Fig. 1

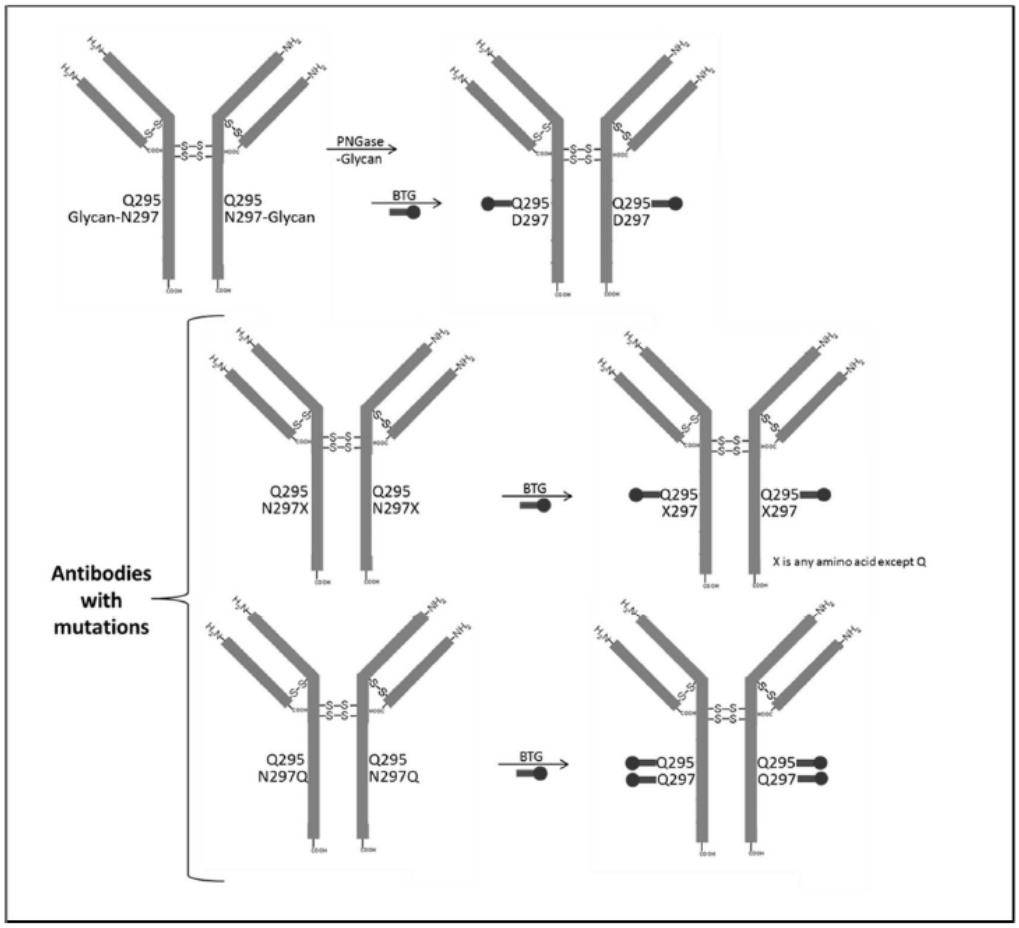

PNGase
-Glycan
BTG
Q295
Glycan-N297
Q295
N297-Glycan
Q295
D297
Q295
D297
Antibodies
with
mutations
Q295
N297X
Q295
N297X
BTG
Q295
X297
Q295
X297
X is any amino acid except Q
Q295
N297Q
Q295
N297Q
BTG
Q295
Q297
Q295
Q297

Fig. 2

```
>TPP-981 VH (PRT)
QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTDYNTPFTSRLSINKDNSKSQVFF
                               |---|              |----HCDR2-----|
                               HCDR1

KMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVTVSA
                 |--HCDR3--|


>TPP-981 VL (PRT)
DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLSINSVES
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDIADYYCQQNNNWPTTFGAGTKLELK
        |-LCDR3-|


>TPP-981 Heavy Chain (PRT)
QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTDYNTPFTSRLSINKDNSKSQVFF
|-------------------------------------------------------------VH--------------------
                               |---|              |----HCDR2-----|
                               HCDR1

KMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
-------------------------------------|
                 |--HCDR3--|


NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGP



SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE



YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL



DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK



>TPP-981 Light Chain (PRT)
DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLSINSVES
|-----------------------------------------------------VL--------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDIADYYCQQNNNWPTTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
--------------------------|
        |-LCDR3-|


ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
```

```
>TPP-1015 VH (PRT)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAY
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS
                  |--HCDR3--|


>TPP-1015 VL (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQP
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQHYTTPPTFGQGTKVEIK
        |-LCDR3-|


>TPP-1015 Heavy Chain (PRT)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAY
|-------------------------------------------------------------VH--------------------
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
---------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV



LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK



>TPP-1015 Light Chain (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQP
|-------------------------------------------------VL----------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
--------------------------|
        |-LCDR3-|


ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
```

```
>TPP-2090 VH (PRT)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNSKNTLY
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSS
                  |--HCDR3--|


>TPP-2090 VL (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTISSLQP
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQSYTSPFITFGQGTKVEIK
        |-LCDR3--|


>TPP-2090 Heavy Chain (PRT)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNSKNTLY
|-------------------------------------------------------------VH--------------------
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
----------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV



LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK



>TPP-2090 Light Chain (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTISSLQP
|-----------------------------------------------------VL--------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQSYTSPFITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
----------------------------|
        |-LCDR3--|


QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
```

```
>TPP-2658 VH (PRT)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNSKNTLY
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSS
                  |--HCDR3--|



>TPP-2658 VL (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTISSLQP
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQSYTSPFITFGQGTKVEIK
        |-LCDR3--|


>TPP-2658 Heavy Chain (PRT)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNSKNTLY
|-------------------------------------------------------------VH--------------------
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
----------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV



LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG



>TPP-2658 Light Chain (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTISSLQP
|-----------------------------------------------------VL--------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQSYTSPFITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
----------------------------|
        |-LCDR3--|
```

```
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC



>TPP-5442 VH (PRT)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNSKNTLY
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSS
                  |--HCDR3--|


>TPP-5442 VL (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTISSLQP
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQSYTSPFITFGQGTKVEIK
        |-LCDR3--|


>TPP-5442 Heavy Chain (PRT)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNSKNTLY
|-------------------------------------------------------------VH--------------------
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
----------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV



LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG



>TPP-5442 Light Chain (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTISSLQP
|-----------------------------------------------------VL--------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQSYTSPFITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
----------------------------|
        |-LCDR3--|
```

```
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC



>TPP-7006 VH (PRT)
QVQLQQSGPELVKPGASVKMSCKASGYTFTDFIIAWVKQRTGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADKSSNTAY
                               |---|              |-----HCDR2-----|
                               HCDR1

MQLSSLTSVDSAVYFCARRTIYYDYDGDYWGQGTTLTVSS
                  |--HCDR3--|


>TPP-7006 VL (PRT)
DIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLASGVPDRFSSSGSGTDFTLRI
                        |----LCDR1-----|               |-----|
                                                      LCDR2

SRVEAEDVGVYYCAHNLELPWTFGGGTKLELK
             |-LCDR3-|



>TPP-7006 Heavy Chain (PRT)
QVQLQQSGPELVKPGASVKMSCKASGYTFTDFIIAWVKQRTGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADKSSNTAY
|-------------------------------------------------------------VH-------------------
                               |---|              |-----HCDR2-----|
                               HCDR1

MQLSSLTSVDSAVYFCARRTIYYDYDGDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
----------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV



LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG



>TPP-7006 Light Chain (PRT)
DIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLASGVPDRFSSSGSGTDFTLRI
|-------------------------------------------------------VL-----------------------
                        |----LCDR1-----|               |-----|
                                                      LCDR2

SRVEAEDVGVYYCAHNLELPWTFGGGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
--------------------------------|
             |-LCDR3-|
```

```
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC



>TPP-7007 VH (PRT)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTSTSTAY
                               |---|              |-----HCDR2-----|
                               HCDR1

MELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSS
                  |--HCDR3--|


>TPP-7007 VL (PRT)
DIVMTQSPLSLPVTPGEPASISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLASGVPDRFSGSGSGTDFTLKI
                        |----LCDR1-----|               |-----|
                                                      LCDR2

SRVEAEDVGVYYCAHNLELPWTFGQGTKVEIK
             |-LCDR3-|



>TPP-7007 Heavy Chain (PRT)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTSTSTAY
|-------------------------------------------------------------VH--------------------
                               |---|              |-----HCDR2-----|
                               HCDR1

MELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
----------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV



LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG



>TPP-7007 Light Chain (PRT)
DIVMTQSPLSLPVTPGEPASISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLASGVPDRFSGSGSGTDFTLKI
|-------------------------------------------------VL------------------------
                        |----LCDR1-----|               |-----|
                                                      LCDR2

SRVEAEDVGVYYCAHNLELPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
--------------------------------|
             |-LCDR3-|
```

```
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC



>TPP-7510 VH (PRT)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAY
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS
                  |--HCDR3--|


>TPP-7510 VL (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQP
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQHYTTPPTFGQGTKVEIK
        |-LCDR3-|


>TPP-7510 Heavy Chain (PRT)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAY
|-------------------------------------------------------------VH--------------------
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
----------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV



LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG



>TPP-7510 Light Chain (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQP
|-------------------------------------------------VL--------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
--------------------------|
```

```
        |-LCDR3-|

ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC



>TPP-7511 VH (PRT)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAY
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS
                  |--HCDR3--|


>TPP-7511 VL (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQP
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQHYTTPPTFGQGTKVEIK
        |-LCDR3-|


>TPP-7511 Heavy Chain (PRT)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAY
|-------------------------------------------------------------VH-------------------
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
---------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV



LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG



>TPP-7511 (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQP
|-----------------------------------------------VL---------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
```

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


ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC



>TPP-8382 VH (PRT)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSISGSGGSTLYADSVKGRFTISRDNSKNTLY
                               |---|              |-----HCDR2-----|
                               HCDR1

LQMNSLRAEDTAVYYCAKLTGTSFDYWGQGTLVTVSS
                  |------|
                  HCDR3

>TPP-8382 VL (PRT)
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNPVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAITGLQ
                       |---LCDR1---|               |-----|
                                                   LCDR2

SEDEADYYCQSFDSSLKKVFGGGTKLTVL
         |-LCDR3--|



>TPP-8382 Heavy Chain (PRT)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSISGSGGSTLYADSVKGRFTISRDNSKNTLY
|-------------------------------------------------------------VH----------------------
                               |---|              |-----HCDR2-----|
                               HCDR1

LQMNSLRAEDTAVYYCAKLTGTSFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
-------------------------------------|
                  |------|
                  HCDR3

GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV



FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK



CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS



DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG



>TPP-8382 Light Chain (PRT)
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNPVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAITGLQ
|-----------------------------------------------------VL--------------------------
                       |---LCDR1---|               |-----|
                                                   LCDR2
```

```
SEDEADYYCQSFDSSLKKVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKA
----------------------------|
         |-LCDR3--|


GVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS



>TPP-8567 VH (PRT)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSISGSGGSTLYADSVKGRFTISRDNSKNTLY
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCAKLTGTSFDYWGQGTLVTVSS
                  |------|
                  HCDR3

>TPP-8567 VL (PRT)
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNPVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAITGLQ
                       |---LCDR1---|               |-----|
                                                   LCDR2

SEDEADYYCQSFDSSLKKVFGGGTKLTVL
         |-LCDR3--|



>TPP-8567 Heavy Chain (PRT)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSISGSGGSTLYADSVKGRFTISRDNSKNTLY
|-------------------------------------------------------------VH----------------------
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCAKLTGTSFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
-------------------------------------|
                  |------|
                  HCDR3

GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV



FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTYRVVSVLTVLHQDWLNGKEYK



CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS



DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG



>TPP-8567 Light Chain (PRT)
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNPVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAITGLQ
|-----------------------------------------------------VL-------------------------
                       |---LCDR1---|               |-----|
                                                   LCDR2
```

```
SEDEADYYCQSFDSSLKKVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKA
----------------------------|
         |-LCDR3--|


GVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS



>TPP-8825 VH (PRT)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNSKNTLY
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSS
                  |--HCDR3--|


>TPP-8825 VL (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTISSLQP
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQSYTSPFITFGQGTKVEIK
        |-LCDR3--|



>TPP-8825 Heavy Chain (PRT)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNSKNTLY
|-------------------------------------------------------------VH--------------------
                              |---|              |-----HCDR2-----|
                              HCDR1

LQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
----------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREENYQSTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV



LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
```

```
>TPP-8825 Light Chain (PRT)
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTISSLQP
|-----------------------------------------------------VL-------------------------
                        |--LCDR1--|               |-----|
                                                  LCDR2

EDFATYYCQQSYTSPFITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
---------------------------|
        |-LCDR3--|


QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC



>TPP-10334 VH (PRT)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTSTSTAY
                               |---|              |-----HCDR2-----|
                               HCDR1

MELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSS
                  |--HCDR3--|


>TPP-10334 VL (PRT)
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNRASGVPDRFSGSGSGTDFTLKI
                        |----LCDR1-----|               |-----|
                                                      LCDR2

SRVEAEDVGVYYCAHNLELPWTFGQGTKVEIK
             |-LCDR3-|



>TPP-10334 Heavy Chain (PRT)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTSTSTAY
|-------------------------------------------------------------VH-------------------
                               |---|              |-----HCDR2-----|
                               HCDR1

MELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
---------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV



LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
```

```
>TPP-10334 Light Chain (PRT)
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNRASGVPDRFSGSGSGTDFTLKI
|-----------------------------------------------------VL------------------------
                       |----LCDR1-----|               |-----|
                                                     LCDR2

SRVEAEDVGVYYCAHNLELPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
--------------------------------|
             |-LCDR3-|


SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC



>TPP-10335 VH (PRT)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTSTSTAY
                               |---|              |-----HCDR2-----|
                               HCDR1

MELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSS
                  |--HCDR3--|


>TPP-10335 VL (PRT)
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGINYLYWYLQKPGQSPQLLIYQMSNRASGVPDRFSGSGSGTDFTLKI
                       |----LCDR1-----|               |-----|
                                                     LCDR2

SRVEAEDVGVYYCAHNLELPWTFGQGTKVEIK
             |-LCDR3-|



>TPP-10335 Heavy Chain (PRT)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTSTSTAY
|-------------------------------------------------------------VH-------------------
                               |---|              |-----HCDR2-----|
                               HCDR1

MELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
----------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV



LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
```

```
>TPP-10335 Light Chain (PRT)
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGINYLYWYLQKPGQSPQLLIYQMSNRASGVPDRFSGSGSGTDFTLKI
|-----------------------------------------------------VL------------------------
                       |----LCDR1-----|               |-----|
                                                     LCDR2

SRVEAEDVGVYYCAHNLELPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
---------------------------------|
             |-LCDR3-|


SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC



>TPP-10336 VH (PRT)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTSTSTAY
                               |---|              |-----HCDR2-----|
                               HCDR1

MELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSS
                  |--HCDR3--|


>TPP-10336 VL (PRT)
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNWINYLYWYLQKPGQSPQLLIYQMSNRASGVPDRFSGSGSGTDFTLKI
                       |----LCDR1-----|               |-----|
                                                     LCDR2

SRVEAEDVGVYYCAHNLELPWTFGQGTKVEIK
             |-LCDR3-|



>TPP-10336 Heavy Chain (PRT)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTSTSTAY
|-------------------------------------------------------------VH-------------------
                               |---|              |-----HCDR2-----|
                               HCDR1

MELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
----------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV



LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
```

```
>TPP-10336 Light Chain (PRT)
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNWINYLYWYLQKPGQSPQLLIYQMSNRASGVPDRFSGSGSGTDFTLKI
|-----------------------------------------------------VL-----------------------
                       |----LCDR1-----|               |-----|
                                                     LCDR2

SRVEAEDVGVYYCAHNLELPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
---------------------------------|
             |-LCDR3-|


SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC



>TPP-10337 VH (PRT)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTSTSTAY
                               |---|              |-----HCDR2-----|
                               HCDR1

MELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSS
                  |--HCDR3--|


>TPP-10337 VL (PRT)
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNWINYLYWYLQKPGQSPQLLIYQGSNRASGVPDRFSGSGSGTDFTLKI
                       |----LCDR1-----|               |-----|
                                                     LCDR2

SRVEAEDVGVYYCAHNLELPWTFGQGTKVEIK
             |-LCDR3-|



>TPP-10337 Heavy Chain (PRT)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTSTSTAY
|-------------------------------------------------------------VH-------------------
                               |---|              |-----HCDR2-----|
                               HCDR1

MELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
---------------------------------------|
                  |--HCDR3--|


WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG



PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK



EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
```

```
LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG



>TPP-10337 Light Chain (PRT)
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNWINYLYWYLQKPGQSPQLLIYQGSNRASGVPDRFSGSGSGTDFTLKI
|-----------------------------------------------------VL-----------------------
                       |----LCDR1-----|               |-----|
                                                     LCDR2

SRVEAEDVGVYYCAHNLELPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
--------------------------------|
             |-LCDR3-|


SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
```

Fig. 3

<SEQ ID NO:1>
QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTDYNTPFTSRLSINKDNSK
SQVFFKMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVTVSA

<SEQ ID NO:2>
NYGVH

<SEQ ID NO:3>
VIWSGGNTDYNTPFTS

<SEQ ID NO:4>
ALTYYDYEFAY

<SEQ ID NO:5>
DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLSI
NSVESEDIADYYCQQNNNWPTTFGAGTKLELK

<SEQ ID NO:6>
RASQSIGTNIH

<SEQ ID NO:7>
YASESIS

<SEQ ID NO:8>
QQNNNWPTT

<SEQ ID NO:9>
QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTDYNTPFTSRLSINKDNSK
SQVFFKMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

<SEQ ID NO:10>
DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLSI
NSVESEDIADYYCQQNNNWPTTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV
DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:11>
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTS
KNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS

<SEQ ID NO:12>
DTYIH

<SEQ ID NO:13>
RIYPTNGYTRYADSVKG

<SEQ ID NO:14>
WGGDGFYAMDY

<SEQ ID NO:15>
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTI
SSLQPEDFATYYCQQHYTTPPTFGQGTKVEIK

<SEQ ID NO:16>
RASQDVNTAVA

<SEQ ID NO:17>
SASFLYS

<SEQ ID NO:18>
QQHYTTPPT

<SEQ ID NO:19>
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTS
KNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

<SEQ ID NO:20>
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTI
SSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV
DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:21>
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSS

<SEQ ID NO:22>
PYPMI

<SEQ ID NO:23>
YISPSGGSTHYADSVKG

<SEQ ID NO:24>
GGDTYFDYFDY

<SEQ ID NO:25>
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTI
SSLQPEDFATYYCQQSYTSPFITFGQGTKVEIK

<SEQ ID NO:26>
RASQSISGYLN

<SEQ ID NO:27>
QASSLQS

<SEQ ID NO:28>
QQSYTSPFIT

<SEQ ID NO:29>
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

<SEQ ID NO:30>

DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTI
SSLQPEDFATYYCQQSYTSPFITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:31>
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSS

<SEQ ID NO:32>
PYPMI

<SEQ ID NO:33>
YISPSGGSTHYADSVKG

<SEQ ID NO:34>
GGDTYFDYFDY

<SEQ ID NO:35>
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTI
SSLQPEDFATYYCQQSYTSPFITFGQGTKVEIK

<SEQ ID NO:36>
RASQSISGYLN

<SEQ ID NO:37>
QASSLQS

<SEQ ID NO:38>
QQSYTSPFIT

<SEQ ID NO:39>
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYA
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:40>
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTI
SSLQPEDFATYYCQQSYTSPFITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:41>
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSS

<SEQ ID NO:42>
PYPMI

<SEQ ID NO:43>
YISPSGGSTHYADSVKG

<SEQ ID NO:44>
GGDTYFDYFDY

<SEQ ID NO:45>

DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTI
SSLQPEDFATYYCQQSYTSPFITFGQGTKVEIK

<SEQ ID NO:46>
RASQSISGYLN

<SEQ ID NO:47>
QASSLQS

<SEQ ID NO:48>
QQSYTSPFIT

<SEQ ID NO:49>
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQ
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:50>
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTI
SSLQPEDFATYYCQQSYTSPFITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:51>
QVQLQQSGPELVKPGASVKMSCKASGYTFTDFIIAWVKQRTGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADKS
SNTAYMQLSSLTSVDSAVYFCARRTIYYDYDGDYWGQGTTLTVSS

<SEQ ID NO:52>
DFIIA

<SEQ ID NO:53>
EIYPGTGRTYYSEKFRG

<SEQ ID NO:54>
RTIYYDYDGDY

<SEQ ID NO:55>
DIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLASGVPDRFSSSGSGTD
FTLRISRVEAEDVGVYYCAHNLELPWTFGGGTKLELK

<SEQ ID NO:56>
RSSKSLLHSNGITYLY

<SEQ ID NO:57>
QMSNLAS

<SEQ ID NO:58>
AHNLELPWT

<SEQ ID NO:59>
QVQLQQSGPELVKPGASVKMSCKASGYTFTDFIIAWVKQRTGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADKS
SNTAYMQLSSLTSVDSAVYFCARRTIYYDYDGDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:60>
DIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLASGVPDRFSSSGSGTD
FTLRISRVEAEDVGVYYCAHNLELPWTFGGGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:61>
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTS
TSTAYMELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSS

<SEQ ID NO:62>
DFIIA

<SEQ ID NO:63>
EIYPGTGRTYYSEKFRG

<SEQ ID NO:64>
RTIYYDYDGDY

<SEQ ID NO:65>
DIVMTQSPLSLPVTPGEPASISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLASGVPDRFSGSGSGTD
FTLKISRVEAEDVGVYYCAHNLELPWTFGQGTKVEIK

<SEQ ID NO:66>
RSSKSLLHSNGITYLY

<SEQ ID NO:67>
QMSNLAS

<SEQ ID NO:68>
AHNLELPWT

<SEQ ID NO:69>
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTS
TSTAYMELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:70>
DIVMTQSPLSLPVTPGEPASISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLASGVPDRFSGSGSGTD
FTLKISRVEAEDVGVYYCAHNLELPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:71>
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTS
KNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS

<SEQ ID NO:72>
DTYIH

<SEQ ID NO:73>
RIYPTNGYTRYADSVKG

<SEQ ID NO:74>
WGGDGFYAMDY

<SEQ ID NO:75>
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTI
SSLQPEDFATYYCQQHYTTPPTFGQGTKVEIK

<SEQ ID NO:76>
RASQDVNTAVA

<SEQ ID NO:77>
SASFLYS

<SEQ ID NO:78>
QQHYTTPPT

<SEQ ID NO:79>
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTS
KNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYA
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:80>
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTI
SSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV
DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:81>
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTS
KNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS

<SEQ ID NO:82>
DTYIH

<SEQ ID NO:83>
RIYPTNGYTRYADSVKG

<SEQ ID NO:84>
WGGDGFYAMDY

<SEQ ID NO:85>
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTI
SSLQPEDFATYYCQQHYTTPPTFGQGTKVEIK

<SEQ ID NO:86>
RASQDVNTAVA

<SEQ ID NO:87>
SASFLYS

<SEQ ID NO:88>
QQHYTTPPT

<SEQ ID NO:89>
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTS
KNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQ

STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:90>
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTI
SSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV
DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:91>
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSISGSGGSTLYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCAKLTGTSFDYWGQGTLVTVSS

<SEQ ID NO:92>
SYAMS

<SEQ ID NO:93>
SISGSGGSTLYADSVKG

<SEQ ID NO:94>
LTGTSFDY

<SEQ ID NO:95>
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNPVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLA
ITGLQSEDEADYYCQSFDSSLKKVFGGGTKLTVL

<SEQ ID NO:96>
SGSSSNIGSNPVN

<SEQ ID NO:97>
SNNQRPS

<SEQ ID NO:98>
QSFDSSLKKV

<SEQ ID NO:99>
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSISGSGGSTLYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCAKLTGTSFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:100>
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNPVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLA
ITGLQSEDEADYYCQSFDSSLKKVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA
WKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

<SEQ ID NO:101>
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSISGSGGSTLYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCAKLTGTSFDYWGQGTLVTVSS

<SEQ ID NO:102>
SYAMS

<SEQ ID NO:103>
SISGSGGSTLYADSVKG

<SEQ ID NO:104>

LTGTSFDY

<SEQ ID NO:105>
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNPVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLA
ITGLQSEDEADYYCQSFDSSLKKVFGGGTKLTVL

<SEQ ID NO:106>
SGSSSNIGSNPVN

<SEQ ID NO:107>
SNNQRPS

<SEQ ID NO:108>
QSFDSSLKKV

<SEQ ID NO:109>
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSISGSGGSTLYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCAKLTGTSFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:110>
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNPVNWYQQLPGTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLA
ITGLQSEDEADYYCQSFDSSLKKVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA
WKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

<SEQ ID NO:111>
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSS

<SEQ ID NO:112>
PYPMI

<SEQ ID NO:113>
YISPSGGSTHYADSVKG

<SEQ ID NO:114>
GGDTYFDYFDY

<SEQ ID NO:115>
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTI
SSLQPEDFATYYCQQSYTSPFITFGQGTKVEIK

<SEQ ID NO:116>
RASQSISGYLN

<SEQ ID NO:117>
QASSLQS

<SEQ ID NO:118>
QQSYTSPFIT

<SEQ ID NO:119>
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYPMIWVRQAPGKGLEWVSYISPSGGSTHYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCARGGDTYFDYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK

THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREENYQ
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:120>
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTI
SSLQPEDFATYYCQQSYTSPFITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:121>
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTS
TSTAYMELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSS

<SEQ ID NO:122>
DFIIA

<SEQ ID NO:123>
EIYPGTGRTYYSEKFRG

<SEQ ID NO:124>
RTIYYDYDGDY

<SEQ ID NO:125>
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNRASGVPDRFSGSGSGTD
FTLKISRVEAEDVGVYYCAHNLELPWTFGQGTKVEIK

<SEQ ID NO:126>
RSSQSLLHSNGITYLY

<SEQ ID NO:127>
QMSNRAS

<SEQ ID NO:128>
AHNLELPWT

<SEQ ID NO:129>
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTS
TSTAYMELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:130>
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNRASGVPDRFSGSGSGTD
FTLKISRVEAEDVGVYYCAHNLELPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:131>
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTS
TSTAYMELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSS

<SEQ ID NO:132>
DFIIA

<SEQ ID NO:133>
EIYPGTGRTYYSEKFRG

<SEQ ID NO:134>
RTIYYDYDGDY

<SEQ ID NO:135>
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGINYLYWYLQKPGQSPQLLIYQMSNRASGVPDRFSGSGSGTD
FTLKISRVEAEDVGVYYCAHNLELPWTFGQGTKVEIK

<SEQ ID NO:136>
RSSQSLLHSNGINYLY

<SEQ ID NO:137>
QMSNRAS

<SEQ ID NO:138>
AHNLELPWT

<SEQ ID NO:139>
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTS
TSTAYMELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:140>
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGINYLYWYLQKPGQSPQLLIYQMSNRASGVPDRFSGSGSGTD
FTLKISRVEAEDVGVYYCAHNLELPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:141>
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTS
TSTAYMELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSS

<SEQ ID NO:142>
DFIIA

<SEQ ID NO:143>
EIYPGTGRTYYSEKFRG

<SEQ ID NO:144>
RTIYYDYDGDY

<SEQ ID NO:145>
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNWINYLYWYLQKPGQSPQLLIYQMSNRASGVPDRFSGSGSGTD
FTLKISRVEAEDVGVYYCAHNLELPWTFGQGTKVEIK

<SEQ ID NO:146>
RSSQSLLHSNWINYLY

<SEQ ID NO:147>
QMSNRAS

<SEQ ID NO:148>
AHNLELPWT

<SEQ ID NO:149>
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTS
TSTAYMELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK

DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:150>
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNWINYLYWYLQKPGQSPQLLIYQMSNRASGVPDRFSGSGSGTD
FTLKISRVEAEDVGVYYCAHNLELPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:151>
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTS
TSTAYMELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSS

<SEQ ID NO:152>
DFIIA

<SEQ ID NO:153>
EIYPGTGRTYYSEKFRG

<SEQ ID NO:154>
RTIYYDYDGDY

<SEQ ID NO:155>
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNWINYLYWYLQKPGQSPQLLIYQGSNRASGVPDRFSGSGSGTD
FTLKISRVEAEDVGVYYCAHNLELPWTFGQGTKVEIK

<SEQ ID NO:156>
RSSQSLLHSNWINYLY

<SEQ ID NO:157>
QGSNRAS

<SEQ ID NO:158>
AHNLELPWT

<SEQ ID NO:159>
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDFIIAWVKQAPGQGLEWIGEIYPGTGRTYYSEKFRGKATLTADTS
TSTAYMELSSLRSEDTAVYFCARRTIYYDYDGDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

<SEQ ID NO:160>
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNWINYLYWYLQKPGQSPQLLIYQGSNRASGVPDRFSGSGSGTD
FTLKISRVEAEDVGVYYCAHNLELPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

<SEQ ID NO:161>
HSDAVFTDNYTRLRKQMAVKKYLNSILN

<SEQ ID NO:162>
ATEPRKQYATPRVFWTDAPG

<SEQ ID NO:163>
LQWRRDDNVHNFGVWARYRL

<SEQ ID NO:164>
MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCAAAPPAPF
RLLWPILGGALSLTFVLGLLSGFLVWRRCRRREKFTTPIEETGGEGCPAVALIQ

<SEQ ID NO:165>
MLRRRGSPGMGVHVGAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPEPGFSLAQLNLIWQLTDTKQL
VHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLE
PNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNP
VLQQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEG
RDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRP
GDTVTITCSSYRGYPEAEVFWQDGQGVPLTGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAH
GSVTITGQPMTFPPEALWVTVGLSVCLIALLVALAFVCWRKIKQSCEEENAGAEDQDGEGEGSKTALQPLKHSDS
KEDDGQEIA

<SEQ ID NO:166>
MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQ
DIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTEILK
GGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA
RCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLA
FLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGI
SWLGLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGP
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