	0.237	0.188
16	0.691	0.614	0.680	0.566	0.597	0.578	0.191	0.231	0.206
18	0.720	0.711	0.778	0.631	0.684	0.683	0.216	0.222	0.210
20	0.800	0.884	0.814	0.719	0.783	0.732	0.221	0.223	0.241
22	0.825	0.898	0.881	0.846	0.868	0.774	0.252	0.244	0.295
24	0.911	0.863	0.797	0.873	0.791	0.801	0.248	0.281	0.279

```
            NC          DSg          Global (shared)
Comparison of Fits
   Null hypothesis                               3 parameters same for all data sets
   Alternative hypothesis                                    3 parameters different for each data set
   P value                           P<0.0001
   Conclusion (alpha = 0.05)                                 Reject null hypothesis
   Preferred model                               3 parameters different for each data set
   F (DFn, DFd)                                  17.58 (3,53)

3 parameters different for each data set
Best-fit values
   OD       0.1060      0.1060       0.1060
   C        0.8113      0.8044
   MUE      0.06922     0.06253
   LAG      7.226       8.180
Std. Error
   OD       0.01399     0.01399      0.01399
   C        0.03151     0.04155
   MUE      0.004449    0.004033
   LAG      0.4182      0.4622
95% Confidence Intervals
   OD       0.07793 to 0.1341        0.07793 to 0.1341       0.07793 to 0.1341
   C        0.7480 to 0.8745         0.7210 to 0.8878
   MUE      0.06029 to 0.07815       0.05443 to 0.07062
   LAG      6.387 to 8.066           7.252 to 9.107
Goodness of Fit
   Degrees of Freedom                                        53
   R²       0.9808      0.9874       0.9842
   Absolute Sum of Squares           0.04276     0.02562     0.06838
   Sy.x                              0.03592
Normality of Residuals
   Kolmogorov-Smirnov distance 0.09566     0.1336
   P value  P > 0.10    P > 0.10
   D'Agostino & Pearson omnibus K2         0.5372      1.621
   P value  0.7645      0.4447
   Shapiro-Wilk W       0.9752       0.9560
   P value  0.6894      0.2439
Constraints
   OD       OD is shared             OD is shared
```

L. plantarum DPC206:

DPC206	NC			DSg			PC		
Time(h)	OD			OD			OD		
0	0.110	0.111	0.114	0.114	0.111	0.112	0.109	0.111	0.112
8	0.119	0.121	0.126	0.113	0.109	0.107	0.108	0.108	0.110
10	0.202	0.210	0.217	0.172	0.129	0.130	0.113	0.113	0.113
12	0.318	0.303	0.305	0.361	0.229	0.259	0.119	0.117	0.117
14	0.425	0.411	0.474	0.360	0.453	0.474	0.131	0.129	0.125
16	0.517	0.630	0.648	0.457	0.512	0.503	0.149	0.149	0.138
18	0.627	0.676	0.744	0.676	0.647	0.633	0.168	0.167	0.152
20	0.778	0.753	0.875	0.725	0.734	0.799	0.208	0.183	0.172
22	0.894	0.776	1.020	0.860	0.836	0.766	0.238	0.208	0.192
24	0.829	0.887	0.987	0.852	0.843	0.814	0.220	0.224	0.187

```
                     NC         DSg        Global (shared)
Comparison of Fits
  Null hypothesis                          3 parameters same for all data sets
  Alternative hypothesis                              3 parameters different for each data set
  P value                       0.0037
  Conclusion (alpha = 0.05)                           Reject null hypothesis
  Preferred model                          3 parameters different for each data set
  F (DFn, DFd)                             5.056 (3,53)

3 parameters different for each data set
Best-fit values
  OD      0.1040     0.1040     0.1040
  C       0.9220     0.8271
  MUE     0.07084    0.06974
  LAG     9.170      9.773
Std. Error
  OD      0.01645    0.01645    0.01645
  C       0.06360    0.05858
  MUE     0.005340   0.005978
  LAG     0.5255     0.5535
95% Confidence Intervals
  OD      0.07096 to 0.1370     0.07096 to 0.1370     0.07096 to 0.1370
  C       0.7943 to 1.050       0.7095 to 0.9447
  MUE     0.06013 to 0.08156    0.05774 to 0.08174
  LAG     8.115 to 10.22        8.662 to 10.88
Goodness of Fit
  Degrees of Freedom                                  53
  R²      0.9713     0.9818     0.9763
  Absolute Sum of Squares       0.07686    0.04275    0.1196
  Sy.x                          0.04750
Normality of Residuals
  Kolmogorov-Smirnov distance   0.1098     0.1588
  P value  P > 0.10  0.0516
  D'Agostino & Pearson omnibus K2          4.320      3.377
  P value  0.1153    0.1848
  Shapiro-Wilk W     0.9612     0.9403
  P value  0.3318    0.0925
Constraints
  OD      OD is shared          OD is shared
```

P. acidilactici DPC209:

DPC209	NC			DSg			PC		
Time(h)	OD			OD			OD		
0	0.157	0.128	0.130	0.112	0.245	0.123	0.111	0.137	0.110
8	0.133	0.130	0.135	0.123	0.122	0.126	0.118	0.102	0.116
10	0.267	0.237	0.253	0.240	0.209	0.249	0.155	0.135	0.161
12	0.338	0.328	0.317	0.265	0.342	0.270	0.199	0.167	0.187
14	0.412	0.382	0.390	0.470	0.432	0.434	0.165	0.178	0.162
16	0.500	0.560	0.528	0.498	0.565	0.527	0.197	0.161	0.207
18	0.617	0.624	0.637	0.628	0.644	0.654	0.198	0.169	0.208
20	0.794	0.795	0.711	0.733	0.651	0.768	0.265	0.282	0.279
22	0.991	1.013	0.881	0.897	0.838	0.845	0.290	0.295	0.350
24	1.098	0.975	0.893	0.869	0.917	0.833	0.321	0.256	0.398

```
                        NC          DSg         Global (shared)
Comparison of Fits
  Null hypothesis                               3 parameters same for all data sets
  Alternative hypothesis                                    3 parameters different for each data set
  P value                           0.0012
  Conclusion (alpha = 0.05)                                 Reject null hypothesis
  Preferred model                               3 parameters different for each data set
  F (DFn, DFd)                                  6.132 (3,53)

3 parameters different for each data set
Best-fit values
  OD        0.1335      0.1335      0.1335
  C         1.418       0.9016
  MUE       0.06507     0.06072
  LAG       10.01       9.338
Std. Error
  OD        0.01726     0.01726     0.01726
  C         0.2453      0.08574
  MUE       0.002837    0.004572
  LAG       0.5265      0.6003
95% Confidence Intervals
  OD        0.09886 to 0.1681       0.09886 to 0.1681       0.09886 to 0.1681
  C         0.9253 to 1.910         0.7294 to 1.074
  MUE       0.05938 to 0.07077      0.05154 to 0.06990
  LAG       8.955 to 11.07          8.133 to 10.54
Goodness of Fit
  Degrees of Freedom                                        53
  R²        0.9766      0.9772      0.9769
  Absolute Sum of Squares           0.06455     0.04923     0.1138
  Sy.x                              0.04633
Normality of Residuals
  Kolmogorov-Smirnov distance 0.09884     0.09791
  P value  P > 0.10    P > 0.10
  D'Agostino & Pearson omnibus K2         1.769       2.493
  P value  0.4130      0.2875
  Shapiro-Wilk W        0.9696      0.9707
  P value  0.5277      0.5597
Constraints
  OD        OD is shared            OD is shared
```

***L. reuteri* DPC16:**

DPC16	NC			DSg			PC		
Time(h)	OD			OD			OD		
0	0.107	0.109	0.115	0.107	0.110	0.115	0.105	0.107	0.110
8	0.116	0.120	0.123	0.105	0.108	0.110	0.105	0.108	0.111
10	0.139	0.147	0.148	0.123	0.128	0.130	0.105	0.111	0.111
12	0.216	0.231	0.230	0.194	0.201	0.201	0.100	0.107	0.105
14	0.368	0.394	0.401	0.357	0.372	0.383	0.097	0.104	0.103
16	0.500	0.534	0.547	0.453	0.511	0.532	0.097	0.103	0.105
18	0.667	0.813	0.653	0.588	0.701	0.538	0.097	0.103	0.103
20	0.840	0.916	0.938	0.693	0.843	0.660	0.098	0.101	0.092
22	1.019	1.099	0.912	0.861	0.950	0.866	0.096	0.097	0.088
24	0.968	1.112	0.976	0.920	0.904	0.899	0.097	0.099	0.096

```
                        NC          DSg         Global (shared)
Comparison of Fits
   Null hypothesis                              3 parameters same for all data sets
   Alternative hypothesis                                   3 parameters different for each data set
   P value                          P<0.0001
   Conclusion (alpha = 0.05)                                Reject null hypothesis
   Preferred model                              3 parameters different for each data set
   F (DFn, DFd)                                 13.11 (3,53)

3 parameters different for each data set
Best-fit values
   OD       0.1087      0.1087      0.1087
   C        1.082       0.9587
   MUE      0.09263     0.07578
   LAG      11.19       10.99
Std. Error
   OD       0.01402     0.01402     0.01402
   C        0.07116     0.08146
   MUE      0.006401    0.005834
   LAG      0.4051      0.4837
95% Confidence Intervals
   OD       0.08059 to 0.1369       0.08059 to 0.1369       0.08059 to 0.1369
   C        0.9395 to 1.225         0.7951 to 1.122
   MUE      0.07978 to 0.1055       0.06406 to 0.08749
   LAG      10.38 to 12.00          10.02 to 11.96
Goodness of Fit
   Degrees of Freedom                                       53
   R²       0.9824      0.9800      0.9815
   Absolute Sum of Squares          0.06644     0.05605     0.1225
   Sy.x                             0.04807
Normality of Residuals
   Kolmogorov-Smirnov distance 0.1620           0.1530
   P value  0.0433      0.0712
   D'Agostino & Pearson omnibus K2              0.7995      1.428
   P value  0.6705      0.4896
   Shapiro-Wilk W       0.9496      0.9534
   P value  0.1652      0.2081
Constraints
   OD       OD is shared            OD is shared
```

B. lactis **DR10:**

DR10	NC			DSg			PC		
Time(h)	OD			OD			OD		
0	0.112	0.114	0.113	0.112	0.111	0.111	0.11	0.112	0.108
8	0.126	0.133	0.130	0.110	0.110	0.110	0.105	0.109	0.106
10	0.246	0.288	0.267	0.154	0.171	0.170	0.111	0.116	0.114
12	0.591	0.477	0.466	0.346	0.325	0.304	0.121	0.124	0.123
14	0.605	0.653	0.676	0.355	0.361	0.497	0.127	0.143	0.135
16	0.708	0.761	0.730	0.439	0.524	0.455	0.133	0.156	0.142
18	0.806	0.776	0.832	0.516	0.525	0.546	0.149	0.152	0.138
20	0.901	0.863	0.793	0.620	0.635	0.566	0.145	0.149	0.160
22	0.842	0.905	0.896	0.621	0.797	0.733	0.136	0.180	0.163
24	0.868	0.892	0.887	0.637	0.805	0.814	0.124	0.153	0.138

```
          NC        DSg        Global (shared)
Comparison of Fits
    Null hypothesis                      3 parameters same for all data sets
    Alternative hypothesis                          3 parameters different for each data set
    P value                    P<0.0001
    Conclusion (alpha = 0.05)                       Reject null hypothesis
    Preferred model                      3 parameters different for each data set
    F (DFn, DFd)                         84.00 (3,53)

3 parameters different for each data set
Best-fit values
    OD    0.09673   0.09673    0.09673
    C     0.7883    0.7691
    MUE   0.1009    0.04930
    LAG   8.192     8.319
Std. Error
    OD    0.01739   0.01739    0.01739
    C     0.02784   0.07988
    MUE   0.008473  0.004271
    LAG   0.3954    0.7153
95% Confidence Intervals
    OD    0.06182 to 0.1316    0.06182 to 0.1316    0.06182 to 0.1316
    C     0.7325 to 0.8442     0.6087 to 0.9294
    MUE   0.08392 to 0.1179    0.04073 to 0.05788
    LAG   7.398 to 8.986       6.883 to 9.755
Goodness of Fit
    Degrees of Freedom                              53
    R²    0.9876    0.9504     0.9757
    Absolute Sum of Squares    0.03222   0.07923    0.1114
    Sy.x                       0.04586
Normality of Residuals
    Kolmogorov-Smirnov distance 0.1425   0.1801
    P value  P > 0.10  0.0142
    D'Agostino & Pearson omnibus K2      11.29      1.402
    P value  0.0035    0.4960
    Shapiro-Wilk W  0.9297     0.9624
    P value  0.0483    0.3555
Constraints
    OD    OD is shared         OD is shared
```

***L. rhamnosus* DR20:**

DR20	NC			DSg			PC		
Time(h)	OD			OD			OD		
0	0.113	0.118	0.119	0.113	0.113	0.115	0.114	0.113	0.115
8	0.147	0.144	0.155	0.124	0.126	0.130	0.124	0.122	0.124
10	0.359	0.391	0.313	0.256	0.267	0.270	0.198	0.208	0.198
12	0.413	0.431	0.496	0.289	0.336	0.272	0.149	0.280	0.290
14	0.504	0.477	0.557	0.333	0.410	0.474	0.244	0.217	0.303
16	0.671	0.621	0.607	0.466	0.427	0.444	0.230	0.250	0.241
18	0.672	0.633	0.686	0.571	0.526	0.523	0.225	0.249	0.235
20	0.737	0.699	0.588	0.595	0.648	0.503	0.269	0.268	0.382
22	0.767	0.692	0.633	0.547	0.653	0.696	0.301	0.286	0.394
24	0.698	0.775	0.686	0.552	0.689	0.684	0.287	0.279	0.369

```
                              NC        DSg       Global (shared)
Comparison of Fits
  Null hypothesis                       3 parameters same for all data sets
  Alternative hypothesis                          3 parameters different for each data set
  P value                     P<0.0001
  Conclusion (alpha = 0.05)                       Reject null hypothesis
  Preferred model                       3 parameters different for each data set
  F (DFn, DFd)                          24.54 (3,53)

3 parameters different for each data set
Best-fit values
  OD      0.1055    0.1055    0.1055
  C       0.6101    0.6009
  MUE     0.06888   0.04312
  LAG     7.018     7.297
Std. Error
  OD      0.01864   0.01864   0.01864
  C       0.02937   0.05639
  MUE     0.007713  0.004947
  LAG     0.5744    0.8639
95% Confidence Intervals
  OD      0.06804 to 0.1429   0.06804 to 0.1429   0.06804 to 0.1429
  C       0.5511 to 0.6690    0.4877 to 0.7141
  MUE     0.05340 to 0.08436  0.03319 to 0.05305
  LAG     5.865 to 8.171      5.563 to 9.031
Goodness of Fit
  Degrees of Freedom                              53
  R²      0.9605    0.9453    0.9560
  Absolute Sum of Squares     0.05568   0.06050   0.1162
  Sy.x                        0.04682
Normality of Residuals
  Kolmogorov-Smirnov distance 0.1119    0.09905
  P value P > 0.10  P > 0.10
  D'Agostino & Pearson omnibus K2       0.1180    0.8277
  P value 0.9427    0.6611
  Shapiro-Wilk W  0.9785    0.9764
  P value 0.7849    0.7243
Constraints
  OD      OD is shared        OD is shared
```

2.3.5 Tolerance of *L. reuteri* DPC16 to pH and bile salts in simulated GI environment

Nutrient-sufficient conditions:

DPC201	Log CFU/mL			Mean	SD
control	8.78	8.95	8.48	8.74	0.24
Ph2	8.90	8.48	8.71	8.70	0.21
Ph2;0.05%BS	8.48	8.45	9.30	8.74	0.48
Ph2;0.1%BS	9.08	9.32	7.85	8.75	0.79
Ph2;0.5%BS	8.48	8.41	8.30	8.40	0.09
Ph2;1%BS	7.30	7.00	6.95	7.09	0.19

DPC206	Log CFU/mL			Mean	SD
control	8.85	9.04	8.79	8.89	0.13
Ph2	9.00	9.41	8.36	8.93	0.53
Ph2;0.05%BS	8.60	9.46	8.53	8.87	0.52
Ph2;0.1%BS	8.60	9.28	8.46	8.78	0.44
Ph2;0.5%BS	8.30	8.26	8.60	8.39	0.19
Ph2;1%BS	7.48	6.00	7.26	6.91	0.80

DPC209	Log CFU/mL			Mean	SD
control	9.11	9.04	8.61	8.92	0.27
Ph2	8.90	8.78	8.40	8.69	0.26
Ph2;0.05%BS	8.70	9.28	8.51	8.83	0.40
Ph2;0.1%BS	8.90	9.32	8.43	8.89	0.45
Ph2;0.5%BS	8.70	9.20	8.28	8.73	0.46
Ph2;1%BS	7.30	7.15	6.95	7.13	0.17

DPC16	Log CFU/mL			Mean	SD
control	9.46	9.6	8.91	9.32	0.36
Ph2	9.08	9.26	9.56	9.30	0.24
Ph2;0.05%BS	8.95	9.23	8.52	8.90	0.36
Ph2;0.1%BS	9.08	8.70	8.28	8.69	0.40
Ph2;0.5%BS	8.30	8.95	8.53	8.59	0.33
Ph2;1%BS	7.48	7.30	7.28	7.35	0.11

DR10	Log CFU/mL			Mean	SD
control	9.26	9.23	8.66	9.05	0.34
Ph2	9.15	9.32	8.46	8.98	0.45
Ph2;0.05%BS	8.30	9.04	8.41	8.59	0.40
Ph2;0.1%BS	7.60	8.04	8.28	7.97	0.34
Ph2;0.5%BS	7.95	8.04	8.04	8.01	0.05
Ph2;1%BS	7.00	7.00	6.20	6.73	0.46

DR20	Log CFU/mL			Mean	SD
control	9.18	9.08	8.72	8.99	0.24
Ph2	8.95	9.00	8.60	8.85	0.22
Ph2;0.05%BS	8.70	8.74	8.60	8.68	0.07
Ph2;0.1%BS	8.60	8.48	8.41	8.50	0.10
Ph2;0.5%BS	8.30	8.60	8.40	8.43	0.15
Ph2;1%BS	8.52	6.53	6.82	7.29	1.07

```
          Parameter
Table Analyzed      Probiotics

Two-way ANOVA

Source of Variation % of total variation P value
  Interaction       4.45       0.8712
  Treatment         72.84      P<0.0001
  Strain    3.52    0.0303

Source of Variation P value summary      Significant?
  Interaction       ns         No
  Treatment         ***        Yes
  Strain    *       Yes

Source of Variation Df         Sum-of-squares       Mean square          F
  Interaction       25         2.728      0.1091    0.6669
  Treatment         5          44.68      8.935     54.62
  Strain    5       2.156      0.4312     2.636
  Residual  72      11.78      0.1636

Number of missing values       0

Bonferroni posttests

NC vs. Ph2
Strain    NC        Ph2        Difference 95% CI of diff.
  DPC201  8.737     8.697      -0.04000   -1.119 to 1.039
  DPC206  8.893     8.923      0.03000    -1.049 to 1.109
  DPC209  8.920     8.693      -0.2267    -1.306 to 0.8522
  DPC16   9.323     9.300      -0.02333   -1.102 to 1.056
  DR10    9.050     8.977      -0.07333   -1.152 to 1.006
  DR20    8.993     8.850      -0.1433    -1.222 to 0.9356

Strain    Difference t         P value    Summary
  DPC201  -0.04000  0.1211     P > 0.05   ns
  DPC206  0.03000   0.09084    P > 0.05   ns
  DPC209  -0.2267   0.6864     P > 0.05   ns
  DPC16   -0.02333  0.07066    P > 0.05   ns
  DR10    -0.07333  0.2221     P > 0.05   ns
  DR20    -0.1433   0.4340     P > 0.05   ns

NC vs. Ph2;0.05%BS
Strain    NC        Ph2;0.05%BS           Difference 95% CI of diff.
  DPC201  8.737     8.743      0.006666   -1.072 to 1.086
  DPC206  8.893     8.863      -0.03000   -1.109 to 1.049
  DPC209  8.920     8.830      -0.09000   -1.169 to 0.9889
  DPC16   9.323     8.900      -0.4233    -1.502 to 0.6556
  DR10    9.050     8.583      -0.4667    -1.546 to 0.6122
  DR20    8.993     8.680      -0.3133    -1.392 to 0.7656

Strain    Difference t         P value    Summary
  DPC201  0.006666  0.02019    P > 0.05   ns
  DPC206  -0.03000  0.09084    P > 0.05   ns
  DPC209  -0.09000  0.2725     P > 0.05   ns
  DPC16   -0.4233   1.282      P > 0.05   ns
  DR10    -0.4667   1.413      P > 0.05   ns
  DR20    -0.3133   0.9488     P > 0.05   ns
```

NC vs. Ph2;0.1%BS

Strain	NC	Ph2;0.1%BS		Difference 95% CI of diff.
DPC201	8.737	8.750	0.01333	-1.066 to 1.092
DPC206	8.893	8.780	-0.1133	-1.192 to 0.9656
DPC209	8.920	8.883	-0.03667	-1.116 to 1.042
DPC16	9.323	8.687	-0.6367	-1.716 to 0.4422
DR10	9.050	7.973	-1.077	-2.156 to 0.002233
DR20	8.993	8.497	-0.4967	-1.576 to 0.5822

Strain	Difference	t	P value	Summary
DPC201	0.01333	0.04037	P > 0.05	ns
DPC206	-0.1133	0.3432	P > 0.05	ns
DPC209	-0.03667	0.1110	P > 0.05	ns
DPC16	-0.6367	1.928	P > 0.05	ns
DR10	-1.077	3.260	P < 0.05	*
DR20	-0.4967	1.504	P > 0.05	ns

NC vs. Ph2;0.5%BS

Strain	NC	Ph2;0.5%BS		Difference 95% CI of diff.
DPC201	8.737	8.397	-0.3400	-1.419 to 0.7389
DPC206	8.893	8.387	-0.5067	-1.586 to 0.5722
DPC209	8.920	8.727	-0.1933	-1.272 to 0.8856
DPC16	9.323	8.593	-0.7300	-1.809 to 0.3489
DR10	9.050	8.010	-1.040	-2.119 to 0.03890
DR20	8.993	8.433	-0.5600	-1.639 to 0.5189

Strain	Difference	t	P value	Summary
DPC201	-0.3400	1.030	P > 0.05	ns
DPC206	-0.5067	1.534	P > 0.05	ns
DPC209	-0.1933	0.5854	P > 0.05	ns
DPC16	-0.7300	2.211	P > 0.05	ns
DR10	-1.040	3.149	P < 0.05	*
DR20	-0.5600	1.696	P > 0.05	ns

NC vs. Ph2;1%BS

Strain	NC	Ph2;1%BS	Difference	95% CI of diff.
DPC201	8.737	7.083	-1.653	-2.732 to -0.5744
DPC206	8.893	6.913	-1.980	-3.059 to -0.9011
DPC209	8.920	7.133	-1.787	-2.866 to -0.7078
DPC16	9.323	7.353	-1.970	-3.049 to -0.8911
DR10	9.050	6.733	-2.317	-3.396 to -1.238
DR20	8.993	7.290	-1.703	-2.782 to -0.6244

Strain	Difference	t	P value	Summary
DPC201	-1.653	5.006	P<0.001	***
DPC206	-1.980	5.996	P<0.001	***
DPC209	-1.787	5.410	P<0.001	***
DPC16	-1.970	5.965	P<0.001	***
DR10	-2.317	7.015	P<0.001	***
DR20	-1.703	5.158	P<0.001	***

Nutrient-deficient conditions:

Strain	NC			pH2			0.05% BS		
	(LogCFU/mL)			(LogCFU/mL)			LogCFU/mL		
DPC201	10.90	10.70	11.04	11.18	11.04	10.70	7.60	7.70	7.85
DPC206	11.18	11.20	11.30	9.00	8.00	8.30	3.74	4.24	4.67
DPC209	11.15	11.28	11.04	6.48	6.30	5.70	7.95	8.00	8.15
DPC16	11.36	11.23	11.40	11.45	11.15	10.95	10.30	10.48	10.78
DR10	10.90	10.95	11.08	6.45	6.04	6.34	4.00	4.00	4.30
DR20	11.23	11.34	11.11	7.30	6.48	6.30	7.23	6.78	6.90

Parameter	
Table Analyzed	GI condition in PBS

```
Two-way ANOVA

Source of Variation   % of total variation   P value
  Interaction         24.06        P<0.0001
  Treatment           48.86        P<0.0001
  Strain     26.29    P<0.0001

Source of Variation   P value summary        Significant?
  Interaction         ***          Yes
  Treatment           ***          Yes
  Strain     ***      Yes

Source of Variation   Df           Sum-of-squares         Mean square          F
  Interaction         10           81.67       8.167      109.1
  Treatment           2            165.9       82.94      1108
  Strain     5        89.25        17.85       238.4
  Residual   36       2.695        0.07486

Number of missing values           0

Bonferroni posttests

NC vs. pH2
Strain       NC       pH2          Difference  95% CI of diff.
  DPC201     10.88    10.97        0.09333     -0.5902 to 0.7769
  DPC206     11.23    8.433        -2.793      -3.477 to -2.110
  DPC209     11.16    6.160        -4.997      -5.680 to -4.313
  DPC16      11.33    11.18        -0.1467     -0.8302 to 0.5369
  DR10       10.98    6.277        -4.700      -5.384 to -4.016
  DR20       11.23    6.693        -4.533      -5.217 to -3.850

Strain       Difference t          P value     Summary
  DPC201     0.09333  0.4178       P > 0.05    ns
  DPC206     -2.793   12.50        P<0.001     ***
  DPC209     -4.997   22.37        P<0.001     ***
  DPC16      -0.1467  0.6565       P > 0.05    ns
  DR10       -4.700   21.04        P<0.001     ***
  DR20       -4.533   20.29        P<0.001     ***

NC vs. 0.05%BS
Strain       NC       0.05%BS      Difference  95% CI of diff.
  DPC201     10.88    7.717        -3.163      -3.847 to -2.480
  DPC206     11.23    4.217        -7.010      -7.694 to -6.326
  DPC209     11.16    8.033        -3.123      -3.807 to -2.440
  DPC16      11.33    10.52        -0.8100     -1.494 to -0.1264
  DR10       10.98    4.100        -6.877      -7.560 to -6.193
  DR20       11.23    6.970        -4.257      -4.940 to -3.573

Strain       Difference t          P value     Summary
  DPC201     -3.163   14.16        P<0.001     ***
  DPC206     -7.010   31.38        P<0.001     ***
  DPC209     -3.123   13.98        P<0.001     ***
  DPC16      -0.8100  3.626        P<0.01      **
  DR10       -6.877   30.78        P<0.001     ***
  DR20       -4.257   19.05        P<0.001     ***
```

2.3.6 Adhesion of *L. reuteri* DPC16 to an intestinal epithelial Caco-2 monolayer

Strain	Added cells (LogCFU/cm2)	Adhered cells (LogCFU/cm2)			Mean	SD
DPC16	9.72	7.41	7.34	7.60	7.45	0.13
	8.48	5.60	6.00	5.60	5.73	0.23
	7.48	4.00	4.12	4.10	4.08	0.06

```
                    DPC16
Sigmoidal dose-response (variable slope)
Best-fit values
   BOTTOM          3.839
   TOP      7.573
   LOGEC50         8.466
   HILLSLOPE       1.183
   EC50     2.924e+008
Std. Error
   BOTTOM          6.466e+006
   TOP      3.750e+006
   LOGEC50         605976
   HILLSLOPE       1.081e+007
95% Confidence Intervals
   BOTTOM          -16620000 to 1.662e+007
   TOP      -9640000 to 9.640e+006
   LOGEC50         -1558000 to 1.558e+006
   HILLSLOPE       -27780000 to 2.778e+007
   EC50
Goodness of Fit
   Degrees of Freedom          5
   R²       0.9913
   Absolute Sum of Squares     0.1499
   Sy.x     0.1731
Normality of Residuals
   Kolmogorov-Smirnov distance 0.1663
   P value  P > 0.10
   D'Agostino & Pearson omnibus K2          2.014
   P value  0.3653
   Shapiro-Wilk W    0.8960
   P value  0.2299
```

Strain	Number of bacteria added			Adhered			Adhesion		
	Log CFU/cm2			Log CFU/cm2			% of control		
DPC201	9.75	9.60	9.64	7.51	7.70	8.00	0.57	1.25	2.27
DPC206	9.38	9.62	9.58	7.34	7.48	7.78	0.92	0.71	1.58
DPC209	9.45	9.62	9.51	7.48	7.64	8.20	1.07	1.05	5.00
DPC16	9.75	9.75	9.72	7.41	7.34	7.60	0.46	0.39	0.77
DR10	8.60	8.90	8.72	6.30	6.78	6.60	0.50	0.75	0.77
DR20	9.38	9.38	8.48	6.78	7.41	7.34	0.25	1.08	7.33

```
Parameter Value
Table Analyzed
Adhesion
One-way analysis of variance
  P value     0.5925
  P value summary      ns
  Are means signif. different? (P < 0.05)         No
  Number of groups     6
  F           0.7645
  R squared0.2416

ANOVA Table              SS           df           MS
  Treatment (between columns)  13.48       5             2.696
  Residual (within columns)    42.31       12            3.526
  Total       55.79        17

No post tests. P > 0.05
```

2.3.7 Mucin degradation assessment of *L. reuteri* DPC16 and other bacteria

Strain	Size of zone (diameter)			Mean	Size(grade)	Discolor(grade)	Mucin degradation activity(grade)
DPC201	8.50	9.00	8.50	8.67	1	1	2
DPC206	9.00	9.00	9.00	9.00	1	2	3
DPC209	8.50	9.00	9.00	8.83	1	1	2
DPC16	8.50	8.50	8.50	8.50	1	1	2
DR10	8.50	8.50	9.00	8.67	1	2	3
DR20	8.50	8.50	8.50	8.50	1	1	2
FF	N/A	N/A	N/A	N/A	N/A	3	N/A
LM	11.50	12.00	10.50	11.33	2	4	6
SA	11.00	10.00	12.00	11.00	2	4	6
ST	18.00	17.50	18.00	17.83	4	4	8
EC	13.00	13.00	12.50	12.83	3	3	6

Chapter 3

3.3.1 The effects of bovine lactoferrin on the growth of some pathogenic and probiotic bacteria

Bacterial turbidity assays:

Lf	LM			SA		
Conc.	Growth(% of control)			Growth(% of control)		
0.625	106.65	103.90	100.56	103.28	97.61	103.28
1.25	96.50	97.09	97.93	102.39	98.21	101.29
2.5	100.68	96.14	103.78	97.91	94.83	98.31
5	95.90	97.69	96.97	90.75	93.33	92.44
10	94.59	94.71	94.82	78.51	88.46	80.10
20	70.22	64.85	65.68	55.32	59.10	59.90
NC	106.03	94.90	99.07	99.80	98.98	99.83
PC	36.18	37.29	38.40	8.46	27.07	18.44

Lf	ST			EC		
Conc.	Growth(% of control)			Growth(% of control)		
0.625	94.16	95.63	97.59	112.66	111.38	93.84
1.25	95.14	95.63	95.14	101.05	108.48	100.81
2.5	95.27	97.10	96.61	108.25	107.08	99.65
5	92.94	95.51	93.55	101.97	106.74	103.14
10	81.18	84.12	85.71	95.35	98.84	100.81
20	58.29	60.73	67.96	52.61	59.81	70.96
NC	97.72	101.31	100.97	92.59	100.77	106.64
PC	16.25	15.58	17.71	13.07	13.19	16.61

Lf	DPC201			DPC206			DPC209		
Conc.	Growth(% of control)			Growth(% of control)			Growth(% of control)		
0.625	99.09	101.20	100.94	103.30	101.06	95.46	107.51	108.75	108.27
1.25	101.47	106.31	103.14	104.70	103.76	96.21	112.74	112.26	111.79
2.5	90.47	98.83	100.76	102.46	96.77	97.70	104.09	111.22	99.90
5	97.68	101.64	101.73	101.06	97.70	94.06	110.55	106.56	107.51
10	96.36	99.35	101.73	97.33	92.75	90.89	111.50	107.89	107.60
20	93.55	100.59	100.94	96.67	88.74	92.38	108.94	112.45	105.80
NC	100.50	97.95	101.55	101.80	95.46	102.74	98.10	102.85	99.05
PC	26.22	28.60	33.00	28.37	28.46	29.02	27.09	29.18	31.94

Lf	DPC16			DR10			DR20		
Conc.	Growth(% of control)			Growth(% of control)			Growth(% of control)		
0.625	117.69	101.67	104.67	98.70	97.52	98.97	98.58	100.54	89.94
1.25	110.23	107.56	111.12	100.88	94.34	98.70	96.85	97.89	88.33
2.5	99.56	96.55	105.12	95.24	91.25	93.88	93.51	95.47	86.03
5	97.55	100.33	108.23	95.52	92.24	93.79	91.79	91.21	95.70
10	97.22	99.56	106.23	94.34	85.34	90.88	87.87	92.71	86.95
20	100.11	93.10	102.78	89.70	79.25	87.34	82.80	82.11	90.75
NC	101.56	96.44	102.00	99.52	100.33	100.15	99.04	100.08	100.88
PC	36.48	36.37	36.15	24.81	24.36	26.17	45.83	45.60	44.22

```
Parameter
Table Analyzed      Lf on all bacteria

Two-way ANOVA

Source of Variation % of total variation P value
 Interaction        6.69      P<0.0001
 Treatment          87.62     P<0.0001
 Strain    4.12     P<0.0001

Source of Variation P value summary      Significant?
 Interaction        ***       Yes
 Treatment          ***       Yes
 Strain    ***      Yes

Source of Variation Df        Sum-of-squares       Mean square         F
 Interaction        63        10100     160.4     10.86
 Treatment          7         132200    18890     1279
 Strain    9        6222      691.3     46.80
 Residual  160      2363      14.77

Number of missing values      0

Bonferroni posttests

NC vs. 0.625
Strain    NC        0.625     Difference 95% CI of diff.
 LM       100.0     103.7     3.703     -7.126 to 14.53
 SA       99.54     101.4     1.853     -8.976 to 12.68
 ST       100.0     95.79     -4.207    -15.04 to 6.623
 EC       100.0     106.0     5.960     -4.870 to 16.79
 DPC201   100.0     100.4     0.4100    -10.42 to 11.24
 DPC206   100.0     99.94     -0.06000  -10.89 to 10.77
 DPC209   100.0     108.2     8.177     -2.653 to 19.01
 DPC16    100.0     108.0     8.010     -2.820 to 18.84
 DR10     100.0     98.40     -1.603    -12.43 to 9.226
 DR20     100.0     96.35     -3.647    -14.48 to 7.183

Strain    Difference t        P value   Summary
```

LM	3.703	1.180	P > 0.05	ns
SA	1.853	0.5906	P > 0.05	ns
ST	-4.207	1.341	P > 0.05	ns
EC	5.960	1.899	P > 0.05	ns
DPC201	0.4100	0.1307	P > 0.05	ns
DPC206	-0.06000	0.01912	P > 0.05	ns
DPC209	8.177	2.606	P > 0.05	ns
DPC16	8.010	2.553	P > 0.05	ns
DR10	-1.603	0.5109	P > 0.05	ns
DR20	-3.647	1.162	P > 0.05	ns

NC vs. 1.25

Strain	NC	1.25	Difference	95% CI of diff.
LM	100.0	97.17	-2.827	-13.66 to 8.003
SA	99.54	100.6	1.093	-9.736 to 11.92
ST	100.0	95.30	-4.697	-15.53 to 6.133
EC	100.0	103.4	3.447	-7.383 to 14.28
DPC201	100.0	103.6	3.640	-7.190 to 14.47
DPC206	100.0	101.6	1.557	-9.273 to 12.39
DPC209	100.0	112.3	12.26	1.434 to 23.09
DPC16	100.0	109.6	9.637	-1.193 to 20.47
DR10	100.0	97.97	-2.027	-12.86 to 8.803
DR20	100.0	94.36	-5.643	-16.47 to 5.186

Strain	Difference	t	P value	Summary
LM	-2.827	0.9008	P > 0.05	ns
SA	1.093	0.3484	P > 0.05	ns
ST	-4.697	1.497	P > 0.05	ns
EC	3.447	1.098	P > 0.05	ns
DPC201	3.640	1.160	P > 0.05	ns
DPC206	1.557	0.4961	P > 0.05	ns
DPC209	12.26	3.908	P<0.01	**
DPC16	9.637	3.071	P < 0.05	*
DR10	-2.027	0.6458	P > 0.05	ns
DR20	-5.643	1.798	P > 0.05	ns

NC vs. 2.5

Strain	NC	2.5	Difference	95% CI of diff.
LM	100.0	100.2	0.2000	-10.63 to 11.03
SA	99.54	97.02	-2.520	-13.35 to 8.310
ST	100.0	96.33	-3.673	-14.50 to 7.156
EC	100.0	105.0	4.993	-5.836 to 15.82
DPC201	100.0	96.69	-3.313	-14.14 to 7.516
DPC206	100.0	98.98	-1.023	-11.85 to 9.806
DPC209	100.0	105.1	5.070	-5.760 to 15.90
DPC16	100.0	100.4	0.4100	-10.42 to 11.24
DR10	100.0	93.46	-6.543	-17.37 to 4.286
DR20	100.0	91.67	-8.330	-19.16 to 2.500

Strain	Difference	t	P value	Summary
LM	0.2000	0.06373	P > 0.05	ns
SA	-2.520	0.8030	P > 0.05	ns
ST	-3.673	1.171	P > 0.05	ns
EC	4.993	1.591	P > 0.05	ns
DPC201	-3.313	1.056	P > 0.05	ns
DPC206	-1.023	0.3261	P > 0.05	ns
DPC209	5.070	1.616	P > 0.05	ns
DPC16	0.4100	0.1307	P > 0.05	ns
DR10	-6.543	2.085	P > 0.05	ns
DR20	-8.330	2.654	P > 0.05	ns

NC vs. 5

Strain	NC	5	Difference	95% CI of diff.
LM	100.0	96.85	-3.147	-13.98 to 7.683
SA	99.54	92.17	-7.363	-18.19 to 3.466
ST	100.0	94.00	-6.000	-16.83 to 4.830
EC	100.0	104.0	3.950	-6.880 to 14.78
DPC201	100.0	100.4	0.3500	-10.48 to 11.18
DPC206	100.0	97.61	-2.393	-13.22 to 8.436
DPC209	100.0	108.2	8.207	-2.623 to 19.04
DPC16	100.0	102.0	2.037	-8.793 to 12.87

DR10	100.0	93.85	-6.150	-16.98 to 4.680
DR20	100.0	92.90	-7.100	-17.93 to 3.730

Strain	Difference	t	P value	Summary
LM	-3.147	1.003	P > 0.05	ns
SA	-7.363	2.346	P > 0.05	ns
ST	-6.000	1.912	P > 0.05	ns
EC	3.950	1.259	P > 0.05	ns
DPC201	0.3500	0.1115	P > 0.05	ns
DPC206	-2.393	0.7627	P > 0.05	ns
DPC209	8.207	2.615	P > 0.05	ns
DPC16	2.037	0.6490	P > 0.05	ns
DR10	-6.150	1.960	P > 0.05	ns
DR20	-7.100	2.263	P > 0.05	ns

NC vs. 10

Strain	NC	10	Difference	95% CI of diff.
LM	100.0	94.71	-5.293	-16.12 to 5.536
SA	99.54	82.36	-17.18	-28.01 to -6.350
ST	100.0	83.67	-16.33	-27.16 to -5.500
EC	100.0	98.33	-1.667	-12.50 to 9.163
DPC201	100.0	99.15	-0.8533	-11.68 to 9.976
DPC206	100.0	93.66	-6.343	-17.17 to 4.486
DPC209	100.0	109.0	8.997	-1.833 to 19.83
DPC16	100.0	101.0	1.003	-9.826 to 11.83
DR10	100.0	90.19	-9.813	-20.64 to 1.016
DR20	100.0	89.18	-10.82	-21.65 to 0.006387

Strain	Difference	t	P value	Summary
LM	-5.293	1.687	P > 0.05	ns
SA	-17.18	5.475	P<0.001	***
ST	-16.33	5.204	P<0.001	***
EC	-1.667	0.5311	P > 0.05	ns
DPC201	-0.8533	0.2719	P > 0.05	ns
DPC206	-6.343	2.021	P > 0.05	ns
DPC209	8.997	2.867	P < 0.05	*
DPC16	1.003	0.3197	P > 0.05	ns
DR10	-9.813	3.127	P < 0.05	*
DR20	-10.82	3.449	P<0.01	**

NC vs. 20

Strain	NC	20	Difference	95% CI of diff.
LM	100.0	66.92	-33.08	-43.91 to -22.25
SA	99.54	58.11	-41.43	-52.26 to -30.60
ST	100.0	62.33	-37.67	-48.50 to -26.84
EC	100.0	61.13	-38.87	-49.70 to -28.04
DPC201	100.0	98.36	-1.640	-12.47 to 9.190
DPC206	100.0	92.60	-7.403	-18.23 to 3.426
DPC209	100.0	109.1	9.063	-1.766 to 19.89
DPC16	100.0	98.66	-1.337	-12.17 to 9.493
DR10	100.0	85.43	-14.57	-25.40 to -3.740
DR20	100.0	85.22	-14.78	-25.61 to -3.950

Strain	Difference	t	P value	Summary
LM	-33.08	10.54	P<0.001	***
SA	-41.43	13.20	P<0.001	***
ST	-37.67	12.01	P<0.001	***
EC	-38.87	12.39	P<0.001	***
DPC201	-1.640	0.5226	P > 0.05	ns
DPC206	-7.403	2.359	P > 0.05	ns
DPC209	9.063	2.888	P < 0.05	*
DPC16	-1.337	0.4260	P > 0.05	ns
DR10	-14.57	4.643	P<0.001	***
DR20	-14.78	4.710	P<0.001	***

NC vs. PC

Strain	NC	PC	Difference	95% CI of diff.
LM	100.0	37.29	-62.71	-73.54 to -51.88
SA	99.54	17.99	-81.55	-92.38 to -70.72
ST	100.0	16.51	-83.49	-94.32 to -72.66
EC	100.0	14.29	-85.71	-96.54 to -74.88

DPC201	100.0	29.27	-70.73	-81.56 to -59.90
DPC206	100.0	28.62	-71.38	-82.21 to -60.55
DPC209	100.0	29.40	-70.60	-81.43 to -59.77
DPC16	100.0	36.33	-63.67	-74.50 to -52.84
DR10	100.0	25.11	-74.89	-85.72 to -64.06
DR20	100.0	45.22	-54.78	-65.61 to -43.95

Strain	Difference	t	P value	Summary
LM	-62.71	19.98	P<0.001	***
SA	-81.55	25.99	P<0.001	***
ST	-83.49	26.60	P<0.001	***
EC	-85.71	27.31	P<0.001	***
DPC201	-70.73	22.54	P<0.001	***
DPC206	-71.38	22.75	P<0.001	***
DPC209	-70.60	22.50	P<0.001	***
DPC16	-63.67	20.29	P<0.001	***
DR10	-74.89	23.86	P<0.001	***
DR20	-54.78	17.46	P<0.001	***

BSA	LM			SA		
Conc.	Growth(% of control)			Growth(% of control)		
0.625	110.76	97.12	107.14	100.34	95.94	94.75
1.25	112.43	91.00	96.01	92.89	90.86	89.00
2.5	103.53	83.49	93.23	91.03	82.74	85.79
5	99.91	110.48	88.50	81.56	78.85	92.05
10	102.69	102.41	79.87	80.88	86.63	97.63
20	98.24	102.97	88.22	73.27	88.49	92.22
NC	106.03	94.90	99.07	99.80	98.98	99.83
PC	36.18	37.29	38.40	8.46	27.07	18.44

BSA	ST			EC		
Conc.	Growth(% of control)			Growth(% of control)		
0.625	91.62	92.73	91.53	91.67	98.95	102.54
1.25	100.77	97.86	96.41	91.78	102.76	106.35
2.5	99.74	102.99	97.86	87.19	98.06	104.00
5	104.36	103.34	105.05	90.10	103.88	104.56
10	108.73	108.04	109.84	92.79	100.64	106.24
20	112.49	111.89	110.27	94.14	97.61	105.57
NC	97.72	101.31	100.97	92.59	100.77	106.64
PC	16.25	15.58	17.71	13.07	13.19	16.61

BSA	DPC201			DPC206			DPC209		
Conc.	Growth(% of control)			Growth(% of control)			Growth(% of control)		
0.625	105.69	106.92	110.27	112.63	93.78	113.65	108.75	109.03	111.88
1.25	102.87	96.45	97.86	100.96	97.70	99.75	108.65	107.60	109.70
2.5	103.31	93.37	95.66	104.60	89.86	93.78	98.76	103.61	98.48
5	103.93	98.12	99.09	109.74	101.15	106.19	94.30	108.08	98.76
10	97.86	101.47	102.17	101.43	100.40	97.88	111.50	112.64	114.83
20	96.45	100.32	97.77	104.23	92.75	103.67	110.55	112.45	112.45
NC	100.50	97.95	101.55	101.80	95.46	102.74	98.10	102.85	99.05
PC	26.22	28.60	33.00	28.37	28.46	29.02	27.09	29.18	31.94

BSA	DPC16			DR10			DR20		
Conc.	Growth(% of control)			Growth(% of control)			Growth(% of control)		
0.625	121.80	116.69	114.46	113.97	113.24	111.88	112.74	113.44	114.47
1.25	118.58	117.80	119.02	115.69	111.06	112.51	119.31	116.20	118.85
2.5	107.23	110.23	121.47	113.15	111.78	111.15	123.11	112.51	112.63
5	109.23	111.79	123.14	114.33	109.33	111.97	102.15	109.64	118.39
10	118.46	113.68	114.68	112.69	105.33	110.51	99.96	106.53	110.56
20	103.45	115.24	112.46	105.79	100.70	105.24	113.90	102.73	105.83
NC	101.56	96.44	102.00	99.52	100.33	100.15	99.04	100.08	100.88
PC	36.48	36.37	36.15	24.81	24.36	26.17	45.83	45.60	44.22

```
Parameter
Table Analyzed       BSA on all bacteria

Two-way ANOVA

Source of Variation  % of total variation   P value
  Interaction        3.33        P<0.0001
  Treatment          88.36       P<0.0001
  Strain     5.71    P<0.0001

Source of Variation  P value summary        Significant?
  Interaction        ***         Yes
  Treatment          ***         Yes
  Strain     ***     Yes

Source of Variation  Df          Sum-of-squares         Mean square          F
  Interaction        63          5583        88.61      3.241
  Treatment          7           148300      21180      774.7
  Strain     9       9586        1065        38.95
  Residual   160     4375        27.34

Number of missing values         0

Bonferroni posttests

NC vs. 0.625
Strain       NC          0.625       Difference 95% CI of diff.
  LM         100.0       105.0       5.007       -9.728 to 19.74
  SA         99.54       97.01       -2.527      -17.26 to 12.21
  ST         100.0       91.96       -8.040      -22.77 to 6.695
  EC         100.0       97.72       -2.280      -17.01 to 12.45
  DPC201     100.0       107.6       7.627       -7.108 to 22.36
  DPC206     100.0       106.7       6.687       -8.048 to 21.42
  DPC209     100.0       109.9       9.887       -4.848 to 24.62
  DPC16      100.0       117.7       17.65       2.915 to 32.38
  DR10       100.0       113.0       13.03       -1.705 to 27.76
  DR20       100.0       113.6       13.55       -1.185 to 28.28

Strain       Difference  t           P value     Summary
  LM         5.007       1.173       P > 0.05    ns
  SA         -2.527      0.5918      P > 0.05    ns
  ST         -8.040      1.883       P > 0.05    ns
  EC         -2.280      0.5340      P > 0.05    ns
  DPC201     7.627       1.786       P > 0.05    ns
  DPC206     6.687       1.566       P > 0.05    ns
  DPC209     9.887       2.316       P > 0.05    ns
  DPC16      17.65       4.134       P<0.001     ***
  DR10       13.03       3.052       P < 0.05    *
  DR20       13.55       3.174       P < 0.05    *

NC vs. 1.25
Strain       NC          1.25        Difference 95% CI of diff.
  LM         100.0       99.81       -0.1867     -14.92 to 14.55
  SA         99.54       90.92       -8.620      -23.35 to 6.115
```

ST	100.0	98.35	-1.653	-16.39 to 13.08
EC	100.0	100.3	0.2967	-14.44 to 15.03
DPC201	100.0	99.06	-0.9400	-15.67 to 13.79
DPC206	100.0	99.47	-0.5300	-15.26 to 14.20
DPC209	100.0	108.7	8.650	-6.085 to 23.38
DPC16	100.0	118.5	18.47	3.732 to 33.20
DR10	100.0	113.1	13.09	-1.648 to 27.82
DR20	100.0	118.1	18.12	3.385 to 32.85

Strain	Difference	t	P value	Summary
LM	-0.1867	0.04372	P > 0.05	ns
SA	-8.620	2.019	P > 0.05	ns
ST	-1.653	0.3872	P > 0.05	ns
EC	0.2967	0.06948	P > 0.05	ns
DPC201	-0.9400	0.2202	P > 0.05	ns
DPC206	-0.5300	0.1241	P > 0.05	ns
DPC209	8.650	2.026	P > 0.05	ns
DPC16	18.47	4.325	P<0.001	***
DR10	13.09	3.065	P < 0.05	*
DR20	18.12	4.244	P<0.001	***

NC vs. 2.5

Strain	NC	2.5	Difference	95% CI of diff.
LM	100.0	93.42	-6.583	-21.32 to 8.151
SA	99.54	86.52	-13.02	-27.75 to 1.718
ST	100.0	100.2	0.1967	-14.54 to 14.93
EC	100.0	96.42	-3.583	-18.32 to 11.15
DPC201	100.0	97.45	-2.553	-17.29 to 12.18
DPC206	100.0	96.08	-3.920	-18.65 to 10.81
DPC209	100.0	100.3	0.2833	-14.45 to 15.02
DPC16	100.0	113.0	12.98	-1.758 to 27.71
DR10	100.0	112.0	12.03	-2.708 to 26.76
DR20	100.0	116.1	16.08	1.349 to 30.82

Strain	Difference	t	P value	Summary
LM	-6.583	1.542	P > 0.05	ns
SA	-13.02	3.049	P < 0.05	*
ST	0.1967	0.04606	P > 0.05	ns
EC	-3.583	0.8393	P > 0.05	ns
DPC201	-2.553	0.5980	P > 0.05	ns
DPC206	-3.920	0.9181	P > 0.05	ns
DPC209	0.2833	0.06636	P > 0.05	ns
DPC16	12.98	3.039	P < 0.05	*
DR10	12.03	2.817	P > 0.05	ns
DR20	16.08	3.767	P<0.01	**

NC vs. 5

Strain	NC	5	Difference	95% CI of diff.
LM	100.0	99.63	-0.3700	-15.10 to 14.36
SA	99.54	84.15	-15.38	-30.12 to -0.6488
ST	100.0	104.3	4.250	-10.48 to 18.98
EC	100.0	99.51	-0.4867	-15.22 to 14.25
DPC201	100.0	100.4	0.3800	-14.35 to 15.11
DPC206	100.0	105.7	5.693	-9.041 to 20.43
DPC209	100.0	100.4	0.3800	-14.35 to 15.11
DPC16	100.0	114.7	14.72	-0.01455 to 29.45
DR10	100.0	111.9	11.88	-2.858 to 26.61
DR20	100.0	110.1	10.06	-4.675 to 24.79

Strain	Difference	t	P value	Summary
LM	-0.3700	0.08666	P > 0.05	ns
SA	-15.38	3.603	P<0.01	**
ST	4.250	0.9954	P > 0.05	ns
EC	-0.4867	0.1140	P > 0.05	ns
DPC201	0.3800	0.08900	P > 0.05	ns
DPC206	5.693	1.333	P > 0.05	ns
DPC209	0.3800	0.08900	P > 0.05	ns
DPC16	14.72	3.448	P<0.01	**
DR10	11.88	2.782	P > 0.05	ns
DR20	10.06	2.356	P > 0.05	ns

NC vs. 10

Strain	NC	10	Difference	95% CI of diff.
LM	100.0	94.99	-5.010	-19.74 to 9.725
SA	99.54	88.38	-11.16	-25.89 to 3.578
ST	100.0	108.9	8.870	-5.865 to 23.60
EC	100.0	99.89	-0.1100	-14.84 to 14.62
DPC201	100.0	100.5	0.5000	-14.23 to 15.23
DPC206	100.0	99.90	-0.09667	-14.83 to 14.64
DPC209	100.0	113.0	12.99	-1.745 to 27.72
DPC16	100.0	115.6	15.61	0.8721 to 30.34
DR10	100.0	109.5	9.510	-5.225 to 24.24
DR20	100.0	105.7	5.683	-9.051 to 20.42

Strain	Difference	t	P value	Summary
LM	-5.010	1.173	P > 0.05	ns
SA	-11.16	2.613	P > 0.05	ns
ST	8.870	2.078	P > 0.05	ns
EC	-0.1100	0.02577	P > 0.05	ns
DPC201	0.5000	0.1171	P > 0.05	ns
DPC206	-0.09667	0.02264	P > 0.05	ns
DPC209	12.99	3.042	P < 0.05	*
DPC16	15.61	3.655	P<0.01	**
DR10	9.510	2.227	P > 0.05	ns
DR20	5.683	1.331	P > 0.05	ns

NC vs. 20

Strain	NC	20	Difference	95% CI of diff.
LM	100.0	96.48	-3.523	-18.26 to 11.21
SA	99.54	84.66	-14.88	-29.61 to -0.1421
ST	100.0	111.6	11.55	-3.185 to 26.28
EC	100.0	99.11	-0.8933	-15.63 to 13.84
DPC201	100.0	98.18	-1.820	-16.55 to 12.91
DPC206	100.0	100.2	0.2167	-14.52 to 14.95
DPC209	100.0	111.8	11.82	-2.918 to 26.55
DPC16	100.0	110.4	10.38	-4.351 to 25.12
DR10	100.0	103.9	3.910	-10.82 to 18.64
DR20	100.0	107.5	7.487	-7.248 to 22.22

Strain	Difference	t	P value	Summary
LM	-3.523	0.8252	P > 0.05	ns
SA	-14.88	3.484	P<0.01	**
ST	11.55	2.705	P > 0.05	ns
EC	-0.8933	0.2092	P > 0.05	ns
DPC201	-1.820	0.4263	P > 0.05	ns
DPC206	0.2167	0.05075	P > 0.05	ns
DPC209	11.82	2.768	P > 0.05	ns
DPC16	10.38	2.432	P > 0.05	ns
DR10	3.910	0.9158	P > 0.05	ns
DR20	7.487	1.754	P > 0.05	ns

NC vs. PC

Strain	NC	PC	Difference	95% CI of diff.
LM	100.0	37.29	-62.71	-77.44 to -47.98
SA	99.54	17.99	-81.55	-96.28 to -66.81
ST	100.0	16.51	-83.49	-98.22 to -68.75
EC	100.0	14.29	-85.71	-100.4 to -70.98
DPC201	100.0	29.27	-70.73	-85.46 to -55.99
DPC206	100.0	28.62	-71.38	-86.12 to -56.65
DPC209	100.0	29.40	-70.60	-85.33 to -55.86
DPC16	100.0	36.33	-63.67	-78.40 to -48.93
DR10	100.0	25.11	-74.89	-89.62 to -60.15
DR20	100.0	45.22	-54.78	-69.52 to -40.05

Strain	Difference	t	P value	Summary
LM	-62.71	14.69	P<0.001	***
SA	-81.55	19.10	P<0.001	***
ST	-83.49	19.55	P<0.001	***
EC	-85.71	20.07	P<0.001	***
DPC201	-70.73	16.57	P<0.001	***
DPC206	-71.38	16.72	P<0.001	***
DPC209	-70.60	16.53	P<0.001	***

```
DPC16    -63.67    14.91    P<0.001    ***
DR10     -74.89    17.54    P<0.001    ***
DR20     -54.78    12.83    P<0.001    ***
```

Plate count assays:

Strain	% of control			Mean	SD
DPC201	100.00	97.12	100.00	99.04	1.66
DPC206	100.00	100.78	98.67	99.82	1.06
DPC209	103.96	101.03	96.54	100.51	3.74
DPC16	95.57	104.92	105.37	101.95	5.53
DR10	108.07	100.00	101.93	103.33	4.22
DR20	106.82	108.60	105.98	107.13	1.34
SA	85.90	97.45	72.31	85.22	12.58
EC	92.02	87.73	93.70	91.15	3.08

```
Parameter Value
Table Analyzed
Lf
One-way analysis of variance
  P value    0.0036
  P value summary      **
  Are means signif. different? (P < 0.05)         Yes
  Number of groups    8
  F             5.034
  R squared0.6877

ANOVA Table            SS            df            MS
  Treatment (between columns)    1039          7             148.4
  Residual (within columns)      471.7         16            29.48
  Total        1510         23

Bonferroni's Multiple Comparison Test         Mean Diff. t              P value      95% CI of diff
  EC vs SA  5.927        1.337       P > 0.05     -9.042 to 20.90
  EC vs DPC201           -7.892       1.780        P > 0.05     -22.86 to 7.077
  EC vs DPC206           -8.669       1.956        P > 0.05     -23.64 to 6.299
  EC vs DPC209           -9.361       2.112        P > 0.05     -24.33 to 5.607
  EC vs DPC16            -10.81       2.438        P > 0.05     -25.78 to 4.162
  EC vs DR10             -12.19       2.749        P > 0.05     -27.16 to 2.783
  EC vs DR20             -15.98       3.606        P < 0.05     -30.95 to -1.015
  SA vs DPC201           -13.82       3.117        P > 0.05     -28.79 to 1.150
  SA vs DPC206           -14.60       3.292        P > 0.05     -29.57 to 0.3725
  SA vs DPC209           -15.29       3.449        P < 0.05     -30.26 to -0.3194
  SA vs DPC16            -16.73       3.775        P < 0.05     -31.70 to -1.765
  SA vs DR10             -18.11       4.086        P < 0.05     -33.08 to -3.144
  SA vs DR20             -21.91       4.942        P < 0.01     -36.88 to -6.942
```

3.3.2 The effect of polymyxin B on the growth of selected pathogens and probiotics

Strain	LM			SA		
PB(mg/mL)	Growth(% of control)			Growth(% of control)		
0.975	105.13	111.45	105.13	65.54	63.88	61.09
1.95	105.30	108.03	110.77	63.32	64.89	66.10
3.9	104.96	115.04	110.26	68.97	68.42	69.99
7.8	109.74	116.92	112.31	73.52	70.09	71.66
15	112.14	114.19	105.98	69.16	69.90	69.53
30	113.68	119.15	117.09	79.64	77.78	77.60
60	10.43	9.40	21.37	4.91	5.10	5.10
NC	89.74	110.94	99.32	99.47	104.11	96.42
PC	6.03	5.80	5.80	33.75	6.70	20.09

Strain	ST			EC		
PB(mg/mL)	Growth(% of control)			Growth(% of control)		
0.975	96.74	96.74	86.38	94.57	106.52	107.90
1.95	4.48	4.20	4.20	88.94	84.11	84.11
3.9	4.48	4.48	4.66	5.23	5.13	5.13
7.8	4.76	4.85	5.41	5.33	5.53	5.43
15	4.85	4.76	5.13	6.12	5.73	5.43
30	4.66	4.57	4.57	5.53	5.23	5.43
60	4.94	4.66	4.85	5.43	5.33	5.33
NC	100.84	99.72	99.44	95.56	99.01	105.43
PC	4.92	4.92	5.20	4.26	4.05	4.40

```
                    LM        SA        ST        EC        Global (shared)
Comparison of Fits
  Null hypothesis                                           One curve for all data sets
  Alternative hypothesis                                              Different curve for each data set
  P value                                         P<0.0001
  Conclusion (alpha = 0.05)                                           Reject null hypothesis
  Preferred model                                           Different curve for each data set
  F (DFn, DFd)                                              44.30 (9,72)

Different curve for each data set
Best-fit values
  BOTTOM            -15850    -12310    -6.037    -5.013
  TOP     121.8     75.77     12896     417.6
  LOGEC50           4.041     4.135     -2.204    -0.4451
  EC50    10981     13640     0.006246  0.3588
Std. Error
  BOTTOM            1.616e+006          1.914e+006          5.940     6.226
  TOP     7.487     5.752     938305    400.9
  LOGEC50           45.38     69.26     32.63     0.5539
95% Confidence Intervals
  BOTTOM            -3412000 to 3.380e+006        -4035000 to 4.010e+006        -18.52 to 6.443     -18.10  to  8.068

  TOP     106.1 to 137.6      63.68 to 87.85      -1958000 to 1.984e+006        -424.7 to 1260
  LOGEC50           -91.30 to 99.38     -141.4 to 149.6     -70.77 to 66.36     -1.609 to 0.7187
  EC50                                  0.02460 to 5.232
Goodness of Fit
  Degrees of Freedom          18        18        18        18
  R²      0.7017    0.6086    0.7691    0.8689
  Absolute Sum of Squares     7382      4358      4676      4518
  Sy.x    20.25     15.56     16.12     15.84
Normality of Residuals
  Kolmogorov-Smirnov distance 0.1446    0.1572    0.2264    0.1560
  P value P > 0.10  P > 0.10  0.0063    P > 0.10
  D'Agostino & Pearson omnibus K2       4.112     4.338     4.631     0.02413
  P value 0.1280    0.1143    0.0987    0.9880
  Shapiro-Wilk W    0.8919    0.8713    0.8499    0.9415
  P value 0.0245    0.0101    0.0042    0.2337
```

Strain	DPC201			DPC206		
PB(mg/mL)	Growth(% of control)			Growth(% of control)		
0.975	101.27	100.13	96.52	99.27	99.18	100.37
1.95	97.75	92.72	95.19	91.12	94.41	100.64
3.9	97.28	94.81	96.05	98.26	98.81	100.46
7.8	96.43	94.34	95.76	98.81	96.43	98.63
15	97.18	92.34	96.99	98.35	101.47	102.66
30	94.15	95.29	93.77	101.83	98.90	101.10
60	105.06	101.93	104.02	107.42	104.03	109.34
NC	101.27	99.37	99.37	100.73	97.99	101.28
PC	8.28	8.28	8.44	8.47	8.39	8.55

Strain	DPC209			DPC16		
PB(mg/mL)	Growth(% of control)			Growth(% of control)		
0.975	101.31	102.96	102.41	96.63	96.30	106.41
1.95	96.00	102.87	93.90	88.71	103.99	99.49
3.9	100.85	98.84	100.49	97.07	92.78	93.88
7.8	101.68	99.66	101.77	90.25	107.51	95.42
15	102.87	104.42	99.57	92.89	100.04	92.12
30	100.40	102.68	100.95	92.01	92.56	93.11
60	107.17	107.72	106.80	94.43	93.55	93.99
NC	99.85	99.48	100.67	97.07	93.77	109.16
PC	9.96	9.60	9.42	12.39	13.62	12.73

Strain	DR10			DR20		
PB(mg/mL)	Growth(% of control)			Growth(% of control)		
0.975	101.72	97.99	96.84	98.32	98.32	96.76
1.95	97.32	97.51	95.22	96.07	96.33	96.42
3.9	97.99	96.27	95.50	96.07	95.03	94.77
7.8	97.70	95.22	96.75	94.60	95.55	94.94
15	96.65	95.02	95.31	96.59	95.55	95.03
30	95.79	92.06	91.96	95.90	95.72	96.07
60	97.80	95.69	96.08	102.14	101.79	102.66
NC	100.57	100.10	99.33	98.93	99.36	101.71
PC	8.90	8.64	8.99	8.38	8.54	8.46

```
        DPC201    DPC206    DPC209    DPC16     DR10      DR20
Best-fit values
   Slope  1.311 ± 1.287       4.085 ± 1.144       2.968 ± 1.047       -3.193 ± 1.752      -1.768 ± 0.6646     1.542  ±
0.8434
   Y-intercept when X=0.0     95.93 ± 1.372       96.46 ± 1.220       99.06 ± 1.116       98.69 ± 1.868       97.87  ±
0.7085    95.52 ± 0.8992
   X-intercept when Y=0.0     -73.18    -23.61    -33.38    30.91     55.37     -61.96
   1/slope  0.7628    0.2448    0.3370    -0.3132   -0.5657   0.6486
95% Confidence Intervals
   Slope  -1.383 to 4.005     1.691 to 6.479      0.7764 to 5.159     -6.860 to 0.4751    -3.159 to -0.3767   -0.2235
to 3.307
   Y-intercept when X=0.0     93.06 to 98.81      93.90 to 99.01      96.72 to 101.4      94.78 to 102.6      96.39  to
99.35     93.64 to 97.40
   X-intercept when Y=0.0               -58.30 to -14.56    -130.1 to -18.82              31.37 to 256.5
Goodness of Fit
   r²     0.05177   0.4016    0.2972    0.1487    0.2713    0.1496
   Sy.x   3.508     3.118     2.853     4.776     1.811     2.299
Is slope significantly non-zero?
   F      1.037     12.75     8.035     3.319     7.075     3.342
   DFn, DFd         1.000, 19.00        1.000, 19.00        1.000, 19.00        1.000, 19.00        1.000,        19.00
          1.000, 19.00
   P value  0.3212  0.0020    0.0106    0.0843    0.0155    0.0833
   Deviation from zero?       Not Significant     Significant Significant Not Significant     Significant Not Significant
Data
   Number of X values         21        21        21        21        21
   Maximum number of Y replicates       1         1         1         1         1
   Total number of values     21        21        21        21        21
   Number of missing values   0         0         0         0         0
```

Strain	LM			SA		
PS(%)	Growth(% of control)			Growth(% of control)		
0.0156	52.20	17.85	16.49	106.90	106.20	106.29
0.03125	6.94	5.80	5.69	103.91	103.47	102.94
0.0625	5.57	7.85	2.50	101.00	102.06	100.21
0.125	6.71	6.14	6.37	85.75	91.66	89.98
0.25	7.16	6.25	6.37	42.92	86.63	56.58
0.5	5.69	5.69	5.80	31.37	41.95	29.79
1	6.03	5.80	5.80	33.75	6.70	20.09

Strain	ST			EC		
PS(%)	Growth(% of control)			Growth(% of control)		
0.0156	107.02	105.56	98.81	86.37	88.67	90.00
0.03125	93.16	92.25	82.13	86.58	86.93	86.51
0.0625	54.97	81.59	53.78	62.44	78.70	87.42
0.125	5.38	5.56	5.29	26.51	14.23	33.07
0.25	5.38	5.47	5.38	5.58	15.56	5.79
0.5	5.01	5.10	5.20	4.26	4.33	4.33
1	4.92	4.92	5.20	4.26	4.05	4.40

```
                              LM        SA        ST        EC        Global (shared)
Comparison of Fits
   Null hypothesis                                          One curve for all data sets
   Alternative hypothesis                                             Different curve for each data set
   P value                                        P<0.0001
   Conclusion (alpha = 0.05)                                          Reject null hypothesis
   Preferred model                                          Different curve for each data set
   F (DFn, DFd)                                             150.1 (6,76)

Different curve for each data set
Best-fit values
   LOGIC50            -2.101    -0.4400   -1.154    -1.058
   HILLSLOPE          -1.481    -1.764    -3.984    -2.404
Std. Error
   LOGIC50            0.1555    0.03931   0.01915   0.02714
   HILLSLOPE          0.5250    0.2632    0.7061    0.3142
95% Confidence Intervals
   LOGIC50            -2.426 to -1.775    -0.5223 to -0.3578    -1.194 to -1.114    -1.115 to -1.001
   HILLSLOPE          -2.580 to -0.3824   -2.315 to -1.213      -5.462 to -2.506    -3.062 to -1.747
Goodness of Fit
   Degrees of Freedom           19        19        19        19
   R²       0.4010    0.9189    0.9702    0.9562
   Absolute Sum of Squares      1306      1944      1079      1280
   Sy.x     8.290     10.11     7.534     8.207
Normality of Residuals
   Kolmogorov-Smirnov distance 0.2604     0.2325    0.2464    0.1491
   P value  0.0007    0.0043    0.0017    P > 0.10
   D'Agostino & Pearson omnibus K2        7.603     5.311     2.565     0.7297
   P value  0.0223    0.0703    0.2773    0.6943
   Shapiro-Wilk W     0.8240    0.8800    0.8939    0.9728
   P value  0.0016    0.0146    0.0267    0.7945
```

Strain	DPC201			DPC206		
PS(%)	Growth(% of control)			Growth(% of control)		
0.0156	101.39	100.64	96.96	100.49	94.33	85.28
0.03125	68.88	72.72	67.46	80.51	73.27	74.67
0.0625	15.80	18.14	8.69	11.35	9.38	8.31
0.125	8.53	8.28	8.94	9.87	9.46	9.05
0.25	8.53	8.28	8.86	9.38	8.96	8.47
0.5	8.11	7.86	7.94	8.72	8.47	8.63
1	8.28	8.28	8.44	8.47	8.39	8.55

Strain	DPC209			DPC16		
PS(%)	Growth(% of control)			Growth(% of control)		
0.0156	106.31	105.69	82.84	95.91	105.95	105.73
0.03125	71.56	55.82	63.82	90.44	82.62	92.33
0.0625	18.40	14.31	10.13	13.17	14.51	13.96
0.125	11.11	10.93	10.76	14.18	13.51	14.85
0.25	10.13	9.42	10.13	12.84	11.61	12.62
0.5	9.33	9.96	10.22	11.83	12.17	12.95
1	9.96	9.60	9.42	12.39	13.62	12.73

Strain	DR10			DR20		
PS(%)	Growth(% of control)			Growth(% of control)		
0.0156	95.68	96.11	91.70	79.25	78.26	70.71
0.03125	63.87	75.11	48.31	49.44	49.11	43.61
0.0625	16.85	21.69	14.87	12.07	15.28	11.83
0.125	11.50	11.84	10.98	9.44	9.44	9.53
0.25	9.68	10.20	9.85	9.03	8.79	8.87
0.5	8.64	8.38	8.38	8.13	8.13	8.05
1	8.90	8.64	8.99	8.38	8.54	8.46

```
                  DPC201     DPC206     DPC209     DPC16      DR10       DR20       Global (shared)
Comparison of Fits
   Null hypothesis                                                                  One curve for all data sets
   Alternative hypothesis                                                                      Different  curve  for  each  data
set
   P value                                                               P<0.0001
   Conclusion (alpha = 0.05)                                                                   Reject null hypothesis
   Preferred model                                                                  Different curve for each data set
   F (DFn, DFd)                                                                     6.422 (10,112)

Different curve for each data set
Best-fit values
   LOGIC50        -1.406     -1.400     -1.426     -1.345     -1.396     -1.545
   HILLSLOPE      -3.692     -4.707     -3.256     -5.420     -2.883     -1.873
Std. Error
   LOGIC50        0.01866    0.02000    0.02668    0.03011    0.02607    0.02434
   HILLSLOPE      0.4725     0.7145     0.5698     1.089      0.3979     0.1949
95% Confidence Intervals
   LOGIC50        -1.445 to -1.367      -1.442 to -1.358      -1.482 to -1.370      -1.408 to -1.282      -1.451    to    -1.342
         -1.596 to -1.494
   HILLSLOPE      -4.681 to -2.703      -6.208 to -3.206      -4.449 to -2.063      -7.699 to -3.141      -3.719    to    -2.047
         -2.280 to -1.465
Goodness of Fit
   Degrees of Freedom         19         18         19         19         18         19
   R²      0.9661     0.9555     0.9291     0.9277     0.9502     0.9420
   Absolute Sum of Squares    871.2      980.6      1660       2132       1053       754.4
   Sy.x    6.772      7.381      9.348      10.59      7.647      6.301
Normality of Residuals
   Kolmogorov-Smirnov distance 0.2555    0.3495     0.3402     0.2928     0.3220     0.2183
   P value  0.0009    P<0.0001   P<0.0001   P<0.0001   P<0.0001   0.0102
   D'Agostino & Pearson omnibus K2        5.582      5.438      8.217      4.094      4.131      3.503
   P value  0.0614    0.0659     0.0164     0.1291     0.1268     0.1736
   Shapiro-Wilk W     0.8244     0.7665     0.7370     0.8273     0.7785     0.8343
   P value  0.0016    0.0003     P<0.0001   0.0018     0.0004     0.0023
```

3.3.3 The effect of bovine lactoferrin in combination with a probiotic supernatant on the growth of selected pathogens and probiotics

Treatment	Lf(10mg/mL)			DSg(12.5% v/v)			Lf(10mg/mL)+DSg(12.5% v/v)		
Strain	Growth(% of control)			Growth(% of control)			Growth(% of control)		
LM	61.70	66.42	64.74	70.44	64.86	68.81	8.97	18.05	5.30
SA	42.09	55.34	53.54	54.70	47.94	35.32	19.87	2.22	14.82
ST	77.76	64.52	67.62	80.00	78.07	80.68	20.23	14.53	39.70
EC	53.95	51.02	54.66	76.70	81.95	78.45	21.40	21.53	17.68

```
Parameter
Table Analyzed      Pathogens

Two-way ANOVA

Source of Variation % of total variation  P value
  Interaction       5.10       0.0043
  Treatment         80.17      P<0.0001
  Strain    10.02   P<0.0001

Source of Variation P value summary   Significant?
  Interaction       **         Yes
  Treatment         ***        Yes
  Strain    ***     Yes

Source of Variation Df         Sum-of-squares     Mean square       F
  Interaction       6          1141       190.2      4.326
  Treatment         2          17960      8981       204.2
  Strain    3       2245       748.4      17.02
  Residual  24      1055       43.97

Number of missing values       0

Bonferroni posttests

Lf+DSg vs. Lf
Strain    Lf+DSg    Lf         Difference 95% CI of diff.
  LM      10.77     64.29      53.51      37.29 to 69.74
  SA      12.30     50.32      38.02      21.79 to 54.25
  ST      24.82     69.97      45.15      28.92 to 61.37
  EC      20.20     53.21      33.01      16.78 to 49.23

Strain    Difference t         P value    Summary
  LM      53.51     9.883      P<0.001    ***
  SA      38.02     7.022      P<0.001    ***
  ST      45.15     8.338      P<0.001    ***
  EC      33.01     6.096      P<0.001    ***

Lf+DSg vs. DSg
Strain    Lf+DSg    DSg        Difference 95% CI of diff.
  LM      10.77     68.04      57.26      41.04 to 73.49
  SA      12.30     45.99      33.68      17.46 to 49.91
  ST      24.82     79.58      54.76      38.54 to 70.99
  EC      20.20     79.03      58.83      42.60 to 75.06

Strain    Difference t         P value    Summary
  LM      57.26     10.58      P<0.001    ***
  SA      33.68     6.221      P<0.001    ***
  ST      54.76     10.11      P<0.001    ***
  EC      58.83     10.87      P<0.001    ***
```

Treatment	Lf(10mg/mL)			DSg(12.5% v/v)			Lf(10mg/mL)+DSg(12.5% v/v)		
Strain	Growth(% of control)			Growth(% of control)			Growth(% of control)		
DPC201	94.05	96.20	95.62	104.95	95.61	95.97	97.56	94.45	95.94
DPC206	91.11	93.48	91.48	95.57	93.34	96.69	90.16	92.37	90.95
DPC209	92.06	91.27	90.01	95.09	97.21	91.06	90.64	86.62	89.65
DPC16	86.62	87.49	86.88	95.59	95.49	87.43	91.40	92.70	93.13
DR10	89.57	91.61	91.70	82.97	79.11	94.55	91.08	85.57	86.93
DR20	95.49	92.57	93.95	79.88	87.91	91.20	90.46	90.38	90.62

```
Parameter
Table Analyzed        Probiotics

Two-way ANOVA

Source of Variation   % of total variation   P value
  Interaction         26.96       0.0135
  Treatment           0.97        0.6179
  Strain      36.35   P<0.0001

Source of Variation   P value summary        Significant?
  Interaction         *           Yes
  Treatment           ns          No
  Strain      ***     Yes

Source of Variation   Df          Sum-of-squares         Mean square          F
  Interaction         10          280.6       28.06      2.717
  Treatment           2           10.08       5.039      0.4879
  Strain      5       378.3       75.67       7.326
  Residual    36      371.8       10.33

Number of missing values          0

Bonferroni posttests

Lf+DSg vs. Lf
Strain      Lf+DSg    Lf          Difference  95% CI of diff.
  DPC201    95.98     95.29       -0.6933     -8.722 to 7.336
  DPC206    91.16     92.02       0.8633      -7.166 to 8.892
  DPC209    88.97     91.11       2.143       -5.886 to 10.17
  DPC16     92.41     87.00       -5.413      -13.44 to 2.616
  DR10      87.86     90.96       3.100       -4.929 to 11.13
  DR20      90.49     94.00       3.517       -4.512 to 11.55

Strain      Difference t          P value     Summary
  DPC201    -0.6933   0.2642      P > 0.05    ns
  DPC206    0.8633    0.3290      P > 0.05    ns
  DPC209    2.143     0.8168      P > 0.05    ns
  DPC16     -5.413    2.063       P > 0.05    ns
  DR10      3.100     1.181       P > 0.05    ns
  DR20      3.517     1.340       P > 0.05    ns

Lf+DSg vs. DSg
Strain      Lf+DSg    DSg         Difference  95% CI of diff.
  DPC201    95.98     98.84       2.860       -5.169 to 10.89
  DPC206    91.16     95.20       4.040       -3.989 to 12.07
  DPC209    88.97     94.45       5.483       -2.546 to 13.51
  DPC16     92.41     92.84       0.4267      -7.602 to 8.456
  DR10      87.86     85.54       -2.317      -10.35 to 5.712
  DR20      90.49     86.33       -4.157      -12.19 to 3.872

Strain      Difference t          P value     Summary
  DPC201    2.860     1.090       P > 0.05    ns
  DPC206    4.040     1.540       P > 0.05    ns
  DPC209    5.483     2.090       P > 0.05    ns
  DPC16     0.4267    0.1626      P > 0.05    ns
  DR10      -2.317    0.8829      P > 0.05    ns
  DR20      -4.157    1.584       P > 0.05    ns
```

Chapter 4

4.3.1 Cytotoxicity of human faecal water

Time(min)	5% FW			10% FW			50% FW		
	Viable cells (% of control)			Viable cells (% of control)			Viable cells (% of control)		
0	109.37	100.59	91.57	96.79	91.89	111.32	96.37	109.97	92.32
5	112.84	103.42	96.29	89.99	104.24	109.13	76.56	93.70	98.41
15	102.65	99.76	81.21	90.93	76.97	84.92	76.38	75.32	76.44
60	99.12	83.98	89.05	88.69	64.55	58.02	52.41	48.00	60.37
120	71.91	67.08	71.79	33.57	34.33	36.16	20.73	20.32	21.61

Time(min)	NC			PC		
	Viable cells (% of control)			Viable cells (% of control)		
0	100.32	105.68	96.58	98.62	94.32	106.96
120	102.65	99.70	93.25	14.19	12.19	11.01

```
          5%        10%       50%       Global (shared)
Comparison of Fits
  Null hypothesis                                 PLATEAU same for all data sets
  Alternative hypothesis                                    PLATEAU different for each data set
  P value                               0.0729
  Conclusion (alpha = 0.05)                                 Do not reject null hypothesis
  Preferred model                                 PLATEAU same for all data sets
  F (DFn, DFd)                                    2.818 (2,36)


PLATEAU same for all data sets
Best-fit values
  X0      50.60     35.15     23.94
  PLATEAU           94.42     94.42     94.42     94.42
  K       0.004259  0.01180   0.01571
Std. Error
  X0      19.43     12.35     16.35
  PLATEAU           2.057     2.057     2.057     2.057
  K       0.001851  0.003305  0.005284
95% Confidence Intervals
  X0      11.25 to 89.96      10.14 to 60.17      -9.177 to 57.06
  PLATEAU           90.26 to 98.59      90.26 to 98.59      90.26 to 98.59      90.26 to 98.59
  K       0.0005101 to 0.008008         0.005110 to 0.01849 0.005005 to 0.02641
Goodness of Fit
  Degrees of Freedom                                        38
  R²      0.6086    0.8437    0.8643    0.8533
  Absolute Sum of Squares       1098      1563      1678      4339
  Sy.x                                  10.69
Normality of Residuals
  Kolmogorov-Smirnov distance 0.1066    0.1603    0.2254
  P value P > 0.10  P > 0.10  0.0389
  d'Agostino & Pearson omnibus K2       0.1218    0.4738    0.3229
  P value 0.9409    0.7891    0.8509
  Shapiro-Wilk W    0.9857    0.9512    0.8893
  P value 0.9944    0.5436    0.0654
Constraints
  PLATEAU           PLATEAU is shared   PLATEAU is shared   PLATEAU is shared
```

4.3.2 Genotoxicity of human faecal water and the effects of potential protectants

Treatment	FW1				
	DNA tail moment (% of control)			Mean	SD
NC	28.50	42.75	40.85	37.37	7.74
PC(300uM H_2O_2)	183.35	175.75	254.60	204.57	43.50
2.5% of FW	38.95	67.45	47.50	51.30	14.63
5% FW	68.85	59.50	68.85	65.73	5.40
10% FW	220.72	81.88	174.44	159.01	70.69
50% FW	268.29	231.66	247.50	249.15	18.37

Treatment	FW2				
	DNA tail moment (% of control)			Mean	SD
NC	28.50	42.75	40.85	37.37	7.74
PC(300uM H_2O_2)	183.35	175.75	254.60	204.57	43.50
2.5% of FW	67.32	66.33	68.31	67.32	0.99
5% FW	119.54	59.34	34.40	71.09	43.77
10% FW	172.55	151.30	80.75	134.87	48.06
50% FW	193.05	262.35	156.42	203.94	53.80

Treatment	FW3				
	DNA tail moment (% of control)			Mean	SD
NC	28.50	42.75	40.85	37.37	7.74
PC(300uM H_2O_2)	183.35	175.75	254.60	204.57	43.50
2.5% of FW	30.38	53.90	70.56	51.61	20.19
5% FW	49.50	37.80	50.40	45.90	7.03
10% FW	57.85	76.54	80.99	71.79	12.28
50% FW	145.35	121.60	75.05	114.00	35.76

```
FW1         FW2         FW3         Global (shared)
Comparison of Fits
   Null hypothesis                                          One curve for all data sets
   Alternative hypothesis                                               Different curve for each data set
   P value                                      0.0025
   Conclusion (alpha = 0.05)                                            Reject null hypothesis
   Preferred model                                          Different curve for each data set
   F (DFn, DFd)                                             4.320 (8,24)

Different curve for each data set
Best-fit values
   BOTTOM               50.11       67.20       48.77
   TOP      249.5       204.0       114.0
   LOGEC50              0.9790      1.002       1.026
   HILLSLOPE            3.823       5.061       10.22
   EC50     9.527       10.04       10.61
Std. Error
   BOTTOM               25.62       25.99       12.65
   TOP      21.87       24.41       12.62
   LOGEC50              0.06595     0.07457     1.700
   HILLSLOPE            3.284       13.38       615.1
95% Confidence Intervals
   BOTTOM               -8.969 to 109.2         7.260 to 127.1          19.59 to 77.94
   TOP      199.1 to 299.9          147.7 to 260.3          84.92 to 143.1
   LOGEC50              0.8269 to 1.131         0.8299 to 1.174         -2.895 to 4.947
   HILLSLOPE            -3.750 to 11.40         -25.80 to 35.92         -1408 to 1429
   EC50     6.712 to 13.52          6.759 to 14.92          0.001272 to 88517
```

```
Goodness of Fit
    Degrees of Freedom          8         8         8
    R²      0.8721    0.7237    0.6902
    Absolute Sum of Squares     11156     14241     3823
    Sy.x    37.34     42.19     21.86
Normality of Residuals
    Kolmogorov-Smirnov distance 0.2081    0.1557    0.1819
    P value  P > 0.10  P > 0.10  P > 0.10
    D'Agostino & Pearson omnibus K2       6.156     0.3607    1.173
    P value  0.0461    0.8350    0.5562
    Shapiro-Wilk W    0.8802    0.9542    0.9649
    P value  0.0883    0.6985    0.8506
```

A pre-assessment of antigenotoxicity of testers

Treatment	DNA tail moment (% of control)			Mean	SD
NC	106.78	68.64	124.58	100.00	28.58
PC(300µM H_2O_2)	227.48	191.08	345.76	254.77	80.87
FW	408.01	325.88	476.90	403.59	75.61
FW+MRS	405.92	316.00	434.18	385.37	61.71
FW+BHI	420.62	435.55	253.86	370.01	100.86
FW+DPC16 sup	256.99	140.42	92.73	163.38	84.51
FW+DPC16 HKcells	198.71	74.18	76.83	116.57	71.14
FW+DPC16 viable cells	172.21	182.81	116.57	157.20	35.58
FW+DPC201 sup	216.10	154.68	81.89	150.89	67.19
FW+DPC201 HKcells	122.84	131.94	68.24	107.67	34.45
FW+DPC201 viable cells	171.01	144.51	115.61	143.71	27.71
FW+DR10 sup	93.93	158.97	192.69	148.53	50.20
FW+DR10 HKcells	228.17	139.00	102.28	156.49	64.74
FW+DR10 viable cells	82.21	187.55	120.75	130.17	53.30
FW+E.c supernatant	443.23	372.42	327.83	381.16	58.19
FW+E.c HKcells	286.62	245.67	310.70	281.00	32.88
FW+E.c viable cells	267.89	153.43	241.10	220.80	59.87
FW+S.a supernatant	396.61	251.69	371.19	339.83	77.38
FW+S.a HKcells	94.42	102.28	107.53	101.41	6.60
FW+S.a viable cells	191.45	125.89	157.36	158.23	32.79

The antigenotoxic effects of *L. reuteri* DPC16

Expt-1:

Treatment	DNA tail moment (% of control)			Mean	SD
NC	106.78	68.64	124.58	100.00	28.58
PC(300µM H_2O_2)	227.48	191.08	345.76	254.77	80.87
FW	408.01	325.88	476.90	403.59	75.61
FW+DPC16 sup	256.99	140.42	92.73	163.38	84.50
FW+DPC16 HK cells	198.71	74.18	76.83	116.57	71.14
FW+DPC16 viable cells	172.21	182.81	116.57	157.20	35.58

Expt-2:

Treatment	DNA tail moment(% of control)			Mean	SD
NC	111.29	101.61	87.10	100.00	12.18
FW	282.38	231.95	254.64	256.32	25.25
FW(heat treated)	247.08	128.58	191.61	189.09	59.29
FW+DPC16 sup	249.19	220.16	203.23	224.19	23.25
FW+DPC16 HK cells	176.61	215.32	195.97	195.97	19.35

Expt-3:

DPC16 HK cells	DNA tail moment(% of control)			Mean	SD
NC	124.04	72.12	103.85	100.00	26.17
FW	465.94	652.32	562.14	560.13	93.20
FW+10^5	255.91	154.74	276.74	229.13	65.26
FW+10^6	123.89	216.80	95.50	145.39	63.45
FW+10^7	115.38	83.65	98.08	99.04	15.89
FW+10^8	123.25	66.13	81.16	90.18	29.61

DPC16 sup	DNA tail moment(% of control)			Mean	SD
NC	124.04	72.12	103.85	100.00	26.17
FW	465.94	652.32	562.14	560.13	93.20
FW+6.25%	611.54	250.96	259.62	374.04	205.73
FW+12.50%	325.20	247.77	552.33	375.10	158.29
FW+25%	219.44	186.38	231.47	212.43	23.35
FW+50%	157.41	189.47	230.28	192.39	36.52

Data analysis for antigenotoxicity of *L. reuteri* DPC16 supernatant and HK-cells

Treatment	DNA tail moment (% of control)			DNA tail moment (% of control)			DNA tail moment (% of control)		
NC	106.78	68.64	124.58	111.29	101.61	87.097	124.04	72.12	103.85
FW	408.01	325.88	476.90	282.38	231.95	254.64	465.94	652.32	562.14
FW+DPC16 sup	256.99	140.42	92.73	249.19	220.16	203.23	157.41	189.47	230.28
FW+DPC16 HK cells	198.71	74.18	76.83	176.61	215.32	195.97	123.25	66.13	81.16

```
           NC         Faecal water                FW+DPC16 sup          FW+DPC16 HK cells
Number of values      9          9          9          9

Minimum    68.64      232.0      92.73      66.13
25% Percentile        79.61      268.5      148.9      75.51
Median     103.9      408.0      203.2      123.3
75% Percentile        117.7      519.5      239.7      197.3
Maximum    124.6      652.3      257.0      215.3

Mean       100.0      406.7      193.3      134.2
Std. Deviation        20.31      145.2      54.29      62.06
Std. Error 6.770      48.39      18.10      20.69

Lower 95% CI of mean             84.39      295.1      151.6      86.53
Upper 95% CI of mean             115.6      518.3      235.1      181.9
```

```
D'Agostino & Pearson omnibus normality test
K2          0.8160      0.7534      1.023       5.269
P value     0.6650      0.6861      0.5997      0.0717
Passed normality test (alpha=0.05)?             Yes         Yes         Yes         Yes
P value summary         ns          ns          ns          ns

Sum         900.0       3660        1740        1208

Parameter Value
Table Analyzed
Antigenotoxicity
One-way analysis of variance
  P value     P<0.0001
  P value summary       ***
  Are means signif. different? (P < 0.05)       Yes
  Number of groups      4
  F           24.10
  R squared             0.6932

Bartlett's test for equal variances
  Bartlett's statistic (corrected)      24.58
  P value     P<0.0001
  P value summary       ***
  Do the variances differ signif. (P < 0.05)    Yes

ANOVA Table             SS          df          MS
  Treatment (between columns)     511100      3           170400
  Residual (within columns)       226300      32          7071
  Total       737400      35

Tukey's Multiple Comparison Test                Mean Diff. q            P value     95% CI of diff
  NC vs Faecal water    -306.7      10.94       P < 0.001   -414.2 to -199.2
  NC vs FW+DPC16 sup                -93.32      3.329       P > 0.05    -200.8 to 14.15
  NC vs FW+DPC16 HK cells           -34.24      1.222       P > 0.05    -141.7 to 73.23
  Faecal water vs FW+DPC16 sup 213.4            7.612       P < 0.001   105.9 to 320.8
  Faecal water vs FW+DPC16 HK cells             272.4       9.720       P < 0.001   165.0 to 379.9
  FW+DPC16 sup vs FW+DPC16 HK cells             59.08       2.108       P > 0.05    -48.39 to 166.6
```

4.3.3 Antigenotoxic effects of bovine lactoferrin on faecal water-induced colon epethelium DNA damage

Samples	DNA tail moment(% of control)			Mean	SD
NC	121.62	94.59	83.78	100.00	19.49
FW	564.15	666.29	816.79	682.41	127.09
FW+ BLf (0.02mg/mL)	639.20	485.23	891.15	671.86	204.92
FW+ BLf (0.2mg/mL)	502.53	578.44	701.45	594.14	100.39
FW+ BLf (2mg/mL)	640.83	534.42	510.24	561.83	69.47
FW+ BLf (10mg/mL)	345.95	156.76	186.49	229.73	101.74
FW+ BLf (20mg/mL)	159.52	268.39	121.54	183.15	76.23
FW+ BSA(0.02mg/mL)	704.13	560.48	405.58	556.73	149.31
FW+ BSA(0.2mg/mL)	440.54	559.46	537.84	512.61	63.35
FW+ BSA(2mg/mL)	729.73	394.59	559.46	561.26	167.57
FW+ BSA(10mg/mL)	535.31	548.96	568.08	550.78	16.46
FW+ BSA(20mg/mL)	344.35	701.37	563.79	536.50	180.06

```
            Table Analyzed
Anti-genotoxicity-Lf
One-way analysis of variance
  P value     P<0.0001
```

```
  P value summary      ***
  Are means signif. different? (P < 0.05)        Yes
  Number of groups     7
  F            14.71
  R squared0.8631

ANOVA Table            SS             df             MS
  Treatment (between columns)   1129000  6              188200
  Residual (within columns)     179200   14             12800
  Total        1309000  20

Tukey's Multiple Comparison Test               Mean Diff. q             P value       95% CI of diff
  NC vs FW -582.4       8.917          P < 0.001  -897.8 to -267.0
  NC vs 0.02 mg/mL      -571.9         8.755         P < 0.001  -887.3 to -256.5
  NC vs 0.2 mg/mL       -494.1         7.565         P < 0.01   -809.6 to -178.7
  NC vs 2 mg/mL         -461.8         7.071         P < 0.01   -777.2 to -146.4
  NC vs 10 mg/mL        -129.7         1.986         P > 0.05   -445.1 to 185.7
  NC vs 20 mg/mL        -83.15         1.273         P > 0.05   -398.6 to 232.3
  FW vs 0.02 mg/mL      10.55          0.1615        P > 0.05   -304.9 to 326.0
  FW vs 0.2 mg/mL       88.27          1.351         P > 0.05   -227.1 to 403.7
  FW vs 2 mg/mL         120.6          1.846         P > 0.05   -194.8 to 436.0
  FW vs 10 mg/mL        452.7          6.931         P < 0.01   137.3 to 768.1
  FW vs 20 mg/mL        499.3          7.644         P < 0.01   183.9 to 814.7
  0.02 mg/mL vs 0.2 mg/mL       77.72          1.190         P > 0.05      -237.7 to 393.1
  0.02 mg/mL vs 2 mg/mL         110.0          1.685         P > 0.05      -205.4 to 425.4
  0.02 mg/mL vs 10 mg/mL        442.1          6.769         P < 0.01      126.7 to 757.5
  0.02 mg/mL vs 20 mg/mL        488.7          7.482         P < 0.01      173.3 to 804.1
  0.2 mg/mL vs 2 mg/mL          32.31          0.4947        P > 0.05      -283.1 to 347.7
  0.2 mg/mL vs 10 mg/mL         364.4          5.579         P < 0.05      49.00 to 679.8
  0.2 mg/mL vs 20 mg/mL         411.0          6.292         P < 0.01      95.58 to 726.4
  2 mg/mL vs 10 mg/mL           332.1          5.084         P < 0.05      16.69 to 647.5
  2 mg/mL vs 20 mg/mL           378.7          5.798         P < 0.05      63.27 to 694.1
  10 mg/mL vs 20 mg/mL          46.58          0.7132        P > 0.05      -268.8 to 362.0

Table Analyzed
Anti-genotoxicity-BSA
One-way analysis of variance
  P value   0.0014
  P value summary      **
  Are means signif. different? (P < 0.05)        Yes
  Number of groups     7
  F            6.902
  R squared0.7473

ANOVA Table            SS             df             MS
  Treatment (between columns)   613000   6              102200
  Residual (within columns)     207200   14             14800
  Total        820200   20

Tukey's Multiple Comparison Test               Mean Diff. q             P value       95% CI of diff
  NC vs FW -582.4       8.291          P < 0.001  -921.6 to -243.2
  NC vs 0.02 mg/mL      -456.7         6.502         P < 0.01   -795.9 to -117.5
  NC vs 0.2 mg/mL       -412.6         5.874         P < 0.05   -751.8 to -73.41
  NC vs 2 mg/mL         -461.3         6.567         P < 0.01   -800.5 to -122.1
  NC vs 10 mg/mL        -450.8         6.418         P < 0.01   -790.0 to -111.6
  NC vs 20 mg/mL        -436.5         6.214         P < 0.01   -775.7 to -97.30
  FW vs 0.02 mg/mL      125.7          1.789         P > 0.05   -213.5 to 464.9
  FW vs 0.2 mg/mL       169.8          2.417         P > 0.05   -169.4 to 509.0
  FW vs 2 mg/mL         121.2          1.725         P > 0.05   -218.1 to 460.4
  FW vs 10 mg/mL        131.6          1.874         P > 0.05   -207.6 to 470.8
  FW vs 20 mg/mL        145.9          2.077         P > 0.05   -193.3 to 485.1
  0.02 mg/mL vs 0.2 mg/mL       44.12          0.6281        P > 0.05      -295.1 to 383.3
  0.02 mg/mL vs 2 mg/mL         -4.530         0.06449       P > 0.05      -343.7 to 334.7
  0.02 mg/mL vs 10 mg/mL        5.947          0.08466       P > 0.05      -333.3 to 345.1
  0.02 mg/mL vs 20 mg/mL        20.23          0.2880        P > 0.05      -319.0 to 359.4
  0.2 mg/mL vs 2 mg/mL          -48.65         0.6925        P > 0.05      -387.8 to 290.6
  0.2 mg/mL vs 10 mg/mL         -38.17         0.5434        P > 0.05      -377.4 to 301.0
  0.2 mg/mL vs 20 mg/mL         -23.89         0.3401        P > 0.05      -363.1 to 315.3
  2 mg/mL vs 10 mg/mL           10.48          0.1491        P > 0.05      -328.7 to 349.7
  2 mg/mL vs 20 mg/mL           24.76          0.3524        P > 0.05      -314.4 to 364.0
  10 mg/mL vs 20 mg/mL          14.28          0.2033        P > 0.05      -324.9 to 353.5
```

4.3.4 Indole determination

Time	Indole in FW (% of control)			Indole in FW+E.coli(% of control)			Indole in FW+DPC16(% of control)		
24h	103.5	98.6	97.9	112.9	107.2	121.2	70.6	72.8	67.6

```
Table Analyzed
Indole level
One-way analysis of variance
  P value    P<0.0001
  P value summary      ***
  Are means signif. different? (P < 0.05)         Yes
  Number of groups    3
  F            67.32
  R squared0.9573

ANOVA Table              SS              df              MS
  Treatment (between columns)    2957         2               1479
  Residual (within columns)        131.8        6               21.96
  Total        3089         8

Tukey's Multiple Comparison Test               Mean Diff.  q               P value       95% CI of diff
  FW vs FW+E.coli        -13.77        5.089         P < 0.05      -25.51 to -2.030
  FW vs FW+DPC16        29.67         10.97         P < 0.001   17.93 to 41.41
  FW+E.coli vs FW+DPC16             43.44         16.06          P < 0.001   31.70 to 55.18
```

Chapter 5

5.3.1.1 Effects of *L. reuteri* DPC16 and lactoferrin on the cytokine profile of RAW 264.7 cells

Cytokine	NC		LPS		DPC16		BLf	
TNF-α	31.27	30.45	557.94	603.18	209.33	220.38	37.09	35.72
IL-6	8.60	8.15	35.80	37.83	22.36	23.26	19.65	18.74
IFN-γ	1.67	1.54	4.87	4.63	6.01	5.89	5.72	5.23
IL-10	2.58	2.78	12.66	13.85	12.29	12.91	10.24	10.38

5.3.1.2 Effect of *L. reuteri* DPC16 and bovine lactoferrin on nitric oxide production by RAW 264.7 cells

Expt-1:

Treatment	Nitric Oxide(μg/mL)			Mean	SD
Control	0.82	-0.56	-0.26	0.00	0.72
LPS	46.33	45.87	44.03	45.41	1.22
0.20% sup	0.51	-0.10	0.05	0.15	0.32
0.39% sup	0.97	0.97	4.34	2.09	1.95
0.78% sup	6.49	5.72	3.73	5.31	1.42
1.56% sup	18.90	19.82	19.97	19.56	0.58
3.13% sup	37.29	38.51	33.76	36.52	2.47
6.25% sup	57.36	56.14	52.00	55.17	2.81
12.50% sup	53.99	70.08	65.79	63.29	8.33

Expt-2:

Treatment	Nitric Oxide(µg/mL)			Mean	SD
Control	1.26	0.13	-1.39	0.00	1.33
LPS	37.37	43.27	38.76	39.80	3.08
0.20% sup	0.58	3.15	-0.82	0.97	2.01
0.39% sup	10.42	5.65	3.37	6.48	3.60
0.78% sup	6.16	17.70	3.37	9.08	7.60
1.56% sup	19.46	15.13	15.49	16.69	2.40
3.13% sup	25.27	25.71	19.54	23.50	3.44
6.25% sup	18.29	26.52	24.53	23.11	4.29
12.50% sup	16.96	17.85	18.95	17.92	0.99

```
Parameter Value
Table Analyzed
Expt-2
One-way analysis of variance
  P value    P<0.0001
  P value summary       ***
  Are means signif. different? (P < 0.05)         Yes
  Number of groups    9
  F            35.47
  R squared0.9403

ANOVA Table          SS          df          MS
  Treatment (between columns)    3880        8           485.0
  Residual (within columns)      246.1       18          13.67
  Total       4126        26

Tukey's Multiple Comparison Test                 Mean Diff.  q           P value     95% CI of diff
  NC vs 0.2% sup         -0.9696     0.4542      P > 0.05    -11.55 to 9.611
  NC vs 0.39% sup        -6.481      3.036       P > 0.05    -17.06 to 4.100
  NC vs 0.78% sup        -9.077      4.252       P > 0.05    -19.66 to 1.504
  NC vs 1.56% sup        -16.69      7.820       P < 0.001   -27.28 to -6.114
  NC vs 3.13% sup        -23.50      11.01       P < 0.001   -34.08 to -12.92
  NC vs 6.25% sup        -23.11      10.83       P < 0.001   -33.69 to -12.53
  NC vs 12.5% sup        -17.92      8.393       P < 0.001   -28.50 to -7.339
  NC vs LPS -39.80       18.64       P < 0.001   -50.38 to -29.22
  0.2% sup vs 0.39% sup              -5.511      2.581       P > 0.05    -16.09 to 5.069
  0.2% sup vs 0.78% sup              -8.107      3.798       P > 0.05    -18.69 to 2.473
  0.2% sup vs 1.56% sup              -15.72      7.366       P < 0.01    -26.31 to -5.144
  0.2% sup vs 3.13% sup              -22.53      10.56       P < 0.001   -33.11 to -11.95
  0.2% sup vs 6.25% sup              -22.14      10.37       P < 0.001   -32.72 to -11.56
  0.2% sup vs 12.5% sup              -16.95      7.939       P < 0.001   -27.53 to -6.369
  0.2% sup vs LPS        -38.83      18.19       P < 0.001   -49.41 to -28.25
  0.39% sup vs 0.78% sup             -2.596      1.216       P > 0.05    -13.18 to 7.984
  0.39% sup vs 1.56% sup             -10.21      4.784       P > 0.05    -20.79 to 0.3667
  0.39% sup vs 3.13% sup             -17.02      7.974       P < 0.001   -27.60 to -6.443
  0.39% sup vs 6.25% sup             -16.63      7.790       P < 0.001   -27.21 to -6.051
  0.39% sup vs 12.5% sup             -11.44      5.358       P < 0.05    -22.02 to -0.8580
  0.39% sup vs LPS       -33.32      15.61       P < 0.001   -43.90 to -22.74
  0.78% sup vs 1.56% sup             -7.618      3.568       P > 0.05    -18.20 to 2.963
  0.78% sup vs 3.13% sup             -14.43      6.758       P < 0.01    -25.01 to -3.846
  0.78% sup vs 6.25% sup             -14.03      6.574       P < 0.01    -24.62 to -3.454
  0.78% sup vs 12.5% sup             -8.842      4.142       P > 0.05    -19.42 to 1.738
  0.78% sup vs LPS       -30.72      14.39       P < 0.001   -41.30 to -20.14
  1.56% sup vs 3.13% sup             -6.809      3.190       P > 0.05    -17.39 to 3.771
  1.56% sup vs 6.25% sup             -6.417      3.006       P > 0.05    -17.00 to 4.163
  1.56% sup vs 12.5% sup             -1.225      0.5737      P > 0.05    -11.81 to 9.356
  1.56% sup vs LPS       -23.10      10.82       P < 0.001   -33.68 to -12.52
  3.13% sup vs 6.25% sup             0.3919      0.1836      P > 0.05    -10.19 to 10.97
  3.13% sup vs 12.5% sup             5.585       2.616       P > 0.05    -4.996 to 16.17
  3.13% sup vs LPS       -16.29      7.632       P < 0.01    -26.87 to -5.714
  6.25% sup vs 12.5% sup             5.193       2.432       P > 0.05    -5.388 to 15.77
```

6.25% sup vs LPS	-16.69	7.816	P < 0.001	-27.27 to -6.105
12.5% sup vs LPS	-21.88	10.25	P < 0.001	-32.46 to -11.30

Expt-3:

Treatment	Nitric Oxide(µg/mL)			Mean	SD
Control	1.14	0.38	-1.51	0.01	1.36
LPS	53.37	59.43	55.32	56.04	3.10
1.56x10^6	26.09	13.95	8.74	16.26	8.90
3.13x10^6	19.15	19.15	17.42	18.57	1.00
6.25x10^6	20.89	13.95	13.95	16.26	4.01
1.25x10^7	31.30	24.36	22.62	26.09	4.59
2.5x10^7	29.56	24.36	29.56	27.83	3.00
5x10^7	36.50	36.50	34.77	35.92	1.00
1x10^8	39.97	29.56	43.44	37.66	7.22

Expt-4:

Treatment	Nitric Oxide(µg/mL)			Mean	SD
Control	2.28	-0.37	-1.51	0.13	1.94
LPS	79.38	83.53	67.73	76.88	8.19
1.56x10^6	24.36	22.62	19.15	22.04	2.65
3.13x10^6	31.30	13.95	19.15	21.47	8.90
6.25x10^6	43.44	33.03	36.50	37.66	5.30
1.25x10^7	59.06	34.77	39.97	44.60	12.79
2.5x10^7	76.40	46.91	62.53	61.95	14.76
5x10^7	78.14	71.20	72.93	74.09	3.61
1x10^8	98.96	72.93	95.49	89.13	14.13

Expt-5:

Treatment	Nitric Oxide(µg/mL)			Mean	SD
Control	1.26	0.13	-1.39	0.00	1.33
LPS	37.37	43.27	38.76	39.80	3.08
2x10^5	2.65	0.00	-1.13	0.50	1.94
4x10^5	3.28	2.90	1.64	2.61	0.86
8x10^5	3.66	6.43	5.55	5.21	1.42
1.56x10^6	7.31	10.34	9.96	9.21	1.65
3.13x10^6	16.77	17.53	17.65	17.32	0.48
6.25x10^6	30.64	15.01	27.36	24.34	8.25
1.25x10^7	36.57	34.43	33.04	34.68	1.78
2.5x10^7	45.65	38.59	37.07	40.44	4.58
5x10^7	42.37	44.51	47.41	44.77	2.53
1x10^8	37.45	45.02	43.88	42.12	4.08

Parameter Value
Table Analyzed
Expt-5
One-way analysis of variance
P value P<0.0001
P value summary ***

```
  Are means signif. different? (P < 0.05)        Yes
  Number of groups    12
  F           85.12
  R squared0.9750

ANOVA Table             SS            df            MS
  Treatment (between columns)   10600         11            964.0
  Residual (within columns)     271.8         24            11.32
  Total       10880       35

Tukey's Multiple Comparison Test             Mean Diff. q             P value       95% CI of diff
  NC vs 10^5.3 Cells    -0.5044     0.2596      P > 0.05    -10.41 to 9.403
  NC vs 10^5.6 Cells    -2.606      1.341       P > 0.05    -12.51 to 7.301
  NC vs 10^5.9 Cells    -5.212      2.683       P > 0.05    -15.12 to 4.695
  NC vs 10^6.2 Cells    -9.205      4.738       P > 0.05    -19.11 to 0.7017
  NC vs 10^6.5 Cells    -17.32      8.913       P < 0.001   -27.22 to -7.411
  NC vs 10^6.8 Cells    -24.34      12.53       P < 0.001   -34.24 to -14.43
  NC vs 10^7.1 Cells    -34.68      17.85       P < 0.001   -44.58 to -24.77
  NC vs 10^7.4 Cells    -40.44      20.81       P < 0.001   -50.34 to -30.53
  NC vs 10^7.7 Cells    -44.77      23.04       P < 0.001   -54.67 to -34.86
  NC vs 10^8.0 Cells    -42.12      21.68       P < 0.001   -52.02 to -32.21
  NC vs LPS -39.80      20.48       P < 0.001   -49.70 to -29.89
  10^5.3 Cells vs 10^5.6 Cells      -2.102      1.082       P > 0.05    -12.01 to 7.805
  10^5.3 Cells vs 10^5.9 Cells      -4.708      2.423       P > 0.05    -14.61 to 5.199
  10^5.3 Cells vs 10^6.2 Cells      -8.701      4.478       P > 0.05    -18.61 to 1.206
  10^5.3 Cells vs 10^6.5 Cells      -16.81      8.654       P < 0.001   -26.72 to -6.906
  10^5.3 Cells vs 10^6.8 Cells      -23.83      12.27       P < 0.001   -33.74 to -13.93
  10^5.3 Cells vs 10^7.1 Cells      -34.17      17.59       P < 0.001   -44.08 to -24.27
  10^5.3 Cells vs 10^7.4 Cells      -39.93      20.55       P < 0.001   -49.84 to -30.02
  10^5.3 Cells vs 10^7.7 Cells      -44.26      22.78       P < 0.001   -54.17 to -34.35
  10^5.3 Cells vs 10^8.0 Cells      -41.61      21.42       P < 0.001   -51.52 to -31.71
  10^5.3 Cells vs LPS   -39.29      20.22       P < 0.001   -49.20 to -29.39
  10^5.6 Cells vs 10^5.9 Cells      -2.606      1.341       P > 0.05    -12.51 to 7.301
  10^5.6 Cells vs 10^6.2 Cells      -6.599      3.397       P > 0.05    -16.51 to 3.308
  10^5.6 Cells vs 10^6.5 Cells      -14.71      7.572       P < 0.001   -24.62 to -4.805
  10^5.6 Cells vs 10^6.8 Cells      -21.73      11.18       P < 0.001   -31.64 to -11.82
  10^5.6 Cells vs 10^7.1 Cells      -32.07      16.51       P < 0.001   -41.98 to -22.16
  10^5.6 Cells vs 10^7.4 Cells      -37.83      19.47       P < 0.001   -47.74 to -27.92
  10^5.6 Cells vs 10^7.7 Cells      -42.16      21.70       P < 0.001   -52.07 to -32.25
  10^5.6 Cells vs 10^8.0 Cells      -39.51      20.34       P < 0.001   -49.42 to -29.60
  10^5.6 Cells vs LPS   -37.19      19.14       P < 0.001   -47.10 to -27.28
  10^5.9 Cells vs 10^6.2 Cells      -3.993      2.055       P > 0.05    -13.90 to 5.914
  10^5.9 Cells vs 10^6.5 Cells      -12.11      6.231       P < 0.01    -22.01 to -2.199
  10^5.9 Cells vs 10^6.8 Cells      -19.13      9.843       P < 0.001   -29.03 to -9.218
  10^5.9 Cells vs 10^7.1 Cells      -29.47      15.17       P < 0.001   -39.37 to -19.56
  10^5.9 Cells vs 10^7.4 Cells      -35.22      18.13       P < 0.001   -45.13 to -25.32
  10^5.9 Cells vs 10^7.7 Cells      -39.55      20.36       P < 0.001   -49.46 to -29.65
  10^5.9 Cells vs 10^8.0 Cells      -36.91      18.99       P < 0.001   -46.81 to -27.00
  10^5.9 Cells vs LPS   -34.59      17.80       P < 0.001   -44.49 to -24.68
  10^6.2 Cells vs 10^6.5 Cells      -8.112      4.175       P > 0.05    -18.02 to 1.795
  10^6.2 Cells vs 10^6.8 Cells      -15.13      7.788       P < 0.001   -25.04 to -5.225
  10^6.2 Cells vs 10^7.1 Cells      -25.47      13.11       P < 0.001   -35.38 to -15.57
  10^6.2 Cells vs 10^7.4 Cells      -31.23      16.07       P < 0.001   -41.14 to -21.32
  10^6.2 Cells vs 10^7.7 Cells      -35.56      18.30       P < 0.001   -45.47 to -25.65
  10^6.2 Cells vs 10^8.0 Cells      -32.91      16.94       P < 0.001   -42.82 to -23.01
  10^6.2 Cells vs LPS   -30.59      15.75       P < 0.001   -40.50 to -20.69
  10^6.5 Cells vs 10^6.8 Cells      -7.020      3.613       P > 0.05    -16.93 to 2.887
  10^6.5 Cells vs 10^7.1 Cells      -17.36      8.935       P < 0.001   -27.27 to -7.453
  10^6.5 Cells vs 10^7.4 Cells      -23.12      11.90       P < 0.001   -33.03 to -13.21
  10^6.5 Cells vs 10^7.7 Cells      -27.45      14.13       P < 0.001   -37.35 to -17.54
  10^6.5 Cells vs 10^8.0 Cells      -24.80      12.76       P < 0.001   -34.71 to -14.89
  10^6.5 Cells vs LPS   -22.48      11.57       P < 0.001   -32.39 to -12.57
  10^6.8 Cells vs 10^7.1 Cells      -10.34      5.322       P < 0.05    -20.25 to -0.4332
  10^6.8 Cells vs 10^7.4 Cells      -16.10      8.286       P < 0.001   -26.01 to -6.192
  10^6.8 Cells vs 10^7.7 Cells      -20.43      10.51       P < 0.001   -30.34 to -10.52
  10^6.8 Cells vs 10^8.0 Cells      -17.78      9.151       P < 0.001   -27.69 to -7.873
  10^6.8 Cells vs LPS   -15.46      7.957       P < 0.001   -25.37 to -5.554
  10^7.1 Cells vs 10^7.4 Cells      -5.759      2.964       P > 0.05    -15.67 to 4.148
  10^7.1 Cells vs 10^7.7 Cells      -10.09      5.192       P < 0.05    -20.00 to -0.1810
  10^7.1 Cells vs 10^8.0 Cells      -7.440      3.829       P > 0.05    -17.35 to 2.467
  10^7.1 Cells vs LPS   -5.120      2.635       P > 0.05    -15.03 to 4.787
```

```
  10^7.4 Cells vs 10^7.7 Cells        -4.329      2.228       P > 0.05     -14.24 to 5.578
  10^7.4 Cells vs 10^8.0 Cells        -1.681      0.8654      P > 0.05     -11.59 to 8.226
  10^7.4 Cells vs LPS    0.6383       0.3285      P > 0.05    -9.269 to 10.55
  10^7.7 Cells vs 10^8.0 Cells        2.648       1.363       P > 0.05     -7.259 to 12.56
  10^7.7 Cells vs LPS    4.968        2.557       P > 0.05    -4.939 to 14.87
  10^8.0 Cells vs LPS    2.320        1.194       P > 0.05    -7.587 to 12.23
```

5.3.1.3 Effect of bovine lactoferrin on LPS-induced nitric oxide production and cell proliferation in RAW 264.7 cells

Expt-1:

Treatment	Nitric Oxide(µg/mL)			Mean	SD
Control	6.60	8.44	8.73	7.93	1.15
LPS					
Lf(mg/mL)	1.31	3.81	3.88	3.00	1.46
0.020	1.46	3.22	4.25	2.98	1.41
0.040	3.44	2.27	1.97	2.56	0.78
0.080	3.81	3.81	4.18	3.93	0.21
0.156	1.75	3.15	6.38	3.76	2.37
0.315	0.21	0.50	0.21	0.31	0.17
0.625	0.87	0.14	0.28	0.43	0.39
1.250	6.60	8.44	8.73	7.93	1.15

Expt-2:

Treatment	Nitric Oxide(µg/mL)			Mean	SD
Control	4.19	2.81	3.12	3.38	0.72
LPS					
Lf(mg/mL)	4.96	4.96	4.04	4.65	0.53
0.020	5.73	4.65	4.96	5.11	0.55
0.040	5.73	4.50	4.81	5.01	0.64
0.080	5.42	4.04	4.65	4.70	0.69
0.156	4.19	2.97	3.27	3.48	0.64
0.315	3.58	2.35	2.81	2.92	0.62
0.625	2.97	1.90	2.20	2.35	0.55
1.250	4.19	2.81	3.12	3.38	0.72

```
Parameter Value
Table Analyzed
EXPT-2
One-way analysis of variance
  P value     P<0.0001
  P value summary      ***
  Are means signif. different? (P < 0.05)         Yes
  Number of groups     9
  F            1325
  R squared0.9983

ANOVA Table             SS              df              MS
  Treatment (between columns)   5384       8             673.0
  Residual (within columns)     9.143      18            0.5079
  Total        5393        26

Tukey's Multiple Comparison Test              Mean Diff.  q           P value      95% CI of diff
  NC vs Lf (0.02 mg/mL)               -1.277      3.104       P > 0.05     -3.316 to 0.7622
  NC vs Lf (0.04 mg/mL)               -1.737      4.221       P > 0.05     -3.776 to 0.3025
  NC vs Lf (0.08 mg/mL)               -1.635      3.973       P > 0.05     -3.674 to 0.4047
```

NC vs Lf (0.16 mg/mL)	-1.328	3.228	P > 0.05	-3.367 to 0.7112
NC vs Lf (0.32 mg/mL)	-0.1022	0.2483	P > 0.05	-2.141 to 1.937
NC vs Lf (0.63 mg/mL)	0.4597	1.117	P > 0.05	-1.580 to 2.499
NC vs Lf (1.25 mg/mL)	1.022	2.483	P > 0.05	-1.018 to 3.061
NC vs LPS	-45.41	110.4	P < 0.001	-47.45 to -43.37
Lf (0.02 mg/mL) vs Lf (0.04 mg/mL)	-0.4597	1.117	P > 0.05	-2.499 to 1.580
Lf (0.02 mg/mL) vs Lf (0.08 mg/mL)	-0.3576	0.8690	P > 0.05	-2.397 to 1.682
Lf (0.02 mg/mL) vs Lf (0.16 mg/mL)	-0.05108	0.1241	P > 0.05	-2.090 to 1.988
Lf (0.02 mg/mL) vs Lf (0.32 mg/mL)	1.175	2.855	P > 0.05	-0.8644 to 3.214
Lf (0.02 mg/mL) vs Lf (0.63 mg/mL)	1.737	4.221	P > 0.05	-0.3025 to 3.776
Lf (0.02 mg/mL) vs Lf (1.25 mg/mL)	2.299	5.586	P < 0.05	0.2594 to 4.338
Lf (0.02 mg/mL) vs LPS	-44.13	107.3	P < 0.001	-46.17 to -42.09
Lf (0.04 mg/mL) vs Lf (0.08 mg/mL)	0.1022	0.2483	P > 0.05	-1.937 to 2.141
Lf (0.04 mg/mL) vs Lf (0.16 mg/mL)	0.4086	0.9931	P > 0.05	-1.631 to 2.448
Lf (0.04 mg/mL) vs Lf (0.32 mg/mL)	1.635	3.973	P > 0.05	-0.4047 to 3.674
Lf (0.04 mg/mL) vs Lf (0.63 mg/mL)	2.196	5.338	P < 0.05	0.1572 to 4.236
Lf (0.04 mg/mL) vs Lf (1.25 mg/mL)	2.758	6.704	P < 0.01	0.7191 to 4.798
Lf (0.04 mg/mL) vs LPS	-43.67	106.1	P < 0.001	-45.71 to -41.63
Lf (0.08 mg/mL) vs Lf (0.16 mg/mL)	0.3065	0.7448	P > 0.05	-1.733 to 2.346
Lf (0.08 mg/mL) vs Lf (0.32 mg/mL)	1.532	3.724	P > 0.05	-0.5068 to 3.572
Lf (0.08 mg/mL) vs Lf (0.63 mg/mL)	2.094	5.090	P < 0.05	0.05504 to 4.134
Lf (0.08 mg/mL) vs Lf (1.25 mg/mL)	2.656	6.455	P < 0.01	0.6169 to 4.695
Lf (0.08 mg/mL) vs LPS	-43.78	106.4	P < 0.001	-45.81 to -41.74
Lf (0.16 mg/mL) vs Lf (0.32 mg/mL)	1.226	2.979	P > 0.05	-0.8133 to 3.265
Lf (0.16 mg/mL) vs Lf (0.63 mg/mL)	1.788	4.345	P > 0.05	-0.2514 to 3.827
Lf (0.16 mg/mL) vs Lf (1.25 mg/mL)	2.350	5.710	P < 0.05	0.3104 to 4.389
Lf (0.16 mg/mL) vs LPS	-44.08	107.1	P < 0.001	-46.12 to -42.04
Lf (0.32 mg/mL) vs Lf (0.63 mg/mL)	0.5619	1.366	P > 0.05	-1.477 to 2.601
Lf (0.32 mg/mL) vs Lf (1.25 mg/mL)	1.124	2.731	P > 0.05	-0.9155 to 3.163
Lf (0.32 mg/mL) vs LPS	-45.31	110.1	P < 0.001	-47.35 to -43.27
Lf (0.63 mg/mL) vs Lf (1.25 mg/mL)	0.5619	1.366	P > 0.05	-1.477 to 2.601
Lf (0.63 mg/mL) vs LPS	-45.87	111.5	P < 0.001	-47.91 to -43.83
Lf (1.25 mg/mL) vs LPS	-46.43	112.8	P < 0.001	-48.47 to -44.39

Expt-3:

Treatment (BLf mg/mL)	Nitric Oxide(µg/mL)			Cell proliferation(% of control)		
NC	4.19	2.81	3.12	101.58	100.36	98.06
LPS(1µg/mL)	49.71	49.25	47.41	63.49	65.02	66.85
LPS+0.02BLf	48.94	44.04	51.09	69.45	74.96	66.55
LPS+0.04BLf	47.71	48.02	55.38	74.04	78.63	75.11
LPS+0.08BLf	51.70	48.17	50.93	84.29	79.40	71.90
LPS+0.156BLf	51.54	50.32	56.75	89.95	84.75	81.23
LPS+0.313BLf	53.08	45.87	46.49	93.32	87.51	87.51
LPS+0.625BLf	41.12	30.09	42.35	95.31	84.75	95.16
LPS+1.25BLf	25.03	28.71	39.90	80.32	87.81	97.91

	NO	Cell proliferation
Sigmoidal dose-response (variable slope)		
Best-fit values		
BOTTOM	40.11	69.43
TOP	50.34	90.77
LOGEC50	-0.3621	-1.082
HILLSLOPE	-5.015	1.707
EC50	0.4344	0.08279
Std. Error		
BOTTOM	3.664	6.425
TOP	1.005	2.767
LOGEC50	0.1681	0.2107
HILLSLOPE	4.986	1.311
95% Confidence Intervals		
BOTTOM	32.25 to 47.97	55.87 to 82.98

```
  TOP      48.18 to 52.50                        84.93 to 96.60
  LOGEC50           -0.7226 to -0.001591                  -1.527 to -0.6375
  HILLSLOPE         -15.71 to 5.680                       -1.059 to 4.474
  EC50     0.1894 to 0.9963                      0.02975 to 0.2304
Goodness of Fit
  Degrees of Freedom          14                          17
  R²       0.5588                    0.7130
  Absolute Sum of Squares     163.1                       451.8
  Sy.x     3.414                     5.155
Normality of Residuals
  Kolmogorov-Smirnov distance 0.1653                      0.1689
  P value  P > 0.10                  P > 0.10
  D'Agostino & Pearson omnibus K2    0.9732                        0.9656
  P value  0.6147                    0.6171
  Shapiro-Wilk W     0.9531                  0.9470
  P value  0.4753                    0.2990
```

5.3.1.4 Effects of *L. reuteri* DPC16 bacterial cells and cell-free supernatants on LPS-induced nitric oxide production by RAW 264.7 cells

Expt-1:

Treatment	Nitric Oxide (µg/mL)		Mean	SD
Control	0.66	0.49	0.57	0.13
LPS	28.10	26.13	27.12	1.39
LPS+DPC16sup	22.47	23.63	23.05	0.82

Expt-2:

Treatment	Nitric Oxide (µg/mL)			Mean	SD
Control	12.79	13.37	12.55	12.90	0.42
LPS	19.82	21.11	22.28	21.07	1.23
LPS+DPC16HK	22.40	23.22		22.81	0.58

Expt-3:

Treatment	Nitric Oxide (µg/mL)				Mean	SD
Control	1.95	2.91			2.43	0.67
LPS	35.08	35.17	34.13	38.72	35.77	2.02
LPS+DPC16sup	30.14	28.23			29.18	1.35

Expt-4:

Treatment	Nitric Oxide (µg/mL)		Mean	SD
Control	7.57	10.97	9.27	2.40
LPS	52.00	56.97	54.48	3.51
LPS+DPC16 sup	18.94	10.97	14.96	5.64
LPS+DPC16HK	31.49	45.86	38.67	10.16

Expt-5:

Treatment	Nitric Oxide (µg/mL)			Mean	SD
Control	0.89	-0.25	-1.76	-0.37	1.33
LPS	37.37	43.27	38.76	39.80	3.08
LPS+DPC16HK	46.22	50.38	55.24	50.61	4.52

```
Parameter Value
Table Analyzed
NO
One-way analysis of variance
  P value    0.0017
  P value summary      **
  Are means signif. different? (P < 0.05)        Yes
  Number of groups    4
  F          9.454
  R squared0.7027

ANOVA Table             SS            df            MS
  Treatment (between columns)   3034    3             1011
  Residual (within columns)     1284    12            107.0
  Total       4318         15

Tukey's Multiple Comparison Test               Mean Diff. q              P value      95% CI of diff
  NC vs LPS (1mg/mL)  -30.69       6.634          P < 0.01     -50.11 to -11.26
  NC vs LPS+DPC16 sup              -17.44         3.264        P > 0.05     -39.86 to 4.993
  NC vs LPS+DPC16 HK cells         -32.40         6.067        P < 0.01     -54.83 to -9.976
  LPS (1mg/mL) vs LPS+DPC16 sup                   13.25        2.481        P > 0.05     -9.176 to 35.68
  LPS (1mg/mL) vs LPS+DPC16 HK cells              -1.716       0.3213       P > 0.05     -24.14 to 20.71
  LPS+DPC16 sup vs LPS+DPC16 HK cells             -14.97       2.507        P > 0.05     -40.04 to 10.11
```

5.3.2.1 Conditions for differentiation of THP-1 cells

PMA (nM)	TNF-α(pg/mL)	
Untreated cells	-2.69	-12.29
10	-15.63	-11.51
50	139.08	127.12

5.3.2.2 Selection of the LPS concentration for the THP-1 system

LPS (ng/mL)	TNF-α(pg/mL)	
NC	-15.63	-11.51
50	215.75	216.92
100	224.37	224.57
250	261.04	275.94
500	300.65	326.33

5.3.3 Effects of bovine lactoferrin on LPS-induced TNF-α production in THP-1 cells

Treatment		TNF-α(pg/mL)	
NC		2.43	3.12
LPS(100ng/mL)		398.94	450.99
LPS+BLf(mg/mL)	0.125	87.76	93.10
	0.25	37.80	40.83
	0.5	24.43	26.08
	1	19.96	22.48
	2	16.06	15.49
LPS+BSA(mg/mL)	0.125	395.94	422.37
	0.25	379.76	457.34
	0.5	398.38	423.49
	1	411.00	353.71
	2	394.62	381.20

```
        LPS+Lf     LPS+BSA    Global (shared)
Comparison of Fits
   Null hypothesis                       One curve for all data sets
   Alternative hypothesis                          Different curve for each data set
   P value                   P<0.0001
   Conclusion (alpha = 0.05)                       Reject null hypothesis
   Preferred model                       Different curve for each data set
   F (DFn, DFd)                          523.9 (4,20)

Different curve for each data set
Best-fit values
   BOTTOM          25.16      385.1
   TOP     425.8   418.9
   LOGEC50         -1.006     -0.2769
   HILLSLOPE       -6.897     -21.05
   EC50    0.09867 0.5286
Std. Error
   BOTTOM          2.784      16.87
   TOP     5.481   8.483
   LOGEC50         0.03514    530.6
   HILLSLOPE       2.303      435661
95% Confidence Intervals
   BOTTOM          18.96 to 31.37        347.6 to 422.7
   TOP     413.6 to 438.0     400.0 to 437.8
   LOGEC50         -1.084 to -0.9275     -1183 to 1182
   HILLSLOPE       -12.03 to -1.766      -970700 to 970632
   EC50    0.08239 to 0.1182
Goodness of Fit
   Degrees of Freedom         10         10
   R²      0.9986  0.3484
   Absolute Sum of Squares    608.8      5730
   Sy.x    7.802   23.94
Normality of Residuals
   Kolmogorov-Smirnov distance 0.2208    0.2080
   P value  0.0628   P > 0.10
   D'Agostino & Pearson omnibus K2       3.498      0.3398
   P value  0.1740   0.8437
   Shapiro-Wilk W    0.9054   0.9477
   P value  0.1352   0.5259
```

Treatment	TNF-α (% of control)	TNF-α (% of control)	Mean	SD
Control(LPS 100ng/mL)	107.06	92.94	100.00	9.98
Pre-BLf +LPS	81.74	92.47	87.10	7.58
Co-(BLf +LPS)	4.99	5.62	5.30	0.44

5.3.4.1 A study of the inflammation-associated interruption to the intestinal permeability barrier in the co-culture system

Treatment	TNF-α(pg/mL)	
NC	15.24	15.85
PMA(10nM)	21396.48	20861.82
PMA(100nM)	75644.23	77562.05
PMA(200nM)	127211.10	132545.70
PMA(10nM)+LPS(500ng/mL)	18103.98	18259.07

Treatment	TEER change	TEER change	TEER change	Mean	SD
Medium only	-1.8	8.4	-6.3	0.1	7.53
Non-diff THP-1 cell	13.5	-0.6	-1.8	3.7	8.51
LPS	10.8	7.5	3.0	7.1	3.92
10ng/mlTNF-α+10ng/mg IFN-γ	-1.8	-2.1	4.2	0.1	3.55
10nMPMA+LPS	28.2	40.8	28.8	32.6	7.11
10nMPMA	30.9	35.1	47.1	37.7	8.41
200nMPMA	35.1	19.5	17.4	24.0	9.67

```
Parameter Value
Table Analyzed
TEER reduction
One-way analysis of variance
  P value     P<0.0001
  P value summary       ***
  Are means signif. different? (P < 0.05)         Yes
  Number of groups    7
  F            14.50
  R squared0.8614

ANOVA Table              SS              df              MS
  Treatment (between columns)    4620          6               770.1
  Residual (within columns)      743.6         14              53.11
  Total         5364          20

Tukey's Multiple Comparison Test                 Mean Diff. q             P value     95% CI of diff
  Medium vs Non-diff THP-1          -3.600        0.8556        P > 0.05     -23.92 to 16.72
  Medium vs 500ng/mL of LPS         -7.000        1.664         P > 0.05     -27.32 to 13.32
  Medium vs 10ng/mL TNF-a+10ng/mL INF-g0.0000     0.0000        P > 0.05     -20.32 to 20.32
  Medium vs 10nM PMA+500ng/mL of LPS    -32.50    7.724         P < 0.01     -52.82 to -12.18
  Medium vs 10nM PMA                -37.60        8.936         P < 0.001   -57.92 to -17.28
  Medium vs 200nM PMA               -23.90        5.680         P < 0.05     -44.22 to -3.581
  Non-diff THP-1 vs 500ng/mL of LPS              -3.400        0.8081        P > 0.05     -23.72 to 16.92
  Non-diff THP-1 vs 10ng/mL TNF-a+10ng/mL INF-g  3.600         0.8556        P > 0.05     -16.72 to 23.92
  Non-diff THP-1 vs 10nM PMA+500ng/mL of LPS     -28.90        6.868         P < 0.01     -49.22 to -8.581
  Non-diff THP-1 vs 10nM PMA    -34.00        8.081         P < 0.001   -54.32 to -13.68
  Non-diff THP-1 vs 200nM PMA   -20.30        4.825         P > 0.05     -40.62 to 0.01872
  500ng/mL of LPS vs 10ng/mL TNF-a+10ng/mL INF-g   7.000         1.664         P > 0.05     -13.32 to 27.32
```

```
500ng/mL of LPS vs 10nM PMA+500ng/mL of LPS        -25.50      6.060       P < 0.05     -45.82 to -5.181
500ng/mL of LPS vs 10nM PMA  -30.60       7.272       P < 0.01     -50.92 to -10.28
500ng/mL of LPS vs 200nM PMA                -16.90      4.016       P > 0.05     -37.22 to 3.419
10ng/mL TNF-a+10ng/mL INF-g vs 10nM PMA+500ng/mL of LPS  -32.50     7.724      P < 0.01     -52.82 to -12.18
10ng/mL TNF-a+10ng/mL INF-g vs 10nM PMA            -37.60      8.936       P < 0.001   -57.92 to -17.28
10ng/mL TNF-a+10ng/mL INF-g vs 200nM PMA           -23.90      5.680       P < 0.05     -44.22 to -3.581
10nM PMA+500ng/mL of LPS vs 10nM PMA               -5.100      1.212       P > 0.05     -25.42 to 15.22
10nM PMA+500ng/mL of LPS vs 200nM PMA              8.600       2.044       P > 0.05     -11.72 to 28.92
10nM PMA vs 200nM PMA        13.70        3.256       P > 0.05     -6.619 to 34.02
```

Treatment	LDH (% control)			Mean	SD
Medium only	102.44	99.57	97.99	100.00	2.26
Non-diff THP-1 cell	103.32	127.78	103.98	111.70	13.94
LPS	105.61	101.65	94.28	100.51	5.75
10ng/mlTNF-α+10ng/mg IFN-γ	108.74	101.82	106.76	105.77	3.56
10nMPMA+LPS	105.26	99.13	132.15	112.18	17.56
10nMPMA	104.11	100.68	121.13	108.64	10.95
200nMPMA	112.67	119.14	116.28	116.03	3.25

```
Parameter  Value
Table Analyzed
LDH
One-way analysis of variance
  P value    0.3947
  P value summary       ns
  Are means signif. different? (P < 0.05)        No
  Number of groups    7
  F            1.130
  R squared                  0.3263

ANOVA Table            SS              df              MS
  Treatment (between columns)    662.5          6               110.4
  Residual (within columns)        1368           14              97.71
  Total        2030          20

No post tests. P > 0.05
```

Treatment	TEER reduction						Mean	SD
Medium only				-45.9	-53.7	-55.5	-51.7	5.10
Non-diff THP-1		21.9	27.9	38.1	33.6	36.6	31.6	6.69
Diff THP-1	101.1	87.3	71.1	102.3	105.6	110.1	96.3	14.51

```
Parameter  Value
Table Analyzed
TEER
One-way analysis of variance
  P value    P<0.0001
  P value summary       ***
  Are means signif. different? (P < 0.05)        Yes
  Number of groups    3
  F            190.9
  R squared                  0.9720

ANOVA Table            SS              df              MS
  Treatment (between columns)    44530         2               22270
  Residual (within columns)        1283           11              116.6
  Total        45820        13

Tukey's Multiple Comparison Test                Mean Diff.q              P value       95% CI of diff
  Medium vs Non-diff THP-1       -83.32         14.94         P < 0.001   -104.6 to -62.01
  Medium vs Diff THP-1             -148.0         27.40         P < 0.001   -168.6 to -127.3
  Non-diff THP-1 vs Diff THP-1   -64.63         13.98         P < 0.001   -82.30 to -46.96
```

5.3.4.2 The effects of *L. reuteri* DPC16 and lactoferrin on the inflammation-associated interruption to the intestinal permeability barrier in the co-culture system

Treatment	TEER reduction						Mean	SD
Non-diff THP-1		21.9	27.9	38.1	33.6	36.6	31.6	6.69
Diff THP-1	101.1	87.3	71.1	102.3	105.6	110.1	96.3	14.51
SCFA control				99.0	98.4	87.9	95.1	6.24
MRS				110.7	109.5	108.6	109.6	1.05
DPC16				94.8	83.4	80.7	86.3	7.48
Lf				97.8	87.3	80.4	88.5	8.76

```
Parameter Value
Table Analyzed
TEER reduction
One-way analysis of variance
  P value    P<0.0001
  P value summary      ***
  Are means signif. different? (P < 0.05)          Yes
  Number of groups     6
  F            36.41
  R squared0.9146

ANOVA Table            SS             df             MS
  Treatment (between columns)   16890          5              3377
  Residual (within columns)     1577           17             92.75
  Total        18460        22

Tukey's Multiple Comparison Test              Mean Diff.  q            P value     95% CI of diff
  Non-diff THP-1 vs Diff THP-1      -64.63       15.67        P < 0.001   -83.29 to -45.97
  Non-diff THP-1 vs SCFA control    -63.48       12.76        P < 0.001   -85.98 to -40.98
  Non-diff THP-1 vs MRS             -77.98       15.68        P < 0.001   -100.5 to -55.48
  Non-diff THP-1 vs DPC16           -54.68       10.99        P < 0.001   -77.18 to -32.18
  Non-diff THP-1 vs BLf-56.88       11.44        P < 0.001   -79.38 to -34.38
  Diff THP-1 vs SCFA control        1.150        0.2388       P > 0.05    -20.63 to 22.93
  Diff THP-1 vs MRS     -13.35       2.772        P > 0.05     -35.13 to 8.435
  Diff THP-1 vs DPC16   9.950        2.066        P > 0.05     -11.83 to 31.73
  Diff THP-1 vs BLf     7.750        1.609        P > 0.05     -14.03 to 29.53
  SCFA control vs MRS   -14.50       2.608        P > 0.05     -39.65 to 10.65
  SCFA control vs DPC16              8.800        1.583        P > 0.05    -16.35 to 33.95
  SCFA control vs BLf   6.600        1.187        P > 0.05     -18.55 to 31.75
  MRS vs DPC16          23.30        4.190        P > 0.05     -1.855 to 48.45
  MRS vs BLf            21.10        3.795        P > 0.05     -4.055 to 46.25
  DPC16 vs BLf          -2.200       0.3957       P > 0.05     -27.35 to 22.95
```

Appendix III

Chapter 2

Resulting sequences (Primer M27F)

GCTAGTTGGTAAGGTAACGGCTTACCAAGGCGATGTATGCATAGCCGAGTTGAGAGACTGATC
GGCCACAATGGAACTGAGACACGGTCCATACTCCTACGGGAGGCAGCAGTAGGGAATCTTCC
ACAATGGGCGCAAGCCTGATGGAGCAACACCGCGTGAGGTGAAGAAGGGTTTCGGCTCGTA
AAGCTCTGTTGTTGGAGAAAGAACGTGCGTGAGGAGTAACTGTTCACGCAGTGACGGTATCC
AACCAGAAAGTCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTT
ATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTGCTTAGGTCTGATGTGAAAGCCTTC
GGCTTAACCGAAGAAGTGCATCGGAAACCGGGCGACTTGAGTGCAGAAGAGGACAGTGGAA
CTCCATGTGTAGCGGTGGAATGCGTAGATATATGGAAGAACACCAGTGGCGAAAGCGGCTGTC
TGGTCTGCAACTGACGCTGAGGCTCGAAAGCATGGGTAGCGAACAGGATTAGATACCCTGGT
AGTCCATGCCGTAAACGATGAGTGCTAGGTGTTGGAGGGTTTCCGCCCTTCAGTGCCGGAGCT
AACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACG
GGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCTACGCGAAGAACCTTACCAG
GTCTTGACATCTTGCGCTAACCTTAGAGATAAGGCGTTCCCTTCGGGGACGCAATGACAGGTG
GTGCATGGTCGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCSCAACC
CTTGTTACTAGTTGCCAGCAT

Resulting sequences (Primer 1522R)

ATGCTGGCAACTAGTAACAAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACA
CGAGCTGACGACGACCATGCACCACCTGTCATTGCGTCCCCGAAGGGAACGCCTTATCTCTAA
GGTTAGCGCAAGATGTCAAGACCTGGTAAGGTTCTTCGCGTAGCTTCGAATTAAACCACATGC
TCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCA
GGCGGAGTGCTTAATGCGTTAGCTCCGGCACTGAAGGGCGGAAACCCTCCAACACCTAGCAC
TCATCGTTTACGGCATGGACTACCAGGGTATCTAATCCTGTTCGCTACCCATGCTTTCGAGCCT
CAGCGTCAGTTGCAGACCAGACAGCCGCCTTCGCCACTGGTGTTCTTCCATATATCTACGCATT
CCACCGCTACACATGGAGTTCCACTGTCCTCTTCTGCACTCAAGTCGCCCGGTTTCCGATGCA
CTTCTTCGGTTAAGCCGAAGGCTTTCACATCAGACCTAAGCAACCGCCTGCGCTCGCTTTACG
CCCAATAAATCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCC
GTGACTTTCTGGTTGGATACCGTCACTGCGTGAACAGTTACTCCTCACGCCCGTTCTTTCTCCA
ACAACAGAGCTTTACGAGCCGAAACCCTTCTTCACCTCACGGGGGTTGCTCCATCAGGCTTG
CGCCCATTGGGGAAGATTCCCTACTGCTGCCCCCGTAGGAGTATGGACCGTGTCTCAGTTCCA
TTGTGGCCGATCAGTCTCTCAACTCGGCTATGCATCACTCGCCTTGGTAAGCCGTTACCTTACC
AACTAGC

Geneious Pro 4.8.4 software was used to assemble above sequence data into two contigs below. The contigs were subjected to similarity to *L. reuteri* DPC16 sequence presented in the patent documents (New Zealand Patent 526544) using the Basic Local Alignment Search Tool (BLAST) programme (http://blast.ncbi.nlm.nih.govt/). It showed a 100% match with the patented 16S rRNA gene sequence for DPC 16.

Consensus contig-1

CCCAGTCATCTGTCCCGCCTTAGGCGGCTCCCTCCATAATGGTTAGGCCACCGACTTTGGGCG
TTACAAACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGC
ATGCTGATCCGCGATTACTAGCGATTCCGACTTCGTGTAGGCGAGTTGCAGCCTACAGTCCGA
ACTGAGAACGGCTTTAAGAGATTAGCTTACTCTCGCGAGCTTGCGACTCGTTGTACCGTCCAT
TGTAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATCTGACGTCGTCCCCACCTTCCT
CCGGTTTGTCACCGGCAGTCTCACTAGAGTGCCCAACTTAATGCTGGCAACTAGTAACAAGG
GTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACGACCATGCAC
CACCTGTCATTGCGTCCCCGAAGGGAACGCCTTATCTCTAAGGTTAGCGCAAGATGTCAAGAC
CTGGTAAGGTTCTTCGCGTAGCTTCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCC
GTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGTGCTTAATGCGTTAG
CTCCGGCACTGAAGGGCGGAAACCCTCCAACACCTAGCACTCATCGTTTACGGCATGGACTA
CCAGGGTATCTAATCCTGTTCGCTACCCATGCTTTCGAG

Consensus contig-2

CCTCAGCGTCAGTTGCAGACCAGACAGCCGCCTTCGCCACTGGTGTTCTTCCATATATCTACG
CATTCCACCGCTACACATGGAGTTCCACTGTCCTCTTCTGCACTCAAGTCGCCCGGTTTCCGAT
GCACTTCTTCGGTTAAGCCGAAGGCTTTCACATCAGACCTAAGCAACCGCCTGCGCTCGCTTT
ACGCCCAATAAATCCGGATAACGCTTGCCACCTACGTATTACCGCGGCTGCTGGCACGTAGTT
AGCCGTGACTTTCTGGTTGGATACCGTCACTGCGTGAACAGTTACTCTCACGCACGTTCTTCT
CCAACAACAGAGCTTTACGAGCCGAAACCCTTCTTCACTCACGCGGTGTTGCTCCATCAGGC
TTGCGCCCATTGTGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTATGGACCGTGTCTCAGT
TCCATTGTGGCCGATCAGTCTCTCAACTCGGCTATGCATCATCGCCTTGGTAAGCCGTTACCTT
ACCAACTAGCTAATGCACCGCAGGTCCATCCCAGAGTGATAGCCAAAGCCATCTTTCAAACAA
AAGCCATGTGGCTTTTGTTGTTATGCGGTATTAGCATCTGTTTCCAAATGTTATCCCCCGCTCCG
GGGCAGGTTACCTACGTGTTACTCACCCGTCCGCCACTCACTGGTGATCCATCGTCAATCAGG
TGCAAGCACCAT

16S rRNA sequences of DPC16 strain (New Zealand patent 526544)

TGGCTCAGGATGACGCCGGCGGTGTGCCTAATACATGCAAGTCGTACGCACTGGCCCAACTGA
TTGATGGTGCTTGCACCTGATTGACGATGGATCACCAGTGAGTGGCGGACGGGTGAGTAACA
CGTAGGTAACCTGCCCCGGAGCGGGGGATAACATTTGGAAACAGATGCTAATACCGCATAACA
ACAAAAGCCACATGGCTTTTGTTTGAAAGATGGCTTTGGCTATCACTCTGGGATGGACCTGCG
GTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCGATGATGCATAGCCGAGTTGAGAG
ACTGATCGGCCACAATGGAACTGAGACACGGTCCATACTCCTACGGGAGGCAGCAGTAGGGA
ATCTTCCACAATGGGCGCAAGCCTGATGGAGCAACACCGCGTGAGTGAAGAAGGGTTTCGGC
TCGTAAAGCTCTGTTGTTGGAGAAGAACGTGCGTGAGAGTAACTGTTCACGCAGTGACGGTA
TCCAACCAGAAAGTCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGC
GTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTGCTTAGGTCTGATGTGAAAGCC
TTCGGCTTAACCGAAGAAGTGCATCGGAAACCGGGCGACTTGAGTGCAGAAGAGGACAGTG
GAACTCCATGTGTAGCGGTGGAATGCGTAGATATATGGAAGAACACCAGTGGCGAAGGCGGC
TGTCTGGTCTGCAACTGACGCTGAGGCTCGAAAGCATGGGTAGCGAACAGGATTAGATACCC
TGGTAGTCCATGCCGTAAACGATGAGTGCTAGGTGTTGGAGGGTTTCCGCCCTTCAGTGCCGG
AGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATT
GACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCTACGCGAAGAACCTTA
CCAGGTCTTGACATCTTGCGCTAACCTTAGAGATAAGGCGTTCCCTTCGGGGACGCAATGACA
GGTGGTGCATGGTCGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCG
CAACCCTTGTTACTAGTTGCCAGCATTAAGTTGGGCACTCTAGTGAGACTGCCGGTGACAAAC
CGGAGGAAGGTGGGGACGACGTCAGATCATCATGCCCCTTATGACCTGGGCTACACACGTGC
TACAATGGACGGTACAACGAGTCGCAAGCTCGCGAGAGTAAGCTAATCTCTTAAAGCCGTTCT
CAGTTCGGACTGTAGGCTGCAACTCGCCTACACGAAGTCGGAATCGCTAGTAATCGCGGATCA
GCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTTG
TAACGCCCAAAGTCGGTGGCCTAACCATTATGGAGGGAGCCGCCTAAGGCGGGACAGATGAC
TGGGGTGAAGTCGTAACAAGGTAGCCGTAGGAGAACCTGCGGCTGGATC

Alignment of 16S rRNA sequences of DPC16 strain

```
>lcl|4177
Length=1547

 Score = 2652 bits (1436),  Expect = 0.0
 Identities = 1436/1436 (100%), Gaps = 0/1436 (0%)
 Strand=Plus/Minus

Query  1
CCCAGTCATCTGTCCCGCCTTAGGCGGCTCCCTCCATAATGGTTAGGCCACCGACTTTGG  60

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Sbjct  1502
CCCAGTCATCTGTCCCGCCTTAGGCGGCTCCCTCCATAATGGTTAGGCCACCGACTTTGG  1443

Query  61
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Sbjct  1442
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Query  121
GCGGCATGCTGATCCGCGATTACTAGCGATTCCGACTTCGTGTAGGCGAGTTGCAGCCTA  180

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Sbjct  1382
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Query  181
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Query  481
GTTAGCGCAAGATGTCAAGACCTGGTAAGGTTCTTCGCGTAGCTTCGAATTAAACCACAT  540

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Sbjct  1022
GTTAGCGCAAGATGTCAAGACCTGGTAAGGTTCTTCGCGTAGCTTCGAATTAAACCACAT  963

Query  541
GCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACT  600

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Sbjct  962
GCTCCACCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACT  903

Query  601
CCCCAGGCGGAGTGCTTAATGCGTTAGCTCCGGCACTGAAGGGCGGAAACCCTCCAACAC  660

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Sbjct  902
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Query  901
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Query  961
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Sbjct  422
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Query  1141
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Sbjct  362
TCCCGTAGGAGTATGGACCGTGTCTCAGTTCCATTGTGGCCGATCAGTCTCTCAACTCGG  303

Query  1201
CTATGCATCATCGCCTTGGTAAGCCGTTACCTTACCAACTAGCTAATGCACCGCAGGTCC  1260

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Sbjct  302
CTATGCATCATCGCCTTGGTAAGCCGTTACCTTACCAACTAGCTAATGCACCGCAGGTCC  243

Query  1261
ATCCCAGAGTGATAGCCAAAGCCATCTTTCAAACAAAAGCCATGTGGCTTTTGTTGTTAT  1320

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Sbjct  242
ATCCCAGAGTGATAGCCAAAGCCATCTTTCAAACAAAAGCCATGTGGCTTTTGTTGTTAT  183

Query  1321
GCGGTATTAGCATCTGTTTCCAAATGTTATCCCCCGCTCCGGGGCAGGTTACCTACGTGT  1380

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Sbjct  182
GCGGTATTAGCATCTGTTTCCAAATGTTATCCCCCGCTCCGGGGCAGGTTACCTACGTGT  123

Query  1381
TACTCACCCGTCCGCCACTCACTGGTGATCCATCGTCAATCAGGTGCAAGCACCAT  1436

||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  122

TACTCACCCGTCCGCCACTCACTGGTGATCCATCGTCAATCAGGTGCAAGCACCAT  67
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