

Peptide Supply Fit For Both

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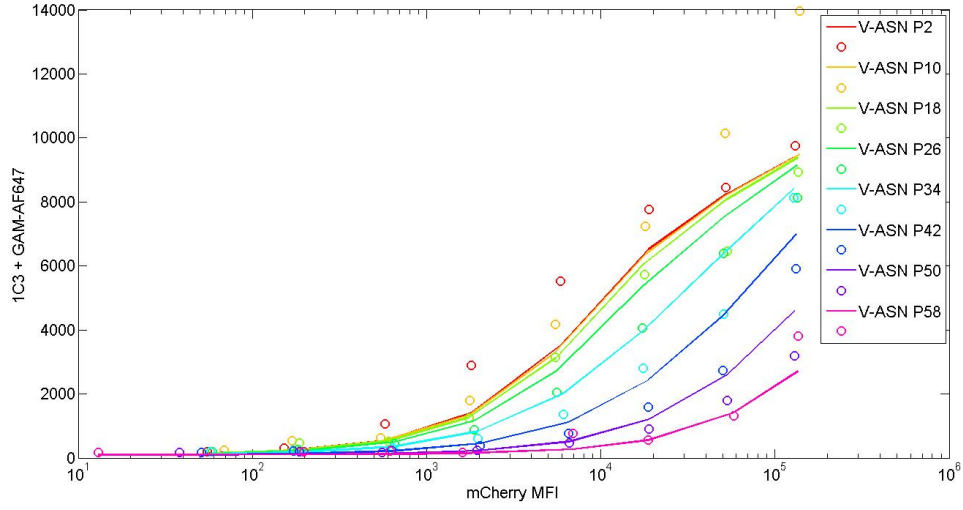
1 150422 ASN SSL IFN none and IFN +

1.1 Attempt 2

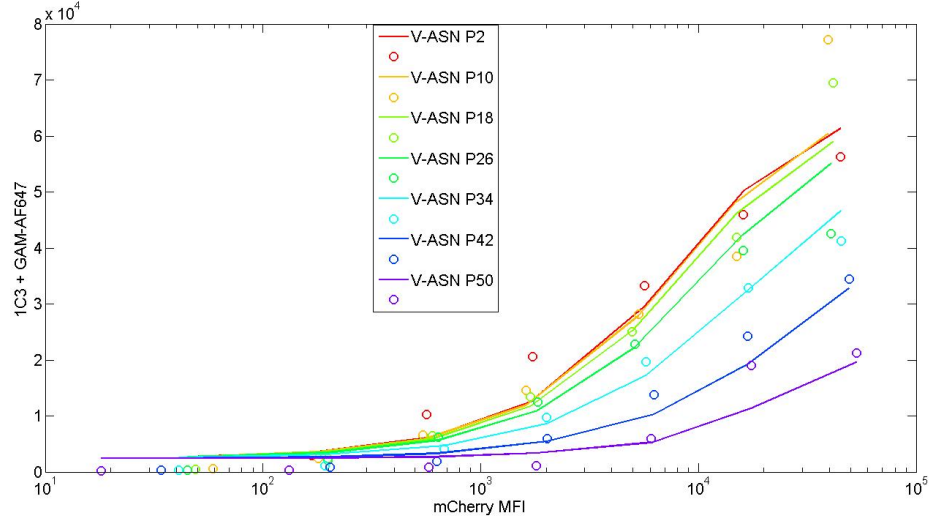
| Parameters | |
|---------------------|---|
| Time to Initialise | 5 hrs |
| Time for Simulation | 24 hrs |
| Self Peptide Supply | 0 molecules/s |
| bP_T | $3.177334 \times 10^{-11} / \text{molecules/s}$ |
| bP_C | $3.177334 \times 10^{-11} / \text{molecules/s}$ |

- Fitting Method 1: Fit for sf1 and sf2 for both $+/-$ IFN (same sf1 and sf2 for both) to fit for supply, and also fit for gM1 and gM2, for - IFN and + IFN respectively (where $gT = 10 * gM$), then scale output cell surface data using polyfit ie $p1 * MeP1 + p2$ to get best fit to data (different polyfit for $+/-$ IFN).
- $err = err_{none} + err_{ifn}$
- $sf0 = [1, 1, 105.5, 10000.5]$

| Best Fit Scale Factors | |
|------------------------|--------------------------|
| sf1 | 0.8008 |
| sf2 | 4.3651 |
| gM1 | 6.6763 |
| gM2 | 102.7993 |
| $p1_{none}$ | 0.0542 |
| $p2_{none}$ | 100.6828 |
| $p1_{ifn}$ | 0.0130 |
| $p2_{ifn}$ | 2.4127×10^3 |
| err | $3.9562 \times 10^{+04}$ |



(a)



(b)

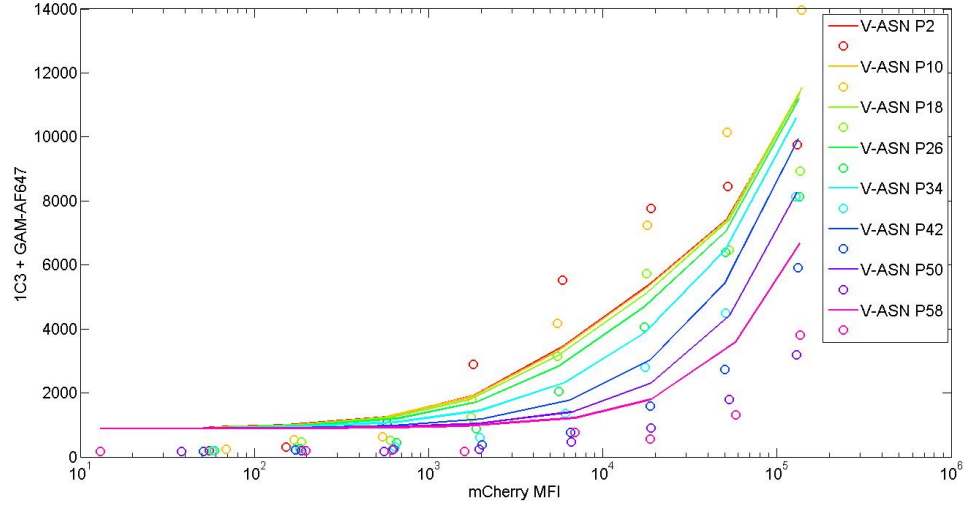
Figure 1: $t_i = 5hrs$, $t_s = 24hrs$, $sf1 = 0.8008$, $sf2 = 4.3651$, $gM1 = 6.6763$, $gM2 = 102.7993$

1.2 Attempt 3

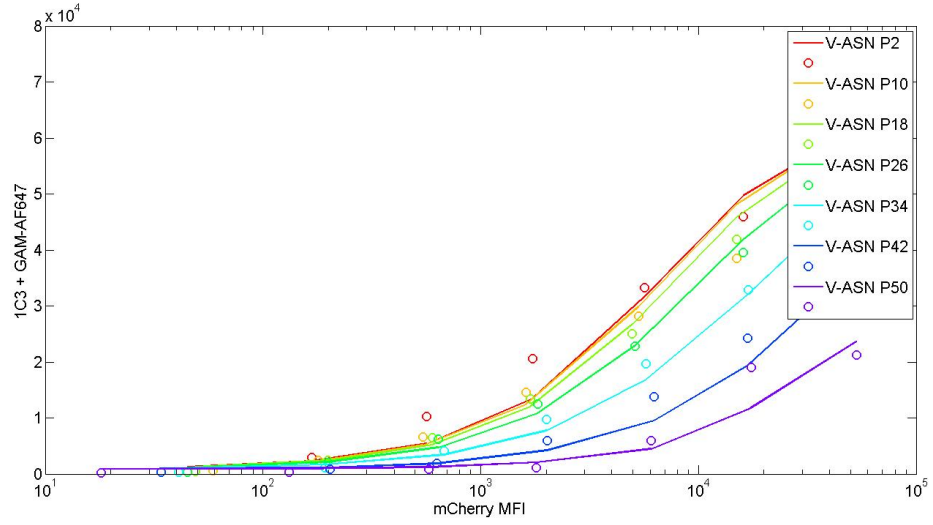
| Parameters | |
|---------------------|--|
| Time to Initialise | 10 hrs |
| Time for Simulation | 5 hrs |
| Self Peptide Supply | $0molecules/s$ |
| bP_T | $3.177334 \times 10^{-11}/molecules/s$ |
| bP_C | $3.177334 \times 10^{-11}/molecules/s$ |

- Fitting Method 2: Fit for $sf1$ and $sf2$ for both $+/-$ IFN (same $sf1$ and $sf2$ for both) to fit for supply, and also fit for $gM1$ and $gM2$, for $-$ IFN and $+$ IFN respectively (where $gT = 10 * gM$), then scale output cell surface data using polyfit ie $p1 * MeP1 + p2$ to get best fit to data, using the same polyfit for polyfit for $+/-$ IFN.
- $sf0 = [1, 1, 105.5, 10000.5]$

| Best Fit Scale Factors | |
|------------------------|--------------------------|
| sf1 | 0.2210 |
| sf2 | 1.0517 |
| gM1 | 0.4256 |
| gM2 | 1.6586 |
| $p1_{both}$ | 3.1581 |
| $p2_{both}$ | 885.7649 |
| err | $3.3076 \times 10^{+04}$ |



(a)



(b)

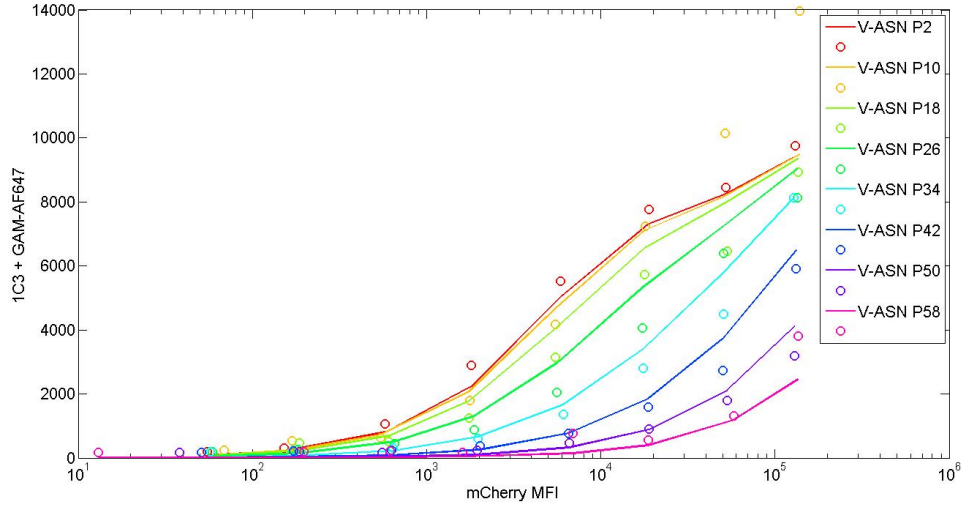
Figure 2: $t_i = 10hrs$, $t_s = 5hrs$, $sf1 = 0.221$, $sf2 = 1.0517$, $gM1 = 0.4256$, $gM2 = 1.6586$

1.3 Attempt 4

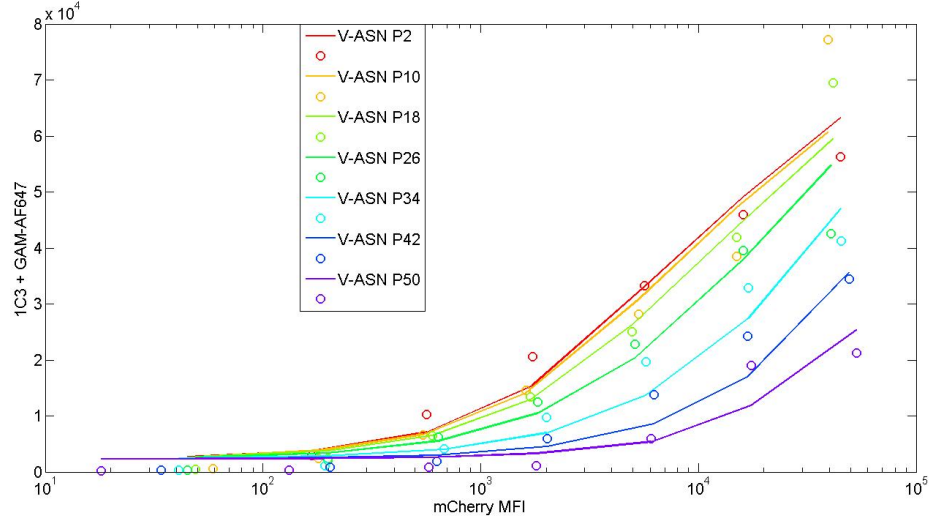
| Parameters | |
|---------------------|---|
| Time to Initialise | 24 hrs |
| Time for Simulation | 5 days |
| Self Peptide Supply | 0 molecules/s |
| bP_T | $3.177334 \times 10^{-11} / \text{molecules/s}$ |
| bP_C | $3.177334 \times 10^{-11} / \text{molecules/s}$ |

- Fitting Method 1: Fit for sf1 and sf2 for both $+/-$ IFN (same sf1 and sf2 for both) to fit for supply, and also fit for gM1 and gM2, for - IFN and + IFN respectively (where $gT = 10 * gM$), then scale output cell surface data using polyfit ie $p1 * MeP1 + p2$ to get best fit to data (different polyfit for $+/-$ IFN).
- $err = err_{none} + err_{ifn}$
- $sf0 = [1, 1, 105.5, 10000.5]$

| Best Fit Scale Factors | |
|------------------------|--------------------------|
| sf1 | 0.2528 |
| sf2 | 2.0310 |
| gM1 | 2.6634 |
| gM2 | 0.7632 |
| $p1_{none}$ | 0.1906 |
| $p2_{none}$ | 2.9975 |
| $p1_{ifn}$ | 11.60 |
| $p2_{ifn}$ | 2.3058×10^3 |
| err | $3.8597 \times 10^{+04}$ |



(a)



(b)

Figure 3: $t_i = 24hrs$, $t_s = 5days$, $sf1 = 0.2528$, $sf2 = 2.0310$, $gM1 = 2.6634$, $gM2 = 0.7632$

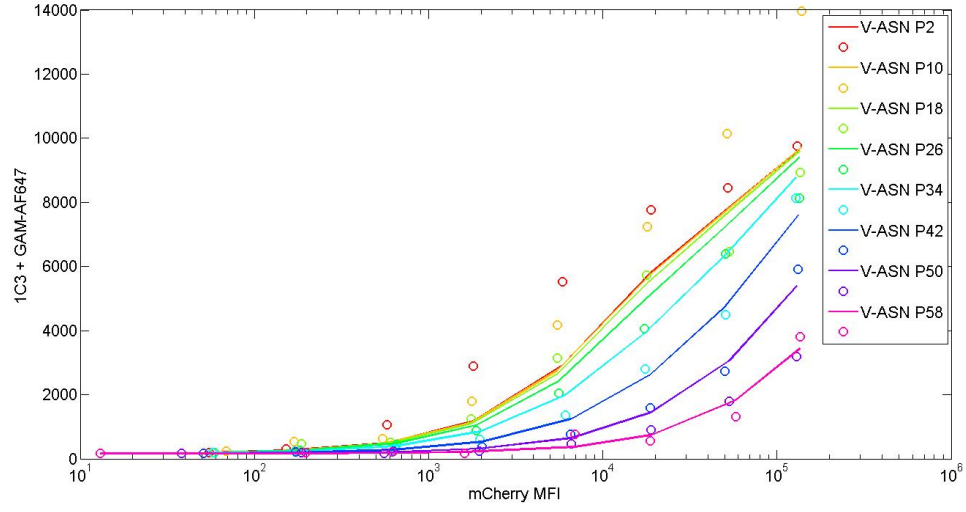
1.4 Attempt 5

| Parameters | |
|---------------------|---|
| Time to Initialise | 24 hrs |
| Time for Simulation | 10 hrs |
| Self Peptide Supply | 0 molecules/s |
| bP_T | $3.177334 \times 10^{-11} / \text{molecules/s}$ |
| bP_C | $3.177334 \times 10^{-11} / \text{molecules/s}$ |

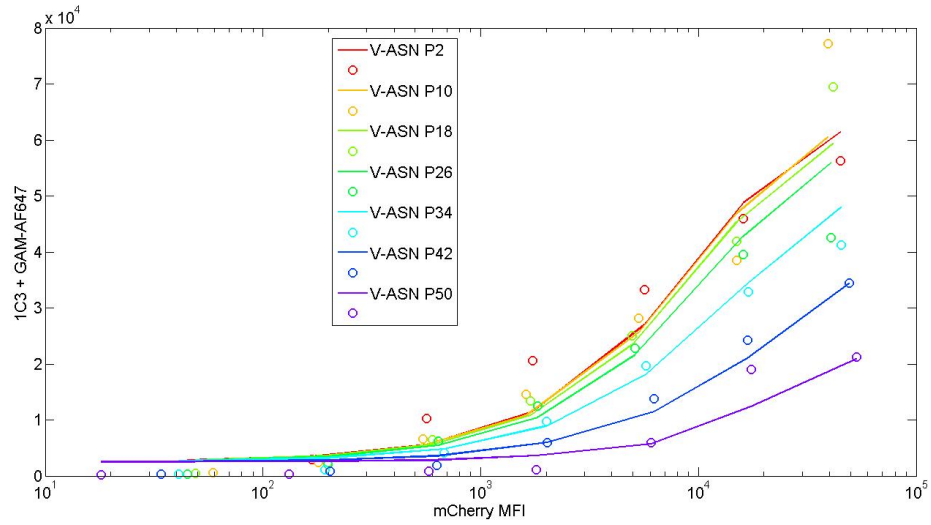
- Fitting Method 1: Fit for $sf1$ and $sf2$ for both $+/-$ IFN (same $sf1$ and $sf2$ for both) to fit for supply, and also fit for $gM1$ and $gM2$, for $-$ IFN and $+$ IFN respectively (where $gT = 10 * gM$), then scale output cell surface data using polyfit ie $p1 * MeP1 + p2$ to get best fit to data (different polyfit for $+/-$ IFN).
- $err = err_{none} + err_{ifn}$

- $sf0 = [1, 1, 105.5, 10000.5]$

| Best Fit Scale Factors | |
|------------------------|--------------------------|
| sf1 | 1.2203 |
| sf2 | 5.6610 |
| gM1 | 2.0098 |
| gM2 | 39.8554 |
| $p1_{none}$ | 0.2275 |
| $p2_{none}$ | 163.3102 |
| $p1_{ifn}$ | 0.0240 |
| $p2_{ifn}$ | 2.5125×10^3 |
| err | $4.0792 \times 10^{+04}$ |



(a)



(b)

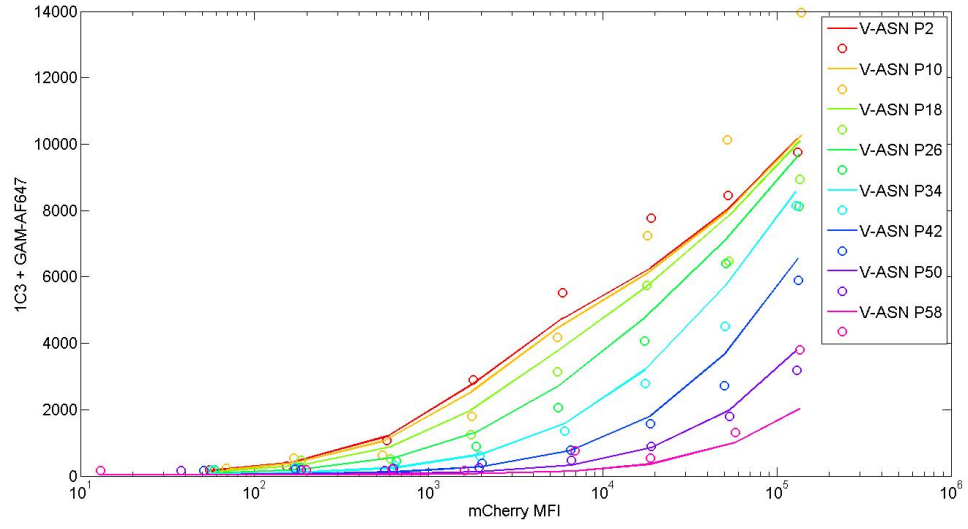
Figure 4: Best fit to the data for a) Fitting method 1, b) Fitting method 2, where the best fit scale factors are given in tables 2 and 3 respectively

1.5 Attempt 6

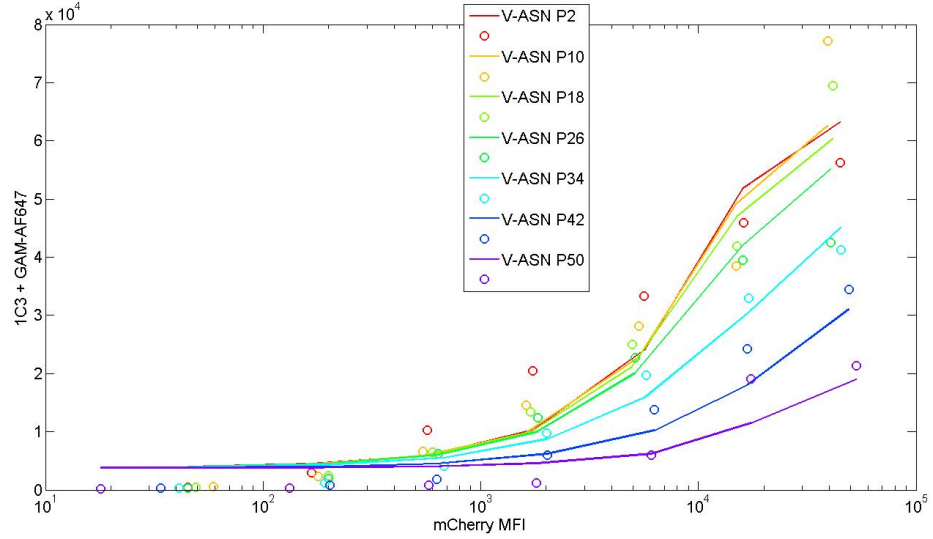
| Parameters | |
|---------------------|---|
| Time to Initialise | 0 hrs |
| Time for Simulation | 24 hrs |
| Self Peptide Supply | 0 molecules/s |
| bP_T | $3.177334 \times 10^{-11} / \text{molecules/s}$ |
| bP_C | $3.177334 \times 10^{-11} / \text{molecules/s}$ |

- Fitting Method 1: Fit for sf1 and sf2 for both $+/-$ IFN (same sf1 and sf2 for both) to fit for supply, and also fit for gM1 and gM2, for - IFN and + IFN respectively (where $gT = 10 * gM$), then scale output cell surface data using polyfit ie $p1 * MeP1 + p2$ to get best fit to data (different polyfit for $+/-$ IFN).
- $err = err_{none} + err_{ifn}$
- $sf0 = [10, 20, 100, 1e6]$

| Best Fit Scale Factors | |
|------------------------|--------------------------|
| sf1 | 4.6506 |
| sf2 | 28.6018 |
| gM1 | 4.9436 |
| gM2 | $6.2284 \times 10^{+04}$ |
| $p1_{none}$ | 0.0628 |
| $p2_{none}$ | 37.8125 |
| $p1_{ifn}$ | 2.0892×10^{-05} |
| $p2_{ifn}$ | $3.7830e \times 10^3$ |
| err | $4.2644 \times 10^{+04}$ |



(a)



(b)

Figure 5: $t_i = 0hrs$, $t_s = 24hrs$, $sf1 = 4.6506$, $sf2 = 28.6018$, $gM1 = 4.9436$, $gM2 = 6.2284 \times 10^{+04}$