

Supporting Information

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* To whom correspondence should be addressed. ytalgan@unr.edu

Experimental details

Solid Phase Peptide Synthesis

The resin (0.1 g) was first swelled by suspension in DCM for 30 minutes at room temperature and then drained. The resin was then washed with DMF (3 × 2 mL). Fmoc removal was accomplished with treatment of the resin by 2 mL of 20% piperidine in DMF and shaking at 200 rpm for 7.5 minutes. This process was then repeated once more for a total of 15 minutes deprotection time and then washed with DMF (3 × 2 mL). To couple each amino acid, Fmoc protected amino acids (2 equiv. relative to the resin loading) was dissolved in 2 mL DMF and mixed with 2-(1H-benzotriazol-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (HBTU; 2 equiv.) and diisopropylethylamine (DIPEA; 2 equiv.). The solution was allowed to pre-activate for 1 minute prior to being added to the resin and shaken at 200 rpm for 1 hour at room temperature. After each coupling step, the resin was drained and washed with DMF (2 × 2 mL).

Final cleavage

The resin containing the final peptide product was washed with 5 mL diethyl ether and air dried for 10 minutes before transferring it into a 15 mL falcon tube. 3 mL of 2.5% water and 2.5% TIPS in TFA was then added and the tube was shaken for 3 hours. The cleaved peptide was filtered through a cotton ball into a 50 mL falcon tube. A cooled solution of diethyl ether:hexane (1:1, 45 mL, -20 °C) was added to the filtrate, and the peptide was allowed to precipitate in a freezer at -20 °C for 10 minutes. The 50 mL tube was centrifuged in a Beckman Coulter Allegra 6 centrifuge equipped with a GH3.8 rotor at 3000 rpm for 5 minutes to pellet the crude peptide. The supernatant was decanted off and the remaining crude peptide was dissolved in 10 mL ACN:H₂O (1:1) and lyophilized.

Biological Assays

Beta-Galactosidase Assays

An initial activation screening was performed at a high concentration (10 μM) for all CSP2 analogs. 198 μL bacterial culture were placed in triplicate to a 96-well plate containing 2 μL of CSP2 peptides and incubated at 37 °C for 30 minutes. A total of 2 μL of 20 μM solution of CSP1 (200 nM final concentration) were added in triplicate and served as the positive control for the group I strain (D39pcomX::lacZ), while 2 μL of 100 μM solution of CSP2 (1000 nM final concentration) were added as the positive control for the group II strain (TIGR4pcomX::lacZ). These concentrations were chosen to afford full activation of the QS circuit, as determined from the dose-dependent curves created for the native CSPs. 2 μL dimethyl sulfoxide (DMSO) were added in triplicate and served as the negative control. After the incubation time had elapsed, the absorbance at 600_{nm} was read. The wells were then treated with 20 μL 1% Triton X-100 in water for 30 minutes at 37 °C to lyse the bacterial cells. In a new plate, 100 μL Z-buffer solution (60.2 mM Na₂HPO₄, 45.8 mM NaH₂PO₄, 10 mM KCl, and 1.0 mM MgSO₄ in 18 MΩ H₂O; pH was adjusted to 7.0 and the buffer was sterilized before use) containing 2-Nitrophenyl-Beta-D-galactopyranoside (ONPG) at a final concentration of 0.4 mg/mL were added, followed by 100 μL lysate, and the plate was incubated for 3 hours at 37 °C. After the incubation, the reaction was quenched by adding 50 μL of 1 M sodium carbonate solution, and the OD 420_{nm} and OD 550_{nm} were measured using a plate reader, allowing for the calculation of the activity in Miller units (see below). The final results were reported as percent activation, which is the ratio between the Miller units of the analog and that of the positive control.

$$\text{Miller Unit} = 1000 \times \frac{[Abs_{420} - (1.75 \times Abs_{550})]}{(t \times v \times Abs_{600})}$$

Abs₄₂₀ is the absorbance of o-nitrophenol (ONP). Abs₅₅₀ is the scatter from cell debris, which, when multiplied by 1.75 approximates the scatter observed at 420 nm. t is the duration of incubation with ONPG in minutes, v is volume of lysate in milliliters, and Abs₆₀₀ reflects cell density.

EC₅₀ Experiments

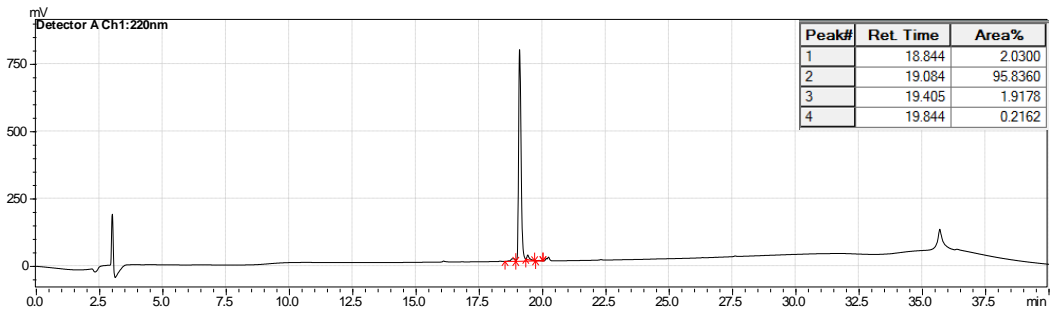
Analogs that exhibited high activity in the initial screening were further evaluated using a dose-dependent assay in which peptide stock solutions were diluted with DMSO in serial dilution and assayed as described above. The EC₅₀ value was then determined through fitting using nonlinear regression with GraphPad Prism 5.

IC₅₀ Experiments

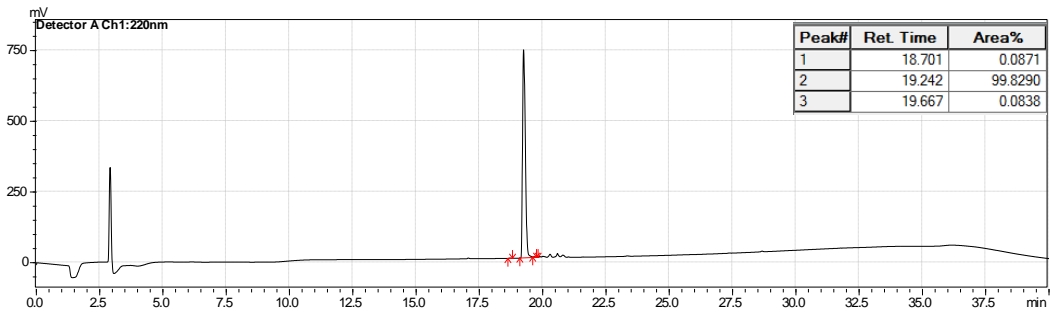
Analogs that exhibited low *comX* activation in the initial screening were evaluated for competitive inhibition. The ability of synthesized CSP2 analogs to inhibit the expression of *comX* by outcompeting CSP for the receptor binding site was evaluated using the same assay conditions as described above, except that in the initial inhibition screening, the native CSP was added to every well in a set concentration (50 nM CSP1 for group I; 250 nM CSP2 for group II) that was chosen to afford full activation of the QS circuit, as determined from the dose-dependent curves created for the native CSPs. 2 μ L of native CSP (5 μ M solution of CSP1 for group I; 25 μ M solution of CSP2 for group II) and 2 μ L of 1 mM solution of CSP analogs were added to the same well in triplicate in a clear 96-well microtiter plate. 2 μ L native CSP (5 μ M solution of CSP1 for group I; 25 μ M solution of CSP2 for group II) and 2 μ L DMSO were added to the same well in triplicate and served as the positive control. 4 μ L DMSO were added in triplicate and served as the negative control. Then, 196 μ L bacterial culture were added to the wells and the plate was incubated at 37 °C for 30 minutes. The procedure for lysis, incubation with ONPG and all the measurements were as described in the beta-galactosidase assay section above. Analogs that exhibited significant competitive inhibition in the initial screening were further evaluated using a dose-dependent assay where peptide stock solutions were diluted with DMSO in serial dilutions and assayed as described above. GraphPad Prism 5 was used to calculate the IC₅₀ values, which are the concentration of an inhibitor where the response (or binding) is reduced by half.

HPLC Traces

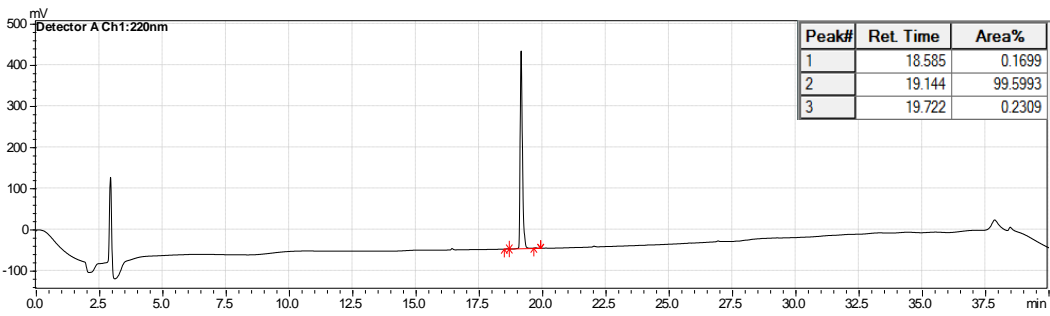
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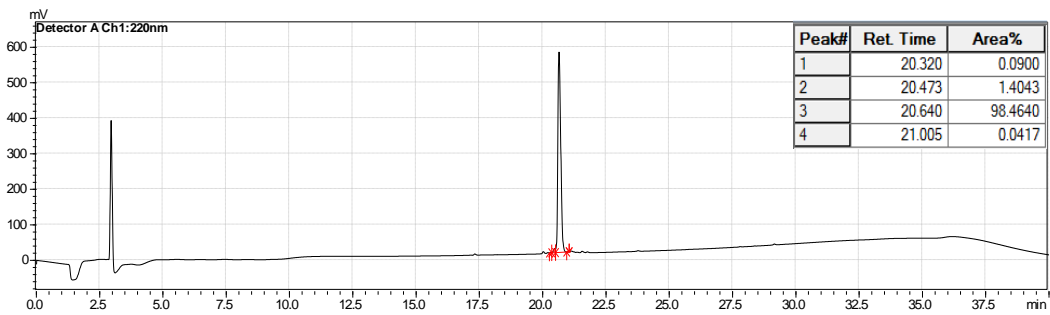
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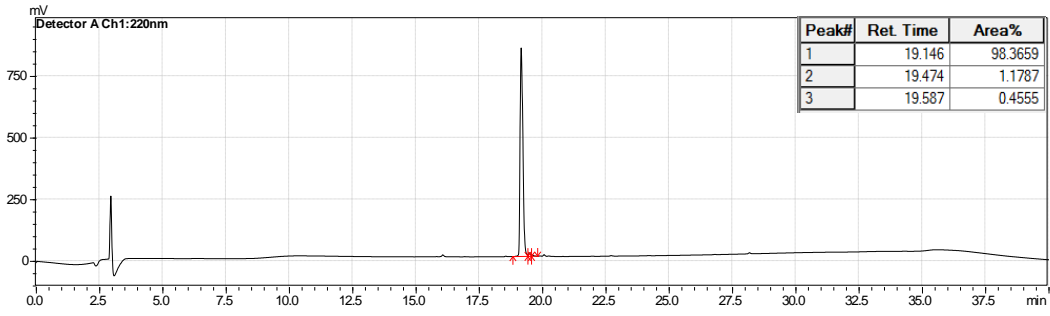
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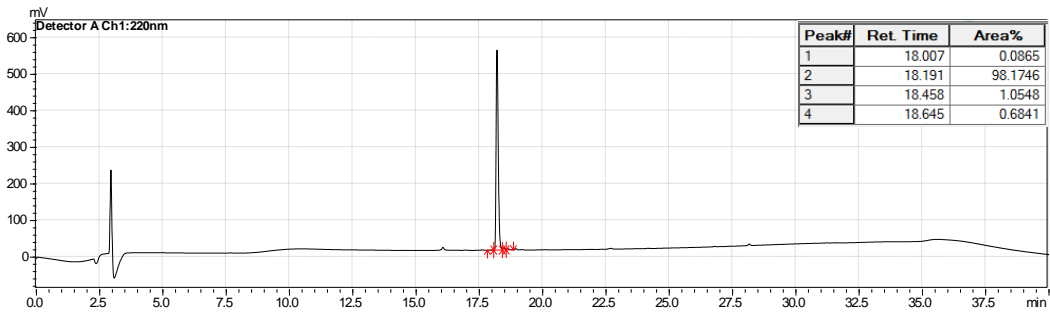
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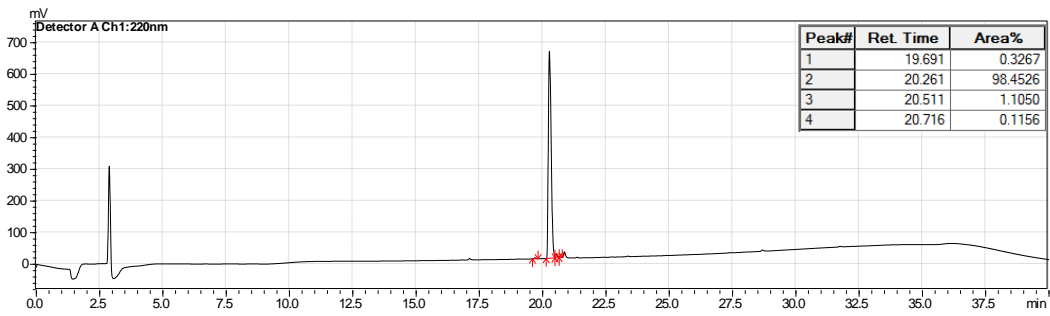
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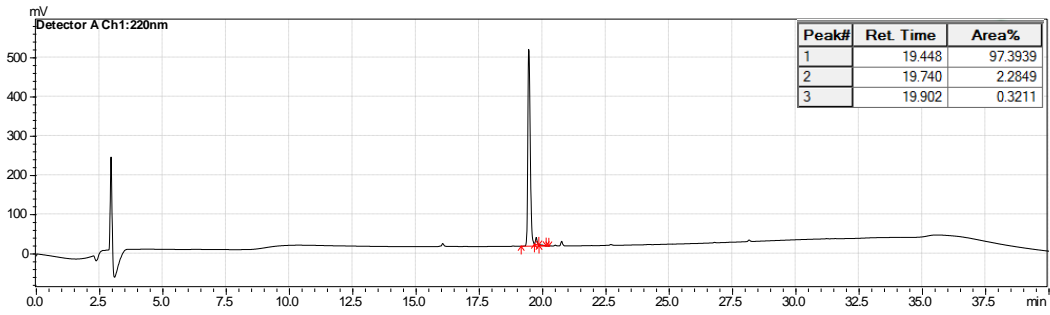
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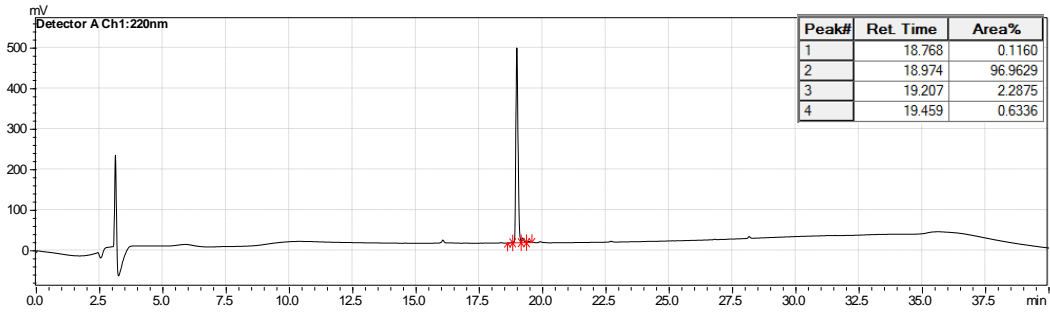
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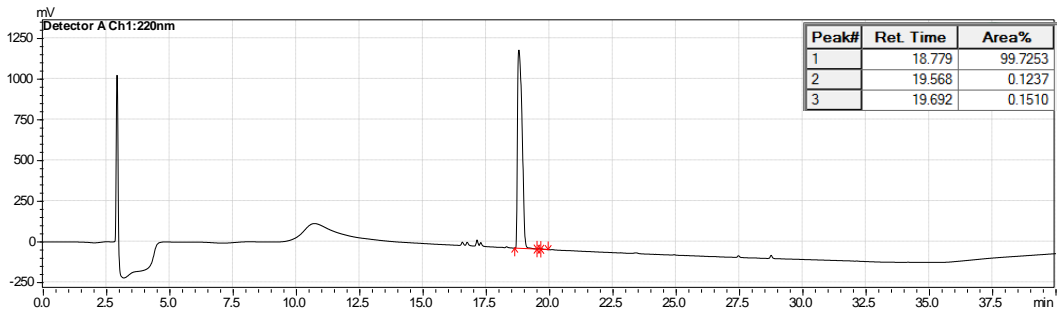
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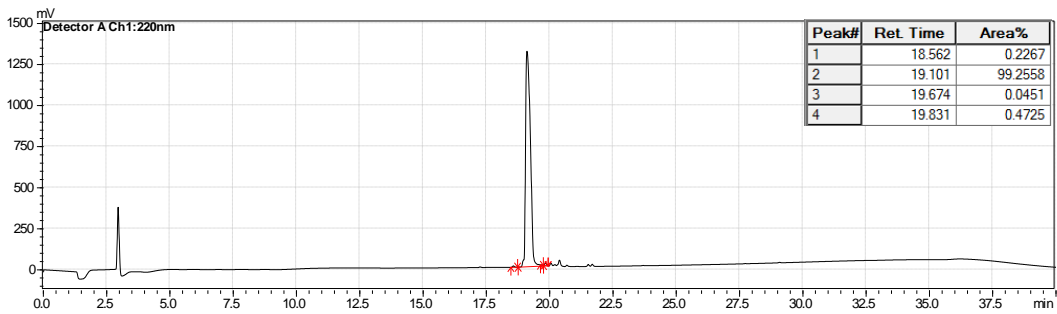
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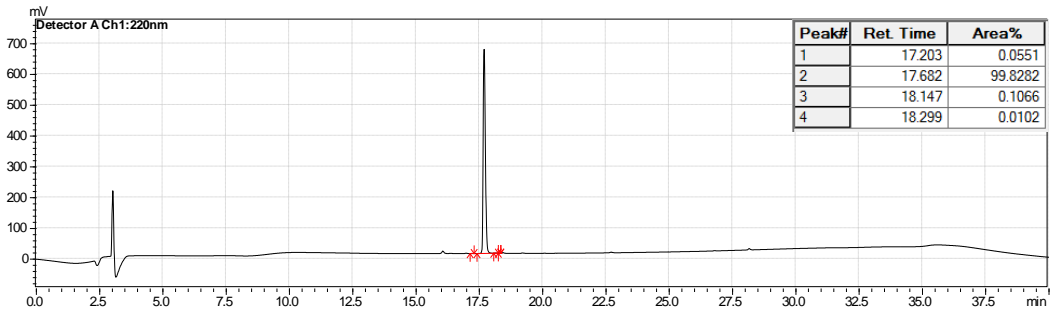
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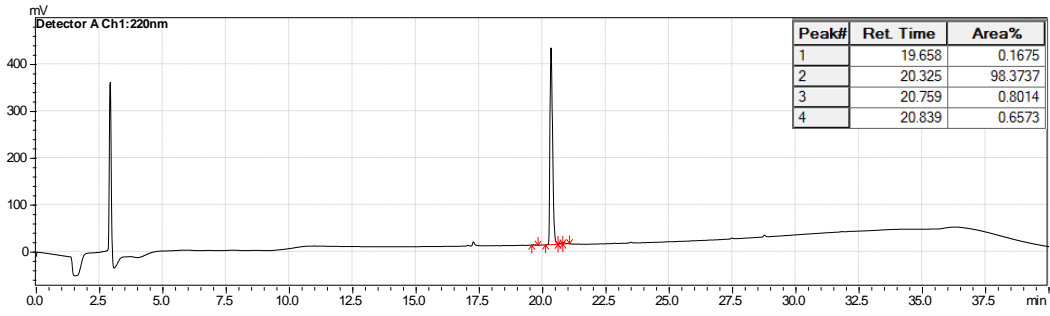
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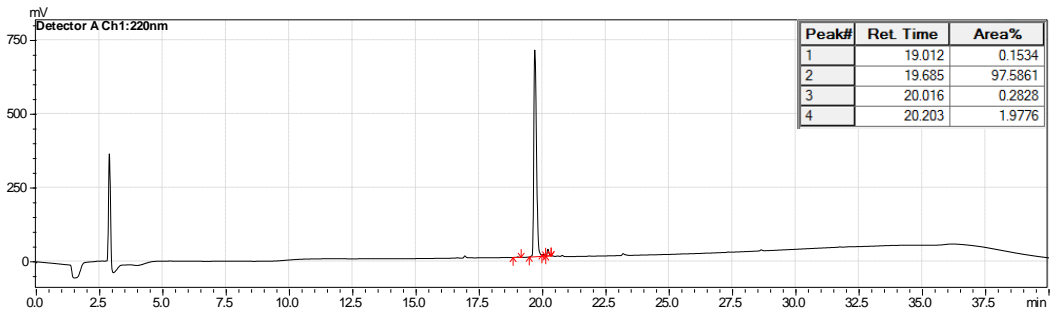
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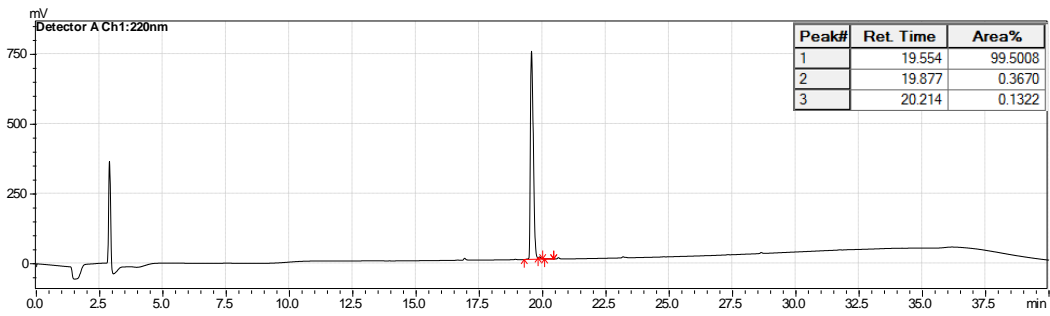
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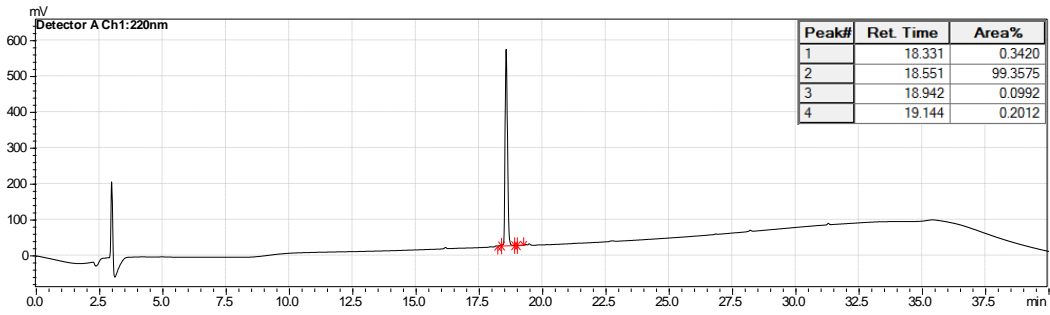
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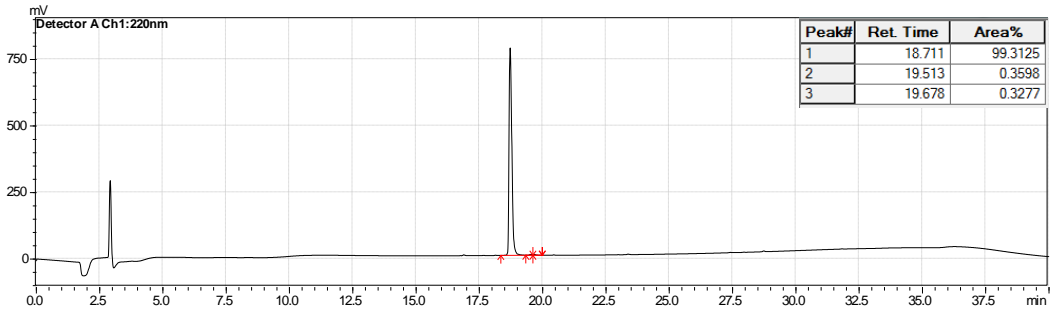
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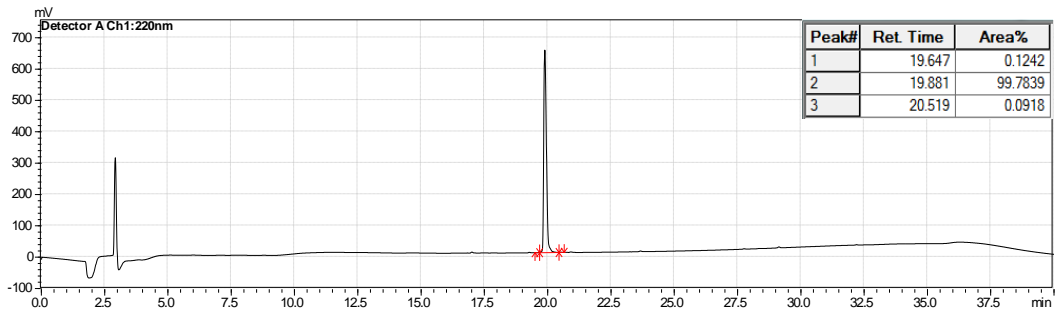
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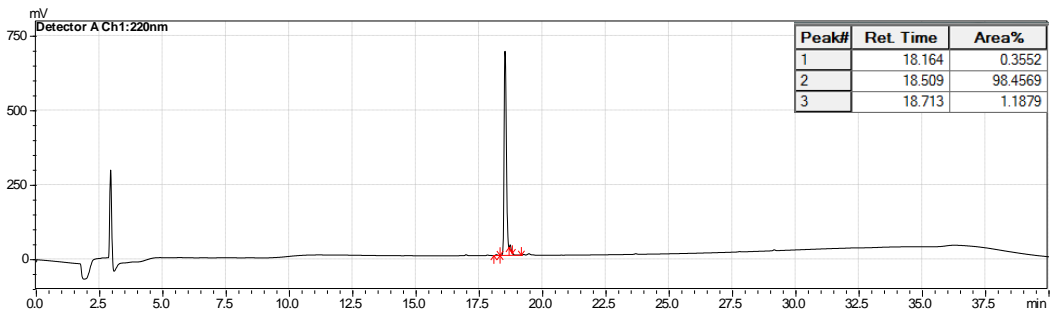
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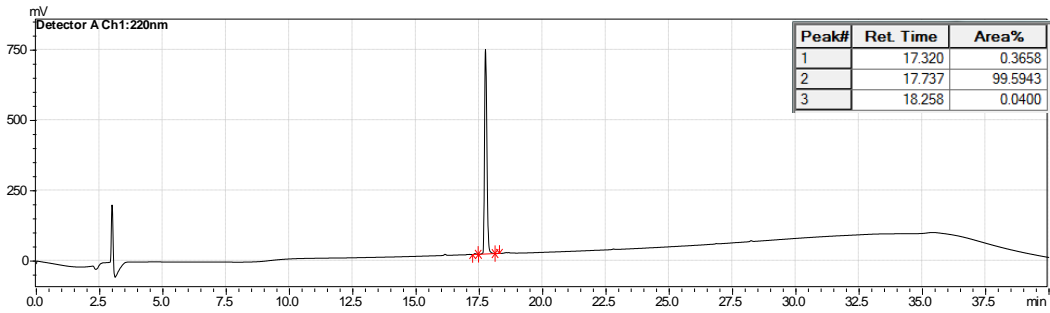
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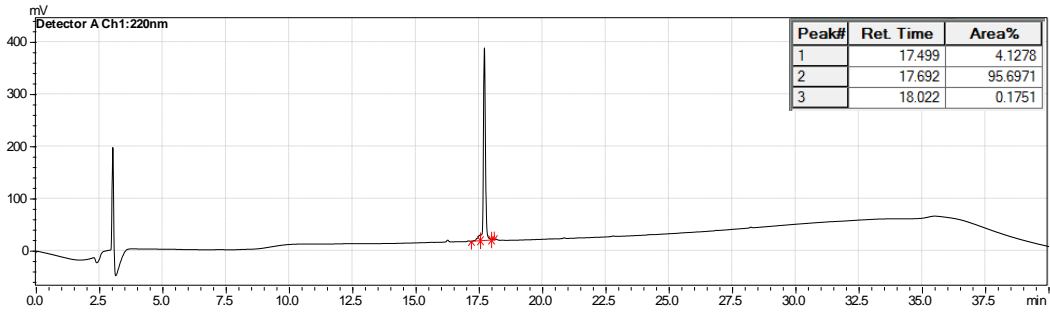
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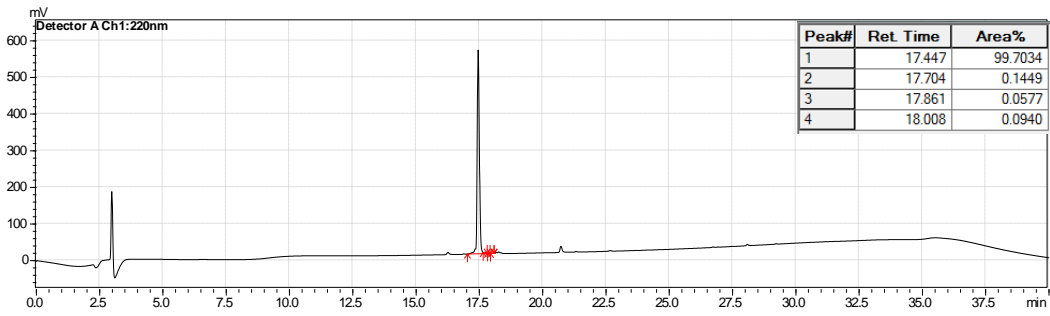
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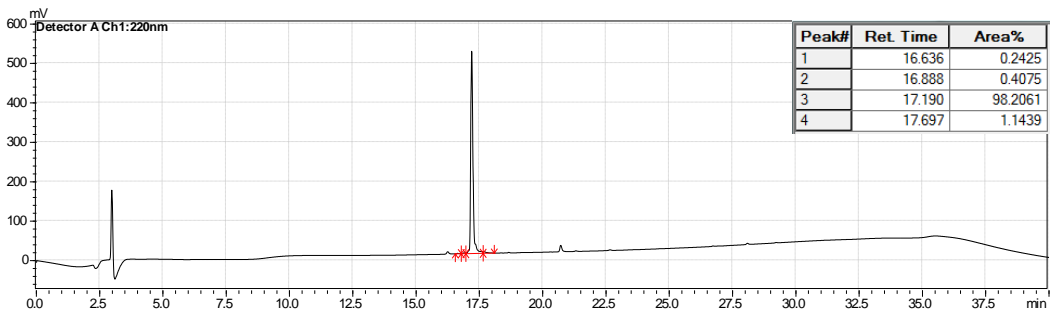
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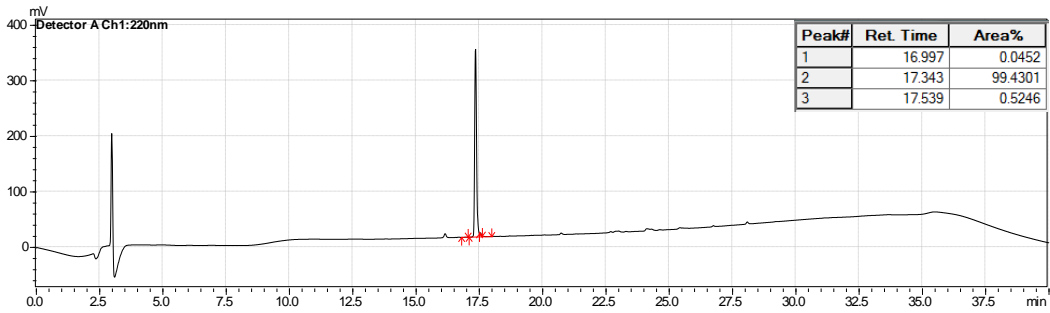
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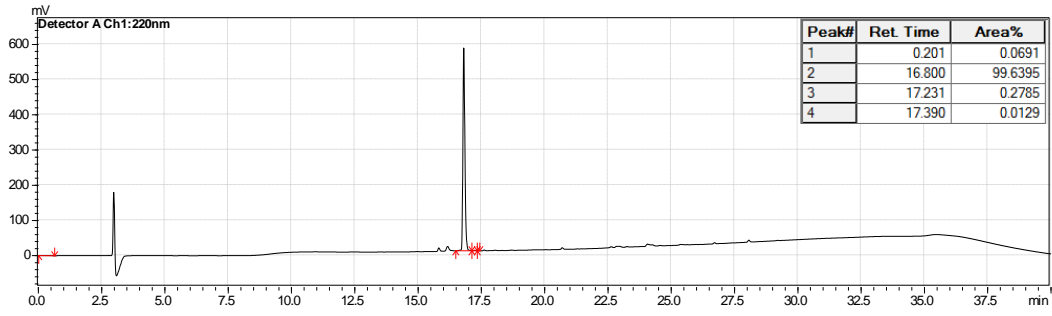
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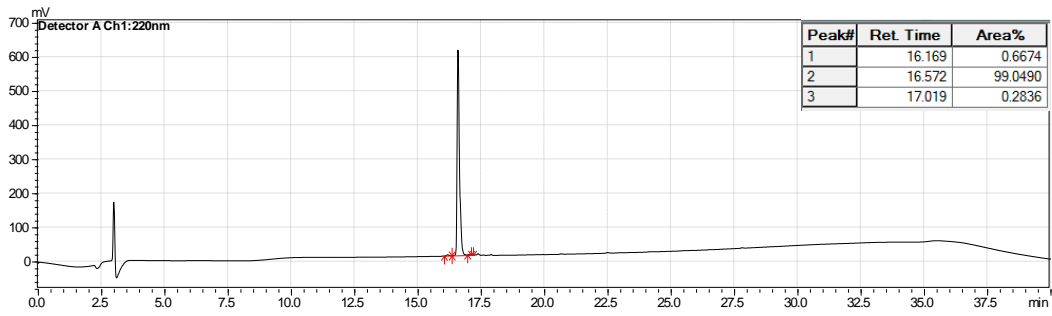
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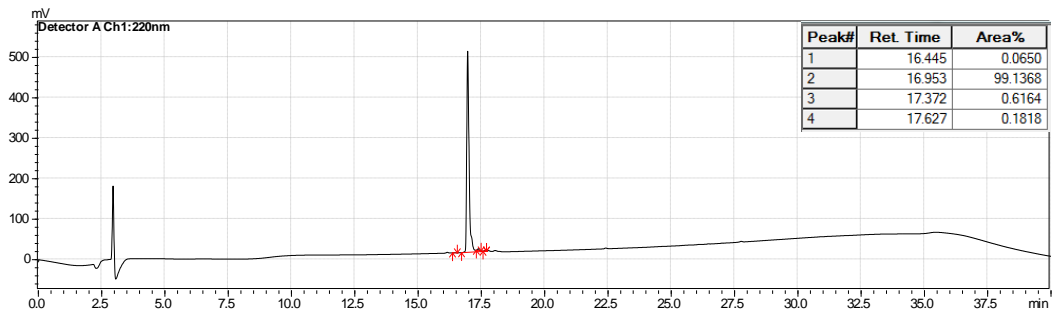
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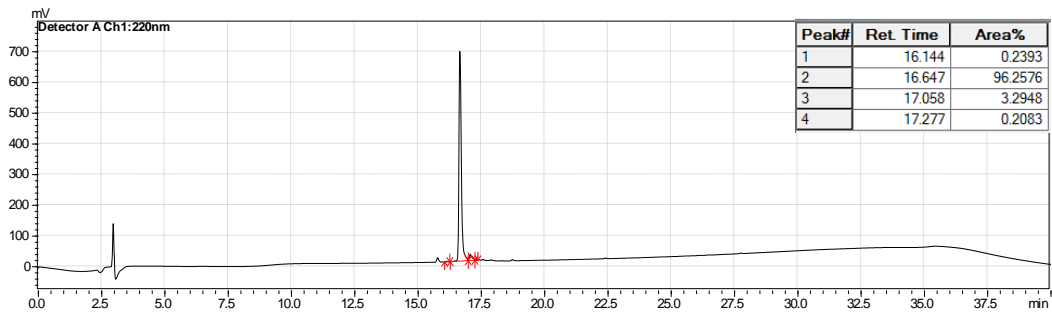
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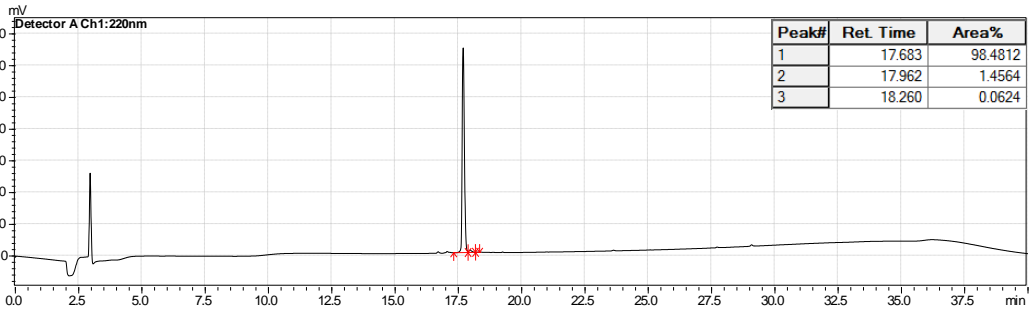
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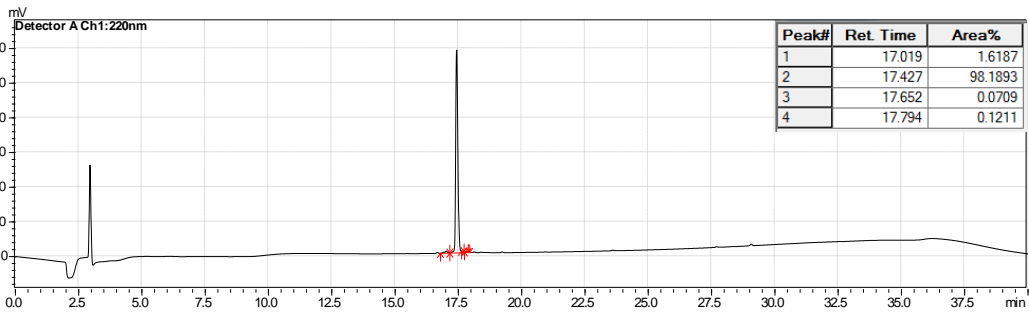
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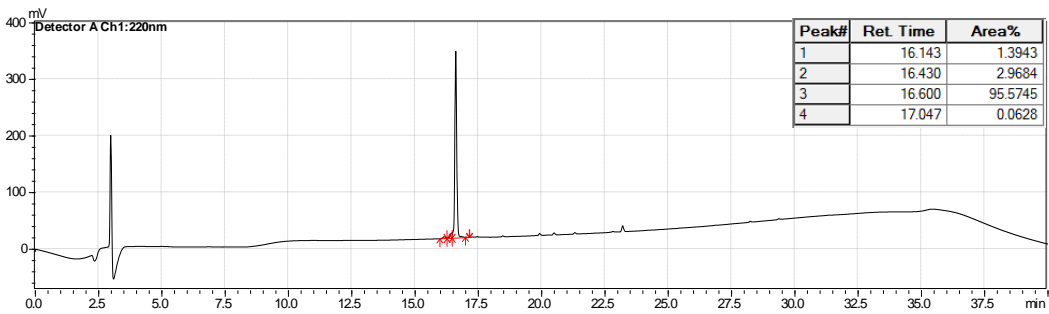
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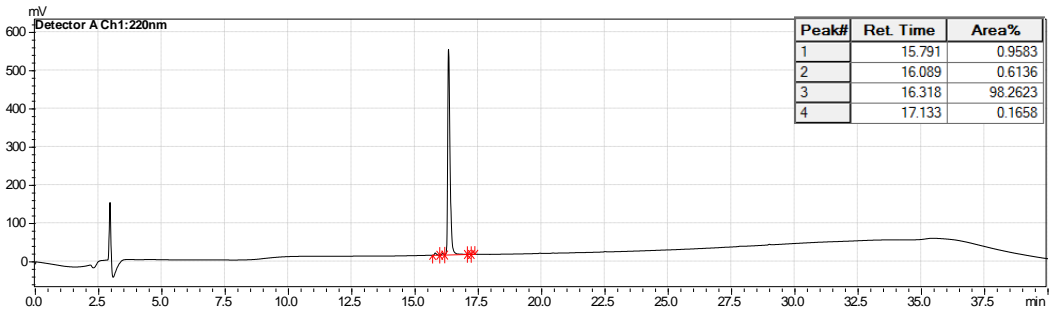
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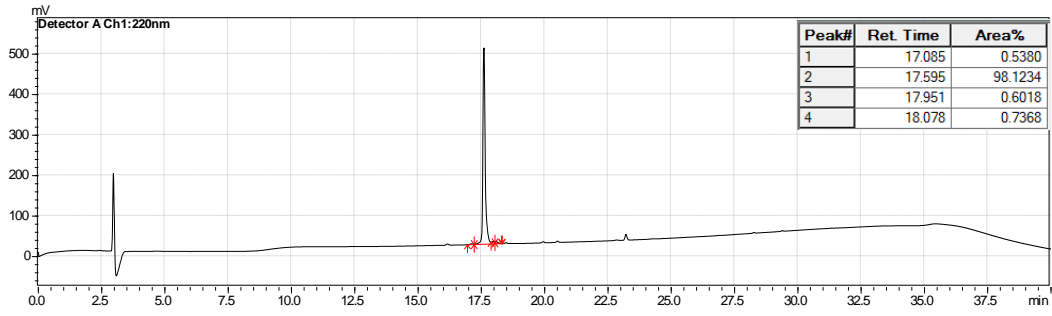
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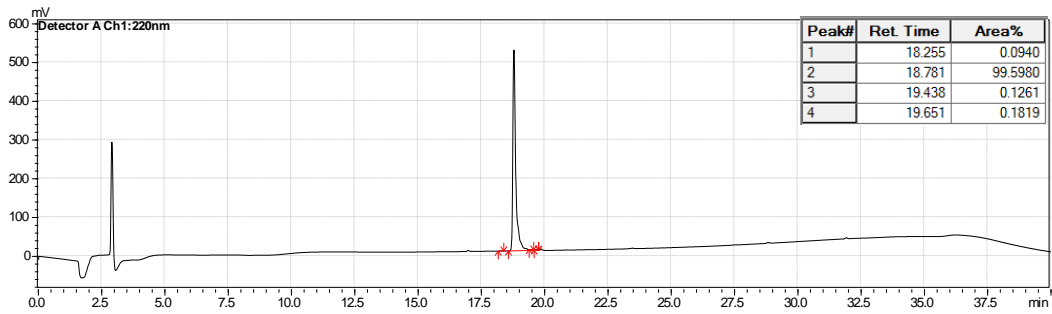
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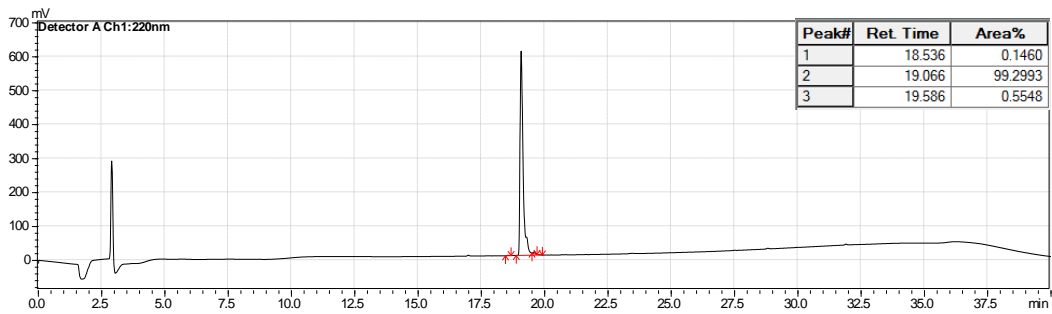
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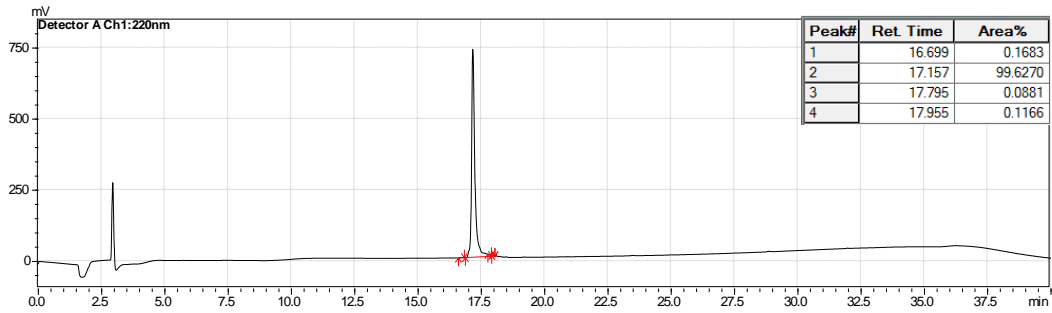
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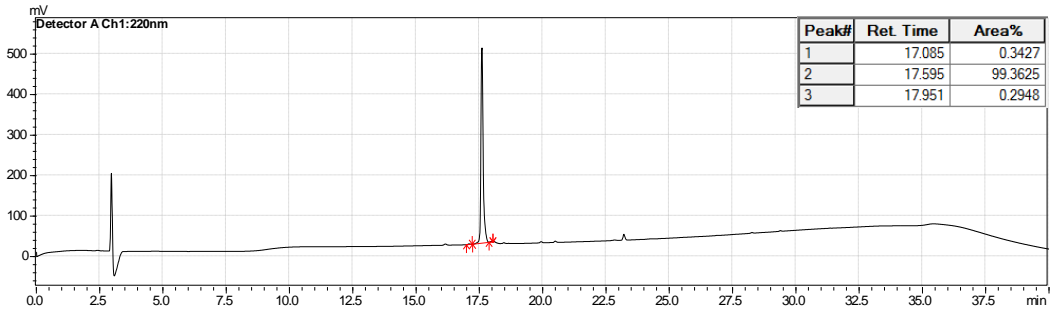
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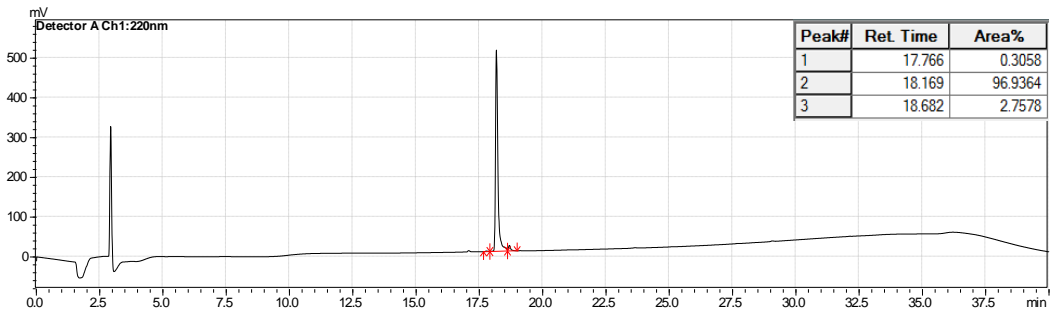
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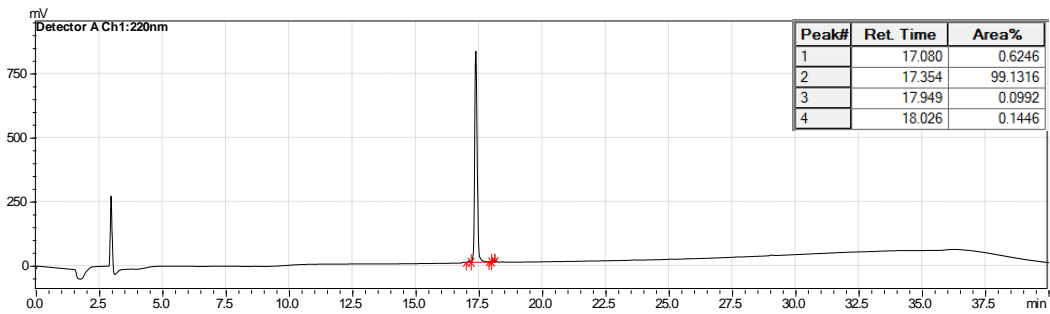
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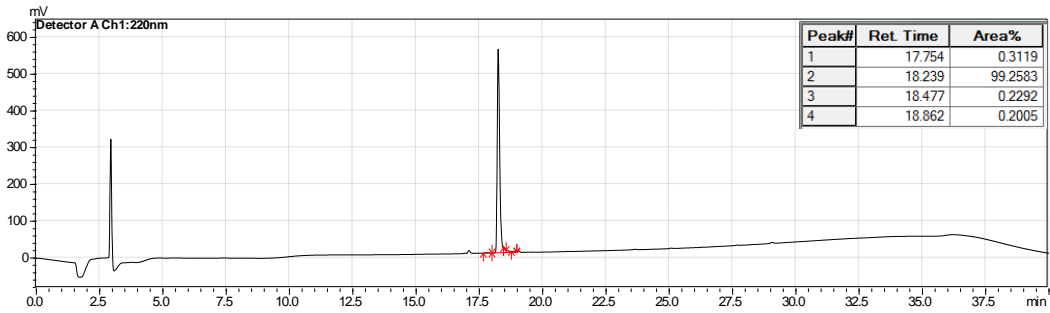
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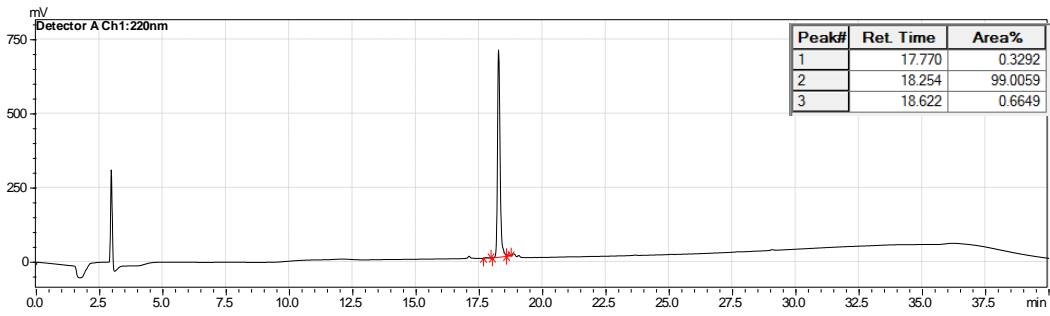
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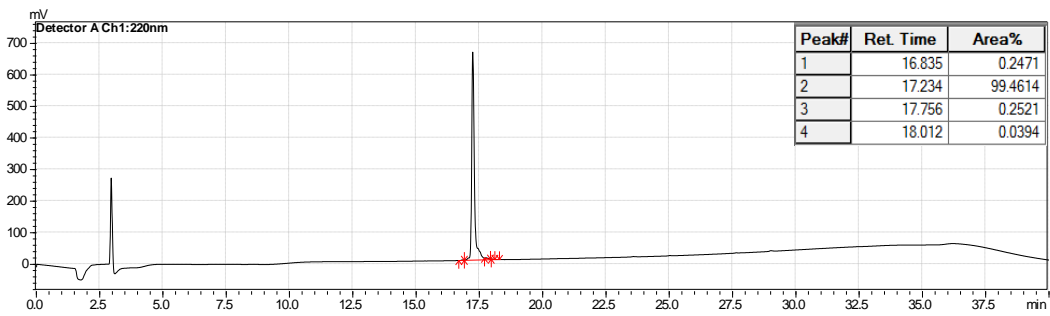
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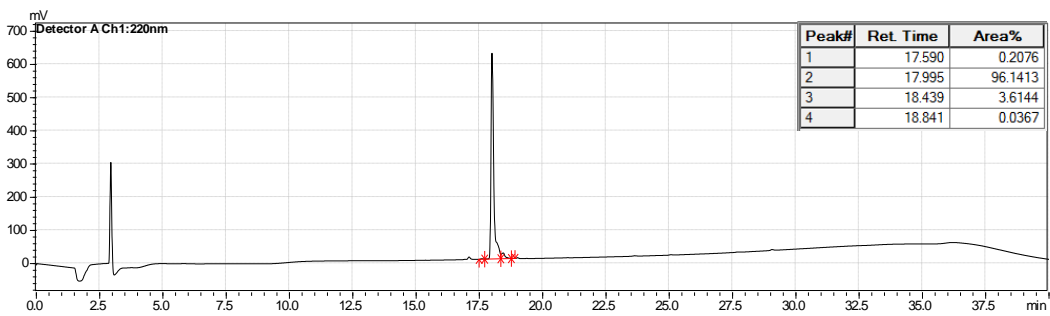
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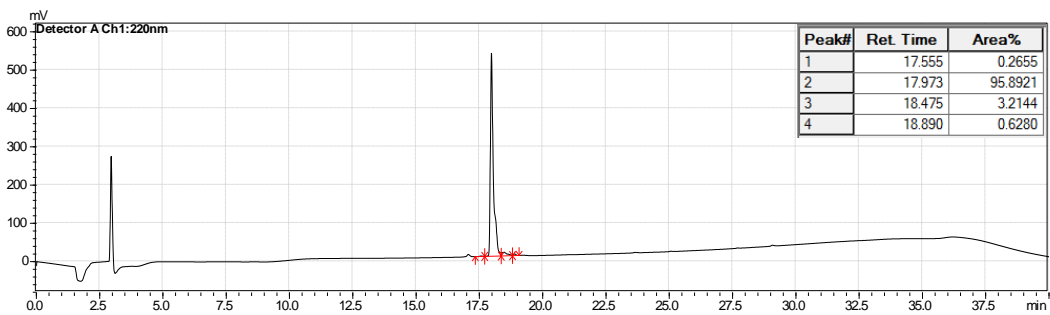
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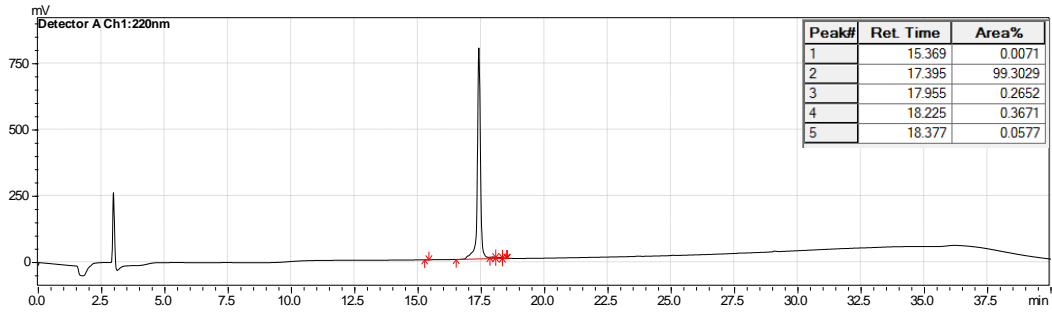
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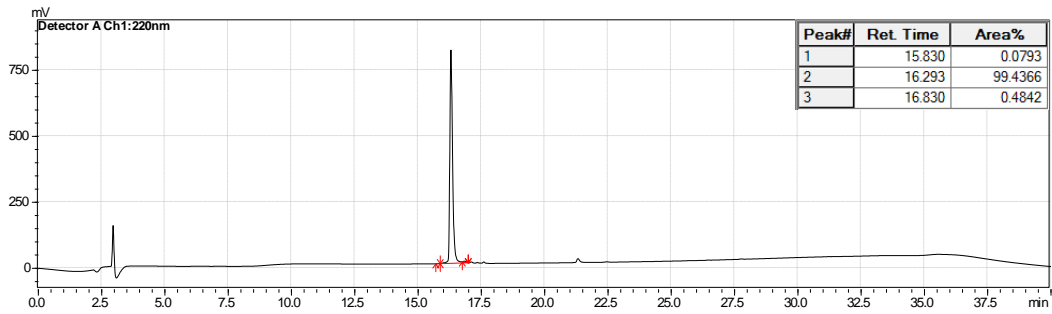
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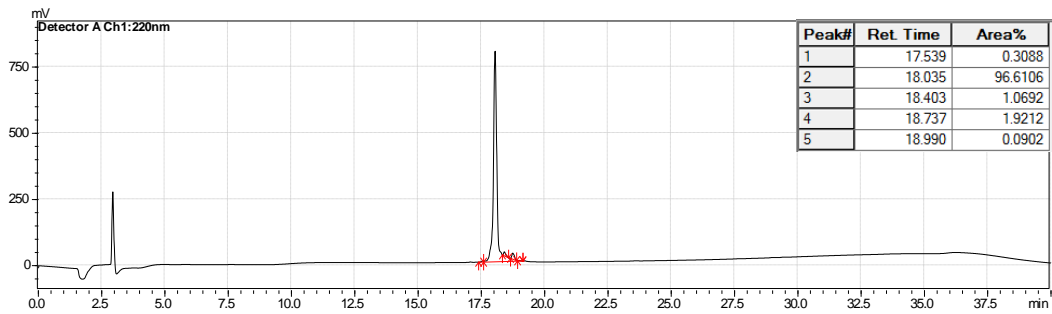
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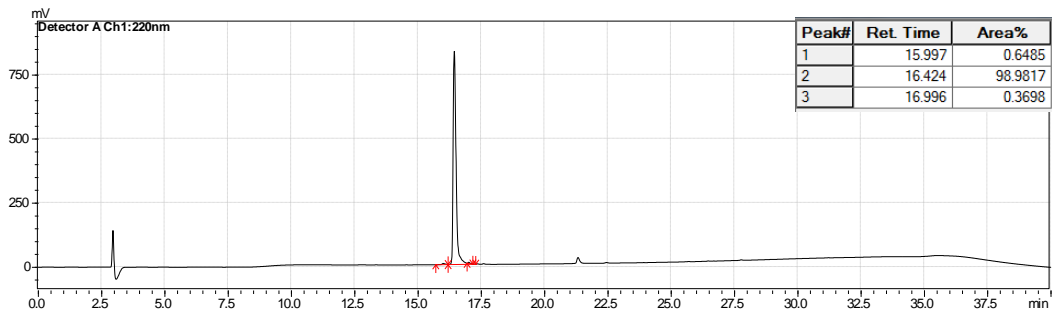
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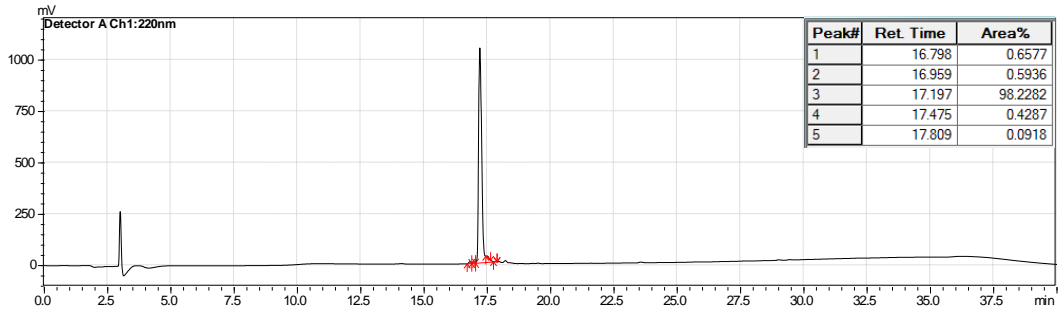
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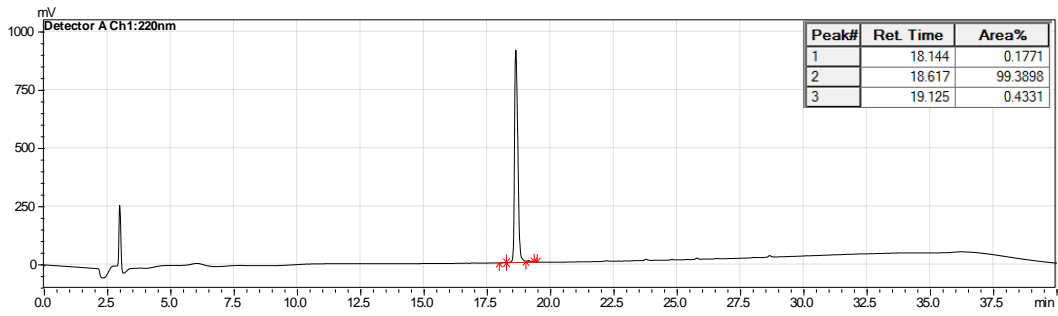
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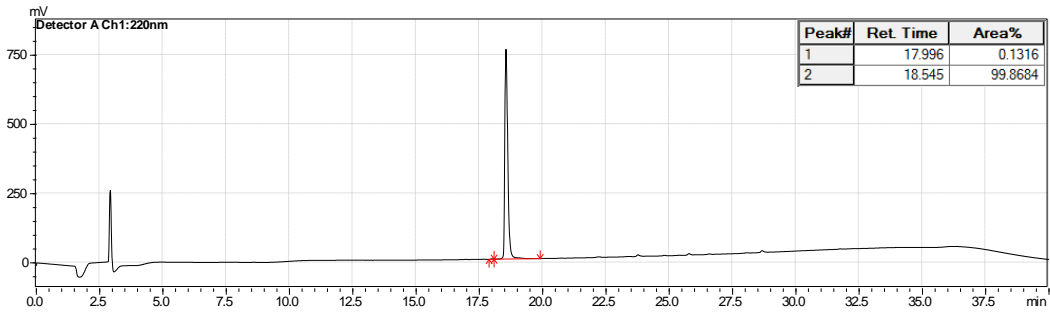
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CSP2-E1Ad10L14Q



CSP2-E1AI4Ld10L14Q



MS and HPLC data for CSP2 analogs

Table S-1. MS and HPLC data for CSP2(15) analogs.

| Compound Name | Calc. EM MH ₂ ²⁺ | Obs. EM MH ₂ ²⁺ | Purity (%) |
|-----------------------------|---|--|---------------|
| CSP2(15)-I4LI7F | 979.0495 | 979.0511 | >96 |
| CSP2(15)-I4LL9R | 983.5658 | 983.5678 | >99 |
| CSP2(15)-I4LL12I | 962.0573 | 962.0558 | >99 |
| CSP2(15)-I4LF13L | 945.0651 | 945.0669 | >98 |
| CSP2(15)-I4LL14Q | 969.5445 | 969.5459 | >98 |
| CSP2(15)-I7FL9R | 1000.5580 | 1000.5534 | >98 |
| CSP2(15)-I7FL12I | 979.0495 | 979.0463 | >98 |
| CSP2(15)-I7FF13L | 962.0573 | 962.0576 | >97 |
| CSP2(15)-I7FL14Q | 986.5367 | 986.5376 | >96 |
| CSP2(15)-L9RL12I | 983.5658 | 983.5390 | >99 |
| CSP2(15)-L9RF13L | 966.5736 | 966.5752 | >99 |
| CSP2(15)-L9RL14Q | 991.0530 | 991.0545 | >99 |
| CSP2(15)-L12IF13L | 948.0886 | 948.0899 | >98 |
| CSP2(15)-L12IL14Q | 969.5445 | 969.5478 | >97 |
| CSP2(15)-F13LL14Q | 952.5524 | 952.5543 | >99 |
| CSP2(15)-I4LL9RF13L | 966.0722 | 966.0735 | >99 |
| CSP2(15)-I4LL9RL14Q | 991.0530 | 991.0525 | >99 |
| CSP2(15)-I4LF13LL14Q | 952.5524 | 952.5542 | >99 |
| CSP2(15)-L9RF13LL14Q | 974.0608 | 974.0622 | >98 |
| CSP2(15)-I4LL9RF13LL14Q | 990.0469 | 990.0482 | >99 |
| CSP2(15)-I4LR6KL9RF13LL14Q | 960.0578 | 960.0545 | >95 |
| CSP2(15)-I4LI7FL9RF13LL14Q | 991.0530 | 991.0563 | >99 |
| CSP2(15)-I4LI8FL9RF13LL14Q | 991.0530 | 991.0568 | >98 |
| CSP2(15)-I4LL9RL12IF13LL14Q | 974.0608 | 974.0612 | >99 |

Table S-2. MS and HPLC data for CSP2 analogs.

| Compound Name | Calc. EM MH₂²⁺ | Obs. EM MH₂²⁺ | Purity (%) |
|--------------------------------|---|--|-----------------------|
| CSP2-E1AL9RL14Q | 1090.1452 | 1090.1468 | >99 |
| CSP2-E1AL9Rd10L14Q | 1090.1452 | 1090.1469 | >99 |
| CSP2-E1AI4LL9RL14Q | 1090.1452 | 1090.1475 | >99 |
| CSP2-E1AI4LL9Rd10L14Q | 1090.1452 | 1090.1448 | >96 |
| CSP2-E1AI4LL9RF13LL14Q | 1073.1531 | 1073.1548 | >98 |
| CSP2-E1AI4LL9Rd10F13LL14Q | 1073.1531 | 1073.1536 | >98 |
| CSP2-E1AI4LI8FL9RF13LL14Q | 1090.1452 | 1090.1415 | >95 |
| CSP2-E1AI4LI8FL9Rd10F13LL14Q | 1090.1452 | 1090.1475 | >98 |
| CSP2-E1AI4Nvad10 | 1054.1417 | 1054.1411 | >98 |
| CSP2-E1AI4Nled10 | 1061.1495 | 1061.1460 | >98 |
| CSP2-E1AI4HLeud10 | 1068.1573 | 1068.1591 | >99 |
| CSP2-E1AI4NvaI8FL9RF13LL14Q | 1083.1374 | 1083.1342 | >99 |
| CSP2-E1AI4NvaI8FL9Rd10F13LL14Q | 1083.1374 | 1083.1343 | >99 |
| CSP2-E1AI4NvaI8Fd10 | 1071.1339 | 1071.1326 | >96 |
| CSP2-E1AI4NvaL9Rd10 | 1075.6502 | 1075.6531 | >99 |
| CSP2-E1AI4Nvad10F13L | 1037.1495 | 1037.1521 | >99 |
| CSP2-E1AI4Nvad10L14Q | 1061.6189 | 1061.6192 | >99 |
| CSP2-E1AI4NvaI8FL9Rd10 | 1092.1384 | 1092.1370 | >99 |
| CSP2-E1AI4NvaI8Fd10F13L | 1054.1417 | 1054.1432 | >96 |
| CSP2-E1AI4NvaI8Fd10L14Q | 1078.6211 | 1078.6198 | >96 |
| CSP2-E1AI4NvaL9Rd10F13L | 1058.6580 | 1058.6596 | >99 |
| CSP2-E1AI4NvaL9Rd10L14Q | 1083.1374 | 1083.1358 | >99 |
| CSP2-E1AI4Nvad10F13LL14Q | 1044.6367 | 1044.6340 | >96 |
| CSP2-E1AI4NvaI8FL9Rd10L14Q | 1100.1296 | 1100.1308 | >98 |
| CSP2-E1AI4NvaI8FL9Rd10F13L | 1054.6501 | 1054.6525 | >99 |
| CSP2-E1Ad10L14Q | 1068.6367 | 1068.6392 | >99 |
| CSP2-E1AI4Ld10L14Q | 1068.6367 | 1068.6395 | >99 |

Bioassay Initial Screening Results

S. pneumoniae D39pcomX::lacZ (ComD1)

Agonism assays were performed at 10 μ M concentration. CSP1 was used as the positive control (100%) while DMSO as the negative control (0%). Percent (%) *comX* activation was measured by normalizing the Miller units obtained for each peptide to that of CSP1. All peptides were screened in triplicates over three separate trials. Error bars indicate standard error of the mean of nine values.

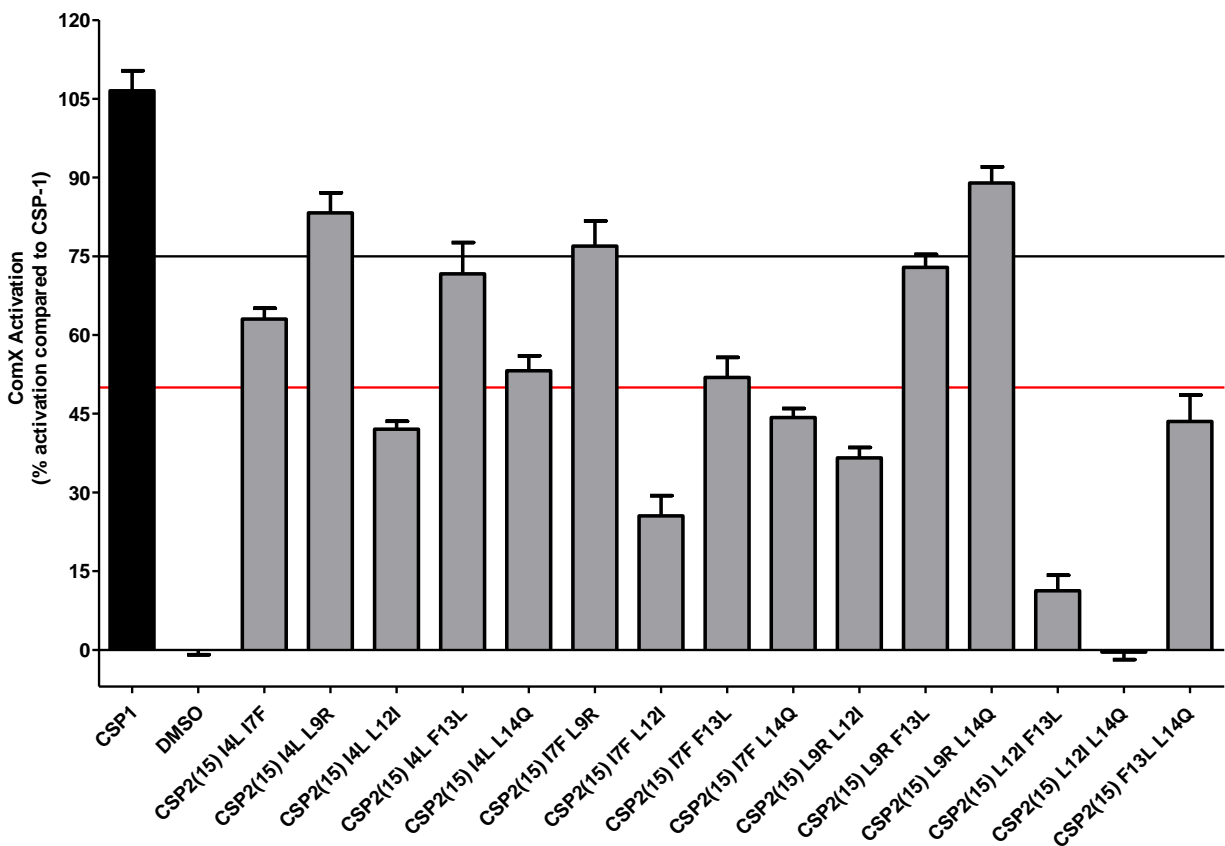


Figure S-1. Primary agonism screening assay data for the CSP2(15) double mutation library. Peptides that exhibited over 75% activation were further evaluated to determine their EC₅₀ while peptides that exhibited less than 50% activation were evaluated as potential competitive inhibitors.

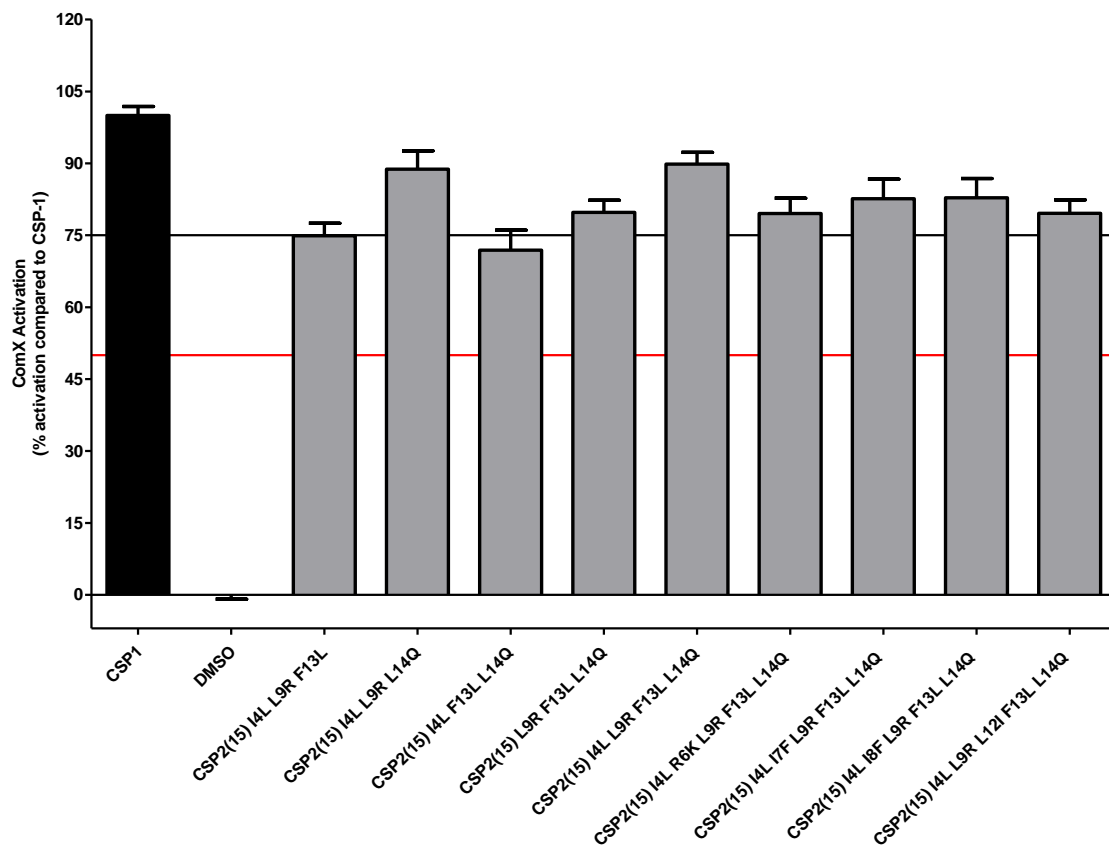


Figure S-2. Primary agonism screening assay data for the CSP2(15) triple, quadruple and quintuple mutation library. Peptides that exhibited over 75% activation were further evaluated to determine their EC₅₀.

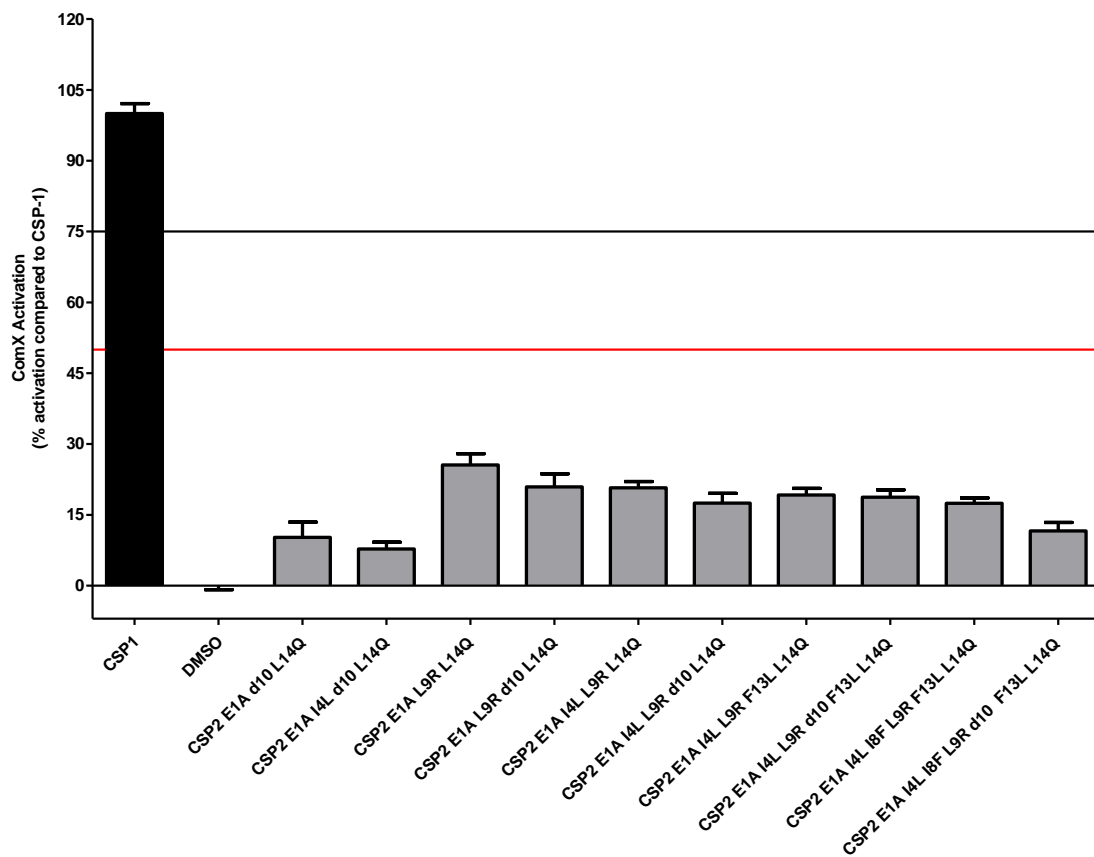


Figure S-3. Primary agonism screening assay data for the CSP2 E1A and d10 modification library. Peptides that exhibited less than 50% activation were evaluated as potential competitive inhibitors.

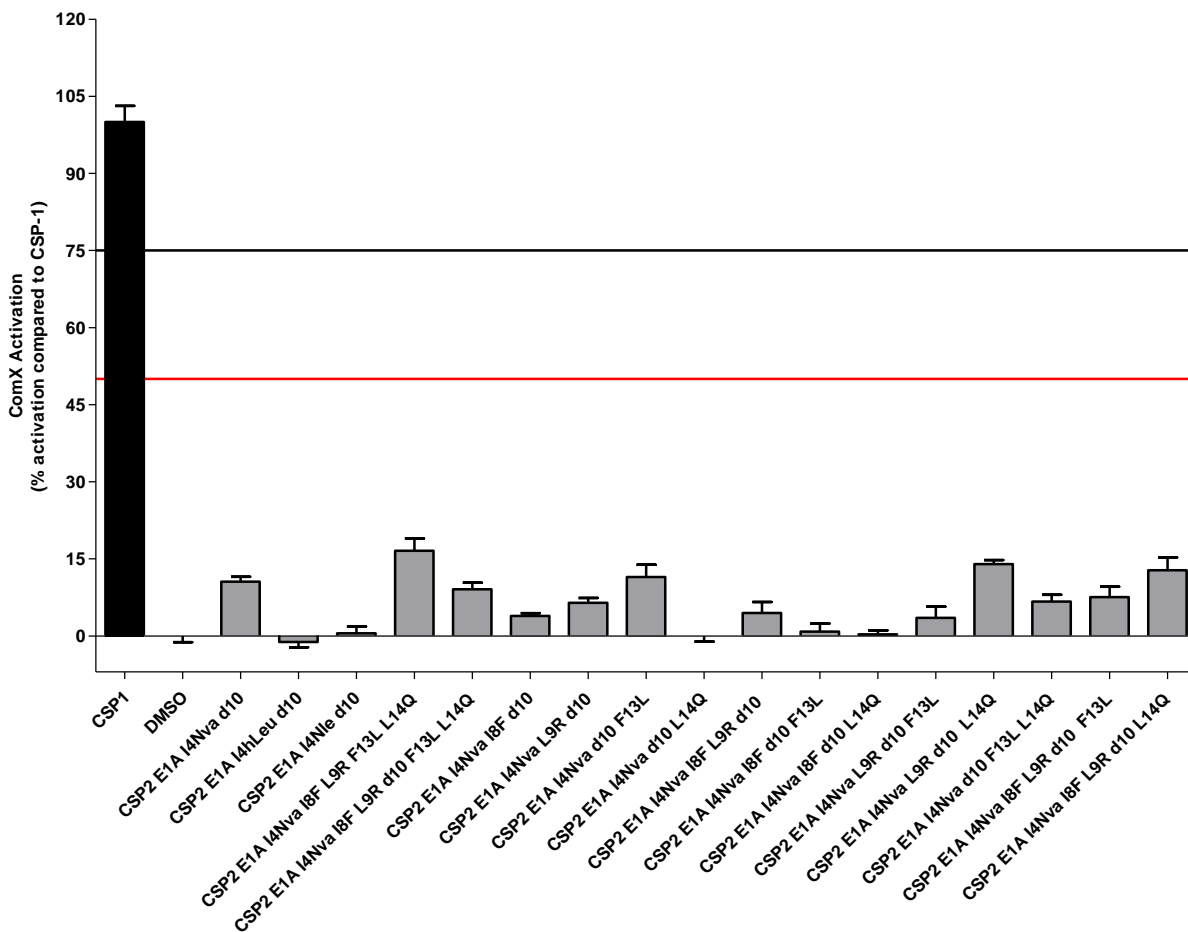


Figure S-4. Primary agonism screening assay data for the CSP2 non-proteogenic modification library. Peptides that exhibited less than 50% activation were evaluated as potential competitive inhibitors.

Antagonism assays were performed at 10 μ M concentration of peptides against 50 nM concentration of CSP1. CSP1 (50 nM) was used as the positive control (100%) while DMSO as the negative control (0%). Percent (%) *comX* activation was measured by normalizing the Miller units obtained for each peptide to that of CSP1. All peptides were screened in triplicates over three separate trials. Error bars indicate standard error of the mean of nine values.

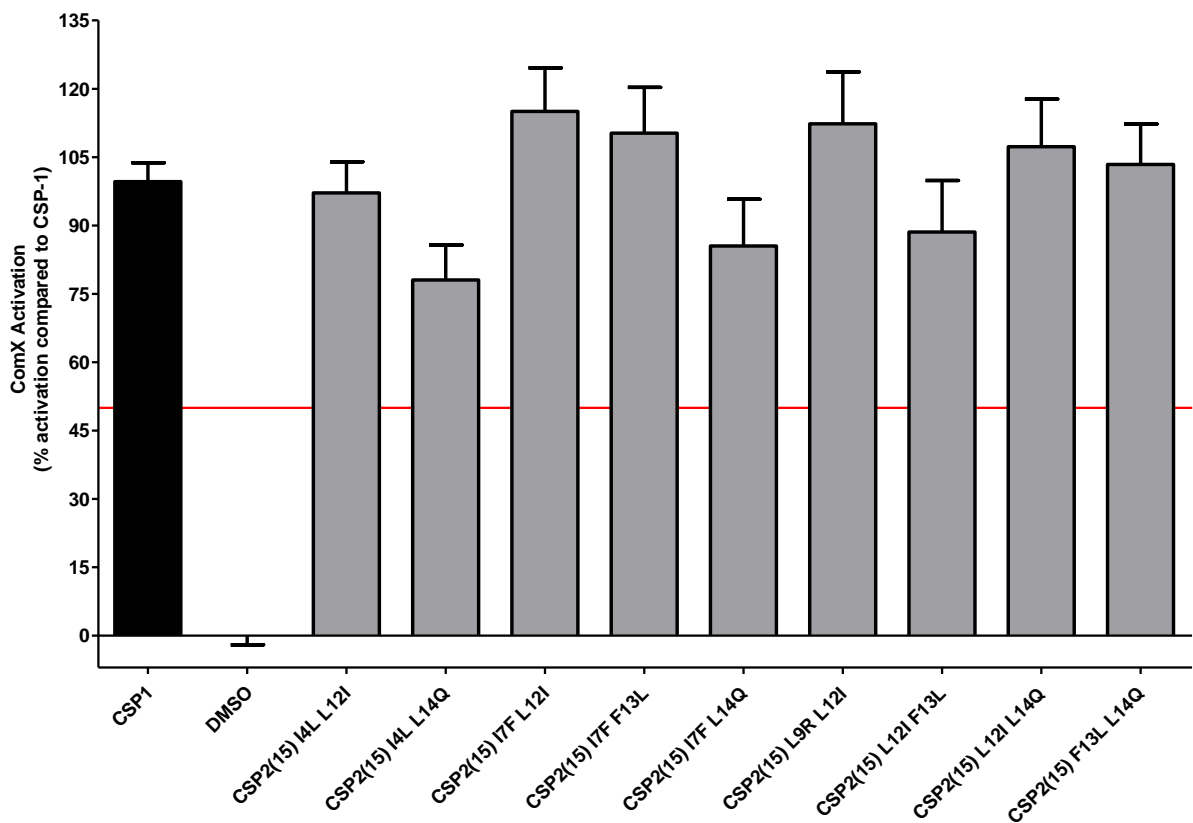


Figure S-5. Primary antagonism screening assay data for the CSP2(15) double mutation library. None of the analogs exhibited less than 50% activation.

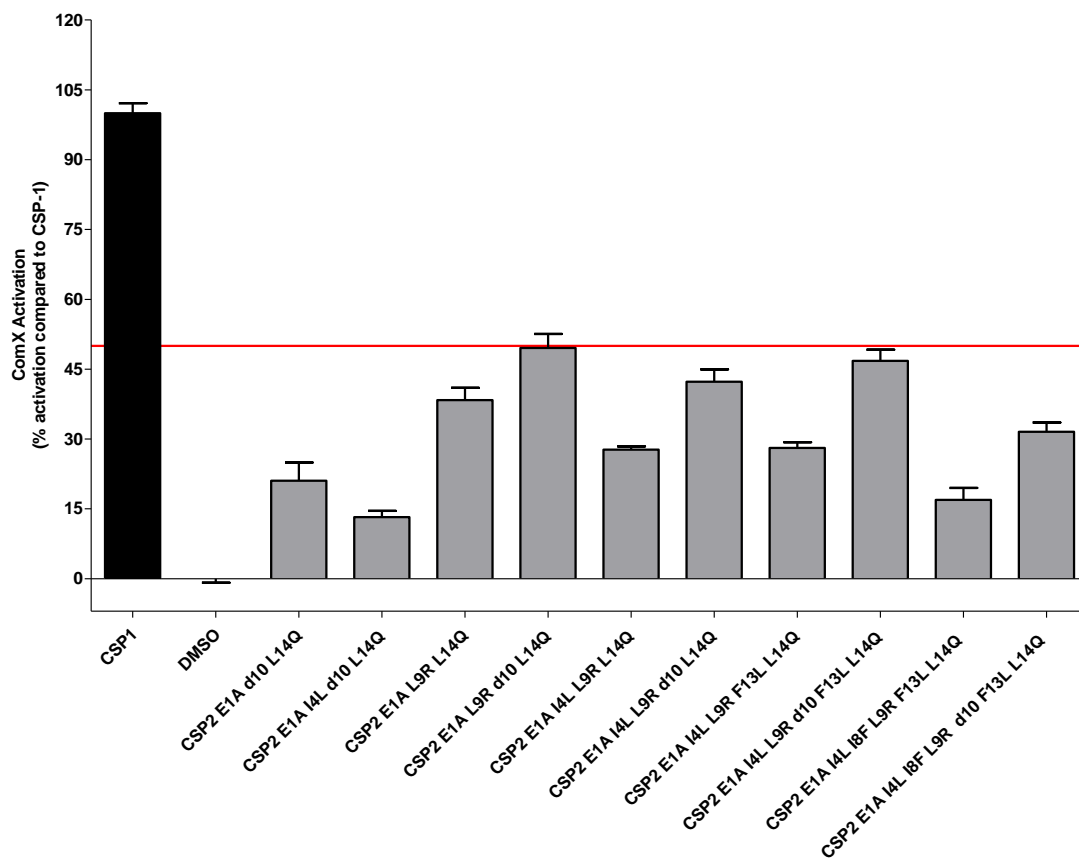


Figure S-6. Primary antagonism screening assay data for the CSP2 E1A and d10 modification library. Peptides that exhibited less than 50% activation were further evaluated to determine their IC_{50} .

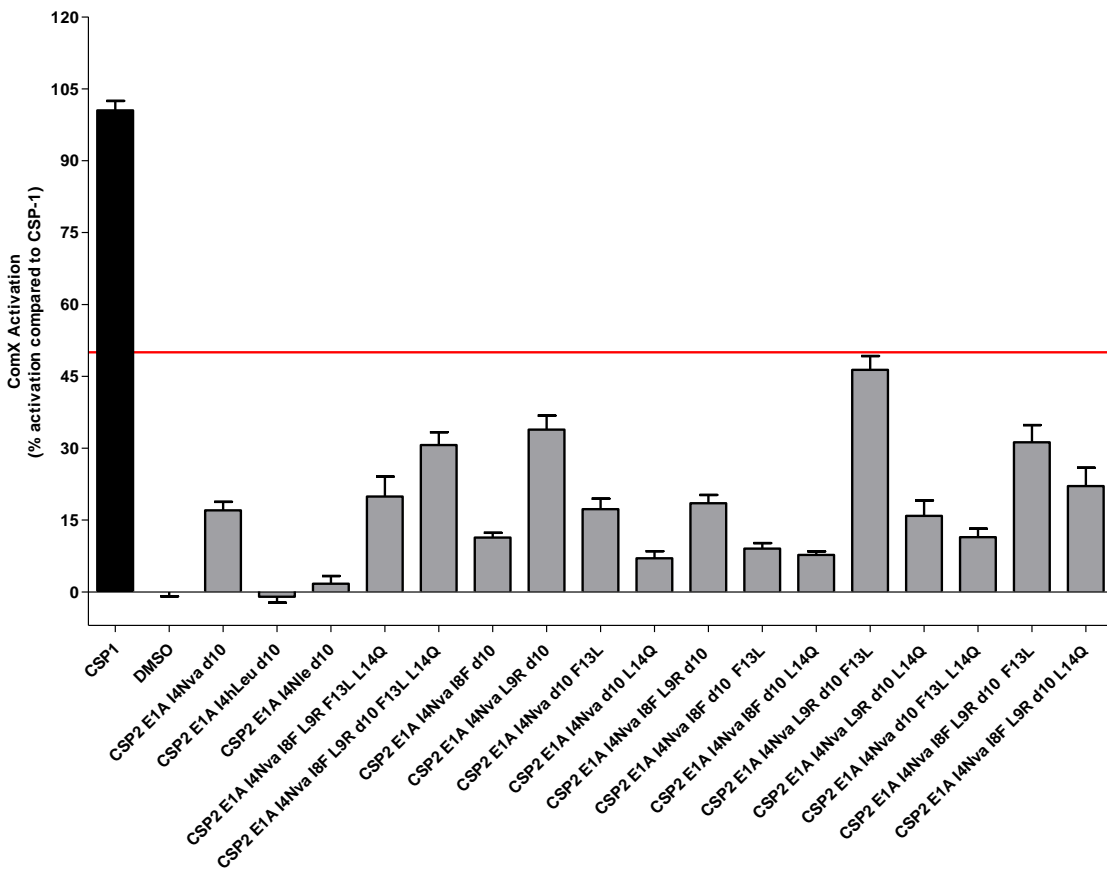


Figure S-7. Primary antagonism screening assay data for the non-proteogenic modification of CSP2 libraries. Peptides that exhibited less than 50% activation were further evaluated to determine their IC₅₀.

***S. pneumoniae* TIGR4pcomX::lacZ (ComD2)**

Agonism assays were performed at 10 μ M concentration. CSP2 was used as the positive control (100%) while DMSO as the negative control (0%). Percent (%) *comX* activation was measured by normalizing the Miller units obtained for each peptide to that of CSP2. All peptides were screened in triplicates over three separate trials. Error bars indicate standard error of the mean of nine values.

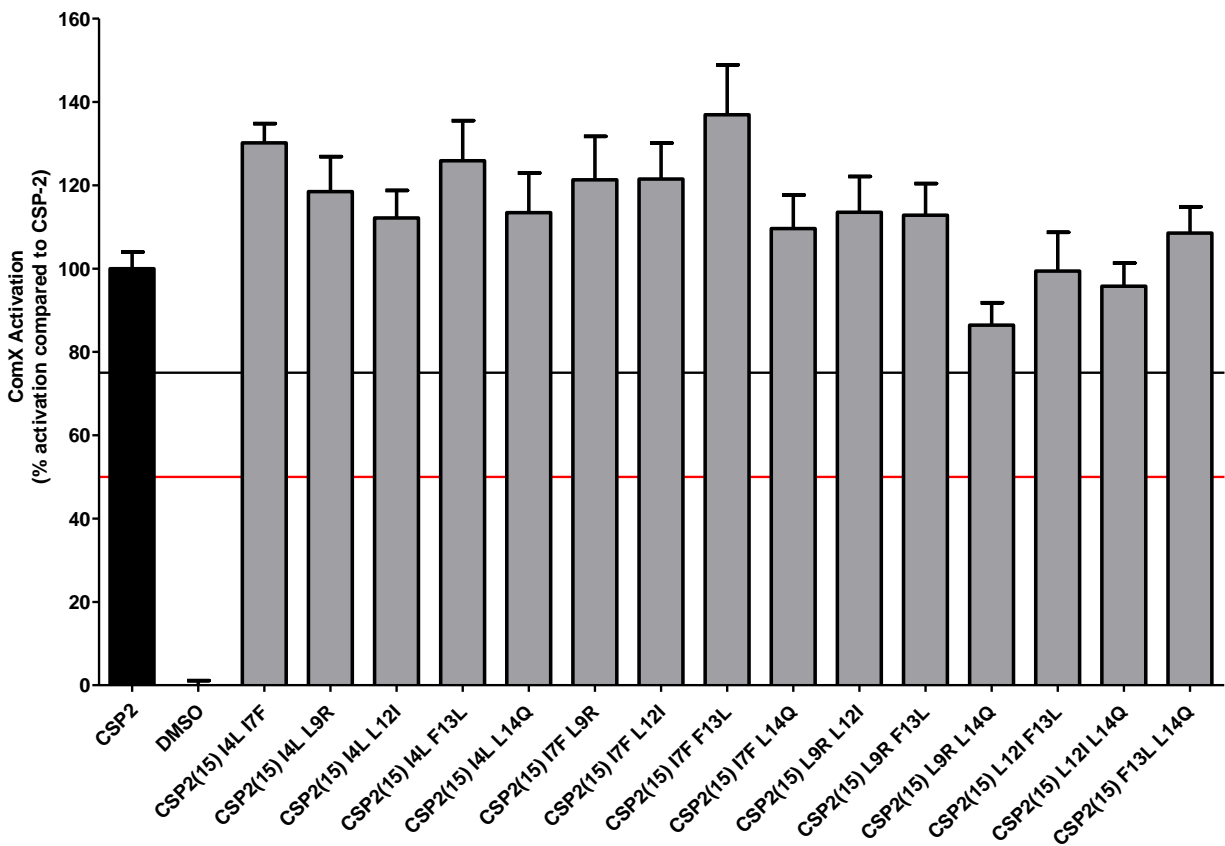


Figure S-8. Primary agonism screening assay data for the CSP2(15) double mutation library. Peptides that exhibited over 75% activation were further evaluated to determine their EC₅₀.

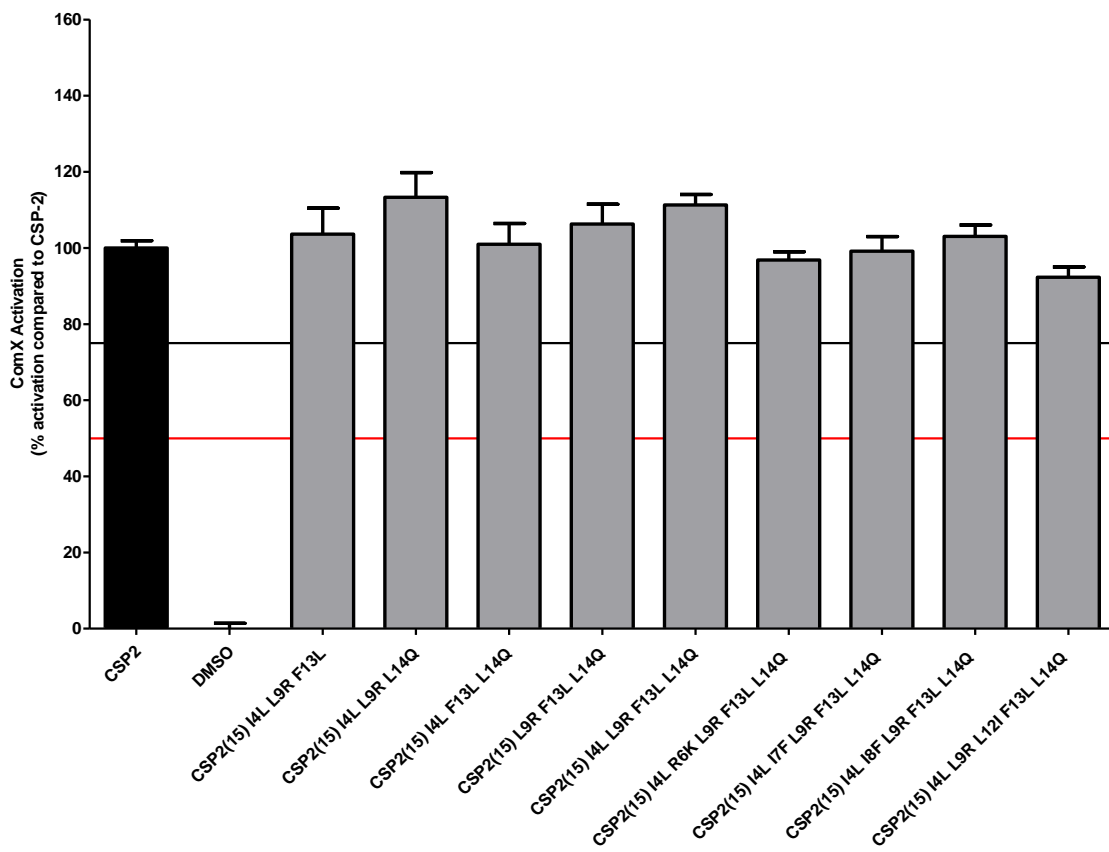


Figure S-9. Primary agonism screening assay data for the CSP2(15) triple, quadruple and quintuple mutation library. Peptides that exhibited over 75% activation were further evaluated to determine their EC₅₀.

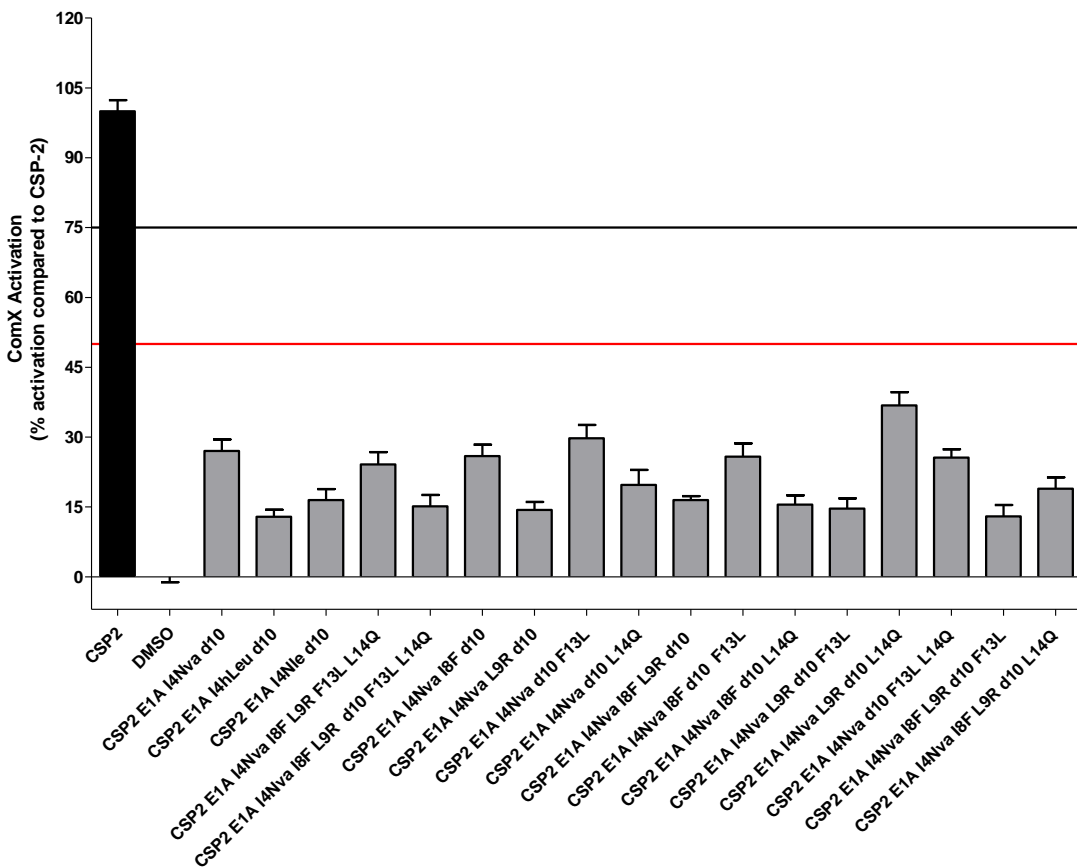


Figure S-10. Primary agonism screening assay data for the CSP2 non-proteogenic modification library. Peptides that exhibited less than 50% activation were evaluated as potential competitive inhibitors.

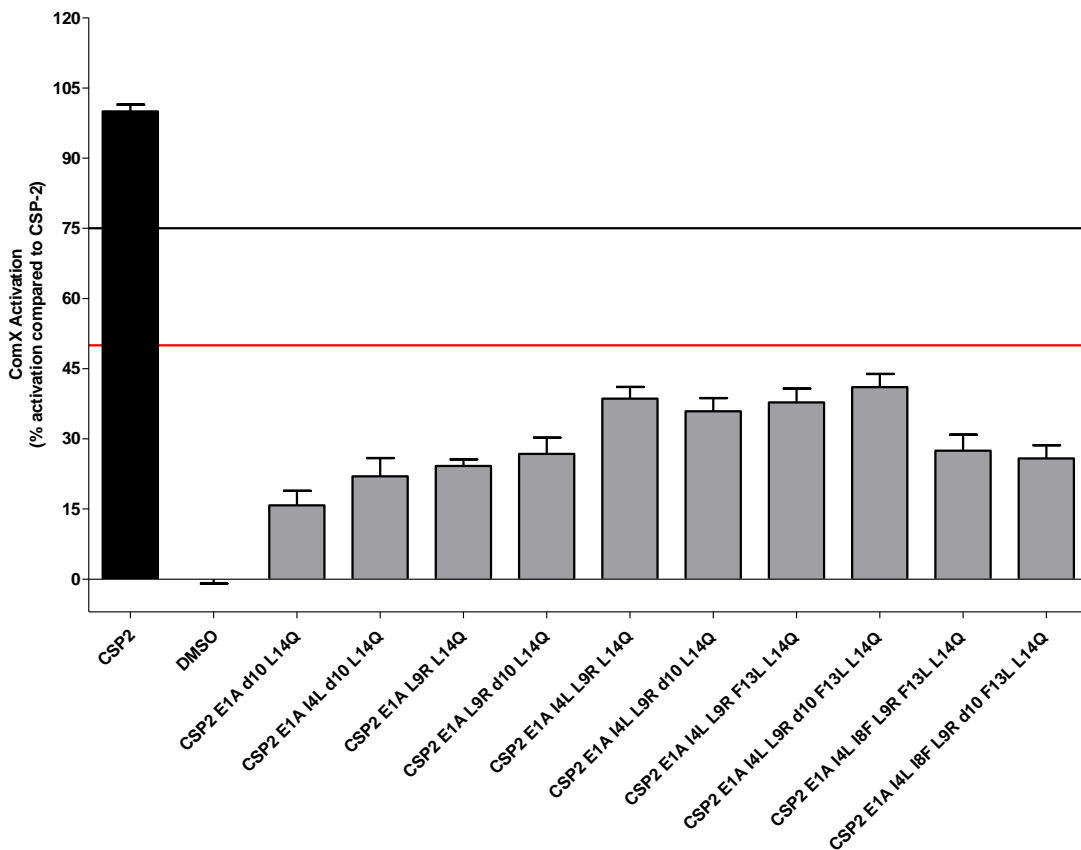


Figure S-11. Primary agonism screening assay data for the CSP2 E1A and d10 modification library. Peptides that exhibited less than 50% activation were evaluated as potential competitive inhibitors.

Antagonism assays were performed at 10 μ M concentration of peptides against 250 nM concentration of CSP2. CSP2 (250 nM) was used as the positive control (100%) while DMSO as the negative control (0%). Percent (%) *comX* activation was measured by normalizing the Miller units obtained for each peptide to that of CSP2. All peptides were screened in triplicates over three separate trials. Error bars indicate standard error of the mean of nine values.

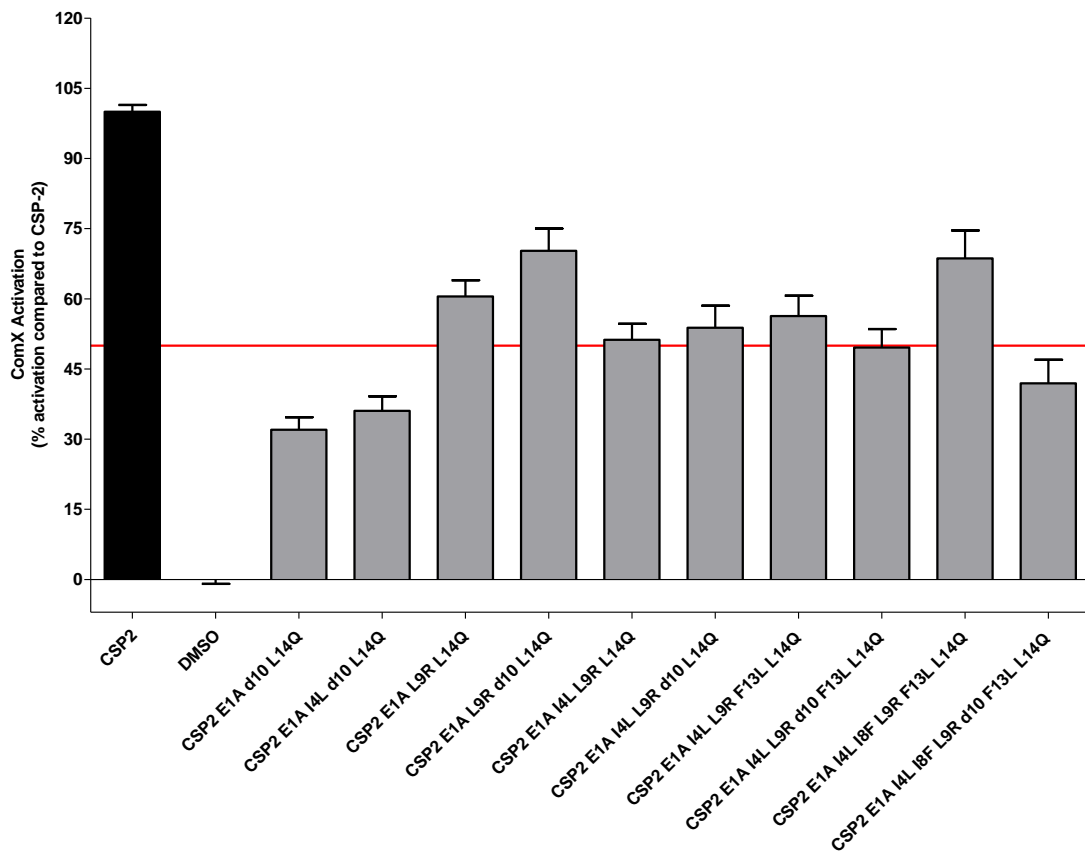


Figure S-12. Primary antagonism screening assay data for the CSP2 E1A and d10 modification library. Peptides that exhibited less than 50% activation were further evaluated to determine their IC₅₀.

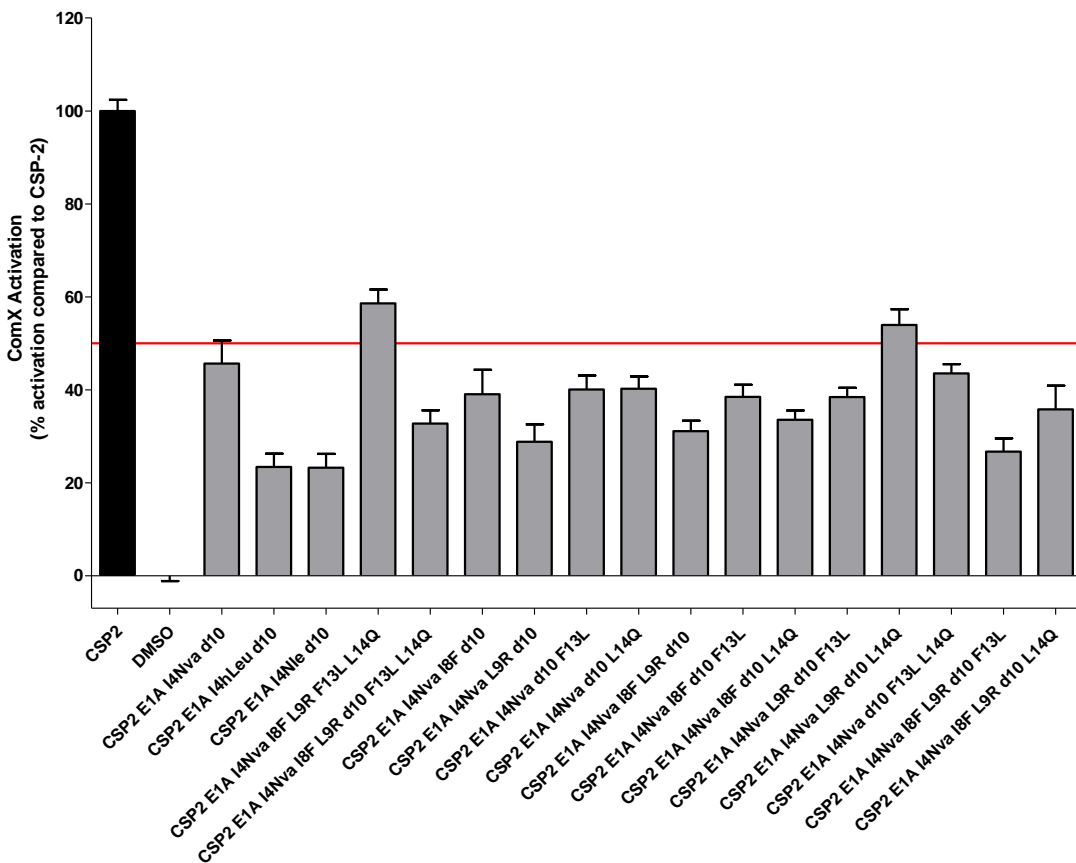
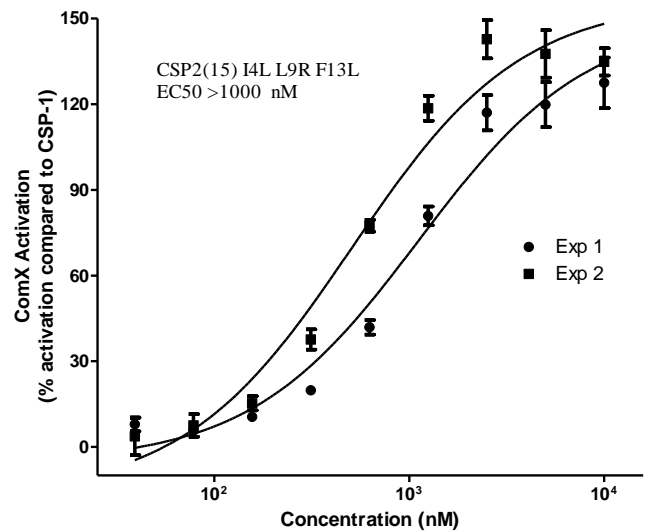
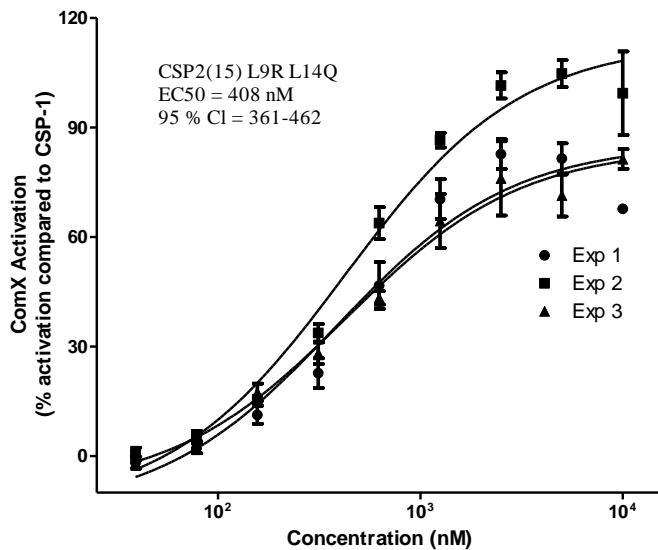
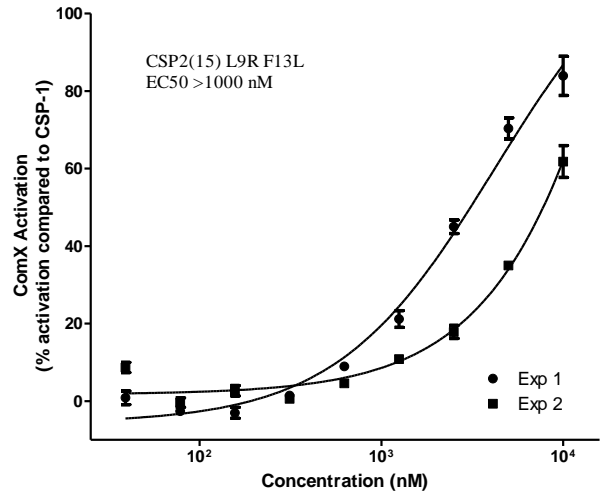
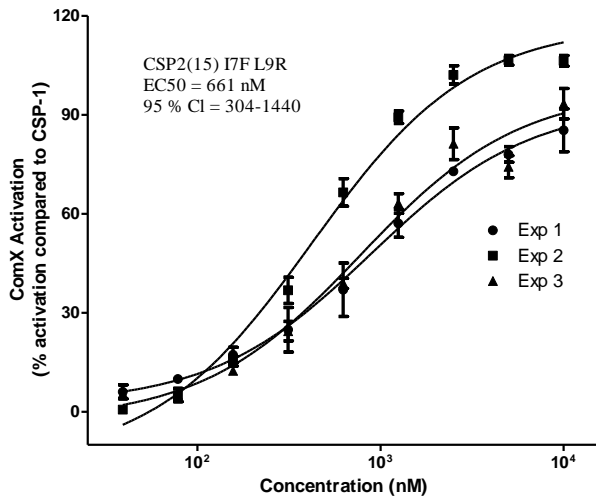
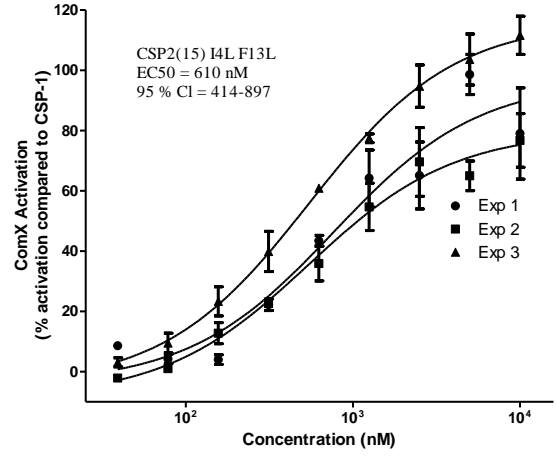
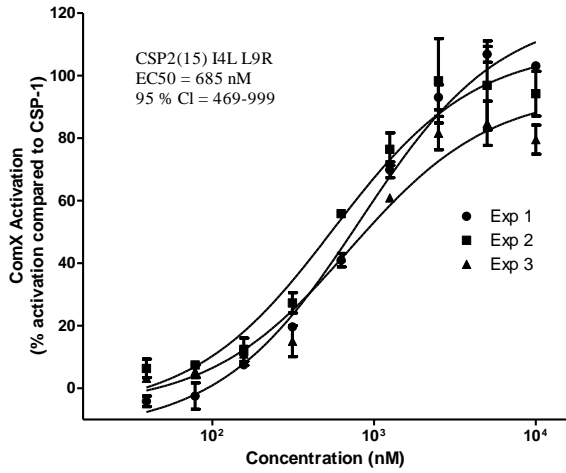
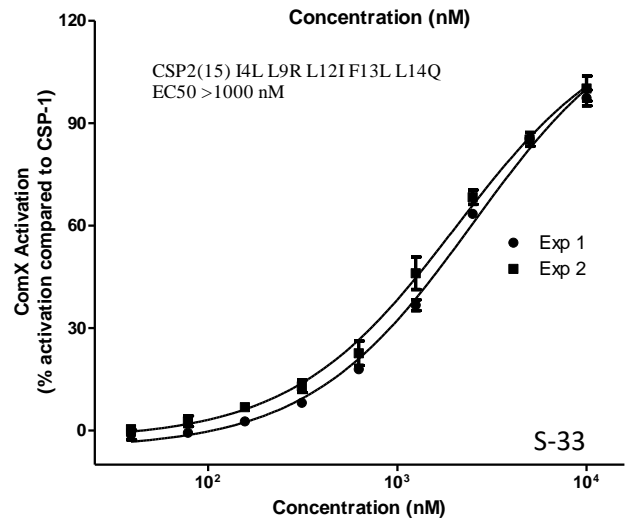
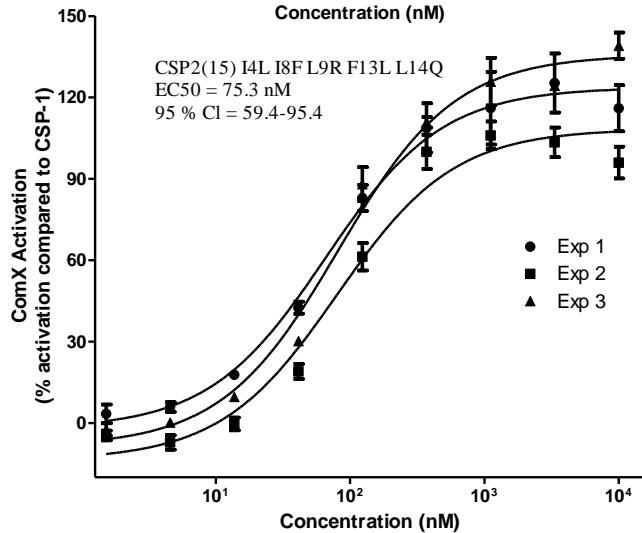
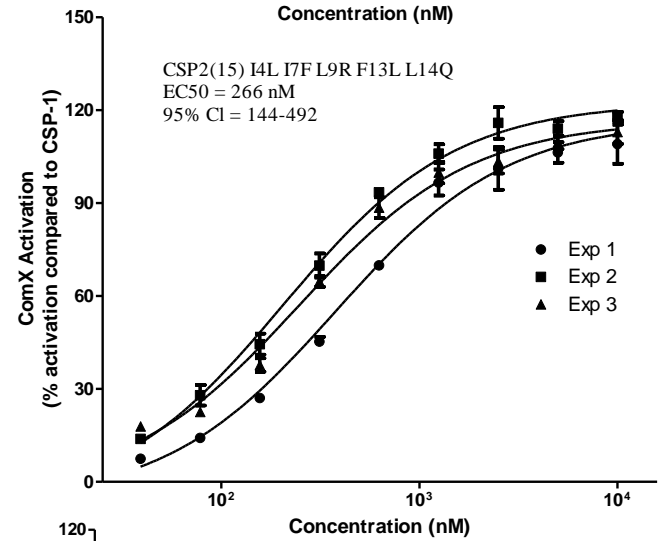
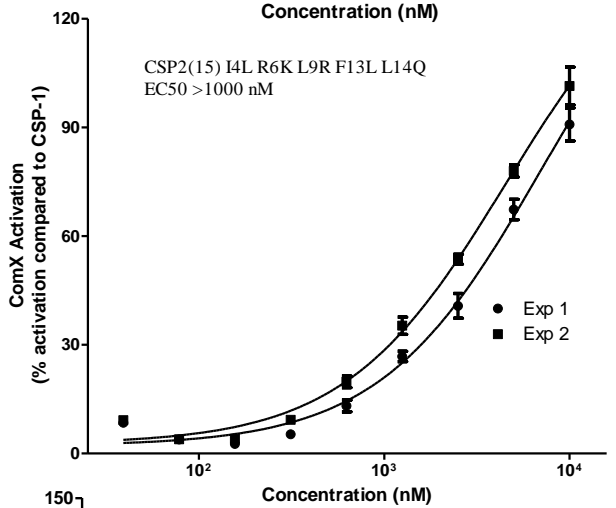
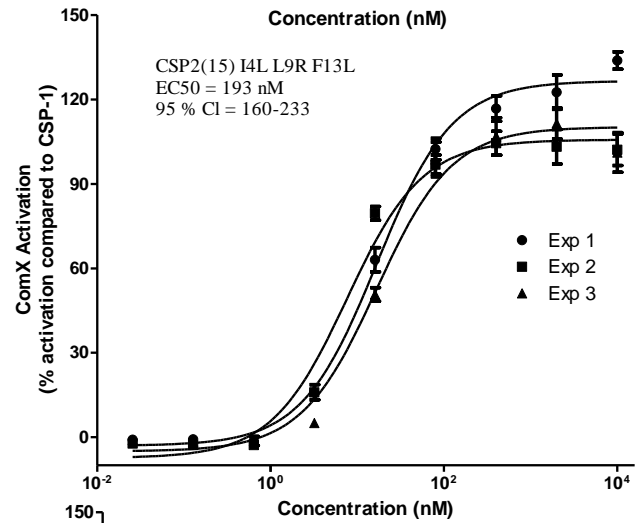
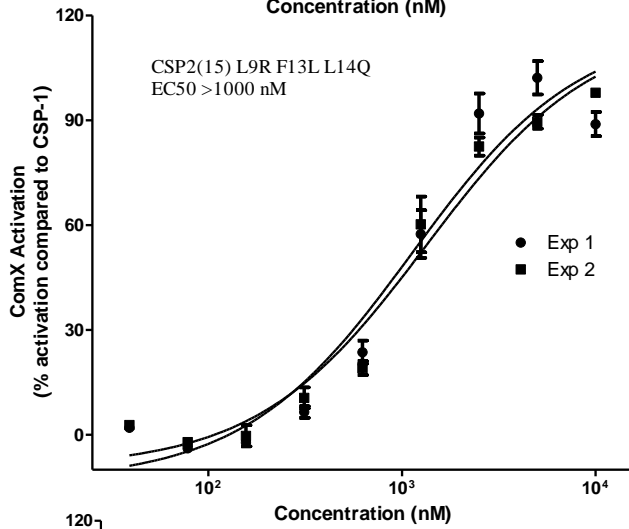
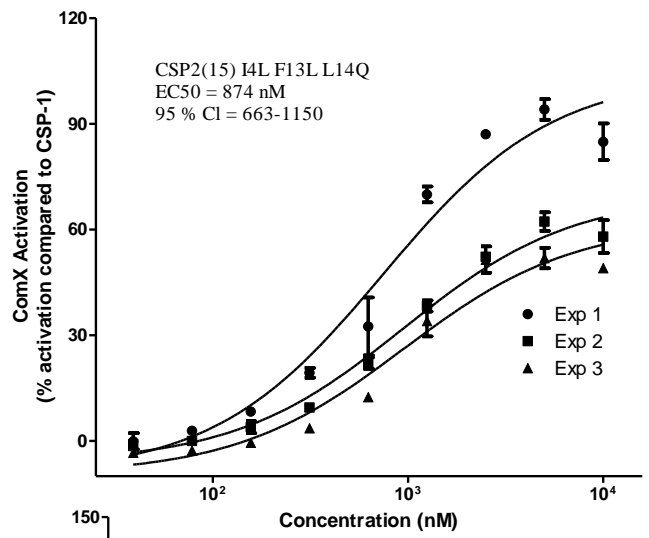
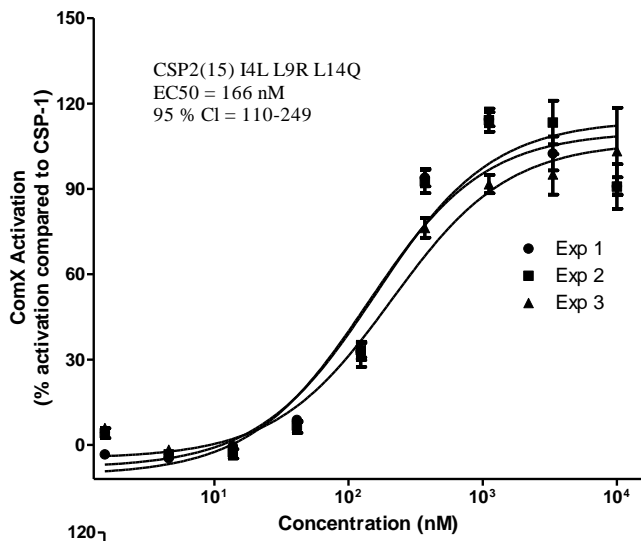


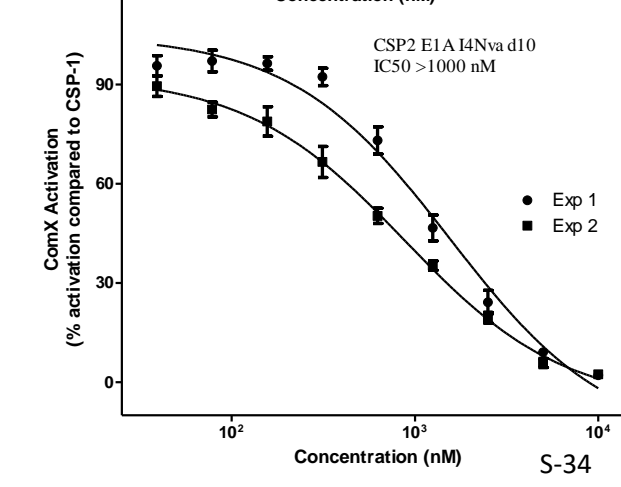
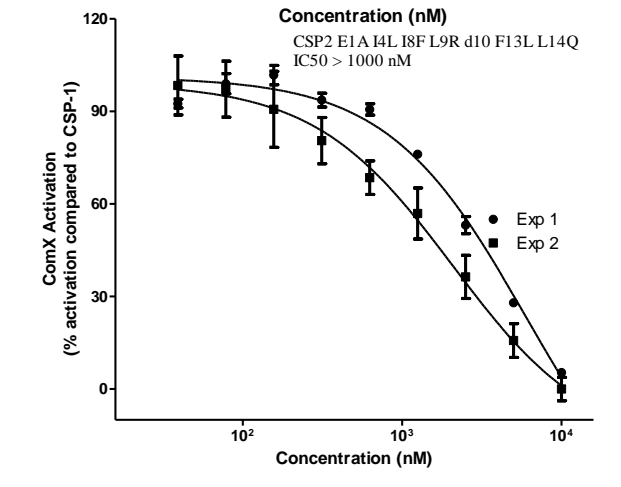
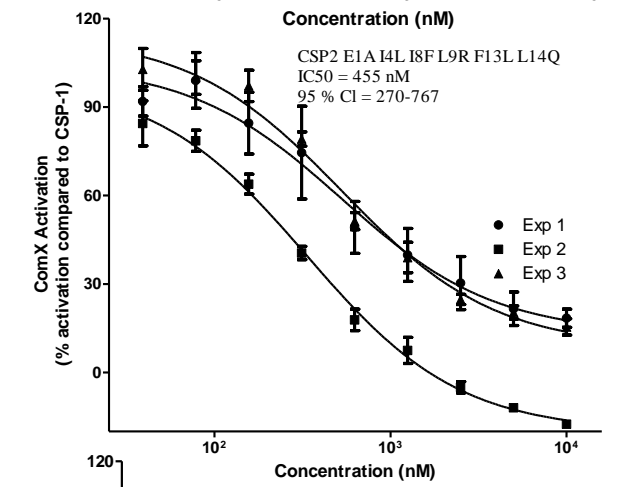
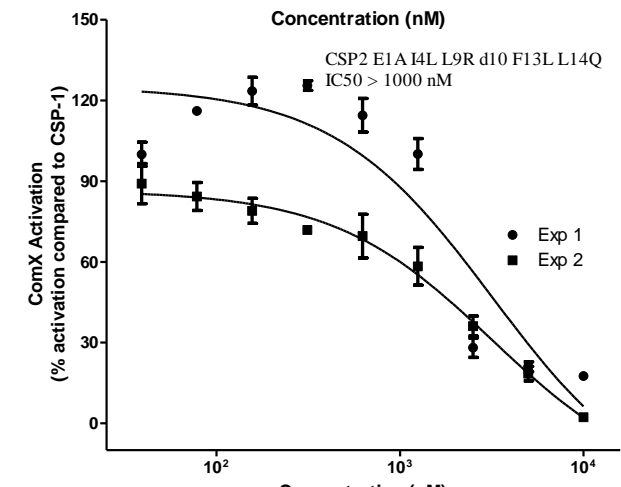
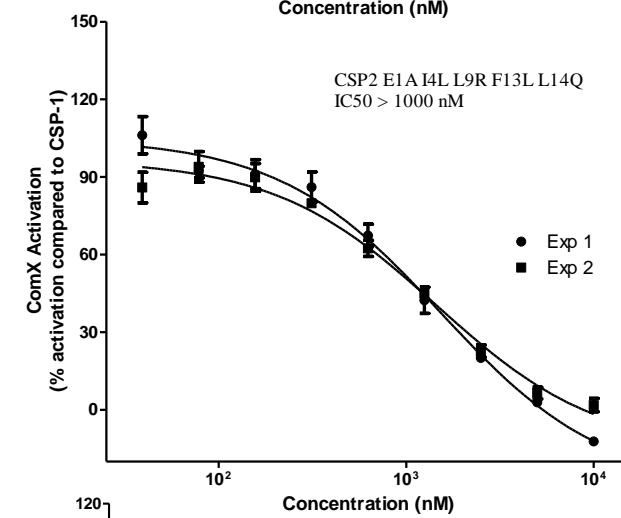
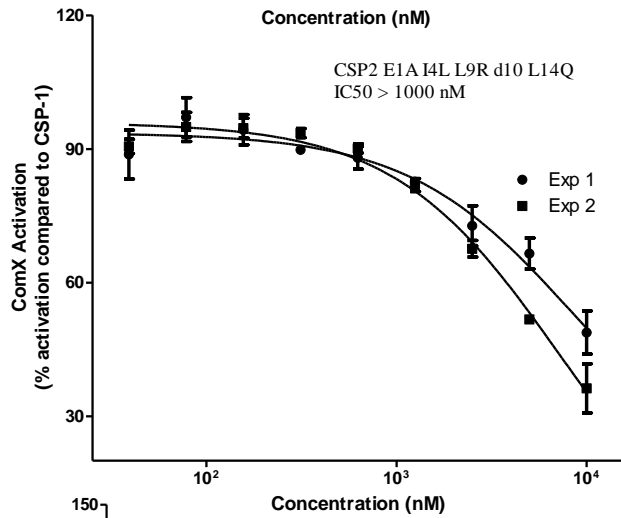
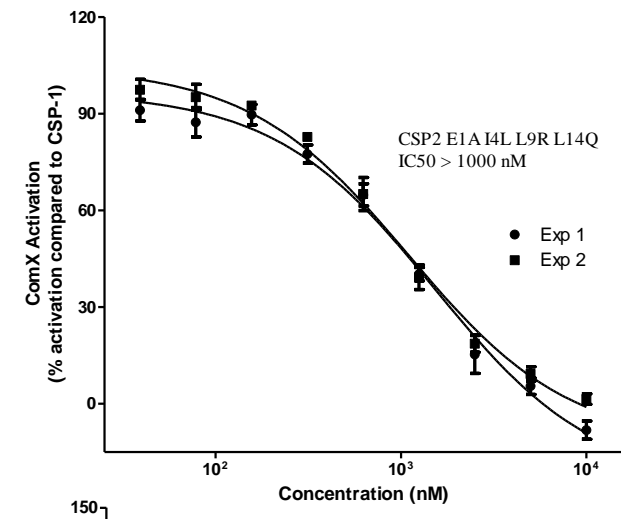
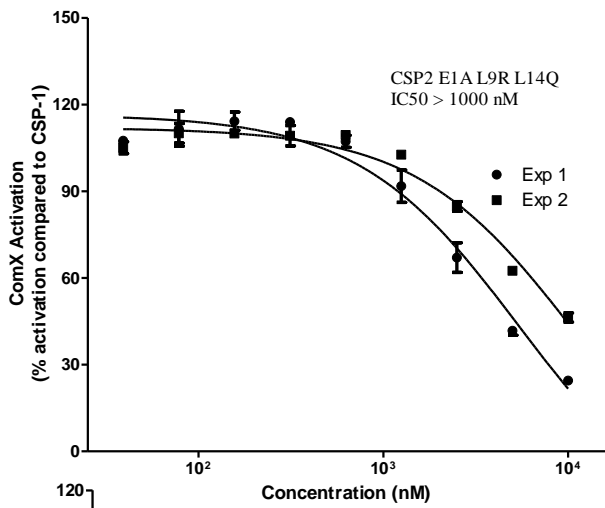
Figure S-13. Primary antagonism screening assay data for the CSP2 non-proteogenic modification library. Peptides that exhibited less than 50% activation were further evaluated to determine their IC₅₀.

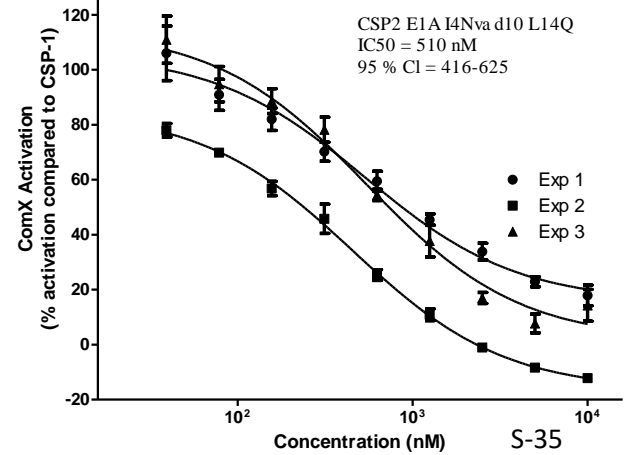
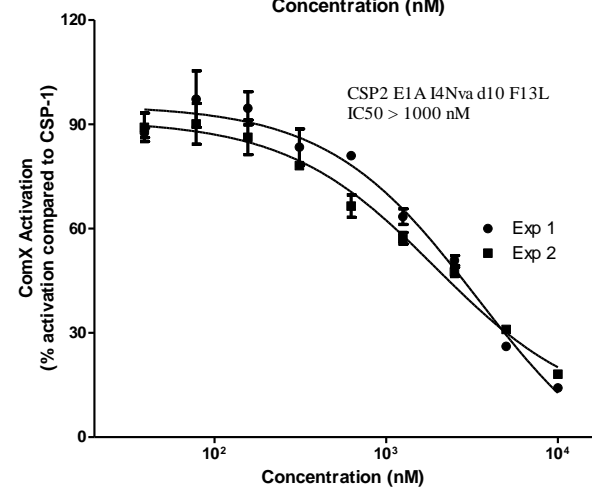
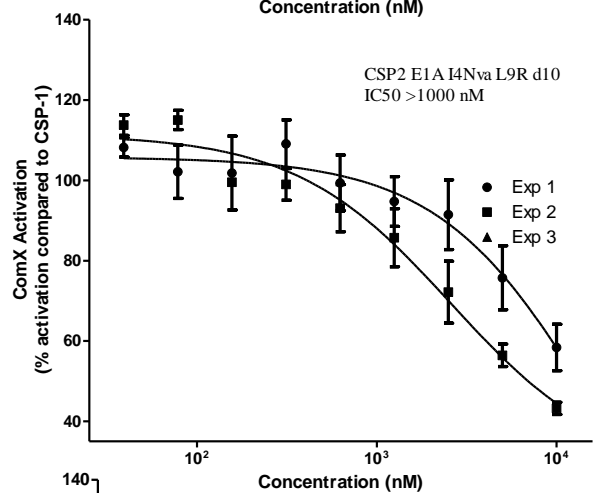
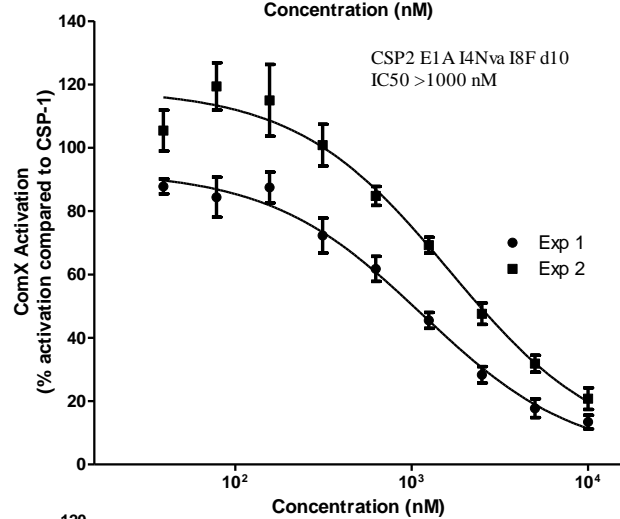
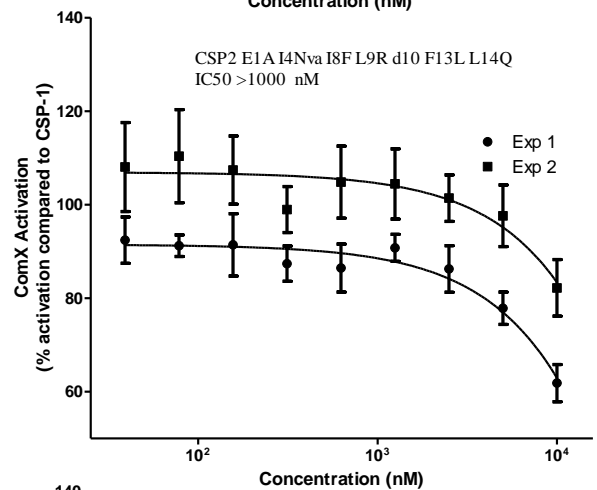
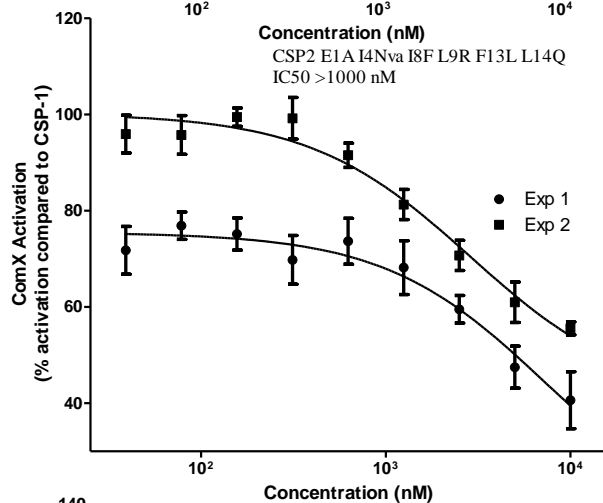
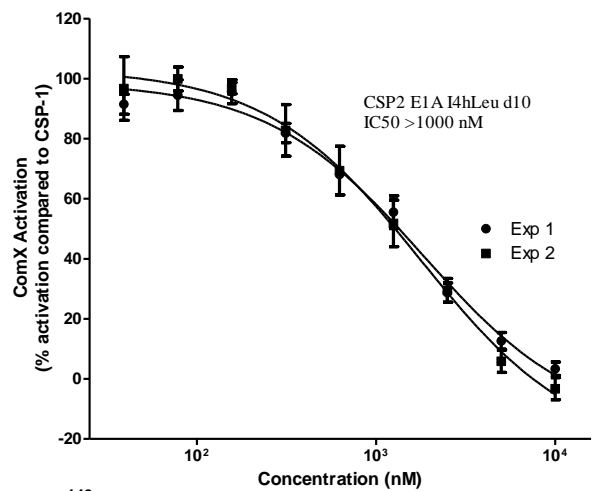
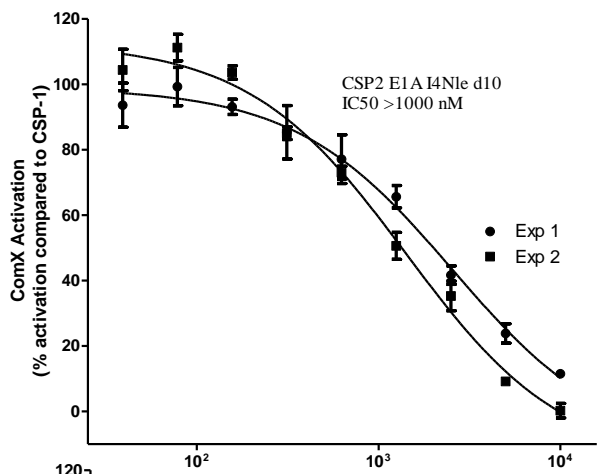
Dose Response Curves

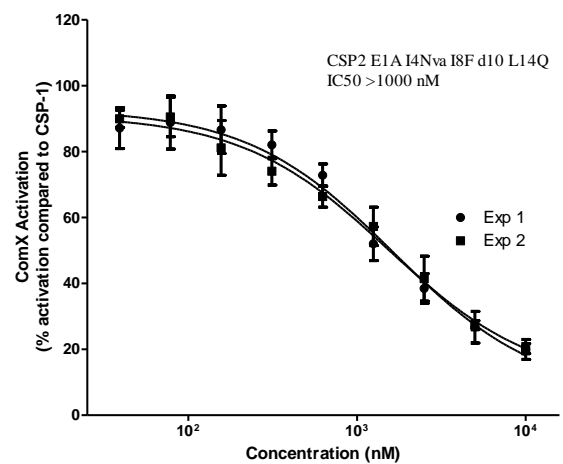
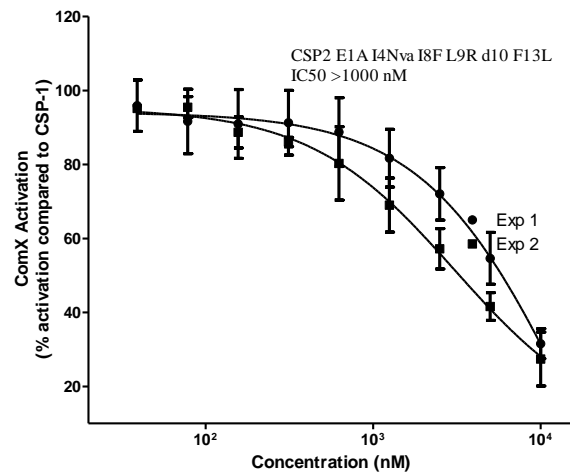
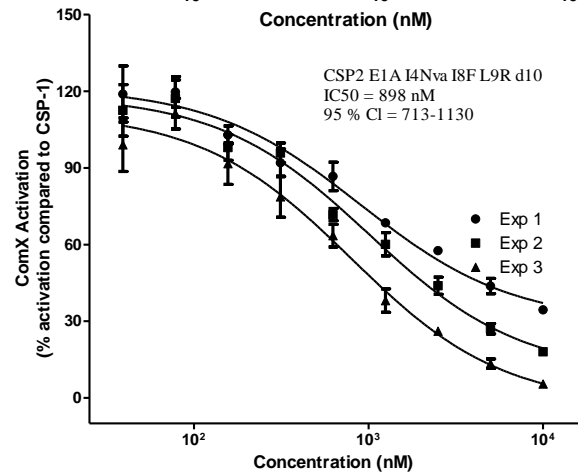
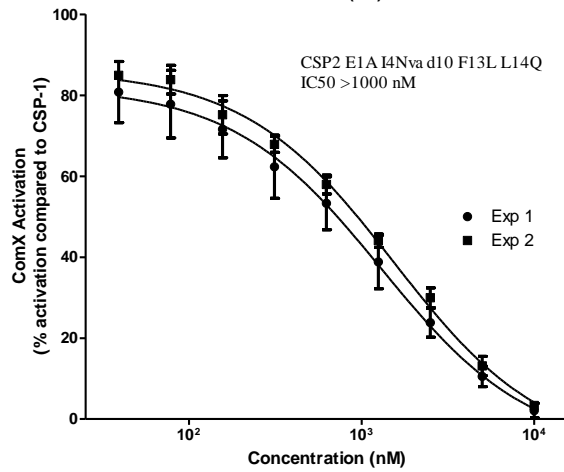
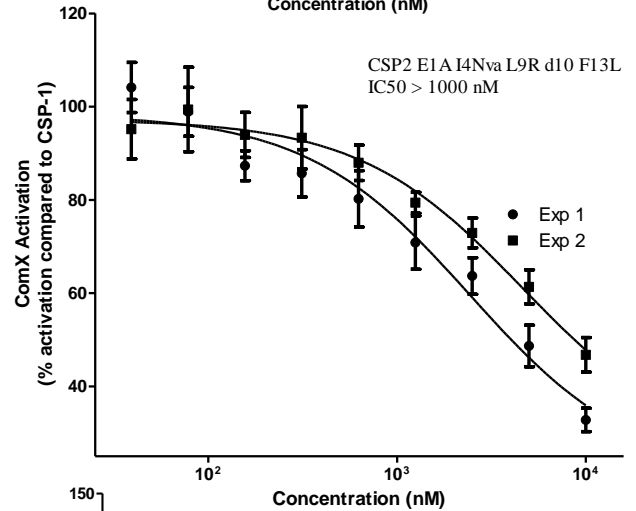
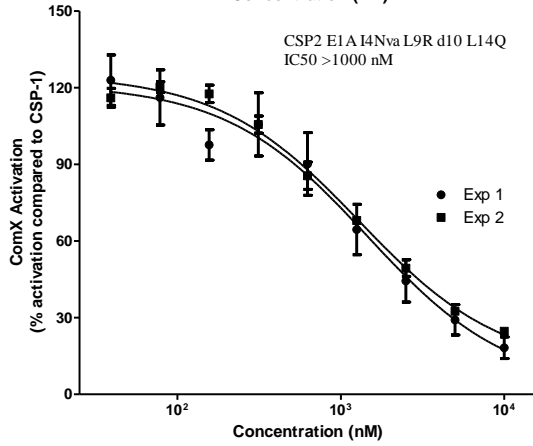
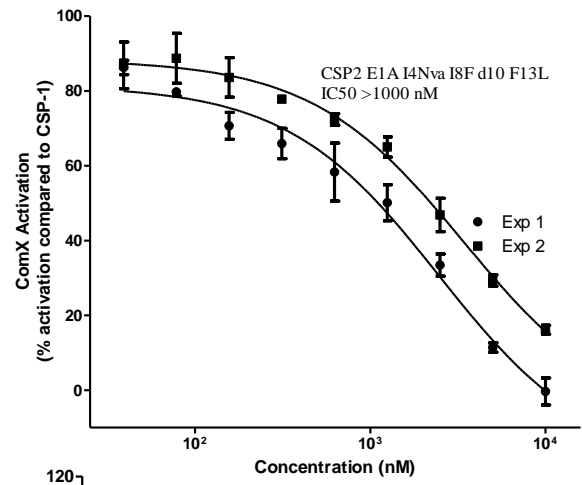
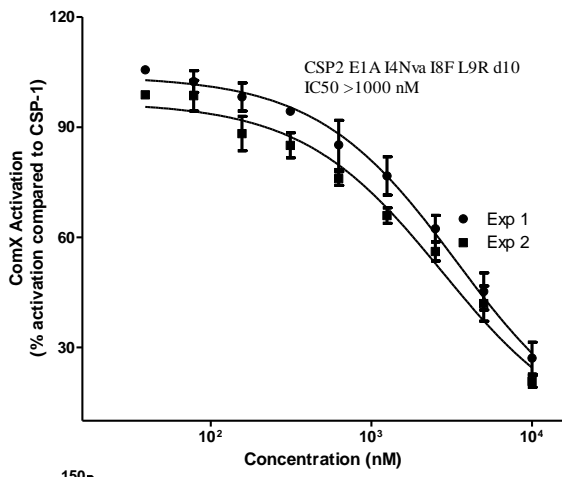
S. pneumoniae D39pcomX::lacZ (ComD1)

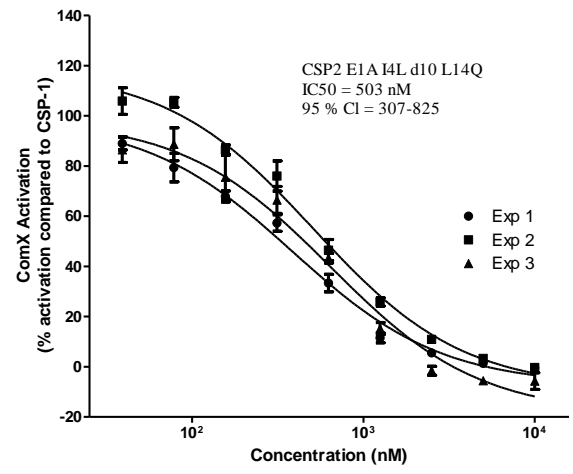
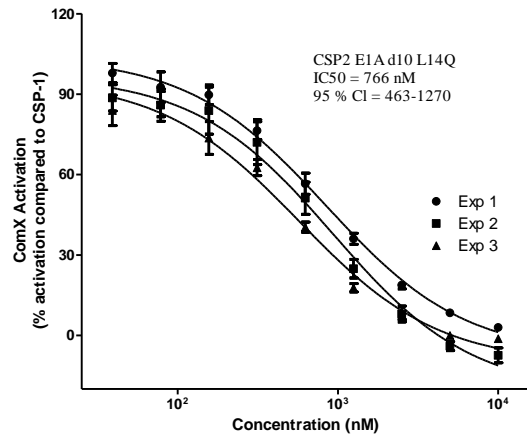












S. pneumoniae TIGR4pcomX::lacZ (ComD2)

