

SEQUENCE LISTING

<110> UDEN Mark
KOTSOPLOULOU, Ekaterina

<120> Production Method

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<150> US60/956772

<151> 2007-08-20

<160> 25

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<213> Artificial Sequence

<220>

<223> Primer/Probe

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27

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<220>

<223> Primer/Probe

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<213> Artificial Sequence

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<400> 4

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<400> 7
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<220>
<223> Primer/Probe

<400> 8
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<220>
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<400> 9
gccctccaat cgggtaactc 20

<210> 10
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<212> DNA
<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 10

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tgtgcagtct ctggattcac cttcagtgac aacggaatgg cgtgggtccg ccaggctcca 180
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<210> 11

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Light chain

<400> 11

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atctcctgca gagttagtca gagcctttta cacagtaatg gatacaccta ttacatttgg 180
tacctgcaga agccagggca gtctccacag ctctgatct ataaagtttc caaccgattt 240
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ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 480
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tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 600
agcagcacc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgctgcgaa 660
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<210> 12

<211> 1392

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon adapted Heavy chain

<400> 12

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ggaaaggggc	tcgagtgggt	gagcttcac	agtaacctgg	cctacagtat	cgactatgct	240
gacaccgtga	ccggccgctt	cactatctct	cgggataatg	ctaagaacag	cctgtacctc	300
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<210> 13

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon adapted Light chain

<400> 13

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atcagctgca	gggtgtccca	gtcgtgtgtc	cattccaacg	ggtacacgta	cctgcattgg	180
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agccgcgtgg	aagctgagga	cgtgggcgtc	tactactgca	gccagaccgc	gcatgtgcc	360
tacaccttcg	gcggcggcac	aaaggtggag	atcaagcgta	cgggtggctgc	accatctgtc	420
ttcatcttcc	cgccatctga	tgagcagttg	aaatctggaa	ctgcctctgt	tgtgtgcctg	480
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agcagcacc	tgacgtgag	caaagcagac	tacgagaaac	acaaagtcta	cgcctgcgaa	660
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<210> 14

<211> 1392

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon adapted Heavy chain

<400> 14

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ggcaagggcc	tggagtgggt	gagcttcac	agcaacctgg	cctacagcat	cgactacgcc	240
gacaccgtga	ccggccgctt	caccatcagc	cgcgacaacg	ccaagaacag	cctgtacctg	300
cagatgaaca	gcctgcgcgc	cgaggacacc	gccgtgtact	actgcgtgag	cggcacctgg	360

ttcgctact	ggggccaggg	cacactagtc	acagtctcct	cagcctccac	caagggccca	420
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<210> 15

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon adapted Light chain

<400> 15

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agcagcacc	tgacgctgag	caaagcagac	tacgagaaac	acaaagtcta	cgctcgcgaa	660
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<210> 16

<211> 1392

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon adapted Heavy chain

<400> 16

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agcgtgttcc	ccctggcccc	cagcagcaag	agcaccagcg	gcggcacagc	cgccctgggc	480
tgcttgggtga	aggactactt	ccccgaaccg	gtgaccgtgt	cctggaacag	cggagccctg	540
accagcggcg	tgcacacctt	ccccgcctgt	ctgcagagca	gcggcctgta	cagcctgagc	600
agcgtgggtga	ccgtgcccag	cagcagcctg	ggcaccacaga	cctacatctg	taacgtgaac	660

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cacaagccca gcaacaccaa ggtggacaag aaggtggagc ccaagagctg tgacaagacc 720
cacacctgcc cccctgcc tgccccgag ctggccggag cccccagcgt gttcctgttc 780
cccccaagc ctaaggacac cctgatgatc agcagaaccc ccgaggtgac ctgtgtggtg 840
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ttcttcctgt acagcaagct gaccgtggac aagagcagat ggcagcaggg caacgtgttc 1320
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tcccctggca ag

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<210> 17

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon adapted Light chain

<400> 17

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gacatcgtga tgaccagag cccctgagc ctgccgtga cccctggcga gcccgccagc 120
atcagctgta gactgagcca gagcctgctg cacagcaacg gctacaccta cctgcactgg 180
tatctgcaga agcctggcca gagccctcag ctgctgatct acaagggtgtc caaccgggttc 240
agcggcgtgc ctgatagatt cagcggcagc ggctccggca ccgacttcac cctgaagatc 300
agcagagtgg aggccgagga tgtgggcgtg tactactgct cccagaccag acacgtgcct 360
tacacctttg gcggcggaac aaagggtggag atcaagcgta cgggtggccgc cccagcgtg 420
ttcatcttcc cccccagcga tgagcagctg aagagcggca ccgccagcgt ggtgtgtctg 480
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agcagcacc tgacctgag caaggccgac tacgagaagc acaagggtgta cgctgtgag 660
gtgaccacc agggcctgtc cagccccgtg accaagagct tcaaccgggg cgagtgc 717

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<210> 18

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> H2L1 Heavy chain

<400> 18

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe Ser Asp Asn
 20           25           30
Gly Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35           40           45
Ser Phe Ile Ser Asn Leu Ala Tyr Ser Ile Asp Tyr Ala Asp Thr Val
 50           55           60
Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser 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
Val Ser Gly Thr Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
100          105          110
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
115          120          125

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Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val
130						135					140				
Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala
145					150					155					160
Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly
			165						170						175
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly
			180						185						190
Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys
		195					200								
Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys
	210					215					220				
Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Ala	Gly	Ala	Pro	Ser	Val	Phe	Leu
225					230					235					240
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
				245					250						255
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys
			260						265						270
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
		275					280					285			
Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
	290					295					300				
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
305					310					315					320
Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys
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Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser
			340						345						350
Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys
		355					360								365
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
	370					375					380				
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
385					390					395					400
Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
				405					410						415
Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn
			420						425						430
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys			
		435					440					445			

<210> 19

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> H2L1 light chain

<400> 19

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Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Val	Ser	Gln	Ser	Leu	Leu	His	Ser
			20					25					30		
Asn	Gly	Tyr	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
		35					40					45			
Pro	Gln	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65					70					75					80

Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Ser	Gln	Thr
				85					90					95	
Arg	His	Val	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys
			100					105					110		
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Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
				165					170					175	
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
			180					185					190		
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
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