

Fig. 1

human CEACAM6	KLTIESPTFNVAEGKEVLLLAHNLQNRIIGYSWYKGERVDGNSLIVGYVIGTQQTATPGPAYSGRETIY	68
cyno CEACAM6	QLTIESRPFNVAEGKEVLLLAHNLQNRIIGYSWYKGERVDGNSLIVGYVIGTQQTATPGPAYSGREMIY	68
human CEACAM5	KLTIESPTFNVAEGKEVLLLVHNLQHLFGYSWYKGERVDGNSLIVGYVIGTQQTATPGPAYSGRETIY	68
human CEACAM1	QLTIESMPFNVAEGKEVLLLVHNLQHLFGYSWYKGERVDGNSLIVGYVIGTQQTATPGPAYSGRETIY	68
human CEACAM3	KLTIESMPLSVAEGKEVLLLVHNLQHLFGYSWYKGERVDGNSLIVGYVIGTQQTATPGPAYSGRETIY	68
human CEACAM6	PNASLLIQNVITQNDIGFYTLQVVKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFICEPE	136
cyno CEACAM6	SNASLLIQNVITQNDIGSYTLQAIKEDLVTEEATGRFWVYPELPKPYITSSNNSNPVEDKDAVDFICEPD	136
human CEACAM5	PNASLLIQNIQNDIGFYTLHVVKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFICEPE	136
human CEACAM1	PNASLLIQNVITQNDIGFYTLQVVKSDLVNEEATGQFHVYPELPKPSISSNNSNPVEDKDAVAFICEPE	136
human CEACAM3	TNASLLIQNVITQNDIGFYTLQVVKSDLVNEEATGQFHVYQEN	110
human CEACAM6	VQNTTYLWVWNGQSLPVSPRLQLSNGNMTLLLSVKRNDAGSYECEIQNPASANRSDPVTNLVLYGPD	204
cyno CEACAM6	IHSITYLWVWVNDQSLPVSPRLQLSNGNRIITLLSVKRNDAGAYECEIQNPVSANLSDPVTNLVLYGPD	204
human CEACAM5	TQDATYLLWVWVNNQSLPVSPRLQLSNGNRIITLLFNVTNRNDTASYKCEIQNPVSARRSDPVTNLVLYGPD	204
human CEACAM1	TQDTTYLWVWVNNQSLPVSPRLQLSNGNRIITLLSVTRNDTGPECEIQNPVSANRSDPVTNLVLYGPD	204
human CEACAM3	APGLPVG.....AVAG.....	121
human CEACAM6	GPTISPSKANYRPGENLNLSCHAASNPPAQYSWFINGTFFQSQSTQELFIPNITVNNSGSMCQAHNSAT	272
cyno CEACAM6	VPTISPSNSNYRPGENLNLSCHAASNPPAQYSWVFNGTFFQSQSTQELFIPNITVNNSGSMCQAYNSAT	272
human CEACAM5	APTISPLNTSYRSGENLNLSCHAASNPPAQYSWVFNGTFFQSQSTQELFIPNITVNNSGSMCQAHNSDT	272
human CEACAM1	TPTISPSDITYRPGANLSLSCYAASNPPAQYSWFINGTFFQSQSTQELFIPNITVNNSGSMCQAHNSVT	272
human CEACAM3		121
human CEACAM6	GLNRTTVMITVSG	286
cyno CEACAM6	GLNRTTVMITVSG	286
human CEACAM5	GLNRTTVMITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWVWNNQSLPVSPRLQL	337
human CEACAM1	GCNRTTVKTIIVTELSPPVAKPQIKASKTTVTGDKDSVNLTCSTNDTGISIRWFKNQSLPSSERMKL	340
human CEACAM3		121
human CEACAM6		286
cyno CEACAM6		286
human CEACAM5	SNDNRITLLSVTRNDVGPYECGIQNKLSVDHSDPVTNLVLYGPD	383
human CEACAM1	SQGNNTLSINPVKREDAGTYWCEVFNPISKNQSDPIMLVNYNALPQENGLSPG	394
human CEACAM3		121

Fig. 2

>TPP-2971_VL

DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYT
GVPDRFTGSGSGTDFTLTISNMQSEDLADYFCQQYSSYPLTFGAGTKLELK

>TPP-2971_VH

QVTLKESGPGILQPSQTLTLTCSFSGFSLSTYGIGVGWIRQPSGKDLEWLAHIWWND
NKYYNTALKSRLTISKDTSNQVFLKIASVDTADTATYYCARISLPYFDYWGQGTTTLTV
SS

>TPP-3187_VL

DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYT
GVPDRFTGSGSGTDFTLTISNMQSEDLADYFCQQYNNYPLTFGAGTKLELK

>TPP-3187_VH

QVTLKESGPGILQPSQTLTLTCSFSGFSLSTYGIGVGWIRQPSGKGLEWLAHIWWND
NKYYNTALKSRLTISKDTSNQVFLKIASVDTADTATYYCARISLPYFDYWGQGTTTLTV
SS

Fig. 3

>TPP-3310_VL

DIQLTQSPSFLSASVGDRVITICKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTG
VPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQYSSYPLTFGGGTKVEIK

>TPP-3310_VH

QVTLRESGPALVKPTQTLTLTCTFSGFSLSYGIGVGWIRQPPGKALEWLAHIWWND
NKYYSTSLKTRLTISKDTSKNQVLTMTNMDPVDATYYCARISLPYFDYWGQGTLT
VSS

>TPP-3714_VL

DIQLTQSPSFLSASVGDRVITICKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTG
VPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQYSSYPLTFGGGTKVEIK

>TPP-3714_VH

QVTLRESGPALVKPTQTLTLTCTFSGFSLSYGIGVGWIRQPPGKALEWLAHIWWND
NKYYSTSLKTRLTISKDTSKNQVLTMTNMDPVDATYYCARISLPYFDYWGQGTLV
VSS

Fig. 4

>TPP-3820_VL

DIQLTQSPSFLSASVGDRVITTCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTG
VPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQYNNYPLTFGGGTKVEIK

>TPP-3820_VH

QVTLRESGPALVKPTQTLTLTCTFSGFSLTTYGIGVGWIRQPPGKGLEWLAHIWWND
NKYYSTSLKTRLTISKDTSKNQVVLMTNMDPVDATYYCARISLPYFDYWGQGLVT
VSS

>TPP-3821_VL

DIQLTQSPSFLSASVGDRVITTCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTG
VPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQYNNYPLTFGGGTKVEIK

>TPP-3821_VH

QVTLRESGPALVKPTQTLTLTCTFSGFSLTTYGIGVGWIRQPPGKALEWLAHIWWND
NKYYSTSLKTRLTISKDTSKNQVVLMTNMDPVDATYYCARISLPYFDYWGQGLVT
VSS

Fig. 5

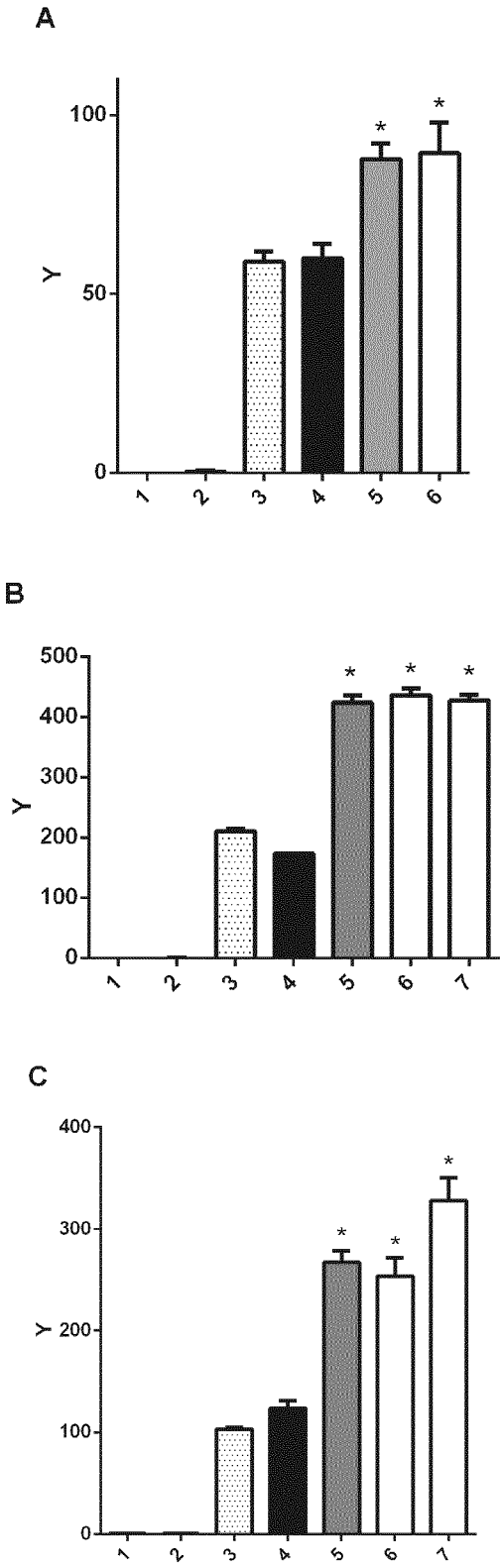


Fig. 6

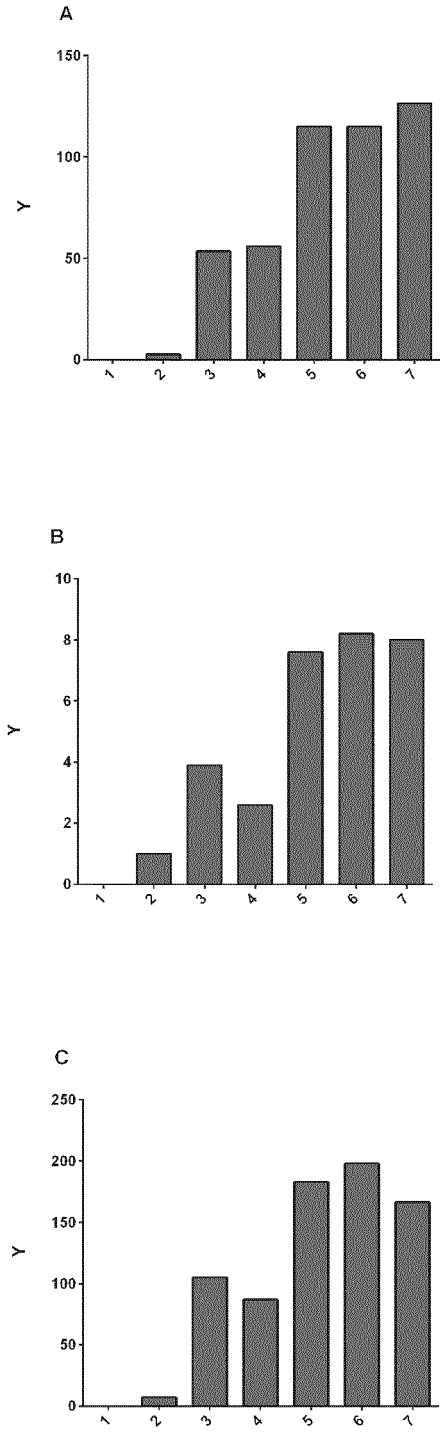


Fig. 7

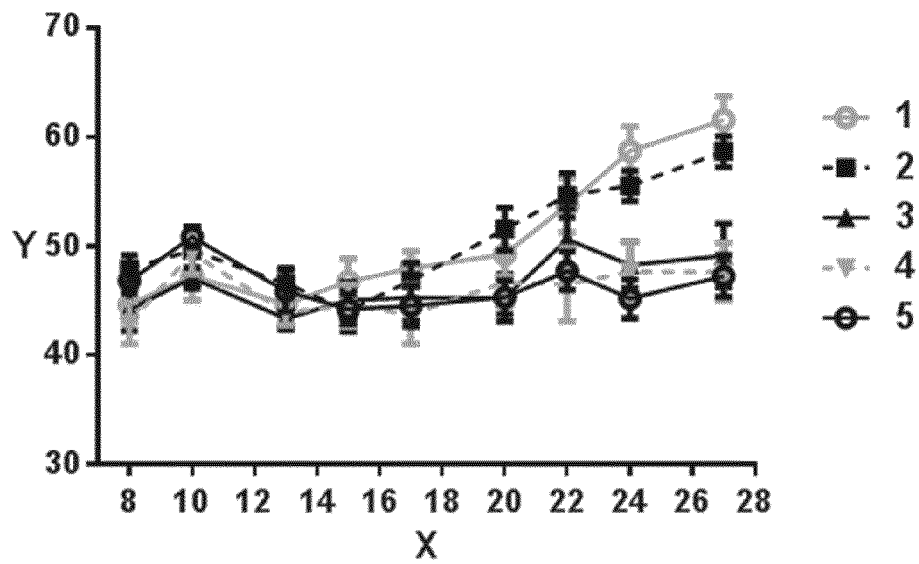


Fig. 8**>TPP-2971 VH (PRT)**

```

QVTLKESGPGILQPSQTLTLTCSFSGFSLSTYGIGVGWIRQPSGKDLEWLAIWWNDNKYYNTALKSRLTISKDTSNNQV
              |-----|               |----HCDR2-----|
              HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLVSS
              |-----|
              HCDR3

```

>TPP-2971 VL (PRT)

```

DIVMTQSQKFMSTSVGDRVSI TCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQS
              |--LCDR1--|               |-----|
              LCDR2

EDLADYFCQQYSSYPITFGAGTKLELK
              |-LCDR3-|

```

>TPP-3186 VH (PRT)

```

QVTLKESGPGILQPSQTLTLTCSFSGFSLSTYGIGVGWIRQPSGKGLEWLAIWWNDNKYYNTALKSRLTISKDTSNNQV
              |-----|               |----HCDR2-----|
              HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLVSS
              |-----|
              HCDR3

```

>TPP-3186 VL (PRT)

```

DIVMTQSQKFMSTSVGDRVSI TCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQS
              |--LCDR1--|               |-----|
              LCDR2

EDLADYFCQQYSSYPITFGAGTKLELK
              |-LCDR3-|

```

>TPP-3187 VH (PRT)

```

QVTLKESGPGILQPSQTLTLTCSFSGFSLSTYGIGVGWIRQPSGKGLEWLAIWWNDNKYYNTALKSRLTISKDTSNNQV
              |-----|               |----HCDR2-----|
              HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLVSS
              |-----|
              HCDR3

```

>TPP-3187 VL (PRT)

```

DIVMTQSQKFMSTSVGDRVSI TCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQS
              |--LCDR1--|               |-----|
              LCDR2

EDLADYFCQQYNNYPITFGAGTKLELK
              |-LCDR3-|

```

>TPP-3308 VH (PRT)

```

QVTLKESGPGILQPSQTLTLTCSFSGFSLSTYGIGVGWIRQPSGKDLEWLAIWWNDNKYYNTALKSRLTISKDTSNNQV
              |-----|               |----HCDR2-----|
              HCDR1

FLKIASVDTADTATYYCARISLPYFDYWGQGTTLVSS
              |-----|
              HCDR3

```

>TPP-3308 VL (PRT)

```

DIVMTQSQKFMSTSVGDRVSI TCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQS

```

```

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

EDLADYFCQQYSSYPITFGAGTKLELK
      | -LCDR3- |

>TPP-3308 Heavy Chain (PRT)
QVTLKESGPGILQPSQTLSTCSFSGFSLSTYIGVGWIRQPSGKDLEWLAHIWVNDNKYYNTALKSRLTISKDTSNNQV
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
                        |-----|      |-----|-----|
                        HCDR1      HCDR2

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

SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPCPAPPVAGPSVFLF
```

```

PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNCKEYKCKV

SNKGLPAPIEKTIKSTKQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSGGS

FFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPG
```

```

>TPP-3308 Light Chain (PRT)
DIVMTQSQKFMTSVGDRVSIITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQS
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
                        |--LCDR1--|      |-----|
                        LCDR2

EDLADYFCQQYSSYPITFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
-----|-----|
      | -LCDR3- |

ESVTEQDSKDSYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
```

```

>TPP-3308 Heavy Chain (DNA)
CAGGTCACACTGAAAAGAGAGCGGCCCTGGCATCCTGCAGCCAGCCAGACCCTGAGCCTGACCTGCAGCTTCAGCGGCTT
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

CAGCCTGAGCACCTACGGCATCGGCGTGGGCTGGATCAGACAGCCAGCGGCAAGGACCTGGAATGGCTGGCCACATCT
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

GGTGAACGACAACAAGTACTACAACACCGCCCTGAAGTCCCGGCTGACCATCAGCAAGGACACCAGCAACAACAGGTG
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
                        VH

TTCCTGAAGATCGCCAGCGTGGACACCGCCGATACCGCCACCTACTACTGCGCCCGGATCAGCCTGCCCTACTTCGACTA
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

CTGGGGCCAGGGCACCACCCTGACCGTGTCTCAGCCAGCACCAAGGGCCCAGCGTGTTCCTCTGGCCCCCTTGTAGCA
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

GAAGCACCAGCGAGTCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCTTGAAC

TCTGGCGCTCTGACAAGCGGCGTGACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCTGTACTCTCTGAGCAGCGTCTG
```

GACAGTGCCCAGCAGCAACTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACA
AGACCGTGGAACGGAAGTGCTGCGTGGAATGCCCCCTTGTCCTGCCCCCTCCAGTGGCTGGCCCTTCCGTGTTCTGTTC
CCCCAAAGCCCAAGGACACCCCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCACAGGA
CCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCA
ACAGCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTG
TCCAAACAAGGGCCTGCCTGCCCCATCGAGAAAACCATCAGCAAGACCAAAGGCCAGCCCCGCGAGCCCCAGGTGTACAC
ACTGCCTCCAAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTCGTGAAAGGCTTCTACCCCTCCGATA
TCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAAACAACCTACAAGACCACCCCCCATGCTGGACAGCGACGGCTCA
TTCTTCTGTACAGCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTGAGCTGCAGCGTGATGCACGA
GGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCTGGC

>TPP-3308 Light Chain (DNA)

GACATCGTGATGACCCAGAGCCAGAAATTCATGAGCACCAGCGTGGGCGACCGGGTGTCCATCACATGCAAGGCCAGCCA
|-----
GAACGTGGGCACCGCGTGGCCTGGTATCAGCAGAAGCCCGGCCAGAGCCCCAAGCTGCTGATCTACAGCGCCAGCAACC
-----v
GGTACACCGCGTGCCCGACAGATTCACAGGCAGCGGCAGCGGCACCGACTTCACCCCTGACCATCAGCAACATGCAGAGC
L-----
GAGGACCTGGCCGACTACTTCTGCCAGCAGTACAGCAGCTACCCCTGACCTTCGGAGCCGGCACCAAGCTGGAACCTGAA

ACGAACCGTGGCCGCTCCAGCGTGTTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTGCTGT
|
GCCTGCTGAACAACCTTCTACCCCGCGAGGCCAAGGTGCAGTGGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAG
GAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCCTGACCTGAGCAAGGCCGACTACGA
GAAGCACAAAGGTGTACGCCCTGCCAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGT
GT

>TPP-3310 VH (PRT)

QVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGIGVGWIRQPPGKALEWLAIHWNDNKYYSTSLKTRLTISKDTSKNQV
|-----| |-----HCDR2-----|
HCDR1
VLTMNMDPVDITATYYCARISLPYFDYWQGTTLTVSS
|-----|
HCDR3

>TPP-3310 VL (PRT)

DIQLTQSPSFLSASVGDVRTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSPRFSGSGSGTEFTLTISLQ
|--LCDR1--| |-----|
LCDR2

EDFATYYCQYSSYP LTFGGG TKVEIK
| -LCDR3- |

>TPP-3310 Heavy Chain (PRT)

QVTLRESGPALVKPTQTLLTCTFSGFSLSTYGIGVGWIRQPPGKALEWLAHIWWDNKYYSTSLKTRLTISKDTSKNQV
|-----VH-----
|-----| |-----HCDR2-----|
HCDR1

VLTMNMDPVDATYYCARISLPYFDYWGQGTTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN

HCDR3

SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLF

PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV

SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPM LSDG S

FFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPG

>TPP-3310 Light Chain (PRT)

DIQLTQSFSFLSASVGDRTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVP SRFSGSGSGTEFTLTISSLQP
|-----VL-----
|--LCDR1--| |-----|
LCDR2

EDFATYYCQYSSYP LTFGGG TKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLN FYPREAKVQWKVDNALQSGNSQ
-----|
| -LCDR3- |

ESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>TPP-3310 Heavy Chain (DNA)

CAAGTGACCCTGAGAGAGTCCGGCCCTGCCCTCGTGAAGCCTACCCAGACCCTGACACTGACCTGCACCTTCTCCGGCTT
|-----

CTCCCTGTCCACCTACGGCATCGGCGTGGGCTGGATCAGACAGCCTCCTGGCAAGGCCCTGGAATGGCTGGCTCACATCT

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

GTGCTGACCATGACCAACATGGACCCCGTGACACCGCCACCTACTACTGCGCCAGAATCTCCCTGCCCTACTTCGACTA

CTGGGGCCAGGGCACCACACTGACCGTCAGCTCAGCTTCCACCAAGGGCCCCCTCCGTGTTCCCTCTGGCCCCCTTGCTCCC
-----|

GGTCCACCTCTGAGTCTACCGCCGCTCTGGGCTGCCTGGTGAAAGACTACTTCCCCGAGCCCGTGACCGTGTCTCTGGAAC

TCTGGCGCCCTGACCTCCGGCGTGACACCTTTCAGCCGTGCTGCAGTCCCTCCGGCCTGTACTCCCTGTCTCTCCGTGGT

GACAGTGCCCTCCTCCAACCTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCTCCAACACCAAGGTGGACA

AGACCGTGGAACGGAAGTGCTGCGTGGAATCCCCACCCTGTCTGCTCCACCTGTGGCTGGCCCCAGCGTGTTCCTGTTTC
CCCCCAAAGCCCAAGGACACCCTGATGATCTCCCGGACCCCCGAAGTGACCTGCGTGGTGGACGTGTCCACAGGGA
CCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCAACAAGCCAAAGCCAGAGAGGAACAGTTCA
ACTCCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTC
TCCAACAAGGGCCTGCCTGCCCCCATCGAAAAGACCATCAGCAAGACCAAGGGCCAGCCCCGCGAGCCCCAGGTGTACAC
ACTGCCCCCAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTGGTGAAAGGCTTCTACCCCTCCGACA
TTGCCGTGGAATGGGAGTCCAACGGACAGCCTGAGAACTACAAGACACCCCCCCCATGCTGGACTCCGACGGCTCA
TTCTTCTGTACTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCTCCTGCTCCGTGATGCACGA
GGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCCCTGAGCCCCGGC

>TPP-3310 Light Chain (DNA)

GATATCCAGCTGACCCAGTCCCCAGCTTCCTGTCTGCCTCTGTGGGCGACAGAGTGACCATCACATGCAAGGCCTCCCA
|-----
GAACGTGGGCACCGCGTGGCTTGGTATCAGCAGAAGCCTGGCAAGGCCCCAAGCTGCTGATCTACTCCGCTCCAACC
-----V
GGTACACCGCGTGCCCTCTAGATTCTCCGGCTCTGGCTCTGGCACCAGCTTTACCCTGACCATCTCCAGCCTGCAGCCC
L-----
GAGGACTTGCACCTACTACTGCCAGCAGTACTCCTCCTACCCCTGACCTTTGGCGGAGGCACCAAGGTGGAATCAA

GCGGACCGTGGCCGCTCCCTCCGTGTTTATCTTCCACCCCTCCGACGAGCAGCTGAAGTCCGGCACAGCTTCCGTGCTGT
|
GCCTGCTGAACAACTTCTACCCCGCGAGGCCAAGGTGCAGTGAAGGTGGACAACGCCCTGCAGTCCGGCAACTCCAG
GAATCCGTGACCGAGCAGGACTCCAAGGACAGCACCTACTCCCTGTCTCCACCTGACCCTGTCCAAGGCCGACTACGA
GAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGTCTTCAACCGGGCGGAGT
GT

>TPP-3322 VH (PRT)

QVTLKESGPGILQPSQTLSTLTCFSFGFSLSTYGIGVGCIRQPSGKGLEWLAIWWNDNKYYNTALKSRLTISKDTSNNQV
|-----| |-----HCDR2-----|
HCDR1
FLKIASVDTADTATYYCARISLPYFDYWGQGTTLVSS
|-----|
HCDR3

>TPP-3322 VL (PRT)

DIVMTQSQKFMSTSVGDRVSIICKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTFTISNMQS
|--LCDR1--| |-----|
LCDR2
EDLADYFCQQYSSYPLTFGAGTKLELK
|-LCDR3-|

>TPP-3322 Heavy Chain (PRT)

```

QVTLKESGPGILQPSQTLTLTCSFSGFSLSTYGIGVGCIRQPSGKGLEWLAHIWWDNKKYYNTALKSRLTISKDTSNNQV
|-----VH-----|
|-----|
|-----HCDR1-----|
|-----HCDR2-----|
FLKIASVDTADTATYYCARISLPYFDYWGQGTTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN
-----|
|-----|
HCDR3
SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTKVERKCCVECPFCPAPPVAGPSVFLF

PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV

SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSDGS

FFLYSKLTVDKSRWQQGNVFSQSVMHREALHNHYTQKSLSLSPG

```

>TPP-3322 Light Chain (PRT)

```

DIVMTQSQKFMSTSVGDRVSIITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTFTISNMQS
|-----VL-----|
|-----LCDR1-----|
|-----|
LCDR2
EDLADYFCQQYSSYPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
-----|
|-----LCDR3-----|
ESVTEQDSKDSSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

```

>TPP-3322 Heavy Chain (DNA)

```

CAGGTACACACTGAAAGAGAGCGGCCCTGGCATCCTGCAGCCAGCCAGACCTGAGCCTGACCTGCAGCTTCAGCGGCTT
|-----|
CAGCCTGAGCACCTACGGCATCGGCTGGGCTGCATCAGACAGCCAGCGGCAAGGGCCTGGAATGGCTGGCCACATCT
-----|
GGTGAACGACAACAAGTACTACAACACCGCCCTGAAGTCCCGGCTGACCATCAGCAAGGACACCAGCAACAACAGGTG
-----VH-----|
TTCCTGAAGATCGCCAGCGTGGACACCGCCGATACCGCCACCTACTACTGCGCCCGGATCAGCCTGCCCTACTTCGACTA
-----|
CTGGGGCCAGGGCACCACCTGACCGTGTCTCAGCCAGCACCAAGGGCCCCAGCGTGTTCCTCTGGCCCCCTTGTAGCA
-----|
GAAGCACCAGCGAGTCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCGTGACCGTGTCTGGAAC
TCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCTGTACTCTCTGAGCAGCGTCGT
GACAGTGGCCAGCAGCAACTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACA
AGACCGTGAACGGAAGTGCTGCGTGAATGCCCCCTTGTCCTGCCCTCCAGTGGCTGGCCCTTCCTGTTCCTGTTTC

```

CCCCAAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCACAGAGGA
CCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGACACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCA
ACAGCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTCAAGGTG
TCCAACAAGGGCCTGCCTGCCCCATCGAGAAAACCATCAGCAAGACCAAGGCCAGCCCCGCGAGCCCCAGGTGTACAC
ACTGCCTCCAAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTCGTGAAGGCTTCTACCCCTCCGATA
TCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCAACCCCCCATGCTGGACAGCGACGGCTCA
TTCTTCTGTACAGCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTGAGCTGCAGCGTGATGCACGA
GGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCTGGC

>TPP-3322 Light Chain (DNA)

GACATCGTGATGACCCAGAGCCAGAAATTCATGAGCACCAGCGTGGGCGACCGGGTGTCCATCACATGCAAGGCCAGCCA
|-----
GAACGTGGGCACCGCGTGGCCTGGTATCAGCAGAAGCCCGGCCAGAGCCCCAAGCTGCTGATCTACAGCGCCAGCAACC
-----V
GGTACACCGCGTGCCCGACAGATTCACAGGCAGCGGCAGCGGCACCGACTTCACCTTCACCATCAGCAACATGCAGAGC
L-----
GAGGACCTGGCCGACTACTTCTGCCAGCAGTACAGCAGCTACCCCTGACCTTCGGAGCCGGCACCAAGCTGGAAGTAA

ACGAACCGTGGCCGCTCCAGCGTGTTCATCTTCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCTGTGT
|
GCCTGTGAACAACTTCTACCCCGCGAGGCCAAGGTGCAGTGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAG
GAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCTGACCTGAGCAAGGCCGACTACGA
GAAGCACAAAGGTGTACGCCTGCCAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGT
GT

>TPP-3323 VH (PRT)

QVTLKESGPGILQPSQTLTLTCSFSGFSLTTYGIGVGWIRQPSGKGLEWLAIWWNDNKYYNTALKSRLTISKDTSNNQV
|-----| |-----HCDR2-----|
HCDR1
FLKIASVDTADTATYYCARISLPYFDYWGQGTTLTVSS
|-----|
HCDR3

>TPP-3323 VL (PRT)

DIVMTQSQKFMSTSVGDRVSIICKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISMQS
|--LCDR1--| |-----|
LCDR2
EDLADYFCQQYNNYPLTFGAGTKLELK
|-LCDR3-|

>TPP-3323 Heavy Chain (PRT)

QVTLKESGPGILQPSQTLTLTCSFSGFSLTTYGIGVGWIRQPSGKGLEWLAIWWNDNKYYNTALKSRLTISKDTSNNQV

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

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

SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTKVERKCCVECPPCPAPPVAGPSVFLF

PPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHQDNLNGKEYKCKV

SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSGGS

FFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPG
```

>TPP-3323 Light Chain (PRT)

```
DIVMTQSQKFMSTSVGDRVSIICKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQS
|-----VL-----|
|---LCDR1---|
|-----|
LCDR2

EDLADYFCQQYNNYPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQ
-----|
|---LCDR3---|

ESVTEQDSKSDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
```

>TPP-3323 Heavy Chain (DNA)

```
CAAGTGACCCTGAAGAGTCCGGCCCTGGCATCCTGCAGCCTTCCCAGACCCTGTCCCTGACCTGCTCCTTCTCCGGCTT
|-----|

CTCCCTGACCACCTACGGCATCGGCGTGGGCTGGATCAGACAGCCTTCTGGCAAGGGCCTGGAATGGCTGGCCACATCT
-----

GGTGAACGACACAAGTACTACAACACCGCCCTGAAGTCCCGGCTGACCATCTCCAAGGACACCTCCAACAACAGGTG
-----VH-----

TTCCTGAAGATCGCCTCCGTGGACACCGCCGATACCGCCACCTACTACTGCGCCCGGATCTCCCTGCCCTACTTCGACTA
-----

TTGGGGCCAGGGCACCACCTGACCGTCAGCTCAGCTTCCACCAAGGGCCCCCTCCGTGTTCCCTCTGGCCCCCTTGCTCCC
-----|

GGTCCACCTCTGAGTCTACCGCGCTCTGGGCTGCCTGGTGAAAGACTACTTCCCCGAGCCCGTGACCGTGTCTTGAAC

TCTGGCGCCCTGACCTCCGGCGTGACACCTTTCCAGCCGTGCTGCAGTCCCTCCGGCCTGTACTCCCTGTCTCTCCGTGGT

GACAGTGCCTCCTCCAACCTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCTCCAACACCAAGGTGGACA

AGACCGTGAACGGAAGTCTGCGTGGAATGCCCCACCCTGTCTGTCCACCTGTGGCTGGCCCCAGCGTGTCTCTGTTT

CCCCCAAAGCCCAAGGACACCCTGATGATCTCCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGACGTGTCCACAGGGA
```

CCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCA
ACTCCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGAAGGTC
TCCAACAAGGGCCTGCCTGCCCCATCGAAAAGACCATCAGCAAGACCAAGGGCCAGCCCCGCGAGCCCCAGGTGTACAC
ACTGCCCCCAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTGGTGAAAGGCTTCTACCCCTCCGACA
TTGCCGTGGAATGGGAGTCCAACGGACAGCCTGAGAACAATAACAAGACCACCCCCCATGCTGGACTCCGACGGCTCA
TTCTTCCTGTACTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCTCCTGCTCCGTGATGCACGA
GGCCTTGACAACCACCTACACCAGAAGTCCCTGTCCCTGAGCCCCGGC

>TPP-3323 Light Chain (DNA)

GACATCGTGATGACCCAGTCCCAGAAATTCATGTCCACCTCCGTGGGCGACCGGGTGTCCATCACATGCAAGGCCTCTCA
|-----
GAACGTGGGCACCGCGTGGCCTGGTATCAGCAGAAGCCTGGCCAGTCCCCAAGCTGCTGATCTACTCCGCCTCCAACC
-----V
GGTACACCGGCGTGCCGATAGATTACCGGCTCTGGCTCTGGCACCAGCTTACCCTGACCATCTCCAACATGCAGTCC
L-----
GAGGACCTGGCCGACTACTTCTGCCAGCAGTACAACAATAACCCCTGACCTTCGGCGCTGGCACCAAGCTGGAAGTAA

GAGAACCGTGGCCGCTCCCTCCGTGTTATCTTCCACCCCTCCGACGAGCAGCTGAAGTCCGGCACAGCTTCCGTGCTGT
|
GCCTGTGAACAACCTTCTACCCCGCGAGGCCAAGGTGCAGTGAAGGTGGACAACGCCCTGCAGTCCGGCAACTCCCAG
GAATCCGTGACCGAGCAGGACTCCAAGGACAGCACCTACTCCCTGTCTCTACCTGACCCTGTCCAAGGCCGATTACGA
GAAGCACAAGGTGTACGCCTGCCAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGTCTTTCAACCGGGCGAGT
GT

>TPP-3705 VH (PRT)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSLYQMHWVRQAPGKGLEWVSWISFSGGNTGYADSVKGRFTISRDN SKNTLY
|---| |-----HCDR2-----|
HCDR1
LQMSLRAEDTAVYYCARATGYSSPWYLDPWGQGTLVTVSS
|--HCDR3--|

>TPP-3705 VL (PRT)

DIQMTQSPSSLSASVGDRVTITCQASHEIDNYLNWYQQKPGKAPKLLIYDAYWLKTGVPSRFSGSGSGTDFTLTISSLQP
|--LCDR1--| |-----|
LCDR2
EDIATYYCQGYDDL SVTFGGGTKVDIK
|-LCDR3-|

>TPP-3705 Heavy Chain (PRT)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSLYQMHWVRQAPGKGLEWVSWISFSGGNTGYADSVKGRFTISRDN SKNTLY
|-----VH-----
|---| |-----HCDR2-----|
HCDR1

DIQMTQSPSSLSASVGDRVITTCQASHEIDNYLNWYQQKFGKAPKLLIYDAYWLKTGVPSTRFSGSGGTDFLTITISLQP
|-----VL-----
 |--LCDR1--| |----|
 LCDR2

EDIATYYCQGYDDLSTVFGGGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQ
-----|
 |-LCDR3-|

ESVTEQDSKSDSTYSLSSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC

[illegible]

AACAGTTCAACTCCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAG
 TGCAAGGTCTCCAACAAGGGCCTGCCTGCCCCATCGAAAAGACCATCAGCAAGACCAAGGGCCAGCCCCGCGAGCCCCA
 GGTGTACACACTGCCCCCAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTGGTGAAAGGCTTCTACC
 CCTCCGACATTGCCGTGGAATGGGAGTCCAACGGACAGCCTGAGAACAATAAGACCACCCCCCATGCTGGACTCC
 GACGGCTCATTCTTCTGTACTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCTCTGCTCCGT
 GATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCCCTGAGCCCCGGC

>TPP-3705 Light Chain (DNA)

GACATCCAGATGACCCAGAGCCCTTCCAGCCTGTCCGCCTCTGTGGGCGACAGAGTGACCATCACCTGTAGGCCTCCCA
 |-----
 CGAGATCGACAACCTACCTGAAGTGGTATCAGCAGAAGCCCGCAAGGCCCCAAGCTGCTGATCTACGATGCCTACTGGC
 -----V
 TGAAAACCGGCGTGCCTCCAGATTCTCCGGCTCTGGCTCTGGCACCAGCTTTACCTGACCATCTCCAGCCTGCAGCCC
 L-----
 GAGGATATCGCCACCTACTATTGTGAGGGCTACGACGACCTGTCCGTGACCTTTGGCGGAGGCACCAAGGTGGACATCAA

 GCGGACAGTGGCCGCTCCCTCCGTGTTTATCTTCCACCCCTCCGACGAGCAGCTGAAGTCCGGCACAGCTTCCGTGCTGT
 |
 GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAGGTGCAGTGGAAAGTGATAACGCCCTGCAGTCCGGCAACTCCAG
 GAATCCGTGACCGAGCAGGACTCCAAGGACAGCACCTACTCCCTGTCTCCACCCCTGACCTGTCCAAGGCCGACTACGA
 GAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGTCTTTCAACCGGGGCGAGT
 GT

>TPP-3707 VH (PRT)

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSLYQMHWVRQAPKGLEWVSWISFSGGNTGYADSVKGRFTISRDNKNTLY
 |---| |-----HCDR2-----|
 HCDR1
 LQMNSLRAEDTAVYYCARATGYSSPWYLDPWGQGTLLTVSS
 |--HCDR3---|

>TPP-3707 VL (PRT)

DIQMTQSPSSLSASVGRVTITCQASHEIDNYLNWYQQKPGKAPKLLIYDAYWSKTGVPSRFSGSGSGTDFTLTISLQF
 |--LCDR1--| |-----|
 LCDR2
 EDIATYYCQGYDDLSTFTGGGTVKDIK
 |--LCDR3--|

>TPP-3707 Heavy Chain (PRT)

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSLYQMHWVRQAPKGLEWVSWISFSGGNTGYADSVKGRFTISRDNKNTLY
 |-----VH-----|
 |---| |-----HCDR2-----|
 HCDR1
 LQMNSLRAEDTAVYYCARATGYSSPWYLDPWGQGTLLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEFVTV
 -----|

|--HCDR3---|

SWNSGALTSGVHTFFAVLQSSGLYSLSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPCPAPPVAGPSV

FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYK

CKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDS

DGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPG

>TPP-3707 Light Chain (PRT)

DIQMTQSPSSLSASVGDRVTITCQASHEIDNYLNWYQQKPGKAPKLLIYDAYWSKTGVPSRFSGSGSGTDFTLTISSLQP

|-----VL-----|
|--LCDR1--| |-----|
LCDR2

EDIATYYCQGYDDLSTFTGGGKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNFFYPREAKVQWKVDNALQSGNSQ

-----|
| -LCDR3- |

ESVTEQDSKSDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>TPP-3707 Heavy Chain (DNA)

GAAGTGCAGCTGGTGAATCCGGCGGAGGCCTGGTGCAGCCTGGCGGATCTCTGAGACTGTCTTGCGCCCTCCGGCTT

-----|
CACCTTCAGCCTGTACCAGATGCACTGGGTGCGACAGGCCCTGGCAAGGACTGGAATGGGTGTCCTGGATCTCCTTCT
-----|

CCGGCGGCAATACCGGCTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAACCTCAAGAACACCCGTGAC
-----VH-----|

CTGCAGATGAACTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCTAGAGCCACCGGCTACTCCTCCCCCTGGTA

-----|
TCTGGATCCTTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCTTCCACCAAGGGCCCCCTCCGTGTTCCCTCTGGCCC
-----|

CTTGCTCCCGGTCCACCTCTGAGTCTACCGCCGCTCTGGGTGCGCTGGTGAAAGACTACTTCCCCGAGCCCGTGACCGTG

TCCTGGAACCTCTGGCGCCCTGACCTCCGGCGTGACACCTTTCAGCCGTGCTGCAGTCCTCCGGCCTGTACTCCCTGTC

CTCCGTGGTGACAGTGCCCTCCTCCAACCTCGGCACCCAGACCTACACCTGTAACTGGACCACAAGCCCTCCAACACCA

AGGTGGACAAGACCGTGGAACGGAAGTGTGCGTGGAATGCCACCCCTGCTCTCCACCTGTGGCTGGCCCCAGCGTG

TTCTGTTCCCCCAAAGCCCAAGGACACCCGTGATGATCTCCCGACCCCGAAGTGACCTGCGTGGTGGTGACGTGTC

CCACGAGGACCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGACAACGCCAAGACCAAGCCCAGAGAGG

AACAGTTCAACTCCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAGAGTACAAG

TGCAAGGTCTCCAACAAGGGCCTGCCTGCCCCATCGAAAAGACCATCAGCAAGACCAAGGGCCAGCCCCGCGAGCCCCA
 GGTGTACACACTGCCCCCAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTGGTGAAAGGCTTCTACC
 CCTCCGACATTGCCGTGGAATGGGAGTCCAACGGACAGCCTGAGAACTACAAGACCACCCCCCATGCTGGACTCC
 GACGGCTCATTCTTCTGTACTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCTCTGCTCCGT
 GATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCCCTGAGCCCCGGC

>TPP-3707 Light Chain (DNA)

GACATCCAGATGACCCAGAGCCCTTCCAGCCTGTCCGCCTCTGTGGGCGACAGAGTGACCATCACCTGTCAGGCCTCCCA
 |-----
 CGAGATCGACAACCTACCTGAACCTGGTATCAGCAGAAGCCCGCAAGGCCCCCAAGCTGCTGATCTACGACGCCTACTGGT
 -----V
 CCAAGACCGCGTGCCCTCCAGATTCTCCGGCTCTGGCTCTGGCACCAGCTTTACCCTGACCATCTCCAGCCTGCAGCCC
 L-----
 GAGGATATCGCCACCTACTATTGTACGGGCTACGACGACCTGTCCGTGACCTTTGGCGGAGGCACCAAGGTGGACATCAA

 GCGGACAGTGGCCGCTCCCTCCGTGTTTATCTTCCACCCCTCCGACGAGCAGCTGAAGTCCGGCACAGCTTCCGTGCTGT
 |
 GCCTGCTGAACAACCTTACCCCCGCGAGGCCAAGGTGCAGTGGAAAGTGGATAACGCCCTGCAGTCCGGCAACTCCAG
 GAATCCGTGACCGAGCAGGACTCCAAGGACAGCACCTACTCCCTGTCTCCACCCCTGACCTGTCCAAGGCCGACTACGA
 GAAGCACAAGGTGTACGCCTGCCAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGTCTTTCAACCGGGGCGAGT
 GT

>TPP-3714 VH (PRT)

QVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGIGVGWIRQPPGKALEWLAHIWVNDNKYYSTSLKTRLTISKDTSKNQV
 |-----| |-----HCDR2-----|
 HCDR1
 VLTMTNMDPVDATYYCARISLPYFDYWQGTLVTVSS
 |-----|
 HCDR3

>TPP-3714 VL (PRT)

DIQLTQSPSFLSASVGDVITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSPRFSGSGSGTEFTLTISLQF
 |--LCDR1--| |-----|
 LCDR2
 EDFATYYCQYSSYPITFGGGTKVEIK
 |--LCDR3--|

>TPP-3714 Heavy Chain (PRT)

QVTLRESGPALVKPTQTLTLTCTFSGFSLSTYGIGVGWIRQPPGKALEWLAHIWVNDNKYYSTSLKTRLTISKDTSKNQV
 |-----VH-----|
 |-----| |-----HCDR2-----|
 HCDR1
 VLTMTNMDPVDATYYCARISLPYFDYWQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN

 |-----|
 HCDR3

SGALTSGVHTFFAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDPKPSNTKVDKTVKCCVECPPCAPPVAGPSVFLF

PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHQDNLNGKEYKCKV

SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPEMLDSGGS

FFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG

>TPP-3714 Light Chain (PRT)

DIQLTQSPSFLSASVGDRTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISLQP
|-----VL-----
|-----L1-----L2-----
|-----L3-----

EDFATYYCQYSSYPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQ
-----L3-----
|-----L3-----

ESVTEQDSKSDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

>TPP-3714 Heavy Chain (DNA)

CAAGTGACCCCTGAGAGAGTCCGGCCCTGCCCTCGTGAAGCCTACCCAGACCCCTGACACTGACCTGCACCTTCTCCGGCTT
|-----
CTCCCTGTCCACCTACGGCATCGGCGTGGGCTGGATCAGACAGCCTCCTGGCAAGGCCCTGGAATGGCTGGCTCACATCT

GGTGAACGACACAAGTACTACTCCACCTCCCTGAAAACCCGGCTGACCATCTCCAAGGACACCTCCAAGAACCAGGTG
-----VH-----
GTGCTGACCATGACCAACATGGACCCCGTGGACACCGCCACCTACTACTGCGCCAGAATCTCCCTGCCCTACTTCGACTA

CTGGGGCCAGGGCACACTCGTGACCGTCAGCTCAGCTTCCACCAAGGGCCCTCCGTGTTCCCTCTGGGCCCTTGCTCCC

GGTCCACCTCTGAGTCTACCGCGCTCTGGGCTGCCTGGTGAAGACTACTTCCCCGAGCCCGTGACCGTGTCTGGAAC

TCTGGCGCCCTGACCTCCGGCGTGACACCTTTCCAGCCGTGCTGCAGTCTCCGGCCTGTACTCCCTGTCTCCGTGGT

GACAGTGCCCTCCTCCAACCTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCTCCAACACCAAGGTGGACA

AGACCGTGAACGGAAGTGTGCGTGAATGCCACCCCTGTCTGCTCCACCTGTGGCTGGCCCCAGCGTGTCTCTGTT

CCCCCAAAGCCCAAGGACACCTGATGATCTCCCGGACCCCGAAGTGACCTGCGTGGTGGTGGACGTGTCCACGAGGA

CCCCGAGGTGCAAGTTCAATTGGTACGTGGACGGCGTGAAGTGACAACGCCAAGACCAAGCCAGAGAGGAACAGTTCA

ACTCCACCTTCCGGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGAAGGTC

TCCAACAAGGGCCTGCCTGCCCCATCGAAAAGACCATCAGCAAGACCAAGGGCCAGCCCCGCGAGCCCCAGGTGTACAC

ACTGCCCCCAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTGGTGAAAGGCTTCTACCCCTCCGACA
TTGCCGTGGAATGGGAGTCCAACGGACAGCCTGAGAACTACAAGACCACCCCCCATGCTGGACTCCGACGGCTCA
TTCTTCCTGTACTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCTCCTGCTCCGTGATGCACGA
GGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCCCTGAGCCCCGGC

>TPP-3714 Light Chain (DNA)

GATATCCAGCTGACCCAGTCCCCAGCTTCTGTCTGCCTCTGTGGGCGACAGAGTGACCATCACATGCAAGGCCTCCCA
|-----
GAACGTGGGCACCGCGTGGCTTGGTATCAGCAGAAGCCTGGCAAGGCCCCAAGCTGCTGATCTACTCCGCCTCCAACC
-----V
GGTACACCGCGTGCCTCTAGATTCTCCGGCTCTGGCTCTGGCACCGAGTTTACCCTGACCATCTCCAGCCTGCAGCCC
L-----
GAGGACTTCGCCACCTACTACTGCCAGCAGTACTCCTCCTACCCCTGACCTTTGGCGGAGGCACCAAGGTGAAATCAA

GCGGACCGTGGCCGCTCCCTCCGTGTTTATCTTCCACCCCTCCGACGAGCAGCTGAAGTCCGGCACAGCTTCCGTGCTGT
|
GCCTGCTGAACAACTTCTACCCCGCGAGGCCAAGGTGCAGTGAAGGTGGACAACGCCCTGCAGTCCGGCAACTCCAG
GAATCCGTGACCGAGCAGGACTCCAAGGACAGCACCTACTCCTGTCTCCACCCCTGACCCTGTCCAAGGCCGACTACGA
GAAGCACAAGGTGTACGCCTGCCAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGTCTTTC AACGGGGCGAGT
GT

>TPP-3820 VH (PRT)

QVTLRESGPALVKPTQTLLTCTFSGFSLTTYGIGVGWIRQPPGKGLEWLAHIWVNDNKYYSTSLKTRLTISKDTSKNQV
|-----| |-----HCDR2-----|
HCDR1
VLTMTNMDPVDATYYCARISLPYFDYWQGTLVTVSS
|-----|
HCDR3

>TPP-3820 VL (PRT)

DIQLTQSPSFLSASVGDRTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSPRFSGSGSGTEFTLTISLQF
|--LCDR1--| |-----|
LCDR2
EDFATYYCQQYNNYPLTFGGGTKVEIK
|-LCDR3-|

>TPP-3820 Heavy Chain (PRT)

QVTLRESGPALVKPTQTLLTCTFSGFSLTTYGIGVGWIRQPPGKGLEWLAHIWVNDNKYYSTSLKTRLTISKDTSKNQV
|-----VH-----
|-----| |-----HCDR2-----|
HCDR1
VLTMTNMDPVDATYYCARISLPYFDYWQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN

HCDR3
SGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPCPAPPVAGPSVFLF

PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV

SNKGLPAPIEKTIKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGS

FFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG

>TPP-3820 Light Chain (PRT)

DIQLTQSPSFSLASVGDRTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQP
|-----VL-----
|-----L-CDR1-----|-----L-CDR2-----|

EDFATYYCQQYNNYPLTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ

|-----L-CDR3-----|

ESVTEQDSKSDSTYSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC

>TPP-3820 Heavy Chain (DNA)

CAAGTGACCCCTGAGAGAGTCCGGCCCTGCCCTCGTGAAGCCTACCCAGACCCCTGACACTGACCTGCACCTTCAGCGGCTT
|-----
CAGCCTGACCACCTACGGCATCGGCGTGGGCTGGATCAGACAGCCTCCTGGCAAGGGCCTGGAATGGCTGGCCACATCT

GGTGAACGACACAAGTACTACAGCACCAGCCTGAAAACCCGGCTGACCATCAGCAAGGACACCAGCAAGAACCAGGTG
-----VH-----
GTGCTGACCATGACCAACATGGACCCCGTGGACACCGCCACCTACTACTGCGCCAGAATCAGCCTGCCCTACTTCGACTA

CTGGGGCCAGGGCACCTCGTGACAGTGTCTATCAGCCAGCACCAAGGGCCCCAGCGTGTTCCTCTGGCCCCCTTGTAGCA
-----|
GAAGCACCAGCGAGTCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCTGGAAC
TCTGGCGCTCTGACAAGCGGCGTGACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCTGTACTCTCTGAGCAGCGTCGT
GACAGTGCCAGCAGCAACTTCGGCACCCAGACCTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACA
AGACCGTGGAACGGAAGTCTGCGTGGAATGCCCCCTTGTCCTGCCCCCTCCAGTGGCTGGCCCTTCCGTGTCTCCTGTT
CCCCCAAGCCCAAGGACACCTGATGATCAGCCGACCCCGAAGTGACCTGCGTGGTGGATGTGTCCACAGGGA
CCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGAAGTGACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCA
ACAGCACCTTCCGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGAAGGTG
TCCAACAAGGGCCTGCCTGCCCCATCGAGAAAACCATCAGCAAGACCAAGGCCAGCCCCGAGCCCCAGGTGTACAC
ACTGCCTCCAAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTCGTGAAAGGCTTCTACCCCTCCGATA

TCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACTACAAGACCACCCCCCATGCTGGACAGCGACGGCTCA
TTCTTCCTGTACAGCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTTCAGCTGCAGCGTGATGCACGA
GGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCTGGC

>TPP-3820 Light Chain (DNA)

GATATCCAGCTGACCCAGAGCCCCAGCTTTCTGAGCGCCAGCGTGGGCGACAGAGTGACCATCACATGCAAGGCCAGCCA
|-----
GAACGTGGGCACAGCCGTGGCCTGGTATCAGCAGAAGCCTGGCAAGGCCCCCAAGCTGCTGATCTACAGCGCCAGCAACC
-----V
GGTACACCGCGGTGCCAGCAGATTTTCTGGCAGCGGCTCCGGCACCGAGTTCACCCCTGACAATCAGCAGCCTGCAGCCC
L-----
GAGGACTTCGCCACCTACTACTGCCAGCAGTACAACAACCTACCCCTGACCTTCGGCGGAGGCACCAAGGTGAAATTAA

ACGAACCGTGGCCGCTCCCAGCGTGTTCATCTTCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCTGTGT
|
GCCTGCTGAACAACCTTACCCCCGCGAGGCCAAGGTGCAGTGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAG
GAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCCTGACCCTGAGCAAGGCCGACTACGA
GAAGCACAAGGTGTACGCCTGCCAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGT
GT

>TPP-3821 VH (PRT)

QVTLRESGPALVKPTQTTLTLCTFSGFSLSTYGIGVGWIRQPPGKALEWLAHIWWDNKKYSTSLKTRLTISKDTSKNQV
|-----|
HCDR1 |-----HCDR2-----|
VLTMTNMDPVDATYYCARISLPYFDYWGQGLVTVSS
|-----|
HCDR3

>TPP-3821 VL (PRT)

DIQLTQSPSFLSASVGDVITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSPRFSGSGSGTEFTLTISLQV
|--LCDR1--| |-----|
LCDR2
EDFATYYCQQYNNYPLTFGGGTKVEIK
|-LCDR3-|

>TPP-3821 Heavy Chain (PRT)

QVTLRESGPALVKPTQTTLTLCTFSGFSLSTYGIGVGWIRQPPGKALEWLAHIWWDNKKYSTSLKTRLTISKDTSKNQV
|-----VH-----
|-----| |-----HCDR2-----|
HCDR1
VLTMTNMDPVDATYYCARISLPYFDYWGQGLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN

|-----|
HCDR3
SGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPCPAPPVAGPSVFLF
PPPKDITLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV

SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGS

FFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPG

>TPP-3821 Light Chain (PRT)

DIQLTQSFSLASVGDVITITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYTGVPSRFSGSGSGTEFTLTISSLQP
|-----VL-----
|-----L1-----L2-----
|-----L3-----
|-----L4-----

EDFATYYCQYNNYPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ

|-----L5-----
|-----L6-----

ESVTEQDSKSDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>TPP-3821 Heavy Chain (DNA)

CAGGTCACACTGAGAGAGTCCGGCCCTGCCCTGGTGAAACCCACCCAGACCCCTGACCCCTGACATGCACCTTCAGCGGCTT
|-----
CAGCCTGAGCACCTACGGCATCGGCGTGGGCTGGATCAGACAGCCCCCTGGCAAGGCCCTGGAATGGCTGGCCACATCT

GGTGGAACGACAACAAGTACTACAGCACCAGCCTGAAACCCGGCTGACCATCAGCAAGGACACCAGCAAGAACCAGGTG
-----VH-----
GTGCTGACCATGACCAACATGGACCCCGTGGACACCGCCACCTACTACTGCGCCCGGATCAGCCTGCCCTACTTCGACTA

CTGGGGCCAGGGCACCCTGGTGACCGTGTCTCAGCCAGCACCAAGGGCCCCAGCGTGTTCCTCTGGCCCCCTTGTAGCA

GAAGCACCAGCGAGTCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCTTGAAC
TCTGGCGCTCTGACAAGCGGCGTGACACCTTTCCAGCCGTGCTGCAGAGCAGCGGCTGTACTCTCTGAGCAGCGTCTGT
GACAGTGGCCAGCAGCAACTTCGGCAGCCAGACCTACACCTGTAACGTGGACCACAAGCCAGCAACACCAAGGTGGACA
AGACCGTGAACGGAAGTGTGCGTGGAATGCCCCCTTGTCTGCCCCCTCCAGTGGCTGGCCCTTCCGTGTTCTCTGTTT
CCCCAAAGCCCAAGGACACCCTGATGATCAGCCGGAACCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCACAGGGA
CCCCGAGGTGAGTTCAATTGGTACGTGGACGGCGTGGAAGTGACACAACGCCAAGACCAAGCCAGAGGGAACAGTTCA
ACAGCACCTTCCGGTGGTGTCCGTGCTGACCGTGGTGCATCAGGACTGGCTGAACGGCAAAGAGTACAAGTGAAGGTG
TCCAACAAGGGCCTGCCTGCCCCATCGAGAAAACCATCAGCAAGACCAAAGGCCAGCCCCGCGAGCCCCAGGTGTACAC
ACTGCCTCCAAGCCGGGAAGAGATGACCAAGAACCAGGTGTCCCTGACCTGTCTCGTGAAGGCTTCTACCCCTCCGATA
TCGCCGTGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCATGTCTGGACAGCGACGGCTCA

TTCTTCCTGTACAGCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTGAGCTGCAGCGTGATGCACGA

GGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCTGGC

>TPP-3821 Light Chain (DNA)

GATATCCAGCTGACCCAGAGCCCCAGCTTTCTGAGCGCCAGCGTGGGCGACAGAGTGACCATCACATGCAAGGCCAGCCA
|-----

GAACGTGGGCACAGCCGTGGCCTGGTATCAGCAGAAGCCTGGCAAGGCCCCAAGCTGCTGATCTACAGCGCCAGCAACC
-----V

GGTACACCGCGTGCCACAGAGATTTCTGGCAGCGGCTCCGGCACCGAGTTCACCCTGACAATCAGCAGCCTGCAGCCC
L-----

GAGGACTTCGCCACCTACTACTGCCAGCAGTACAACAATAACCCCTGACCTTCGGCGGAGGCACCAAGGTGAAATTAA

ACGAACCGTGGCCGCTCCAGCGTGTTCATCTTCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCTGT
|

GCCTGCTGAACAACCTTCTACCCCGCGAGGCCAAGGTGCAGTGGGAAGGTGGACAATGCCCTGCAGAGCGGCAACAGCCAG

GAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCCTGACCCCTGAGCAAGGCCGACTACGA

GAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCGTGACCAAGAGCTTCAACCGGGGCGAGT

GT

Fig. 9

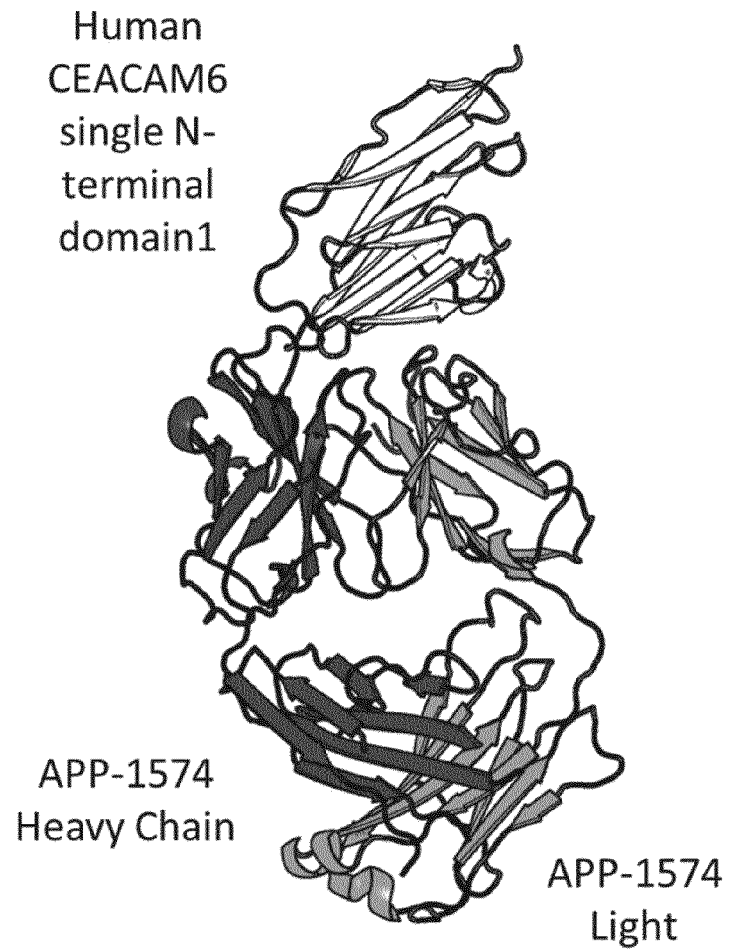


Fig. 10

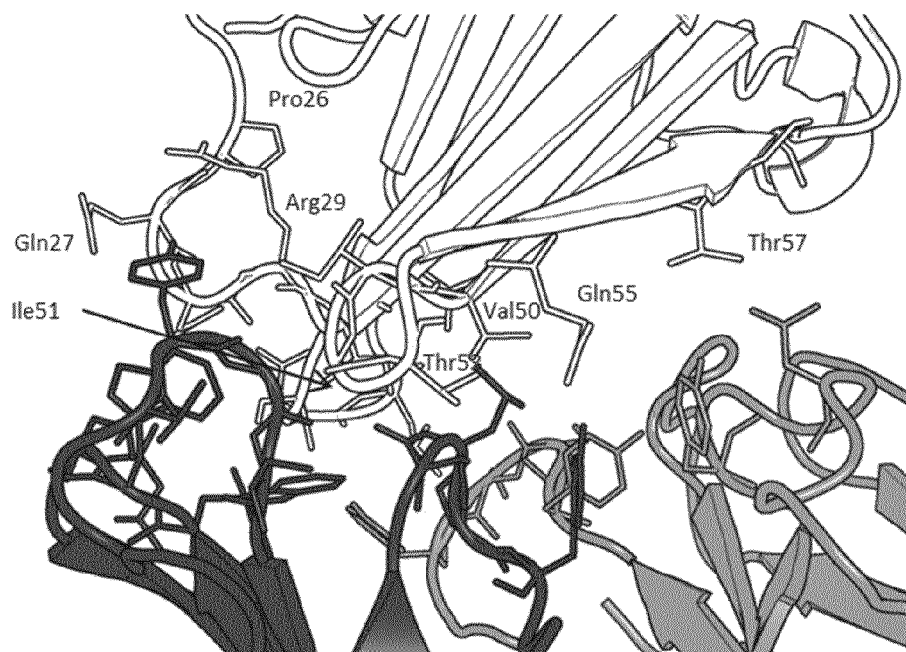
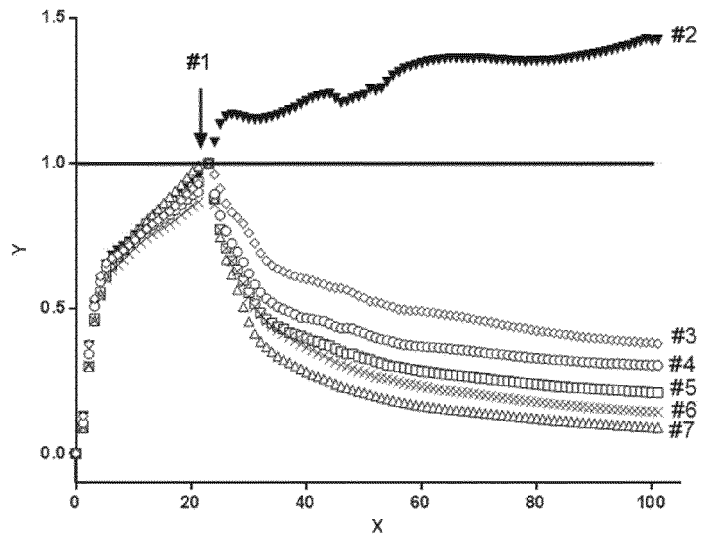


Fig. 11

A



B

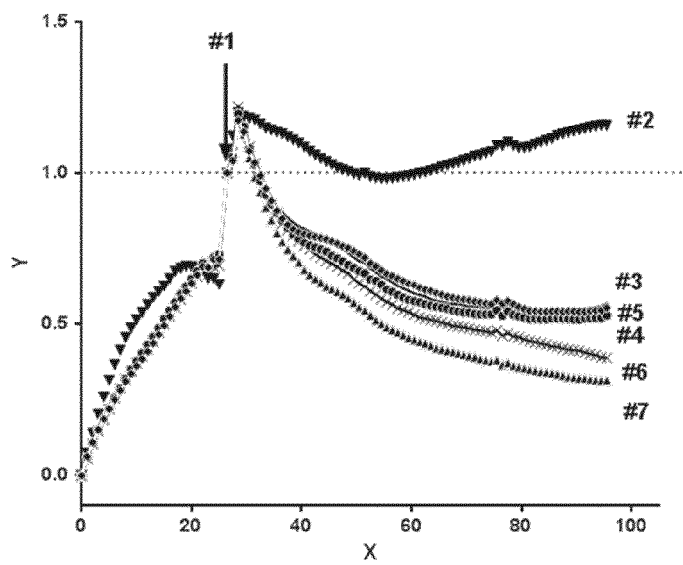
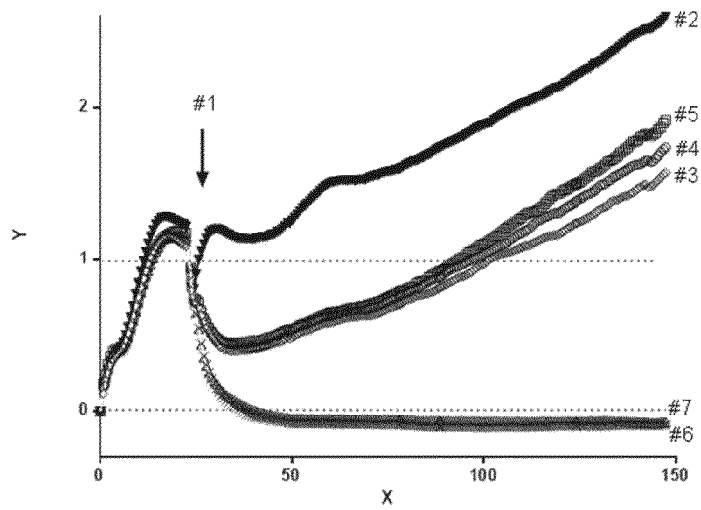


Fig. 12

A



B

