

SEQUENCE-LISTING-17207-0006WOU2
SEQUENCE LISTING

<110> BAYER HEALTHCARE LLC
Jin, Ye
Murphy, John E.
Hermiston, Terry
Myles, Timothy
Dittmer, Frank
Strerath, Michael
Gritzan, Uwe

<120> Monoclonal Antibodies Against Antithrombin Beta

<130> 17207.0006WOU1

<150> US 61/784,590

<151> 2013-03-14

<160> 60

<170> PatentIn version 3.5

<210> 1

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP2009, Light Chain Variable Region

<400> 1

Ala Gln Ser Val Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly
1 5 10 15

Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr
20 25 30

Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile
35 40 45

Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60

Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala
65 70 75 80

Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn
85 90 95

His Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
100 105 110

Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
115 120 125

Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
130 135 140

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Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala
145 150 155 160

Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
165 170 175

Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
180 185 190

Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
195 200 205

Val Ala Pro Ala Glu Cys Ser
210 215

<210> 2
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2009, Heavy Chain Variable Region

<400> 2

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
20 25 30

Arg Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Tyr Ser Ser Gly Gly Arg Thr Arg Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Lys Ala Ser Asp Leu Ser Gly Ser Phe Ser Glu Ala Leu
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 3
<211> 216
<212> PRT
<213> Artificial Sequence

<220>

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<223> TPP2015, Light Chain Variable Region

<400> 3

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser
1 5 10 15

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser
20 25 30

Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
35 40 45

Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
65 70 75 80

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser
85 90 95

Ser Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Arg Arg Thr Val
100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
195 200 205

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 4

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP2015, Heavy Chain Variable Region

SEQUENCE-LISTING-17207-0006WOU2

<400> 4

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
20 25 30

Lys Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Gly Pro Ser Gly Gly Lys Thr Met Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Lys Ala Ser Asp Leu Ser Gly Thr Tyr Ser Glu Ala Leu
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 5

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP2016, Light Chain Variable Region

<400> 5

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser
1 5 10 15

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asn Ile Asn
20 25 30

Arg Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro Arg Leu
35 40 45

Leu Ile His Thr Ala Ser Thr Arg Ala Pro Gly Val Pro Val Arg Ile
50 55 60

Thr Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu
65 70 75 80

Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Ala Ser Pro
85 90 95

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Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
195 200 205

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 6
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2016, Heavy Chain Variable Region

<400> 6

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
20 25 30

Arg Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Gly Pro Ser Gly Gly Lys Thr Thr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Lys Thr Ser Asp Leu Ser Gly Ser Tyr Ser Glu Ala Leu
100 105 110

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Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 7
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2019, Light Chain Variable Region

<400> 7

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser
1 5 10 15

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser
20 25 30

Ser Ser Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
35 40 45

Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
65 70 75 80

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Ser
85 90 95

Thr Pro Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

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Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 8
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2019, Heavy Chain Variable Region

<400> 8

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Ser Pro Ser Gly Gly Lys Thr His Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Ser Gln Thr Gly Tyr Tyr Pro His Tyr His Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 9
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2803, Light Chain Variable Region

<400> 9

Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1 5 10 15

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

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Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
85 90 95

Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala Gly
145 150 155 160

Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
195 200 205

Ala Pro Ala Glu Cys Ser
210

<210> 10
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2803, Heavy Chain Variable Region
<400> 10

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Arg Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Tyr Ser Ser Gly Gly Arg Thr Arg Tyr Ala Asp Ser Val
50 55 60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Lys Ala Ser Asp Leu Ser Gly Ser Phe Ser Glu Ala Leu
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 11
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP2009 Light Chain_V region

<400> 11
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atcacatgcc aaggagacag cctcagaagc tattatgcaa gctggtacca gcagaagcca 120
ggacaggccc ctgtacttgt catctatggt aaaaacaacc ggccctcagg gatcccagac 180
cgattctctg gctccagctc aggaaacaca gcttccttga ccatcactgg ggctcaggcg 240
gaagatgagg ctgactatta ctgtaactcc cgggacagca gtggtaacca tctggtattc 300
ggcggaggga ccaagctgac cgtcctaggt cagcccaagg ctgccccctc ggtcactctg 360
ttcccgccct cctctgagga gcttcaagcc aacaaggcca cactagtgtg tctgatcagt 420
gacttctacc cgggagctgt gacagtggcc tggaaggcag atggcagccc cgtcaaggcg 480
ggagtggaga ccaccaaacc ctcaaacag agcaacaaca agtacgcggc cagcagctac 540
ctgagcctga cgcccagca gtggaagtcc cacagaagct acagctgcca ggtcacgcat 600
gaaggagca ccgtggagaa gacagtggcc cctgcagaat gctct 645

<210> 12
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> TPP2009 Heavy chain

<400> 12
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tcttgcgctg cttccggatt cactttctct gcttaccgta tgggttgggt tcgccaagct 120
cctggtaaag gtttggagtg ggtttctcgt atctattctt ctggtggccg tactcgttat 180
gctgactccg ttaaaggctg cttcactatc tctagagaca actctaagaa tactctctac 240
ttgcagatga acagcttaag ggctgaggac acggccgtgt attactgtgc gagagagaaa 300

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gcgtcggatc	tatcggggag	tttttctgag	gcccttgact	actggggcca	gggaaccctg	360
gtcaccgtct	caagcgcctc	caccaagggc	ccatcgggtct	tcccgcctagc	accagcagc	420
aagagcacca	gcggcggaac	agccgccctg	ggctgcctgg	tgaaagacta	cttccccgag	480
cccgtgaccg	tgtcctggaa	ctctggcgcc	ctgaccagcg	gagtgcatac	cttccccgcc	540
gtgctgcaga	gcagcggcct	gtacagcctg	agcagcgtgg	tgacagtgcc	cagcagcagc	600
ctgggaaccc	agacctacat	ctgcaacgtg	aaccacaagc	ccagcaacac	caaggtggac	660
aagaaggtgg	aaccaagag	ctgcgacaag	acccacacct	gtccccctg	ccctgcccct	720
gaactgctgg	gcggaccag	cgtgttcctg	ttcccccaa	agcccaagga	caccctgatg	780
atcagccgga	ccccgaagt	gacctgcgtg	gtggtggacg	tgtcccacga	ggaccagaa	840
gtgaagtta	attggtacgt	ggacggcgtg	gaagtgcata	acgccaagac	caagcccaga	900
gaggaacagt	acaacagcac	ctaccgggtg	gtgtccgtgc	tgaccgtgct	gcaccaggac	960
tggctgaacg	gcaaagagta	caagtgcaag	gtctccaaca	aggccctgcc	tgccccatc	1020
gagaaaacca	tcagcaaggc	caagggccag	ccccgcgagc	ctcaggtgta	cacactgccc	1080
cccagccggg	atgagctgac	caagaaccag	gtgtccctga	cctgtctggt	gaaaggcttc	1140
taccccagcg	atatcgccgt	ggaatgggag	agcaacggcc	agcccgagaa	caattacaag	1200
accaccccc	ctgtgctgga	cagcgacggc	tcattcttcc	tgtactcaa	gctgaccgtg	1260
gacaagagcc	ggtggcagca	gggcaacgtg	ttcagctgca	gcgtgatgca	cgaggccctg	1320
cacaatcact	acaccagaa	gtccctgagc	ctgagccccg	gc		1362

<210> 13

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> TPP2015 Light Chain_V region

<400> 13

gcacaagaca	tccagatgac	ccagtctcca	ggcaccctgt	ctttgtctcc	aggggaaaga	60
gccaccctct	cctgcagggc	cagtcagagt	gttagcagca	gctacttagc	ctggtaccag	120
cagaaacctg	gccaggctcc	caggctcctc	atctatggtg	catccagcag	ggccactggc	180
atcccagaca	ggttcagtgg	cagtgggtct	gggacagact	tcactctcac	catcagcaga	240
cggagcctga	agattttgca	gtgtattact	gtcagcagta	tggtagctca	acgttcggcc	300
aagggaccaa	ggtggaaatc	agacgaactg	tggtgcaat	ctgtcttcat	cttcccgcca	360
tctgatgagc	agttgaaatc	tggaactgcc	tctgttgtgt	gcctgctgaa	taacttctat	420
cccagagagg	caaagtaca	gtggaagggtg	gataacgccc	tccaatcggg	taactcccag	480
gagagtgtca	cagagcagga	cagcaaggac	agcacctaca	gcctcagcag	caccctgacg	540
ctgagcaaag	cagactacga	gaaacacaaa	gtctacgcct	gcgaagtcac	ccatcagggc	600
ctgagctcgc	ccgtcacaaa	gagcttcaac	aggggagagt	gt		642

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<210> 14
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TPP2015 Heavy Chain

<400> 14
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 tcttgcgctg cttccggatt cactttctct aagtacaaga tggattgggt tcgccaagct 120
 cctggtaaag gtttggagtg ggtttctcgt atcggtcctt ctggtggcaa gactatgtat 180
 gctgactccg ttaaaggctg cttcactatc tctagagaca actctaagaa tactctctac 240
 ttgcagatga acagcttaag ggctgaggac acggccgtgt attactgtgc gagagagaaa 300
 gcgtcggatc tatcggggac ttattctgag gcccttgact actggggcca gggaaccctg 360
 gtcaccgtct caagcgcctc caccaagggc ccatcggctt tcccgttagc acccagcagc 420
 aagagcacca gcggcggaac agccgccctg ggctgcctgg tgaaagacta cttccccgag 480
 cccgtgaccg tgtcctggaa ctctggcgcc ctgaccagcg gagtgcatac cttccccgcc 540
 gtgctgcaga gcagcggcct gtacagcctg agcagcgtgg tgacagtgcc cagcagcagc 600
 ctgggaaccc agacctacat ctgcaacgtg aaccacaagc ccagcaacac caaggtggac 660
 aagaaggtgg aaccaagag ctgcgacaag acccacacct gtccccctg ccctgcccct 720
 gaactgctgg gcggaccag cgtgttcctg tccccccaa agcccaagga caccctgatg 780
 atcagccgga ccccggaagt gacctgcgtg gtggtggacg tgtccacga ggaccagaa 840
 gtgaagtta attggtacgt ggacggcgtg gaagtgcata acgccaagac caagcccaga 900
 gaggaacagt acaacagcac ctaccgggtg gtgtccgtgc tgaccgtgct gcaccaggac 960
 tgggtgaacg gcaaagagta caagtgaag gtctccaaca aggccctgcc tgccccatc 1020
 gagaaaacca tcagcaaggc caagggccag ccccgcgagc ctcaggtgta cactgccc 1080
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 accaccccc ctgtgctgga cagcgacggc tcattcttcc tgtactcaa gctgaccgtg 1260
 gacaagagcc ggtggcagca gggcaacgtg ttcagctgca gcgtgatgca cgaggccctg 1320
 cacaatcact acaccagaa gtccctgagc ctgagccccg gc 1362

<210> 15
 <211> 648
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TPP2016 Light Chain_V region

<400> 15
 gcacaagaca tccagatgac ccagtctcca gccaccctgt ctgtgtctcc aggggaaaga 60

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gccaccctct cctgcagggc cagtcagaat attaatagaa acttggcctg gtaccagcag	120
aagcctggcc gggctcccag actcctcatc cataccgcac ccactagggc ccctggtgtc	180
ccagtcagga tctactggcag tgggtctgga acagagttca ctctcaccat cagcagcctg	240
gaacctgaag attttgcagt gtattttctgt cagcagtatg ctagcccacc tcggacgttc	300
ggccaagggg ccaaggtgga aatcaagcga actgtggctg caccatctgt cttcatcttc	360
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac	420
ttctatccca gagaggccaa agtacagtgg aagggtgata acgccctcca atcgggtaac	480
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc	540
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat	600
cagggcctga gctcgcccggt cacaaagagc ttcaacaggg gagagtgt	648

<210> 16
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TPP2016 Heavy Chain

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cctggtaaag gtttggagtg ggtttctcgt atcggtcctt ctggtggcaa gactacttat	180
gctgactccg ttaaaggctc cttcactatc tctagagaca actctaagaa tactctctac	240
ttgcagatga acagcttaag ggctgaggac acggccgtgt attactgtgc gagagagaaa	300
acgtcggatc tatcggggag ttattctgag gcccttgact actggggcca gggaaccctg	360
gtcaccgtct caagcgcctc caccaagggc ccatcgggtct tcccgtagc acccagcagc	420
aagagcacca gcggcggaac agccgccctg ggctgcctgg tgaaagacta cttccccgag	480
cccgtgaccg tgtcctggaa ctctggcgcc ctgaccagcg gagtgcatac cttccccgcc	540
gtgctgcaga gcagcggcct gtacagcctg agcagcgtgg tgacagtgcc cagcagcagc	600
ctgggaacc agacctacat ctgcaacgtg aaccacaagc ccagcaacac caaggtggac	660
aagaaggtgg aaccgaagag ctgcgacaag acccacacct gtccccctg ccctgcccct	720
gaactgctgg gcggaccag cgtgttcctg ttcccccaa agcccaagga caccctgatg	780
atcagccgga ccccgaagt gacctgcgtg gtggtggacg tgtccacga ggaccagaa	840
gtgaagtta attggtacgt ggacggcgtg gaagtgcata acgccaagac caagcccaga	900
gaggaacagt acaacagcac ctaccgggtg gtgtccgtgc tgaccgtgct gcaccaggac	960
tggctgaacg gcaaagagta caagtgaag gtctccaaca aggccctgcc tgccccatc	1020
gagaaaacca tcagcaaggc caagggccag ccccgcgagc ctgaggtgta cacactgccc	1080
cccagccggg atgagctgac caagaaccag gtgtccctga cctgtctggt gaaaggcttc	1140

SEQUENCE-LISTING-17207-0006WOU2

taccccagcg atatcgccgt ggaatgggag agcaacggcc agcccagagaa caattacaag	1200
accacccccct ctgtgctgga cagcgacggc tcattcttcc tgtactccaa gctgaccgtg	1260
gacaagagcc ggtggcagca gggcaacgtg ttcagctgca gcgtgatgca cgaggccctg	1320
cacaatcact acaccagaa gtcctgagc ctgagccccg gc	1362

<210> 17
 <211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TPP2019 Light Chain_V region

<400> 17	
gcacaagaca tccagatgac ccagtctcca gccaccctgt ctttgtctcc aggggaaaga	60
gccaccctct cctgcagggc cagtcagcgt gttagcagca gctacttaac ctggtaccag	120
cagaaacctg gccaggctcc caggctcctc atctatggtg catccagcag ggccactggc	180
atcccagaca ggttcagtgg cagtgggtct gggacagact tcactctcac catcagcaga	240
ctggagcctg aagattttgc agttttattac tgtcagcagt atgatagtac gcctccgctc	300
accttcggcg gagggaccaa ggtggagatc aaacgaactg tggctgcacc atctgtcttc	360
atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg	420
aataacttct atcccagaga ggccaaagta cagtgggaagg tggataacgc cctccaatcg	480
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc	540
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc	600
acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt	654

<210> 18
 <211> 1365
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TPP2019 Heavy chain

<400> 18	
gaagttcaat tgtagagtc tgggtggcggc cttgttcagc ctggtgggtc tttacgtctt	60
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cctggtaaag gtttgagtg ggtttctcgt atctctcctt ctggtggcaa gactcattat	180
gctgactccg ttaaaggctc cttcactatc tctagagaca actctaagaa tactctctac	240
ttgcagatga acagcttaag ggctgaggac acggccgtgt attactgtgc gagactgtct	300
caaactgggt attaccctca ctaccactac tacggtatgg acgtctgggg ccaagggacc	360
acggtcaccg tctcaagcgc ctccaccaag ggcccatcgg tcttcccgt agcaccacgc	420
agcaagagca ccagcggcgg aacagccgcc ctgggctgcc tggtgaaaga ctacttcccc	480
gagcccgtga ccgtgtcctg gaactctggc gccctgacca gcggagtgc taccttcccc	540

SEQUENCE-LISTING-17207-0006WOU2

gccgtgctgc agagcagcgg cctgtacagc ctgagcagcg tgggtgacagt gcccagcagc	600
agcctgggaa cccagaccta catctgcaac gtgaaccaca agcccagcaa caccaaggtg	660
gacaagaagg tggaacccaa gagctgcgac aagaccacaca cctgtccccc ctgccctgccc	720
cctgaactgc tgggcggaacc cagcgtgttc ctgttccccc caaagcccaa ggacaccctg	780
atgatcagcc ggacccccga agtgacctgc gtgggtggtg acgtgtccca cgaggaccca	840
gaagtgaagt ttaattggta cgtggacggc gtggaagtgc ataacgcaa gaccaagccc	900
agagaggaac agtacaacag cacctaccgg gtgggtgtccg tgctgaccgt gctgcaccag	960
gactggctga acggcaaaga gtacaagtgc aaggtctcca acaaggccct gcctgcccc	1020
atcgagaaaa ccatcagcaa ggccaagggc cagccccgcg agcctcaggt gtacacactg	1080
ccccccagcc gggatgagct gaccaagaac caggtgtccc tgacctgtct ggtgaaaggc	1140
ttctacccca gcgatatcg cgtggaatgg gagagcaacg gccagcccga gaacaattac	1200
aagaccaccc cccctgtgct ggacagcgac ggctcattct tcctgtactc caagctgacc	1260
gtggacaaga gccggtggca gcagggcaac gtgttcagct gcagcgtgat gcacgaggcc	1320
ctgcacaatc actacacca gaagtcctg agcctgagcc ccggc	1365

<210> 19
 <211> 639
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TPP2803 Light Chain_V region

<400> 19 agcgaattga ctcaggaccc tgctgtgtct gtggccttgg gacagacagt caggatcaca	60
tgccaaggag acagcctcag aagctattat gcaagctggt accagcagaa gccaggacag	120
gcccctgtac ttgtcatcta tggtaaaaac aaccggccct cagggatccc agaccgattc	180
tctgggtcca gtcaggaaa cacagcttcc ttgaccatca ctgggggtca ggcggaagat	240
gaggctgact attactgtaa ctcccgggac agcagtggta accatctggt attcggcgga	300
gggaccaagc tgaccgtcct aggtcagccc aaggctgccc cctcggtcac tctgttccc	360
ccctcctctg aggagcttca agccaacaag gccacactag tgtgtctgat cagtgacttc	420
taccggggag ctgtgacagt ggcctggaag gcagatggca gcccgtcaa ggcgggagtg	480
gagaccacca aaccctcaa acagagcaac aacaagtacg cggccagcag ctacctgagc	540
ctgacgccc agcagtggaa gtccacaga agctacagct gccaggtcac gcatgaaggg	600
agcaccgtgg agaagacagt ggcccctgca gaatgctct	639

<210> 20
 <211> 1348
 <212> DNA
 <213> Artificial Sequence

<220>

SEQUENCE-LISTING-17207-0006WOU2

<223> TPP2803 Heavy Chain

<400> 20

gaagtgcagc tgctggaaag cggcggaggc ctggtgcagc ctggcggatc tctgagactg	60
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cctggcaagg gactggaatg ggtgtcccgc atctacagca gcggcggcag aaccagatac	180
gccgacagcg tgaagggccg gttcaccatc tcccgggaca acagcaagaa caccctgtac	240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actattgcgc cagagagaag	300
gccagcgacc tgagcggcag ctttagcgag gccctggatt attggggcca gggcacactc	360
gtgaccgtgt ctagcgccag cacaagggc cccagcgtgt tccctctggc cccttgtagc	420
agaagcacca gcgagtctac agccgccctg ggctgcctcg tgaaggacta ctttcccagag	480
cccgtgacag tgtcctggaa ctctggcgcc ctgacaagcg gcgtgcacac ctttccagcc	540
gtgctgcaga gcagcggcct gtactctctg agcagcgtcg tgactgtgcc cagcagcaac	600
ttcggcaccc agacctacac ctgtaacgtg gaccacaagc ccagcaacac caaggtggac	660
aagaccgtgg aacggaagtg ctgcgtggaa tgccccctt gtcctgcccc tccagtggct	720
ggcccttccg tgttcctgtt cccccaaaag cccaaggaca ccctgatgat cagccggacc	780
ccgaagtgac ctgcgtgggt gtggatgtgt cccacgagga ccccgagggt cagttcaatt	840
ggtacgtgga cggcgtggaa gtgcacaacg ccaagaccaa gccagagag gaacagttca	900
acagcacctt ccgggtgggt tccgtgctga ccgtgggtgca tcaggactgg ctgaacggca	960
aagagtacaa gtgcaagggt tccaacaagg gcctgcctgc ccccatcgag aaaaccatca	1020
gcaagaccaa aggccagccc cgcgagcccc aggtgtacac actgcctcca agccgggaag	1080
agatgaccaa gaaccagggt tccctgacct gtctcgtgaa aggccttctac ccctccgata	1140
tcgccgtgga atgggagagc aacggccagc ccgagaacaa ctacaagacc accccccca	1200
tgctggacag cgcggctcat tcttcctgta cagcaagctg acagtggaca agtcccgggtg	1260
gcagcagggc aacgtgttca gctgcagcgt gatgcacgaa gccctgcaca accactacac	1320
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<210> 21

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP2009 LCDR1

<400> 21

Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	Ser
1				5					10	

<210> 22

<211> 12

<212> PRT

<213> Artificial Sequence

SEQUENCE-LISTING-17207-0006WOU2

<220>

<223> TPP2015 LCDR1

<400> 22

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 23

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP2016 LCDR1

<400> 23

Arg Ala Ser Gln Asn Ile Asn Arg Asn Leu Ala
1 5 10

<210> 24

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP2019 LCDR1

<400> 24

Arg Ala Ser Gln Arg Val Ser Ser Ser Tyr Leu Thr
1 5 10

<210> 25

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP2803 LCDR1

<400> 25

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
1 5 10

<210> 26

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP2009 LCDR2

<400> 26

Gly Lys Asn Asn Arg Pro Ser
1 5

<210> 27

<211> 7

SEQUENCE-LISTING-17207-0006WOU2

<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2015 LCDR2

<400> 27

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 28
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2016 LCDR2

<400> 28

Thr Ala Ser Thr Arg Ala Pro
1 5

<210> 29
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2019 LCDR2

<400> 29

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 30
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2803 LCDR2

<400> 30

Gly Lys Asn Asn Arg Pro Ser
1 5

<210> 31
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2009 LCDR3

<400> 31

Asn Ser Arg Asp Ser Ser Gly Asn His Leu Val
1 5 10

SEQUENCE-LISTING-17207-0006WOU2

<210> 32
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP2015 LCDR3

<400> 32

Gln Gln Tyr Gly Ser Ser Arg Thr
 1 5

<210> 33
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP2016 LCDR3

<400> 33

Gln Gln Tyr Ala Ser Pro Pro Arg Thr
 1 5

<210> 34
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP2019 LCDR3

<400> 34

Gln Gln Tyr Asp Ser Thr Pro Pro Leu Thr
 1 5 10

<210> 35
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP2803 LCDR3

<400> 35

Asn Ser Arg Asp Ser Ser Gly Asn His Leu Val
 1 5 10

<210> 36
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP2009 HCDR1

<400> 36

Ala Tyr Arg Met Gly
 1 5

SEQUENCE-LISTING-17207-0006WOU2

<210> 37
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP2015 HCDR1

<400> 37

Lys Tyr Lys Met Asp
 1 5

<210> 38
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP2016 HCDR1

<400> 38

Lys Tyr Arg Met Asp
 1 5

<210> 39
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP2019 HCDR1

<400> 39

Arg Tyr Ala Met Tyr
 1 5

<210> 40
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP2803 HCDR1

<400> 40

Ser Tyr Arg Met Ser
 1 5

<210> 41
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP2009 HCDR2

<400> 41

SEQUENCE-LISTING-17207-0006WOU2

Arg Ile Tyr Ser Ser Gly Gly Arg Thr Arg Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 42
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2015 HCDR2

<400> 42

Arg Ile Gly Pro Ser Gly Gly Lys Thr Met Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 43
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2016 HCDR2

<400> 43

Arg Ile Gly Pro Ser Gly Gly Lys Thr Thr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 44
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2019 HCDR2

<400> 44

Arg Ile Ser Pro Ser Gly Gly Lys Thr His Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 45
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

SEQUENCE-LISTING-17207-0006WOU2

<223> TPP2803 HCDR2

<400> 45

Arg Ile Tyr Ser Ser Gly Gly Arg Thr Arg Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 46

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP2009 HCDR3

<400> 46

Ala Arg Glu Lys Ala Ser Asp Leu Ser Gly Ser Phe Ser Glu Ala Leu
1 5 10 15

Asp Tyr

<210> 47

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP2015 HCDR3

<400> 47

Ala Arg Glu Lys Ala Ser Asp Leu Ser Gly Thr Tyr Ser Glu Ala Leu
1 5 10 15

Asp Tyr

<210> 48

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP2016 HCDR3

<400> 48

Ala Arg Glu Lys Thr Ser Asp Leu Ser Gly Ser Tyr Ser Glu Ala Leu
1 5 10 15

Asp Tyr

<210> 49

<211> 19

SEQUENCE-LISTING-17207-0006WOU2

<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2019 HCDR3

<400> 49

Ala Arg Leu Ser Gln Thr Gly Tyr Tyr Pro His Tyr His Tyr Tyr Gly
1 5 10 15

Met Asp Val

<210> 50
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2803 HCDR3

<400> 50

Ala Arg Glu Lys Ala Ser Asp Leu Ser Gly Ser Phe Ser Glu Ala Leu
1 5 10 15

Asp Tyr

<210> 51
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2009 , hIgG, Light_Chain

<400> 51

Ala Gln Ser Val Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly
1 5 10 15

Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr
20 25 30

Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile
35 40 45

Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60

Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala
65 70 75 80

Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn
85 90 95

SEQUENCE-LISTING-17207-0006WOU2

His Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
100 105 110

Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
115 120 125

Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
130 135 140

Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala
145 150 155 160

Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
165 170 175

Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
180 185 190

Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
195 200 205

Val Ala Pro Ala Glu Cys Ser
210 215

<210> 52
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP2009, hIgG, Heavy_chain

<400> 52

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
20 25 30

Arg Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Tyr Ser Ser Gly Gly Arg Thr Arg Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Lys Ala Ser Asp Leu Ser Gly Ser Phe Ser Glu Ala Leu
100 105 110

SEQUENCE-LISTING-17207-0006WOU2

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
 115 120 125
 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 130 135 140
 Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 145 150 155 160
 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 165 170 175
 Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 180 185 190
 Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
 195 200 205
 Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
 210 215 220
 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 225 230 235 240
 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 245 250 255
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 260 265 270
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 275 280 285
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 290 295 300
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 305 310 315 320
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 325 330 335
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 340 345 350
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
 355 360 365
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380

SEQUENCE-LISTING-17207-0006WOU2

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
435 440 445

Leu Ser Leu Ser Pro Gly
450

<210> 53
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2015, hIgG, light_chain

<400> 53

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser
1 5 10 15

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser
20 25 30

Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
35 40 45

Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
65 70 75 80

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser
85 90 95

Ser Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Arg Arg Thr Val
100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
130 135 140

SEQUENCE-LISTING-17207-0006WOU2

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
180 185 190

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
195 200 205

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 54

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP-2015, hIgG, heavy_chain

<400> 54

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
20 25 30

Lys Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Gly Pro Ser Gly Gly Lys Thr Met Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Lys Ala Ser Asp Leu Ser Gly Thr Tyr Ser Glu Ala Leu
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

SEQUENCE-LISTING-17207-0006WOU2

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
290 295 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
420 425 430

SEQUENCE-LISTING-17207-0006WOU2

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
435 440 445

Leu Ser Leu Ser Gly
450

<210> 55
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2016, hIgG, light_chain, Kappa

<400> 55

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser
1 5 10 15

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asn Ile Asn
20 25 30

Arg Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro Arg Leu
35 40 45

Leu Ile His Thr Ala Ser Thr Arg Ala Pro Gly Val Pro Val Arg Ile
50 55 60

Thr Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu
65 70 75 80

Glu Pro Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Ala Ser Pro
85 90 95

Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
100 105 110

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
180 185 190

SEQUENCE-LISTING-17207-0006WOU2

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
195 200 205

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 56
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2016, hIgG, heavy_chain

<400> 56

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr
20 25 30

Arg Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Gly Pro Ser Gly Gly Lys Thr Thr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Lys Thr Ser Asp Leu Ser Gly Ser Tyr Ser Glu Ala Leu
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
130 135 140

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
195 200 205

SEQUENCE-LISTING-17207-0006WOU2

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
 210 215 220
 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 225 230 235 240
 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 245 250 255
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 260 265 270
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 275 280 285
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 290 295 300
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 305 310 315 320
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 325 330 335
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 340 345 350
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
 355 360 365
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 385 390 395 400
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 405 410 415
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 420 425 430
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 435 440 445
 Leu Ser Leu Ser Pro Gly
 450

<210> 57
 <211> 218

SEQUENCE-LISTING-17207-0006WOU2

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP-2019, hIgG, light_chain, Kappa

<400> 57

Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser
1 5 10 15

Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser
20 25 30

Ser Ser Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
35 40 45

Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
65 70 75 80

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Ser
85 90 95

Thr Pro Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 58

<211> 455

<212> PRT

<213> Artificial Sequence

SEQUENCE-LISTING-17207-0006WOU2

<220>

<223> TPP-2019, hIgG, heavy_chain

<400> 58

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Ser Pro Ser Gly Gly Lys Thr His Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Ser Gln Thr Gly Tyr Tyr Pro His Tyr His Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser
115 120 125

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
130 135 140

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
145 150 155 160

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
165 170 175

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
180 185 190

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
195 200 205

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
210 215 220

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
225 230 235 240

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
245 250 255

SEQUENCE-LISTING-17207-0006WOU2

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
260 265 270

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
275 280 285

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
290 295 300

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
305 310 315 320

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
325 330 335

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
340 345 350

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
355 360 365

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
370 375 380

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
385 390 395 400

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
405 410 415

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
420 425 430

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
435 440 445

Ser Leu Ser Leu Ser Pro Gly
450 455

<210> 59
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2803, hIgG2, light_chain, lambda

<400> 59

Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1 5 10 15

SEQUENCE-LISTING-17207-0006WOU2

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
85 90 95

Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala Gly
145 150 155 160

Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
195 200 205

Ala Pro Ala Glu Cys Ser
210

<210> 60
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-2803, hIgG2, heavy_chain

<400> 60

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

SEQUENCE-LISTING-17207-0006WOU2

Arg Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Tyr Ser Ser Gly Gly Arg Thr Arg Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Lys Ala Ser Asp Leu Ser Gly Ser Phe Ser Glu Ala Leu
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
130 135 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
195 200 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
210 215 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
290 295 300

SEQUENCE-LISTING-17207-0006WOU2

Arg val val ser val Leu Thr val val His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly
450