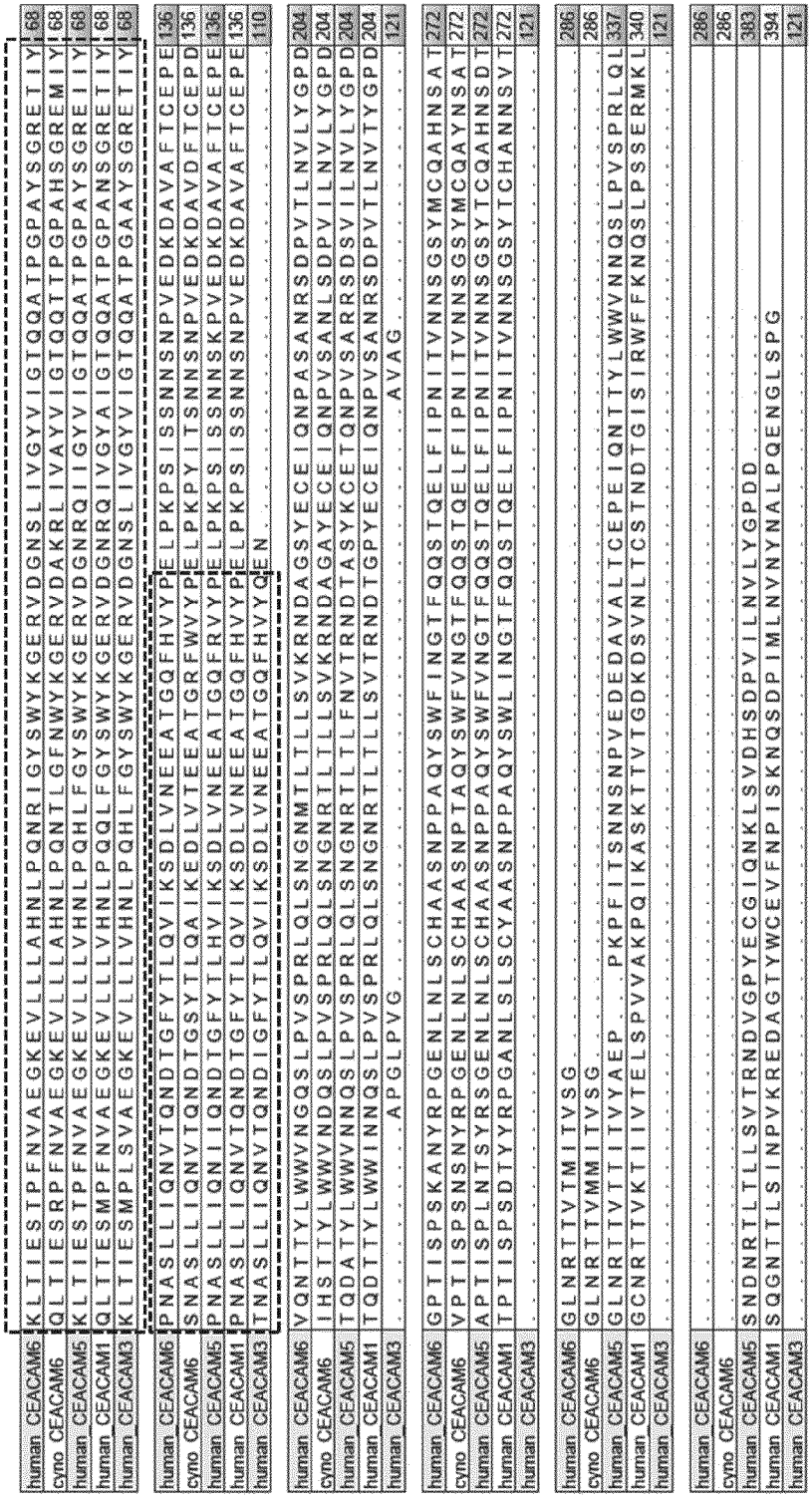
Fig. 1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cyno_CEACAM6
human_CEACAM5
human_CEACAM1
human_CEACAM3

Fig. 2

>TPP-2971_VL

DIVMTQSQKFMSTSVGDRVSITC***KASQNVGTAVA***WYQQKPGQSPKLLIY***SASNRYT***
GVPDRFTGSGSGTDFTLTISNMQSEDLADYFC***QQYSSYPLT***FGAGTKLELK

>TPP-2971_VH

QVTLKESGPGILQPSQTLSLTCSFSGFSLS***TYGIGVG***WIRQPSGKDLEWLA***HIWWND***
NKY*YNTALKS*RLTISKDTSNNQVFLKIASVDTADTATYYCAR***ISLPYFDY***WGQGTTLTV
SS

>TPP-3187_VL

DIVMTQSQKFMSTSVGDRVSITC***KASQNVGTAVA***WYQQKPGQSPKLLIY***SASNRYT***
GVPDRFTGSGSGTDFTLTISNMQSEDLADYFC***QQYNNYPLT***FGAGTKLELK

>TPP-3187_VH

QVTLKESGPGILQPSQTLSLTCSFSGFSLT***TYGIGVG***WIRQPSGKGLEWLA***HIWWND***
NKY*YNTALKS*RLTISKDTSNNQVFLKIASVDTADTATYYCAR***ISLPYFDY***WGQGTTLTV
SS

Fig. 3

>TPP-3310_VL

DIQLTQSPSFLSASVGDRVTITC***KASQNVGTAVA***WYQQKPGKAPKLLIY***SASNRYT***G
VPSRFSGSGSGTEFTLTISSLQPEDFATYYC***QQYSSYPLT***FGGGTKVEIK

>TPP-3310_VH

QVTLRESGPALVKPTQTLTLTCTFSGFSLS***TYGIGVG***WIRQPPGKALEWLA***HIWWND***
NKY*YSTSLKT*RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR***ISLPYFDY***WGQGTTLT
VSS

>TPP-3714_VL

DIQLTQSPSFLSASVGDRVTITC***KASQNVGTAVA***WYQQKPGKAPKLLIY***SASNRYT***G
VPSRFSGSGSGTEFTLTISSLQPEDFATYYC***QQYSSYPLT***FGGGTKVEIK

>TPP-3714_VH

QVTLRESGPALVKPTQTLTLTCTFSGFSLS***TYGIGVG***WIRQPPGKALEWLA***HIWWND***
NKY*YSTSLKT*RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR***ISLPYFDY***WGQGTLVT
VSS

Fig. 4

>TPP-3820_VL

DIQLTQSPSFLSASVGDRVTITC***KASQNVGTAVA***WYQQKPGKAPKLLIY***SASNRYT***G
VPSRFSGSGSGTEFTLTISSLQPEDFATYYC***QQYNNYPLT***FGGGTKVEIK

>TPP-3820_VH

QVTLRESGPALVKPTQTLTLTCTFSGFSLT***TYGIGVG***WIRQPPGKGLEWLA***HIWWND***
NKY*YSTSLKT*RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR***ISLPYFDY***WGQGTLVT
VSS

>TPP-3821_VL

DIQLTQSPSFLSASVGDRVTITC***KASQNVGTAVA***WYQQKPGKAPKLLIY***SASNRYT***G
VPSRFSGSGSGTEFTLTISSLQPEDFATYYC***QQYNNYPLT***FGGGTKVEIK

>TPP-3821_VH

QVTLRESGPALVKPTQTLTLTCTFSGFSLS***TYGIGVG***WIRQPPGKALEWLA***HIWWND***
NKY*YSTSLKT*RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR***ISLPYFDY***WGQGTLVT
VSS

Fig. 5

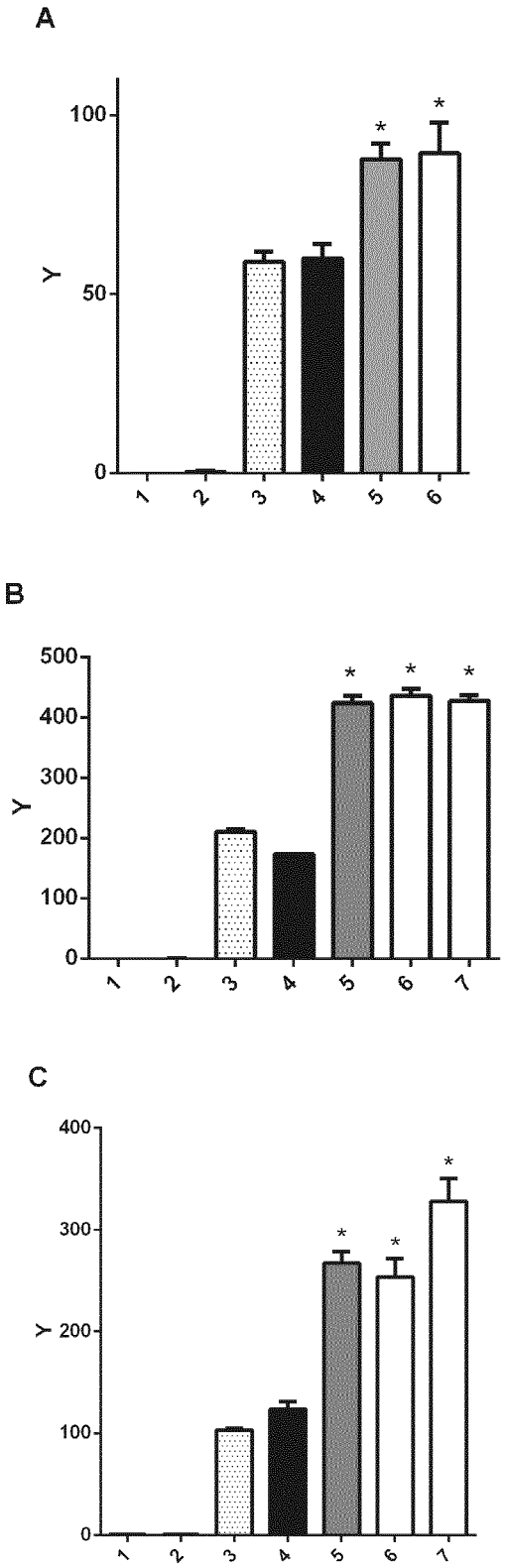
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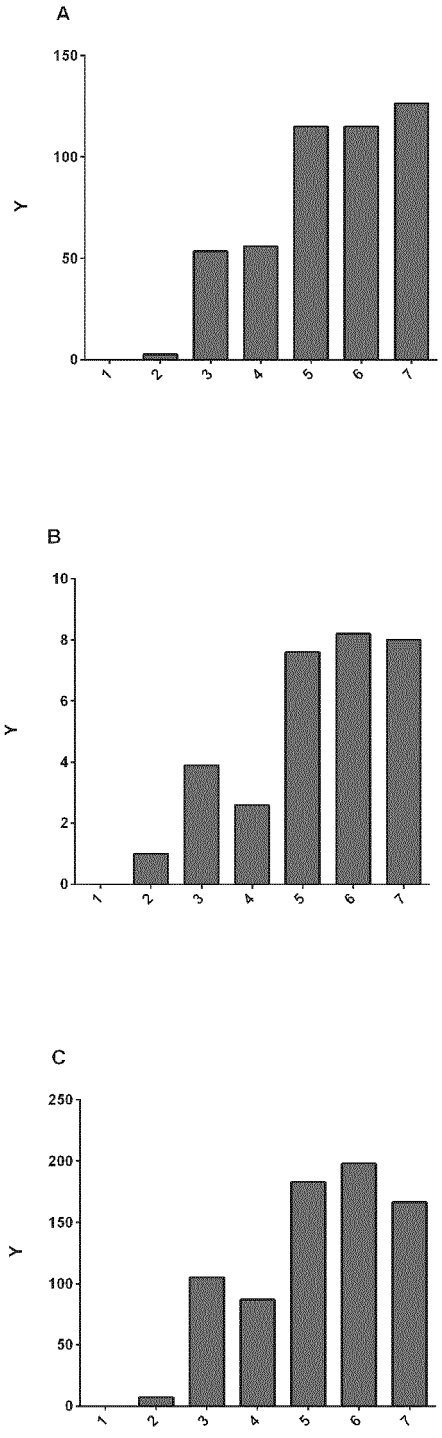
Fig. 6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Y
1
2
3
4
5
6
7
C
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200
150
100
50
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Y
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3
4
5
6
7

Fig. 7

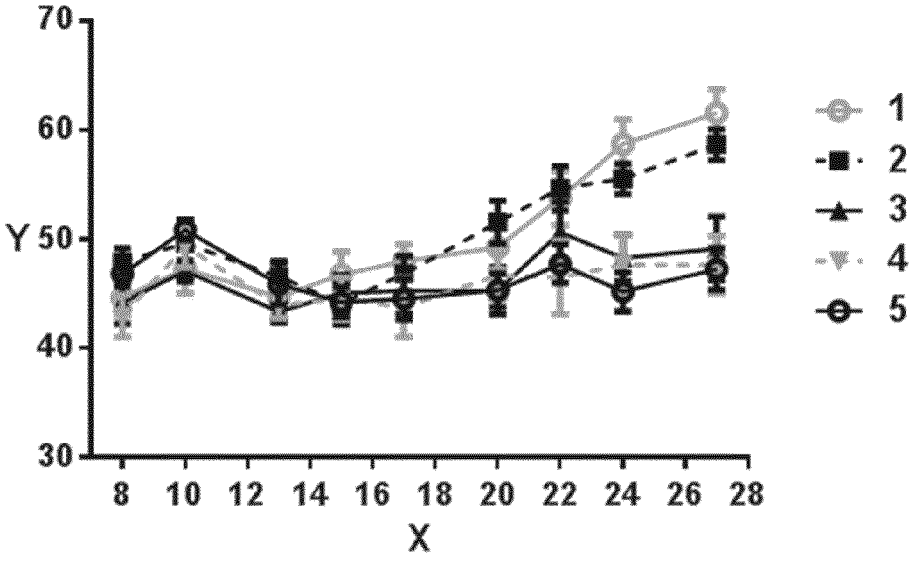


Fig. 8

```
>TPP-2971 VH (PRT)
QVTLKESGPGILQPSQTLSLTCSFSGFSLSTYGIGVGWIRQPSGKDLEWLAHIWWNDNKYYNTALKSRLTISKDTSNNQV
                               |-----|               |----HCDR2-----|
                               HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLTVSS
                   |------|
                   HCDR3

>TPP-2971 VL (PRT)
DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQS
                         |--LCDR1--|               |-----|
                                                   LCDR2

EDLADYFCQQYSSYPLTFGAGTKLELK
        |-LCDR3-|



>TPP-3186 VH (PRT)
QVTLKESGPGILQPSQTLSLTCSFSGFSLSTYGIGVGCIRQPSGKGLEWLAHIWWNDNKYYNTALKSRLTISKDTSNNQV
                               |-----|               |----HCDR2-----|
                               HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLTVSS
                   |------|
                   HCDR3

>TPP-3186 VL (PRT)
DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTFTISNMQS
                         |--LCDR1--|               |-----|
                                                   LCDR2

EDLADYFCQQYSSYPLTFGAGTKLELK
        |-LCDR3-|



>TPP-3187 VH (PRT)
QVTLKESGPGILQPSQTLSLTCSFSGFSLTTYGIGVGWIRQPSGKGLEWLAHIWWNDNKYYNTALKSRLTISKDTSNNQV
                               |-----|               |----HCDR2-----|
                               HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLTVSS
                   |------|
                   HCDR3

>TPP-3187 VL (PRT)
DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQS
                         |--LCDR1--|               |-----|
                                                   LCDR2

EDLADYFCQQYNNYPLTFGAGTKLELK
        |-LCDR3-|



>TPP-3308 VH (PRT)
QVTLKESGPGILQPSQTLSLTCSFSGFSLSTYGIGVGWIRQPSGKDLEWLAHIWWNDNKYYNTALKSRLTISKDTSNNQV
                               |-----|               |----HCDR2-----|
                               HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLTVSS
                   |------|
                   HCDR3

>TPP-3308 VL (PRT)
DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQS
```

```
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDLADYFCQQYSSYPLTFGAGTKLELK
        |-LCDR3-|
```

>TPP-3308 Heavy Chain (PRT)

```
QVTLKESGPGILQPSQTLSLTCSFSGFSLSTYGIGVGWIRQPSGKDLEWLAHIWWNDNKYYNTALKSRLTISKDTSNNQV
|-----------------------------------------------------------VH--------------------
                              |-----|              |----HCDR2-----|
                              HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN
-------------------------------------|
                    |------|
                    HCDR3

SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLF


PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV


SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGS


FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
```

>TPP-3308 Light Chain (PRT)

```
DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQS
|-----------------------------------------------------VL--------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDLADYFCQQYSSYPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
--------------------------|
        |-LCDR3-|

ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
```

>TPP-3308 Heavy Chain (DNA)

```
CAGGTCACACTGAAAGAGAGCGGCCCTGGCATCCTGCAGCCCAGCCAGACCCTGAGCCTGACCTGCAGCTTCAGCGGCTT
|-------------------------------------------------------------------------------

CAGCCTGAGCACCTACGGCATCGGCGTGGGCTGGATCAGACAGCCCAGCGGCAAGGACCTGGAATGGCTGGCCCACATCT
-------------------------------------------------------------------------------

GGTGGAACGACAACAAGTACTACAACACCGCCCTGAAGTCCCGGCTGACCATCAGCAAGGACACCAGCAACAACCAGGTG
----------------VH-----------------------------------------------------------

TTCCTGAAGATCGCCAGCGTGGACACCGCCGATACCGCCACCTACTACTGCGCCCGGATCAGCCTGCCCTACTTCGACTA
-------------------------------------------------------------------------------

CTGGGGCCAGGGCACCACCCTGACCGTGTCCTCAGCCAGCACCAAGGGCCCCAGCGTGTTCCCTCTGGCCCCTTGTAGCA
---------------------------------|

GAAGCACCAGCGAGTCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAAC

TCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGT
```

GACAGTGCCCAGCAGCAACTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACA

AGACCGTGGAACGGAAGTGCTGCGTGGAATGCCCCCCTTGTCCTGCCCCTCCAGTGGCTGGCCCTTCCGTGTTCCTGTTC

CCCCCAAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGA

CCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCA

ACAGCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTG

TCCAACAAGGGCCTGCCTGCCCCCATCGAGAAAACCATCAGCAAGACCAAAGGCCAGCCCCGCGAGCCCCAGGTGTACAC

ACTGCCTCCAAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTCGTGAAAGGCTTCTACCCCTCCGATA

TCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCCCATGCTGGACAGCGACGGCTCA

TTCTTCCTGTACAGCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCAGCGTGATGCACGA

GGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCTGGC

>TPP-3308 Light Chain (DNA)
GACATCGTGATGACCCAGAGCCAGAAATTCATGAGCACCAGCGTGGGCGACCGGGTGTCCATCACATGCAAGGCCAGCCA
|--

GAACGTGGGCACCGCCGTGGCCTGGTATCAGCAGAAGCCCGGCCAGAGCCCCAAGCTGCTGATCTACAGCGCCAGCAACC
--V

GGTACACCGGCGTGCCCGACAGATTCACAGGCAGCGGCAGCGGCACCGACTTCACCCTGACCATCAGCAACATGCAGAGC
L---

GAGGACCTGGCCGACTACTTCTGCCAGCAGTACAGCAGCTACCCCCTGACCTTCGGAGCCGGCACCAAGCTGGAACTGAA

ACGAACCGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT
|

GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAGGTGCAGTGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAG

GAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGA

GAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGT

GT

>TPP-3310 VH (PRT)
QVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGIGVGWIRQPPGKALEWLAHIWWNDNKYYSTSLKTRLTISKDTSKNQV
|-----| |----HCDR2-----|
HCDR1

VLTMTNMDPVDTATYYCARISLPYFDYWGQGTTLTVSS
|------|
HCDR3

>TPP-3310 VL (PRT)
DIQLTQSPSFLSASVGDRVTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQP
|--LCDR1--| |-----|
LCDR2

```
EDFATYYCQQYSSYPLTFGGGTKVEIK
        |-LCDR3-|
```

>TPP-3310 Heavy Chain (PRT)

```
QVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGIGVGWIRQPPGKALEWLAHIWWNDNKYYSTSLKTRLTISKDTSKNQV
|-----------------------------------------------------------VH--------------------
                              |-----|              |----HCDR2-----|
                              HCDR1

VLTMTNMDPVDTATYYCARISLPYFDYWGQGTTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN
-------------------------------------|
                   |------|
                   HCDR3

SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLF


PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV


SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGS


FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
```

>TPP-3310 Light Chain (PRT)

```
DIQLTQSPSFLSASVGDRVTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQP
|-------------------------------------------------VL--------------------------
                       |--LCDR1--|               |-----|
                                                 LCDR2

EDFATYYCQQYSSYPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
-------------------------|
        |-LCDR3-|

ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
```

>TPP-3310 Heavy Chain (DNA)

```
CAAGTGACCCTGAGAGAGTCCGGCCCTGCCCTCGTGAAGCCTACCCAGACCCTGACACTGACCTGCACCTTCTCCGGCTT
|-------------------------------------------------------------------------------

CTCCCTGTCCACCTACGGCATCGGCGTGGGCTGGATCAGACAGCCTCCTGGCAAGGCCCTGGAATGGCTGGCTCACATCT
-------------------------------------------------------------------------------

GGTGGAACGACAACAAGTACTACTCCACCTCCCTGAAAACCCGGCTGACCATCTCCAAGGACACCTCCAAGAACCAGGTG
----------------VH-----------------------------------------------------------

GTGCTGACCATGACCAACATGGACCCCGTGGACACCGCCACCTACTACTGCGCCAGAATCTCCCTGCCCTACTTCGACTA
-------------------------------------------------------------------------------

CTGGGGCCAGGGCACCACACTGACCGTCAGCTCAGCTTCCACCAAGGGCCCCTCCGTGTTCCCTCTGGCCCCTTGCTCCC
---------------------------------|

GGTCCACCTCTGAGTCTACCGCCGCTCTGGGCTGCCTGGTGAAAGACTACTTCCCCGAGCCCGTGACCGTGTCCTGGAAC

TCTGGCGCCCTGACCTCCGGCGTGCACACCTTTCCAGCCGTGCTGCAGTCCTCCGGCCTGTACTCCCTGTCCTCCGTGGT

GACAGTGCCCTCCTCCAACTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCTCCAACACCAAGGTGGACA
```

```
AGACCGTGGAACGGAAGTGCTGCGTGGAATGCCCACCCTGTCCTGCTCCACCTGTGGCTGGCCCCAGCGTGTTCCTGTTC

CCCCCAAAGCCCAAGGACACCCTGATGATCTCCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGACGTGTCCCACGAGGA

CCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCA

ACTCCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTC

TCCAACAAGGGCCTGCCTGCCCCCATCGAAAAGACCATCAGCAAGACCAAGGGCCAGCCCCGCGAGCCCCAGGTGTACAC

ACTGCCCCCCAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTGGTGAAAGGCTTCTACCCCTCCGACA

TTGCCGTGGAATGGGAGTCCAACGGACAGCCTGAGAACAACTACAAGACCACCCCCCCCCATGCTGGACTCCGACGGCTCA

TTCTTCCTGTACTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCTCCTGCTCCGTGATGCACGA

GGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCCCTGAGCCCCGGC
```

>TPP-3310 Light Chain (DNA)

```
GATATCCAGCTGACCCAGTCCCCCAGCTTCCTGTCTGCCTCTGTGGGCGACAGAGTGACCATCACATGCAAGGCCTCCCA
|-----------------------------------------------------------------------------

GAACGTGGGCACCGCCGTGGCTTGGTATCAGCAGAAGCCTGGCAAGGCCCCCAAGCTGCTGATCTACTCCGCCTCCAACC
-----------------------------------------------------------------------------V

GGTACACCGGCGTGCCCTCTAGATTCTCCGGCTCTGGCTCTGGCACCGAGTTTACCCTGACCATCTCCAGCCTGCAGCCC
L----------------------------------------------------------------------------

GAGGACTTCGCCACCTACTACTGCCAGCAGTACTCCTCCTACCCCCTGACCTTTGGCGGAGGCACCAAGGTGGAAATCAA
----------------------------------------------------------------------------

GCGGACCGTGGCCGCTCCCTCCGTGTTTATCTTCCCACCCTCCGACGAGCAGCTGAAGTCCGGCACAGCTTCCGTCGTGT
|

GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCCCTGCAGTCCGGCAACTCCCAG

GAATCCGTGACCGAGCAGGACTCCAAGGACAGCACCTACTCCCTGTCCTCCACCCTGACCCTGTCCAAGGCCGACTACGA

GAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGTCTTTCAACCGGGGCGAGT

GT
```

>TPP-3322 VH (PRT)

```
QVTLKESGPGILQPSQTLSLTCSFSGFSLSTYGIGVGCIRQPSGKGLEWLAHIWWNDNKYYNTALKSRLTISKDTSNNQV
                              |-----|              |----HCDR2-----|
                              HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLTVSS
                  |------|
                  HCDR3
```

>TPP-3322 VL (PRT)

```
DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTFTISNMQS
                        |--LCDR1--|              |-----|
                                                 LCDR2

EDLADYFCQQYSSYPLTFGAGTKLELK
        |-LCDR3-|
```

>TPP-3322 Heavy Chain (PRT)

```
QVTLKESGPGILQPSQTLSLTCSFSGFSLSTYGIGVGCIRQPSGKGLEWLAHIWWNDNKYYNTALKSRLTISKDTSNNQV
|-----------------------------------------------------------VH--------------------
                              |-----|              |----HCDR2-----|
                              HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN
-------------------------------------|
                    |------|
                    HCDR3

SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLF



PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV



SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGS



FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
```

>TPP-3322 Light Chain (PRT)

```
DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTFTISNMQS
|-----------------------------------------------------VL--------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDLADYFCQQYSSYPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
-------------------------|
        |-LCDR3-|

ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
```

>TPP-3322 Heavy Chain (DNA)

```
CAGGTCACACTGAAAGAGAGCGGCCCTGGCATCCTGCAGCCCAGCCAGACCCTGAGCCTGACCTGCAGCTTCAGCGGCTT
|-------------------------------------------------------------------------------

CAGCCTGAGCACCTACGGCATCGGCGTGGGCTGCATCAGACAGCCCAGCGGCAAGGGCCTGGAATGGCTGGCCCACATCT
-------------------------------------------------------------------------------

GGTGGAACGACAACAAGTACTACAACACCGCCCTGAAGTCCCGGCTGACCATCAGCAAGGACACCAGCAACAACCAGGTG
----------------VH-----------------------------------------------------------

TTCCTGAAGATCGCCAGCGTGGACACCGCCGATACCGCCACCTACTACTGCGCCCGGATCAGCCTGCCCTACTTCGACTA
-------------------------------------------------------------------------------

CTGGGGCCAGGGCACCACCCTGACCGTGTCCTCAGCCAGCACCAAGGGCCCCAGCGTGTTCCCTCTGGCCCCTTGTAGCA
----------------------------------|

GAAGCACCAGCGAGTCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAAC

TCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGT

GACAGTGCCCAGCAGCAACTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACA

AGACCGTGGAACGGAAGTGCTGCGTGGAATGCCCCCCTTGTCCTGCCCCTCCAGTGGCTGGCCCTTCCGTGTTCCTGTTC
```

CCCCCAAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGA

CCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCA

ACAGCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTG

TCCAACAAGGGCCTGCCTGCCCCCATCGAGAAAACCATCAGCAAGACCAAAGGCCAGCCCCGCGAGCCCCAGGTGTACAC

ACTGCCTCCAAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTCGTGAAAGGCTTCTACCCCTCCGATA

TCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCCATGCTGGACAGCGACGGCTCA

TTCTTCCTGTACAGCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCAGCGTGATGCACGA

GGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCTGGC

>TPP-3322 Light Chain (DNA)
GACATCGTGATGACCCAGAGCCAGAAATTCATGAGCACCAGCGTGGGCGACCGGGTGTCCATCACATGCAAGGCCAGCCA
|----------

GAACGTGGGCACCGCCGTGGCCTGGTATCAGCAGAAGCCCGGCCAGAGCCCCAAGCTGCTGATCTACAGCGCCAGCAACC
----------V

GGTACACCGGCGTGCCCGACAGATTCACAGGCAGCGGCAGCGGCACCGACTTCACCTTCACCATCAGCAACATGCAGAGC
L----------

GAGGACCTGGCCGACTACTTCTGCCAGCAGTACAGCAGCTACCCCCTGACCTTCGGAGCCGGCACCAAGCTGGAACTGAA

ACGAACCGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT
|

GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAGGTGCAGTGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAG

GAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGA

GAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGT

GT

>TPP-3323 VH (PRT)
QVTLKESGPGILQPSQTLSLTCSFSGFSLTTYGIGVGWIRQPSGKGLEWLAHIWWNDNKYYNTALKSRLTISKDTSNNQV
|-----| |----HCDR2-----|
HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLTVSS
|------|
HCDR3

>TPP-3323 VL (PRT)
DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQS
|--LCDR1--| |-----|
LCDR2

EDLADYFCQQYNNYPLTFGAGTKLELK
|-LCDR3-|

>TPP-3323 Heavy Chain (PRT)
QVTLKESGPGILQPSQTLSLTCSFSGFSLTTYGIGVGWIRQPSGKGLEWLAHIWWNDNKYYNTALKSRLTISKDTSNNQV

```
|-----------------------------------------------------------VH--------------------
                               |-----|              |----HCDR2-----|
                               HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN
-------------------------------------|
                    |------|
                    HCDR3

SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLF



PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV



SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGS



FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
```

>TPP-3323 Light Chain (PRT)

```
DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQS
|-------------------------------------------------VL--------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDLADYFCQQYNNYPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
--------------------------|
        |-LCDR3-|

ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
```

>TPP-3323 Heavy Chain (DNA)

```
CAAGTGACCCTGAAAGAGTCCGGCCCTGGCATCCTGCAGCCTTCCCAGACCCTGTCCCTGACCTGCTCCTTCTCCGGCTT
|-----------------------------------------------------------------------------

CTCCCTGACCACCTACGGCATCGGCGTGGGCTGGATCAGACAGCCTTCTGGCAAGGGCCTGGAATGGCTGGCCCACATCT
-----------------------------------------------------------------------------

GGTGGAACGACAACAAGTACTACAACACCGCCCTGAAGTCCCGGCTGACCATCTCCAAGGACACCTCCAACAACCAGGTG
----------------VH-------------------------------------------------------------

TTCCTGAAGATCGCCTCCGTGGACACCGCCGATACCGCCACCTACTACTGCGCCCGGATCTCCCTGCCCTACTTCGACTA
-----------------------------------------------------------------------------

TTGGGGCCAGGGCACCACCCTGACCGTCAGCTCAGCTTCCACCAAGGGCCCCTCCGTGTTCCCTCTGGCCCCTTGCTCCC
---------------------------------|

GGTCCACCTCTGAGTCTACCGCCGCTCTGGGCTGCCTGGTGAAAGACTACTTCCCCGAGCCCGTGACCGTGTCCTGGAAC

TCTGGCGCCCTGACCTCCGGCGTGCACACCTTTCCAGCCGTGCTGCAGTCCTCCGGCCTGTACTCCCTGTCCTCCGTGGT

GACAGTGCCCTCCTCCAACTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCTCCAACACCAAGGTGGACA

AGACCGTGGAACGGAAGTGCTGCGTGGAATGCCCACCCTGTCCTGCTCCACCTGTGGCTGGCCCCAGCGTGTTCCTGTTC

CCCCCAAAGCCCAAGGACACCCTGATGATCTCCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGACGTGTCCCACGAGGA
```

CCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCA

ACTCCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTC

TCCAACAAGGGCCTGCCTGCCCCCATCGAAAAGACCATCAGCAAGACCAAGGGCCAGCCCCGCGAGCCCCAGGTGTACAC

ACTGCCCCCCAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTGGTGAAAGGCTTCTACCCCTCCGACA

TTGCCGTGGAATGGGAGTCCAACGGACAGCCTGAGAACAACTACAAGACCACCCCCCCCATGCTGGACTCCGACGGCTCA

TTCTTCCTGTACTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCTCCTGCTCCGTGATGCACGA

GGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCCCTGAGCCCCGGC

>TPP-3323 Light Chain (DNA)

```
GACATCGTGATGACCCAGTCCCAGAAATTCATGTCCACCTCCGTGGGCGACCGGGTGTCCATCACATGCAAGGCCTCTCA
|-------------------------------------------------------------------------------

GAACGTGGGCACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGCCAGTCCCCCAAGCTGCTGATCTACTCCGCCTCCAACC
--------------------------------------------------------------------------------V

GGTACACCGGCGTGCCCGATAGATTCACCGGCTCTGGCTCTGGCACCGACTTCACCCTGACCATCTCCAACATGCAGTCC
L-------------------------------------------------------------------------------

GAGGACCTGGCCGACTACTTCTGCCAGCAGTACAACAACTACCCCCTGACCTTCGGCGCTGGCACCAAGCTGGAACTGAA
--------------------------------------------------------------------------------

GAGAACCGTGGCCGCTCCCTCCGTGTTTATCTTCCCACCCTCCGACGAGCAGCTGAAGTCCGGCACAGCTTCCGTCGTGT
|

GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCCCTGCAGTCCGGCAACTCCCAG

GAATCCGTGACCGAGCAGGACTCCAAGGACAGCACCTACTCCCTGTCCTCTACCCTGACCCTGTCCAAGGCCGATTACGA

GAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGTCTTTCAACCGGGGCGAGT

GT
```

>TPP-3705 VH (PRT)

```
EVQLVESGGGLVQPGGSLRLSCAASGFTFSLYQMHWVRQAPGKGLEWVSWISFSGGNTGYADSVKGRFTISRDNSKNTLY
                              |---|              |-----HCDR2-----|
                             HCDR1

LQMNSLRAEDTAVYYCARATGYSSPWYLDPWGQGTLVTVSS
                  |--HCDR3---|
```

>TPP-3705 VL (PRT)

```
DIQMTQSPSSLSASVGDRVTITCQASHEIDNYLNWYQQKPGKAPKLLIYDAYWLKTGVPSRFSGSGSGTDFTLTISSLQP
                        |--LCDR1--|              |-----|
                                                 LCDR2

EDIATYYCQGYDDLSVTFGGGTKVDIK
        |-LCDR3-|
```

>TPP-3705 Heavy Chain (PRT)

```
EVQLVESGGGLVQPGGSLRLSCAASGFTFSLYQMHWVRQAPGKGLEWVSWISFSGGNTGYADSVKGRFTISRDNSKNTLY
|-------------------------------------------------------VH-------------------
                              |---|              |-----HCDR2-----|
                             HCDR1
```

```
LQMNSLRAEDTAVYYCARATGYSSPWYLDPWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTV
----------------------------------------|
                  |--HCDR3---|

SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSV


FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYK


CKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDS


DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
```

>TPP-3705 Light Chain (PRT)

```
DIQMTQSPSSLSASVGDRVTITCQASHEIDNYLNWYQQKPGKAPKLLIYDAYWLKTGVPSRFSGSGSGTDFTLTISSLQP
|-------------------------------------------------VL--------------------------
                       |--LCDR1--|               |-----|
                                                 LCDR2

EDIATYYCQGYDDLSVTFGGGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
-------------------------|
        |-LCDR3-|


ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
```

>TPP-3705 Heavy Chain (DNA)

```
GAAGTGCAGCTGGTGGAATCCGGCGGAGGCCTGGTGCAGCCTGGCGGATCTCTGAGACTGTCTTGTGCCGCCTCCGGCTT
|-------------------------------------------------------------------------------

CACCTTCAGCCTGTACCAGATGCACTGGGTGCGACAGGCCCCTGGCAAGGGACTGGAATGGGTGTCCTGGATCTCCTTCT
--------------------------------------------------------------------------------

CCGGCGGCAATACCGGCTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTAC
--------------------VH------------------------------------------------------

CTGCAGATGAACTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCTAGAGCCACCGGCTACTCCTCCCCCTGGTA
--------------------------------------------------------------------------------

TCTGGATCCTTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCTTCCACCAAGGGCCCCTCCGTGTTCCCTCTGGCCC
-----------------------------------------|

CTTGCTCCCGGTCCACCTCTGAGTCTACCGCCGCTCTGGGCTGCCTGGTGAAAGACTACTTCCCCGAGCCCGTGACCGTG


TCCTGGAACTCTGGCGCCCTGACCTCCGGCGTGCACACCTTTCCAGCCGTGCTGCAGTCCTCCGGCCTGTACTCCCTGTC


CTCCGTGGTGACAGTGCCCTCCTCCAACTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCTCCAACACCA


AGGTGGACAAGACCGTGGAACGGAAGTGCTGCGTGGAATGCCCACCCTGTCCTGCTCCACCTGTGGCTGGCCCCAGCGTG


TTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCTCCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGACGTGTC


CCACGAGGACCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGG
```

```
AACAGTTCAACTCCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAG

TGCAAGGTCTCCAACAAGGGCCTGCCTGCCCCCATCGAAAAGACCATCAGCAAGACCAAGGGCCAGCCCCGCGAGCCCCA

GGTGTACACACTGCCCCCCAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTGGTGAAAGGCTTCTACC

CCTCCGACATTGCCGTGGAATGGGAGTCCAACGGACAGCCTGAGAACAACTACAAGACCACCCCCCCCATGCTGGACTCC

GACGGCTCATTCTTCCTGTACTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCTCCTGCTCCGT

GATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCCCTGAGCCCCGGC
```

>TPP-3705 Light Chain (DNA)

```
GACATCCAGATGACCCAGAGCCCTTCCAGCCTGTCCGCCTCTGTGGGCGACAGAGTGACCATCACCTGTCAGGCCTCCCA
|-------------------------------------------------------------------------------

CGAGATCGACAACTACCTGAACTGGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACGATGCCTACTGGC
--------------------------------------------------------------------------------V

TGAAAACCGGCGTGCCCTCCAGATTCTCCGGCTCTGGCTCTGGCACCGACTTTACCCTGACCATCTCCAGCCTGCAGCCC
L-------------------------------------------------------------------------------

GAGGATATCGCCACCTACTATTGTCAGGGCTACGACGACCTGTCCGTGACCTTTGGCGGAGGCACCAAGGTGGACATCAA
---------------------------------------------------------------------------------

GCGGACAGTGGCCGCTCCCTCCGTGTTTATCTTCCCACCCTCCGACGAGCAGCTGAAGTCCGGCACAGCTTCCGTCGTGT
|

GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAGGTGCAGTGGAAAGTGGATAACGCCCTGCAGTCCGGCAACTCCCAG

GAATCCGTGACCGAGCAGGACTCCAAGGACAGCACCTACTCCCTGTCCTCCACCCTGACCCTGTCCAAGGCCGACTACGA

GAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGTCTTTCAACCGGGGCGAGT

GT
```

>TPP-3707 VH (PRT)

```
EVQLVESGGGLVQPGGSLRLSCAASGFTFSLYQMHWVRQAPGKGLEWVSWISFSGGNTGYADSVKGRFTISRDNSKNTLY
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCARATGYSSPWYLDPWGQGTLVTVSS
                  |--HCDR3---|
```

>TPP-3707 VL (PRT)

```
DIQMTQSPSSLSASVGDRVTITCQASHEIDNYLNWYQQKPGKAPKLLIYDAYWSKTGVPSRFSGSGSGTDFTLTISSLQP
                        |--LCDR1--|              |-----|
                                                 LCDR2

EDIATYYCQGYDDLSVTFGGGTKVDIK
        |-LCDR3-|
```

>TPP-3707 Heavy Chain (PRT)

```
EVQLVESGGGLVQPGGSLRLSCAASGFTFSLYQMHWVRQAPGKGLEWVSWISFSGGNTGYADSVKGRFTISRDNSKNTLY
|-----------------------------------------------------------VH------------------
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCARATGYSSPWYLDPWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTV
----------------------------------------|
```

```
                  |--HCDR3---|

SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSV


FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYK


CKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDS


DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
```

>TPP-3707 Light Chain (PRT)

```
DIQMTQSPSSLSASVGDRVTITCQASHEIDNYLNWYQQKPGKAPKLLIYDAYWSKTGVPSRFSGSGSGTDFTLTISSLQP
|-------------------------------------------------------VL-------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDIATYYCQGYDDLSVTFGGGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
-------------------------|
        |-LCDR3-|


ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
```

>TPP-3707 Heavy Chain (DNA)

```
GAAGTGCAGCTGGTGGAATCCGGCGGAGGCCTGGTGCAGCCTGGCGGATCTCTGAGACTGTCTTGTGCCGCCTCCGGCTT
|-------------------------------------------------------------------------------

CACCTTCAGCCTGTACCAGATGCACTGGGTGCGACAGGCCCCTGGCAAGGGACTGGAATGGGTGTCCTGGATCTCCTTCT
-------------------------------------------------------------------------------

CCGGCGGCAATACCGGCTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTAC
-------------------VH-----------------------------------------------------------

CTGCAGATGAACTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCTAGAGCCACCGGCTACTCCTCCCCCTGGTA
-------------------------------------------------------------------------------

TCTGGATCCTTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCTTCCACCAAGGGCCCCTCCGTGTTCCCTCTGGCCC
-----------------------------------------|

CTTGCTCCCGGTCCACCTCTGAGTCTACCGCCGCTCTGGGCTGCCTGGTGAAAGACTACTTCCCCGAGCCCGTGACCGTG


TCCTGGAACTCTGGCGCCCTGACCTCCGGCGTGCACACCTTTCCAGCCGTGCTGCAGTCCTCCGGCCTGTACTCCCTGTC


CTCCGTGGTGACAGTGCCCTCCTCCAACTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCTCCAACACCA


AGGTGGACAAGACCGTGGAACGGAAGTGCTGCGTGGAATGCCCACCCTGTCCTGCTCCACCTGTGGCTGGCCCCAGCGTG


TTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCTCCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGACGTGTC


CCACGAGGACCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGG


AACAGTTCAACTCCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAG
```

TGCAAGGTCTCCAACAAGGGCCTGCCTGCCCCCATCGAAAAGACCATCAGCAAGACCAAGGGCCAGCCCCGCGAGCCCCA

GGTGTACACACTGCCCCCCAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTGGTGAAAGGCTTCTACC

CCTCCGACATTGCCGTGGAATGGGAGTCCAACGGACAGCCTGAGAACAACTACAAGACCACCCCCCCCATGCTGGACTCC

GACGGCTCATTCTTCCTGTACTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCTCCTGCTCCGT

GATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCCCTGAGCCCCGGC

>TPP-3707 Light Chain (DNA)

```
GACATCCAGATGACCCAGAGCCCTTCCAGCCTGTCCGCCTCTGTGGGCGACAGAGTGACCATCACCTGTCAGGCCTCCCA
|-----------------------------------------------------------------------------
CGAGATCGACAACTACCTGAACTGGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACGACGCCTACTGGT
-----------------------------------------------------------------------------V
CCAAGACCGGCGTGCCCTCCAGATTCTCCGGCTCTGGCTCTGGCACCGACTTTACCCTGACCATCTCCAGCCTGCAGCCC
L----------------------------------------------------------------------------
GAGGATATCGCCACCTACTATTGTCAGGGCTACGACGACCTGTCCGTGACCTTTGGCGGAGGCACCAAGGTGGACATCAA
----------------------------------------------------------------------------
GCGGACAGTGGCCGCTCCCTCCGTGTTTATCTTCCCACCCTCCGACGAGCAGCTGAAGTCCGGCACAGCTTCCGTCGTGT
|
GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAGGTGCAGTGGAAAGTGGATAACGCCCTGCAGTCCGGCAACTCCCAG
GAATCCGTGACCGAGCAGGACTCCAAGGACAGCACCTACTCCCTGTCCTCCACCCTGACCCTGTCCAAGGCCGACTACGA
GAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGTCTTTCAACCGGGGCGAGT
GT
```

>TPP-3714 VH (PRT)

```
QVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGIGVGWIRQPPGKALEWLAHIWWNDNKYYSTSLKTRLTISKDTSKNQV
                              |-----|              |----HCDR2-----|
                              HCDR1

VLTMTNMDPVDTATYYCARISLPYFDYWGQGTLVTVSS
                    |------|
                    HCDR3
```

>TPP-3714 VL (PRT)

```
DIQLTQSPSFLSASVGDRVTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQP
                        |--LCDR1--|              |-----|
                                                 LCDR2

EDFATYYCQQYSSYPLTFGGGTKVEIK
        |-LCDR3-|
```

>TPP-3714 Heavy Chain (PRT)

```
QVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGIGVGWIRQPPGKALEWLAHIWWNDNKYYSTSLKTRLTISKDTSKNQV
|-----------------------------------------------------------VH--------------------
                              |-----|              |----HCDR2-----|
                              HCDR1

VLTMTNMDPVDTATYYCARISLPYFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN
-----------------------------------|
                    |------|
                    HCDR3
```

SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLF

PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV

SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGS

FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

>TPP-3714 Light Chain (PRT)

```
DIQLTQSPSFLSASVGDRVTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQP
|-------------------------------------------------VL--------------------------
                       |--LCDR1--|               |-----|
                                                 LCDR2

EDFATYYCQQYSSYPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
-------------------------|
        |-LCDR3-|
```

ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>TPP-3714 Heavy Chain (DNA)

```
CAAGTGACCCTGAGAGAGTCCGGCCCTGCCCTCGTGAAGCCTACCCAGACCCTGACACTGACCTGCACCTTCTCCGGCTT
|-------------------------------------------------------------------------------

CTCCCTGTCCACCTACGGCATCGGCGTGGGCTGGATCAGACAGCCTCCTGGCAAGGCCCTGGAATGGCTGGCTCACATCT
-------------------------------------------------------------------------------

GGTGGAACGACAACAAGTACTACTCCACCTCCCTGAAAACCCGGCTGACCATCTCCAAGGACACCTCCAAGAACCAGGTG
----------------VH---------------------------------------------------------------

GTGCTGACCATGACCAACATGGACCCCGTGGACACCGCCACCTACTACTGCGCCAGAATCTCCCTGCCCTACTTCGACTA
-------------------------------------------------------------------------------

CTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCTTCCACCAAGGGCCCCTCCGTGTTCCCTCTGGCCCCTTGCTCCC
---------------------------------|

GGTCCACCTCTGAGTCTACCGCCGCTCTGGGCTGCCTGGTGAAAGACTACTTCCCCGAGCCCGTGACCGTGTCCTGGAAC

TCTGGCGCCCTGACCTCCGGCGTGCACACCTTTCCAGCCGTGCTGCAGTCCTCCGGCCTGTACTCCCTGTCCTCCGTGGT

GACAGTGCCCTCCTCCAACTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCTCCAACACCAAGGTGGACA

AGACCGTGGAACGGAAGTGCTGCGTGGAATGCCCACCCTGTCCTGCTCCACCTGTGGCTGGCCCCAGCGTGTTCCTGTTC

CCCCCAAAGCCCAAGGACACCCTGATGATCTCCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGACGTGTCCCACGAGGA

CCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCA

ACTCCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTC

TCCAACAAGGGCCTGCCTGCCCCCATCGAAAAGACCATCAGCAAGACCAAGGGCCAGCCCCGCGAGCCCCAGGTGTACAC
```

```
ACTGCCCCCCAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTGGTGAAAGGCTTCTACCCCTCCGACA

TTGCCGTGGAATGGGAGTCCAACGGACAGCCTGAGAACAACTACAAGACCACCCCCCCCATGCTGGACTCCGACGGCTCA

TTCTTCCTGTACTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCTCCTGCTCCGTGATGCACGA

GGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCCCTGAGCCCCGGC
```

>TPP-3714 Light Chain (DNA)

```
GATATCCAGCTGACCCAGTCCCCCAGCTTCCTGTCTGCCTCTGTGGGCGACAGAGTGACCATCACATGCAAGGCCTCCCA
|-----------------------------------------------------------------------------------

GAACGTGGGCACCGCCGTGGCTTGGTATCAGCAGAAGCCTGGCAAGGCCCCCAAGCTGCTGATCTACTCCGCCTCCAACC
----------------------------------------------------------------------------------V

GGTACACCGGCGTGCCCTCTAGATTCTCCGGCTCTGGCTCTGGCACCGAGTTTACCCTGACCATCTCCAGCCTGCAGCCC
L-----------------------------------------------------------------------------

GAGGACTTCGCCACCTACTACTGCCAGCAGTACTCCTCCTACCCCCTGACCTTTGGCGGAGGCACCAAGGTGGAAATCAA
----------------------------------------------------------------------------------

GCGGACCGTGGCCGCTCCCTCCGTGTTTATCTTCCCACCCTCCGACGAGCAGCTGAAGTCCGGCACAGCTTCCGTCGTGT
|

GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCCCTGCAGTCCGGCAACTCCCAG

GAATCCGTGACCGAGCAGGACTCCAAGGACAGCACCTACTCCCTGTCCTCCACCCTGACCCTGTCCAAGGCCGACTACGA

GAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGTCTTTCAACCGGGGCGAGT

GT
```

>TPP-3820 VH (PRT)

```
QVTLRESGPALVKPTQTLTLTCTFSGFSLTTYGIGVGWIRQPPGKGLEWLAHIWWNDNKYYSTSLKTRLTISKDTSKNQV
                              |-----|              |----HCDR2-----|
                              HCDR1

VLTMTNMDPVDTATYYCARISLPYFDYWGQGTLVTVSS
                   |------|
                   HCDR3
```

>TPP-3820 VL (PRT)

```
DIQLTQSPSFLSASVGDRVTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQP
                        |--LCDR1--|              |-----|
                                                 LCDR2

EDFATYYCQQYNNYPLTFGGGTKVEIK
        |-LCDR3-|
```

>TPP-3820 Heavy Chain (PRT)

```
QVTLRESGPALVKPTQTLTLTCTFSGFSLTTYGIGVGWIRQPPGKGLEWLAHIWWNDNKYYSTSLKTRLTISKDTSKNQV
|-----------------------------------------------------------VH--------------------
                              |-----|              |----HCDR2-----|
                              HCDR1

VLTMTNMDPVDTATYYCARISLPYFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN
-------------------------------------|
                   |------|
                   HCDR3

SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLF
```

PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV

SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGS

FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

>TPP-3820 Light Chain (PRT)

```
DIQLTQSPSFLSASVGDRVTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQP
|-------------------------------------------------VL--------------------------
                       |--LCDR1--|               |-----|
                                                 LCDR2

EDFATYYCQQYNNYPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
-------------------------|
        |-LCDR3-|
```

ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>TPP-3820 Heavy Chain (DNA)

```
CAAGTGACCCTGAGAGAGTCCGGCCCTGCCCTCGTGAAGCCTACCCAGACCCTGACACTGACCTGCACCTTCAGCGGCTT
|-------------------------------------------------------------------------------

CAGCCTGACCACCTACGGCATCGGCGTGGGCTGGATCAGACAGCCTCCTGGCAAGGGCCTGGAATGGCTGGCCCACATCT
--------------------------------------------------------------------------------

GGTGGAACGACAACAAGTACTACAGCACCAGCCTGAAAACCCGGCTGACCATCAGCAAGGACACCAGCAAGAACCAGGTG
----------------VH----------------------------------------------------------

GTGCTGACCATGACCAACATGGACCCCGTGGACACCGCCACCTACTACTGCGCCAGAATCAGCCTGCCCTACTTCGACTA
--------------------------------------------------------------------------------

CTGGGGCCAGGGCACCCTCGTGACAGTGTCATCAGCCAGCACCAAGGGCCCCAGCGTGTTCCCTCTGGCCCCTTGTAGCA
---------------------------------|

GAAGCACCAGCGAGTCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAAC

TCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGT

GACAGTGCCCAGCAGCAACTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACA

AGACCGTGGAACGGAAGTGCTGCGTGGAATGCCCCCCTTGTCCTGCCCCTCCAGTGGCTGGCCCTTCCGTGTTCCTGTTC

CCCCCAAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGA

CCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCA

ACAGCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTG

TCCAACAAGGGCCTGCCTGCCCCCATCGAGAAAACCATCAGCAAGACCAAAGGCCAGCCCCGCGAGCCCCAGGTGTACAC

ACTGCCTCCAAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTCGTGAAAGGCTTCTACCCCTCCGATA
```

```
TCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCCATGCTGGACAGCGACGGCTCA

TTCTTCCTGTACAGCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCAGCGTGATGCACGA

GGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCTGGC
```

>TPP-3820 Light Chain (DNA)

```
GATATCCAGCTGACCCAGAGCCCCAGCTTTCTGAGCGCCAGCGTGGGCGACAGAGTGACCATCACATGCAAGGCCAGCCA
|-------------------------------------------------------------------------------

GAACGTGGGCACAGCCGTGGCCTGGTATCAGCAGAAGCCTGGCAAGGCCCCCAAGCTGCTGATCTACAGCGCCAGCAACC
--------------------------------------------------------------------------------V

GGTACACCGGCGTGCCCAGCAGATTTTCTGGCAGCGGCTCCGGCACCGAGTTCACCCTGACAATCAGCAGCCTGCAGCCC
L-------------------------------------------------------------------------------

GAGGACTTCGCCACCTACTACTGCCAGCAGTACAACAACTACCCCCTGACCTTCGGCGGAGGCACCAAGGTGGAAATTAA
--------------------------------------------------------------------------------

ACGAACCGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT
|

GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAGGTGCAGTGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAG

GAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGA

GAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGT

GT
```

>TPP-3821 VH (PRT)

```
QVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGIGVGWIRQPPGKALEWLAHIWWNDNKYYSTSLKTRLTISKDTSKNQV
                              |-----|              |----HCDR2-----|
                              HCDR1

VLTMTNMDPVDTATYYCARISLPYFDYWGQGTLVTVSS
                    |------|
                    HCDR3
```

>TPP-3821 VL (PRT)

```
DIQLTQSPSFLSASVGDRVTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQP
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQYNNYPLTFGGGTKVEIK
        |-LCDR3-|
```

>TPP-3821 Heavy Chain (PRT)

```
QVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGIGVGWIRQPPGKALEWLAHIWWNDNKYYSTSLKTRLTISKDTSKNQV
|-----------------------------------------------------------VH--------------------
                              |-----|              |----HCDR2-----|
                              HCDR1

VLTMTNMDPVDTATYYCARISLPYFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN
-----------------------------------|
                    |------|
                    HCDR3

SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLF



PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
```

SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGS

FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

>TPP-3821 Light Chain (PRT)

```
DIQLTQSPSFLSASVGDRVTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQP
|-------------------------------------------------VL--------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQYNNYPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
--------------------------|
        |-LCDR3-|
```

ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>TPP-3821 Heavy Chain (DNA)

```
CAGGTCACACTGAGAGAGTCCGGCCCTGCCCTGGTGAAACCCACCCAGACCCTGACCCTGACATGCACCTTCAGCGGCTT
|-----------------------------------------------------------------------------

CAGCCTGAGCACCTACGGCATCGGCGTGGGCTGGATCAGACAGCCCCCTGGCAAGGCCCTGGAATGGCTGGCCCACATCT
-----------------------------------------------------------------------------

GGTGGAACGACAACAAGTACTACAGCACCAGCCTGAAAACCCGGCTGACCATCAGCAAGGACACCAGCAAGAACCAGGTG
----------------VH---------------------------------------------------------

GTGCTGACCATGACCAACATGGACCCCGTGGACACCGCCACCTACTACTGCGCCCGGATCAGCCTGCCCTACTTCGACTA
-----------------------------------------------------------------------------

CTGGGGCCAGGGCACCCTGGTGACCGTGTCCTCAGCCAGCACCAAGGGCCCCAGCGTGTTCCCTCTGGCCCCTTGTAGCA
---------------------------------|

GAAGCACCAGCGAGTCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAAC

TCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGT

GACAGTGCCCAGCAGCAACTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACA

AGACCGTGGAACGGAAGTGCTGCGTGGAATGCCCCCCTTGTCCTGCCCCTCCAGTGGCTGGCCCTTCCGTGTTCCTGTTC

CCCCCAAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGA

CCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCA

ACAGCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTG

TCCAACAAGGGCCTGCCTGCCCCCATCGAGAAAACCATCAGCAAGACCAAAGGCCAGCCCCGCGAGCCCCAGGTGTACAC

ACTGCCTCCAAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTCGTGAAAGGCTTCTACCCCTCCGATA

TCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCCATGCTGGACAGCGACGGCTCA
```

TTCTTCCTGTACAGCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCAGCGTGATGCACGA

GGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCTGGC

>TPP-3821 Light Chain (DNA)

```
GATATCCAGCTGACCCAGAGCCCCAGCTTTCTGAGCGCCAGCGTGGGCGACAGAGTGACCATCACATGCAAGGCCAGCCA
|-----------------------------------------------------------------------------

GAACGTGGGCACAGCCGTGGCCTGGTATCAGCAGAAGCCTGGCAAGGCCCCCAAGCTGCTGATCTACAGCGCCAGCAACC
-----------------------------------------------------------------------------V

GGTACACCGGCGTGCCCAGCAGATTTTCTGGCAGCGGCTCCGGCACCGAGTTCACCCTGACAATCAGCAGCCTGCAGCCC
L----------------------------------------------------------------------------

GAGGACTTCGCCACCTACTACTGCCAGCAGTACAACAACTACCCCCTGACCTTCGGCGGAGGCACCAAGGTGGAAATTAA
-----------------------------------------------------------------------------

ACGAACCGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT
|

GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAGGTGCAGTGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAG

GAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGA

GAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGT

GT
```

Fig. 9

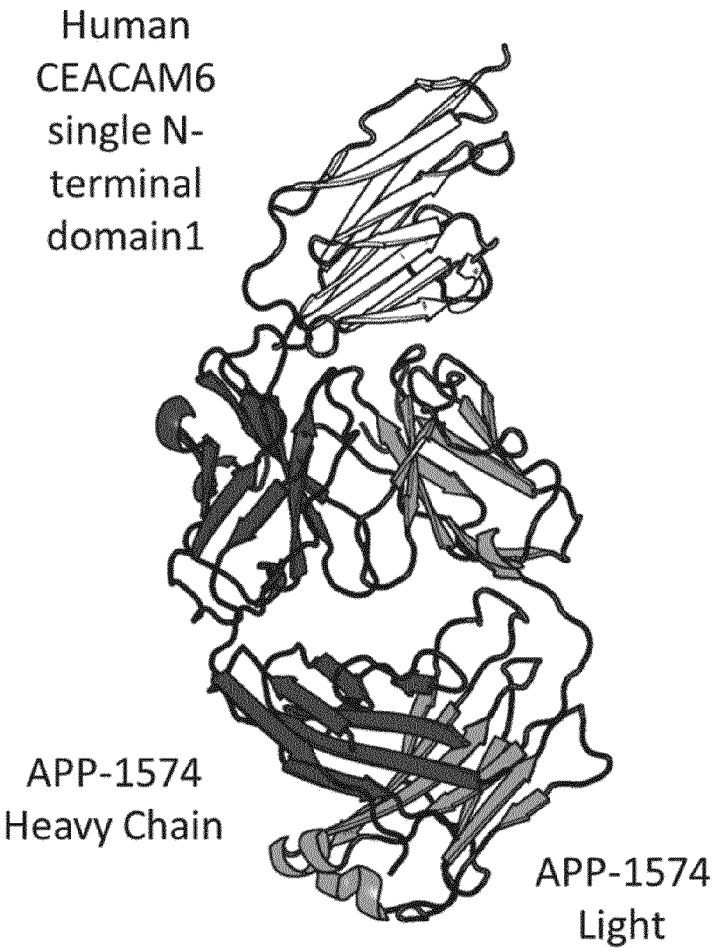

Human
CEACAM6
single N-
terminal
domain1
APP-1574
Heavy Chain
APP-1574
Light

Fig. 10

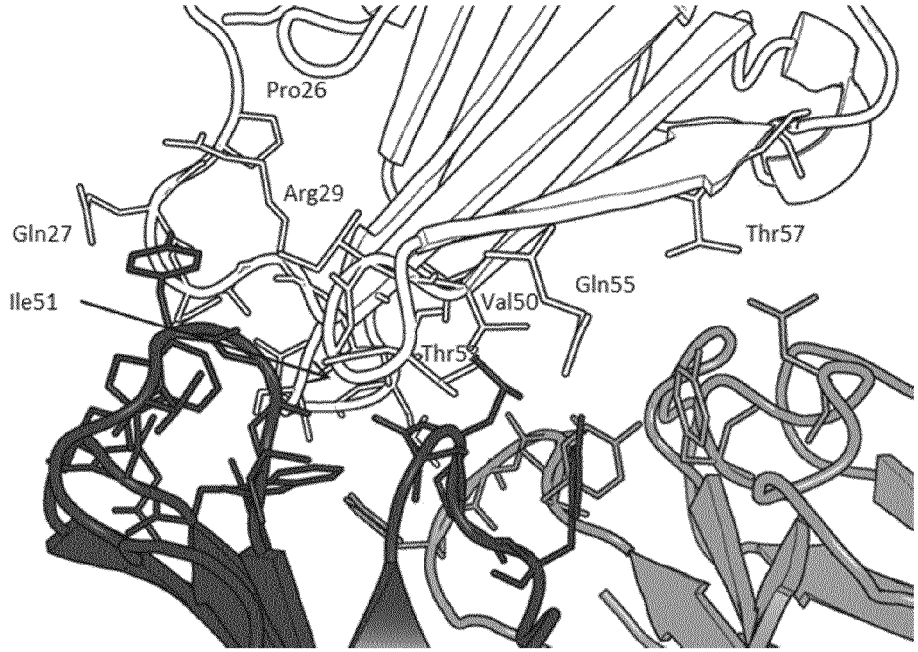
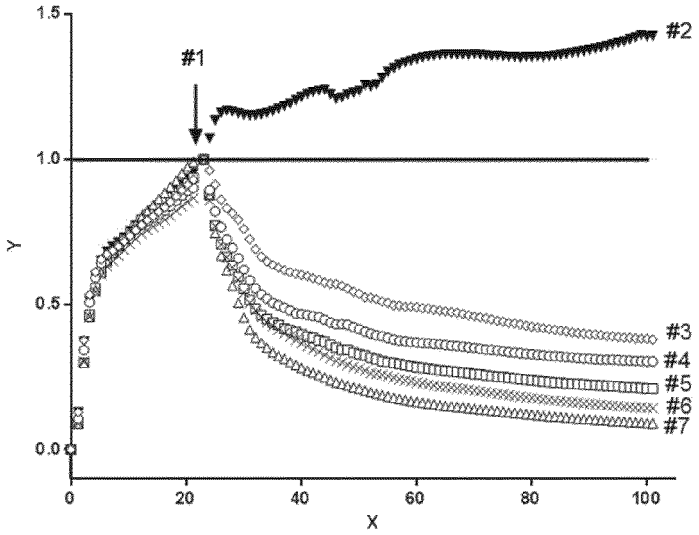


Fig. 11

A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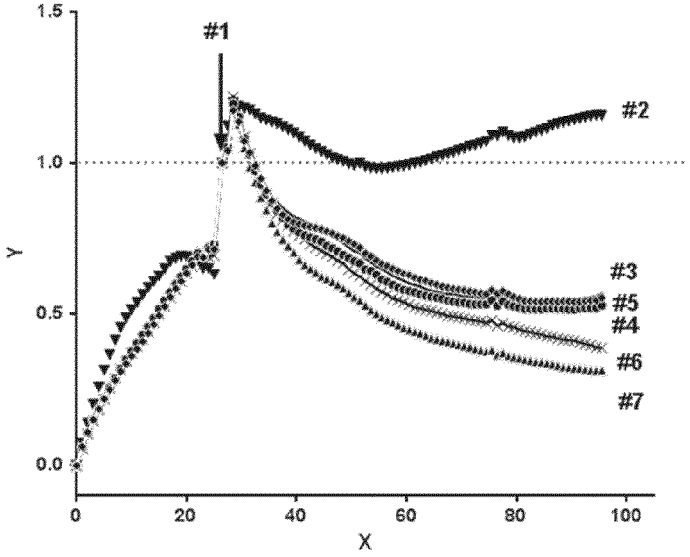
0.5
0.0
Y
0
20
40
60
80
100
X
#1
#2
#3
#4
#5
#6
#7

B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0.5
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100
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#1
#2
#3
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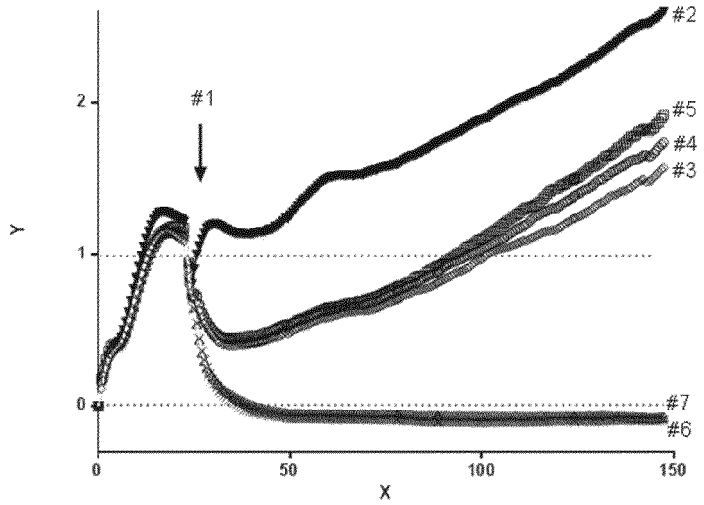
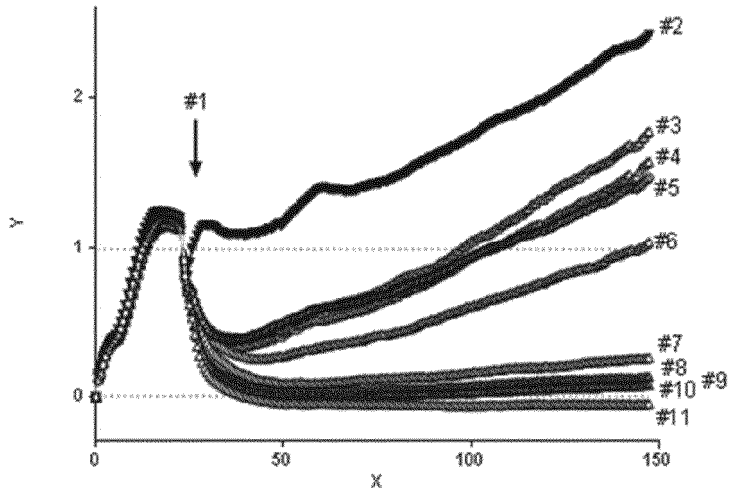
#4
#6
#7

Fig. 12

A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