SEQUENCE LISTING

<110> Kirin Pharma Kabushiki Kaisha (Tokyo, Japan)
La Jolla Institute for Allergy & Immunology (La Jolla, CA)

<120> Antagonistic Human LIGHT-Specific Human Monoclonal Antibodies

<130> 7505-049-228

<140>
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<150> 60/840,774
<151> 2006-08-28

<150> 60/897,875
<151> 2007-01-25

<160> 106

<170> FastSEQ for Windows Version 4.0

<210> 1
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<213> Homo sapiens

<220>
<223> E1 heavy chain variable region

<400> 1

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		20					25					30			
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe
	35					40					45				
Ser	Arg	Phe	Asn	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
50					55					60					
Glu	Trp	Val	Ser	Tyr	Ile	Ser	Ser	Ser	Ser	Tyr	Thr	Ile	Tyr	Tyr	Ala
65				70					75						80
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn
			85					90					95		
Ser	Leu	Asp	Leu	Gln	Met	Asn	Ser	Leu	Arg	Asp	Glu	Asp	Thr	Ala	Val
		100					105					110			
Tyr	Tyr	Cys	Ala	Arg	Ser	Ile	Ala	Ala	Ala	Phe	Asp	Tyr	Trp	Gly	Gln
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Gly	Ala	Leu	Val	Thr	Val	Ser	Ser								
130					135										

<210> 2
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<212> PRT
<213> Homo sapiens

<220>
<223> E13 heavy chain variable region

<400> 2
Met Glu Phe Gly Leu Ser Trp Ile Phe Leu Ala Ala Ile Leu Lys Gly
 1   5   10   15
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
            20   25   30
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu
        35   40   45
Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50   55   60
Glu Trp Val Gly Arg Ile Lys Ser Lys Ile Asp Gly Gly Thr Thr Asp
65   70   75   80
Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
                85   90   95
Lys Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
            100   105   110
Ala Val Tyr Tyr Cys Thr Thr Ala Met Ala Gly Ala Phe Gly Phe Trp
        115   120   125
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130   135

<210> 3
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<223> E63 heavy chain variable region

<400> 3
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1   5   10   15
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
            20   25   30
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ile Val Ser Gly Gly Ser Val
        35   40   45
Ser Ser Gly Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys
    50   55   60
Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr
65   70   75   80
Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
                85   90   95
Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
            100   105   110
Val Tyr Tyr Cys Ala Arg Trp Ile Thr Met Phe Arg Gly Val Gly Phe
        115   120   125
Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130   135   140

<210> 4
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<223> F19 heavy chain variable region

<400> 4
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

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 1               5                  10                  15
Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
            20                  25                  30
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
        35                  40                  45
Ser Gly Tyr Asn Trp His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
    50                  55                  60
Glu Trp Ile Gly Glu Ile Thr His Ser Gly Ser Thr Asn Tyr Asn Pro
65                  70                  75                  80
Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
                85                  90                  95
Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
            100                 105                 110
Tyr Cys Val Arg Glu Ile Ala Val Ala Gly Thr Gly Tyr Tyr Gly Met
        115                 120                 125
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
    130                 135                 140
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<210> 5
<211> 143
<212> PRT
<213> Homo sapiens

<220>
<223> F23 heavy chain variable region

<400> 5

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 1               5                  10                  15
Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Gln
            20                  25                  30
Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
        35                  40                  45
Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Asn Trp Ile Arg
    50                  55                  60
Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn Gln Tyr
65                  70                  75                  80
Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys
                85                  90                  95
Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala
            100                 105                 110
Val Tyr Tyr Cys Ala Arg Glu Ile Ala Thr Ala Asp Lys Gly Tyr Tyr
        115                 120                 125
Gly Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
    130                 135                 140
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<210> 6
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<220>
<223> E1 kappa light chain variable region #2 (E1 kappa(B))

<400> 6

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Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1               5                  10                  15
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
            20                  25                  30
```

```
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45
Val Ser Ser Ser Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
65                  70                  75                  80
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
            100                 105                 110
Gly Ser Ser Met Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
        115                 120                 125


<210> 7
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<223> E13 kappa light chain variable region

<400> 7
Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1               5                  10                  15
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
            20                  25                  30
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45
Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50                  55                  60
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
65                  70                  75                  80
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
            100                 105                 110
Gly Ser Ser Pro Met Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
        115                 120                 125
Lys Arg
    130


<210> 8
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<223> E63 kappa light chain variable region

<400> 8
Met Ser Pro Ser Gln Leu Ile Gly Phe Leu Leu Leu Trp Val Pro Ala
 1               5                  10                  15
Ser Arg Gly Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val
            20                  25                  30
Thr Pro Lys Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile
        35                  40                  45
Gly Ser Ser Leu His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys
    50                  55                  60
Leu Leu Ile Lys Tyr Ala Ser Gln Ser Phe Ser Gly Val Pro Ser Arg
```

```
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser
                85                  90                  95
Leu Glu Ala Glu Asp Ala Ala Ala Tyr Tyr Cys His Gln Ser Ser Ser
            100                 105                 110
Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
        115                 120                 125


<210> 9
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<223> F19 kappa light chain variable region #2

<400> 9
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1               5                  10                  15
Leu Pro Gly Ala Arg Cys Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser
            20                  25                  30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
        35                  40                  45
Glu     Gly Ile Asn Ser Ala Phe Ala Trp Tyr Gln Gln Lys Pro Gly Lys
         50                  55                  60
Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val
65                  70                  75                  80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
                85                  90                  95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
            100                 105                 110
Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
        115                 120                 125
Lys


<210> 10
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<223> F23 kappa light chain variable region

<400> 10
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1               5                  10                  15
Leu Pro Gly Ala Arg Cys Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser
            20                  25                  30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
        35                  40                  45
Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
    50                  55                  60
Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val
65                  70                  75                  80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
                85                  90                  95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
            100                 105                 110
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Phe Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
115 120 125
Lys

<210> 11
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of E1 heavy chain variable region

<400> 11
Arg Phe Asn Met Asn
1 5

<210> 12
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of E1 heavy chain variable region

<400> 12
Tyr Ile Ser Ser Ser Ser Tyr Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 13
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of E1 heavy chain variable region

<400> 13
Ser Ile Ala Ala Phe Asp Tyr
1 5

<210> 14
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of E13 heavy chain variable region

<400> 14
Asn Ala Trp Met Ser
1 5

<210> 15

<211> 19
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of E13 heavy chain variable region

<400> 15
Arg Ile Lys Ser Lys Ile Asp Gly Gly Thr Thr Asp Tyr Ala Ala Pro
 1   5   10   15
Val Lys Gly

<210> 16
<211> 8
<212> PRT
<213> Homo sapiens

<220>
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<400> 16
Ala Met Ala Gly Ala Phe Gly Phe
 1   5

<210> 17
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of E63 heavy chain variable region

<400> 17
Ser Gly Gly Tyr Tyr Trp Ser
 1   5

<210> 18
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of E63 heavy chain variable region

<400> 18
Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser
 1   5   10   15

<210> 19
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of E63 heavy chain variable region

<400> 19
Trp Ile Thr Met Phe Arg Gly Val Gly Phe Asp Pro
 1   5   10

<210> 20
<211> 5
<212> PRT
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<220>
<223> CDR1 of F19 heavy chain variable region #2 (F19 kappa(B))

<400> 20
Gly Tyr Asn Trp His
 1   5

<210> 21
<211> 16
<212> PRT
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<220>
<223> CDR2 of F19 heavy chain variable region #2 (F19 kappa(B))

<400> 21
Glu Ile Thr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser
 1   5   10   15

<210> 22
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of F19 heavy chain variable region #2 (F19 kappa(B))

<400> 22
Glu Ile Ala Val Ala Gly Thr Gly Tyr Tyr Gly Met Asp Val
 1   5   10

<210> 23
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of F23 heavy chain variable region

<400> 23
Gly Tyr Tyr Trp Asn
 1   5

<210> 24
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of F23 heavy chain variable region

<400> 24
Glu Ile Asn Gln Tyr Asn Pro Ser Leu Lys Ser
 1   5   10

<210> 25
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of F23 heavy chain variable region

<400> 25
GLu Ile Ala   Thr Ala Asp Lys Gly Tyr Tyr Gly Leu Asp Val
 1   5   10

<210> 26
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of E1 light chain variable region #2 (E1 kappa(B))

<400> 26
Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Thr
 1   5   10

<210> 27
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of E1 light chain variable region #2 (E1 kappa(B))

<400> 27
Gly Ala Ser Ser Arg Ala Thr
 1   5

<210> 28
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of E1 light chain variable region #2 (E1 kappa(B))

<400> 28
Gln Gln Tyr Gly Ser Ser Met Tyr Thr
 1   5

<210> 29
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of E13 light chain variable region

<400> 29
Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
 1   5   10

<210> 30
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of E13 light chain variable region

<400> 30
Gly Ala Ser Ser Arg Ala Thr
 1   5

<210> 31
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of E13 light chain variable region

<400> 31
Gln Gln Tyr Gly Ser Ser Pro Met Tyr Thr
 1   5   10

<210> 32
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<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of E63 light chain variable region

<400> 32
Arg Ala Ser Gln Ser Ile Gly Ser Ser Leu His
 1   5   10

<210> 33
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of E63 light chain variable region

<400> 33

Tyr Ala Ser Gln Ser Phe Ser
1 5

<210> 34
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of E63 light chain variable region

<400> 34
His Gln Ser Ser Ser Leu Pro Leu Thr
1 5

<210> 35
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of F19 light chain variable region #2 (F19 kappa(B))

<400> 35
Arg Ala Ser Glu Gly Ile Asn Ser Ala Phe Ala
1 5 10

<210> 36
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of F19 light chain variable region #2 (F19 kappa(B))

<400> 36
Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 37
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of F19 light chain variable region #2 (F19 kappa(B))

<400> 37
Gln Gln Phe Asn Ser Tyr Pro Leu Thr
1 5

<210> 38
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of F23 light chain variable region

<400> 38
Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
 1   5   10

<210> 39
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of F23 light chain variable region

<400> 39
Asp Ala Ser Ser Leu Glu Ser
 1   5

<210> 40
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of F23 light chain variable region

<400> 40
Gln Gln Phe Asn Ser Tyr Pro Leu Thr
 1   5

<210> 41
<211> 408
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of E1 heavy chain variable region

<400> 41
atggagttgg ggctgtgctg ggttttcctt gttgctattt tagaaggtgt ccagtgtgag 60
gtgcagctgg tggagtctgg gggaggcttg gtacagcctg gggggtccct gagactctcc 120
tgtgcagcct ctggattcac cttcagtaga tttaacatga actgggtccg ccaggctcca 180
gggaaggggc tggagtgggt ttcatacatt agtagtagta gttataccat atactacgca 240
gactctgtga agggccgatt caccatctcc agagacaatg ccaagaactc actggatctg 300
caaatgaaca gcctgagaga cgaggacacg gctgtgtatt actgtgcgag gagtatagca 360
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<210> 42
<211> 414
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of E13 heavy chain variable region

<400> 42
atggagtttg ggctgagctg gattttcctt gctgcgattt taaaaggtgt ccagtgtgag 60

gtgcagctgg tggagtctgg gggaggcctg gtaaagcctg gggggtccct tagactctcc 120
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tacgctgcac ccgtgaaagg cagattcacc atctcaagag atgattcaaa aaacacgctg 300
tttctgcaaa tgaacagcct gaaaaccgag gacacagccg tgtattactg taccacagca 360
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<210> 43
<211> 423
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of E63 heavy chain variable region

<400> 43
atgaaacacc tgtggttctt cctcctcctg gtggcagctc ccagatgggt cctgtcccag 60
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc 120
tgcattgtct ctggtggctc cgtcagcagt ggtggttact actggagctg gatccggcag 180
cccccaggga agggactgga gtggattggg tatatctatt acagtgggag caccaactac 240
aacccctccc tcaagagtcg agtcaccata tcagtagaca cgtccaagaa ccagttctcc 300
ctgaagctga gctctgtgac cgctgcggac acggccgtgt attactgtgc gagatggatt 360
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tca 423

<210> 44
<211> 423
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of F19 heavy chain variable region

<400> 44
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tgcgctgtct atggtgggtc cttcagtggt tacaactggc actggatccg ccagcccccа 180
gggaaggggc tggagtggat tggggaaatc actcatagtg gaagcaccaa ttacaacccg 240
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ctgagctctg tgaccgccgc ggacacggct gtgtattact gtgtgcgaga gattgcagtg 360
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tca 423

<210> 45
<211> 429
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of F23 heavy chain variable region

<400> 45
atggacctcc tgcacaagaa catgaaacac ctgtggttct tcctcctcct ggtggcagct 60
cccagatggg tcctgtccca ggtgcagcta cagcagtggg gcgcaggact gttgaagcct 120
tcggagaccc tgtccctcac ctgcgctgtc tatggtgggt ccttcagtgg ttactactgg 180
aactggatcc gccagccccc agggaagggg ctggagtgga ttggggaaat caatcagtac 240
aacccgtccc tcaagagtcg agtcaccata tcagtagaca cgtccaagaa ccagttctcc 300
ctgaagctga gctctgtgac cgccgcggac acggctgtgt attactgtgc gagagagata 360
gcaacagctg ataaagggta ctacggtttg gacgtctggg gccaagggac cacggtcacc 420
gtctcctca 429

<210> 46
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of E1 kappa light chain variable region #2 (E1 kappa(B))

<400> 46
atggaaaccc cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctgca gggccagtca gagtgttagc agcagctact taacctggta ccagcagaaa 180
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 240
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caggggacca agctggagat caaa 384

<210> 47
<211> 390
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of E13 kappa light chain variable region

<400> 47
atggaaaccc cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 180
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 240
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 300
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacccat gtacactttt 360
ggccagggga ccaagctgga gatcaaacga 390

<210> 48
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of E63 kappa light chain variable region

<400> 48
atgtcgccat cacaactcat tgggtttctg ctgctctggg ttccagcctc caggggtgaa 60
attgtgctga ctcagtctcc agactttcag tctgtgactc caaaggagaa agtcaccatc 120
acctgccggg ccagtcagag cattggtagt agcttacact ggtaccagca gaaaccagat 180
cagtctccaa agctcctcat caagtatgct tcccagtcct tctcaggggt cccctcgagg 240
ttcagtggca gtggatctgg gacagatttc accctcacca tcaatagcct ggaagctgaa 300
gatgctgcag catattactg tcatcagagt agtagtttac ctctcacttt cggcggaggg 360
accaaggtgg agatcaaa 378

<210> 49
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of F19 kappa light chain variable region #2 (F19 kappa(B))

<400> 49
atggacatga gggtccccgc tcagctcctg gggcttctgc tgctctggct cccaggtgcc 60

```
agatgtgcca tccagttgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccgggc           aagtcagggc attaacagtg cttttgcctg gtatcagcag 180
aaaccaggga aagctcctaa gctcctgatc tatgatgcct ccagtttgga aagtggggtc 240
ccatcaaggt tcagcggcag tggatctggg acagatttca ctctcaccat cagcagcctg 300
cagcctgaag attttgcaac ttattactgt caacagttta atagttaccc tctcactttc 360
ggcggaggga ccaaggtgga gatcaaa                                     387
```

<210> 50
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of F23 kappa light chain variable region

<400> 50
```
atggacatga gggtccccgc tcagctcctg gggcttctgc tgctctggct cccaggtgcc 60
agatgtgcca tccagttgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccgggc aagtcagggc attagcagtg ctttagcctg gtatcagcag 180
aaaccaggga aagctcctaa gctcctgatc tatgatgcct ccagtttgga aagtggggtc 240
ccatcaaggt tcagcggcag tggatctggg acagatttca ctctcaccat cagcagcctg 300
cagcctgaag attttgcaac ttattactgt caacagttta atagttaccc gctcactttc 360
ggcggaggga ccaaggtgga gatcaaa                                     387
```

<210> 51
<211> 723
<212> DNA
<213> Homo sapiens

<220>
<223> Nucleotide sequence of a hLIGHT

<400> 51
```
atggaggaga gtgtcgtacg gccctcagtg tttgtggtgg atggacagac cgacatccca 60
ttcacgaggc tgggacgaag ccaccggaga cagtcgtgca gtgtggcccg ggtgggtctg 120
ggtctcttgc tgttgctgat gggggccggg ctggccgtcc aaggctggtt cctcctgcag 180
ctgcactggc gtctaggaga gatggtcacc cgcctgcctg acggacctgc aggctcctgg 240
gagcagctga tacaagagcg aaggtctcac gaggtcaacc cagcagcgca tctcacaggg 300
gccaactcca gcttgaccgg cagcgggggg ccgctgttat gggagactca gctgggcctg 360
gccttcctga ggggcctcag ctaccacgat ggggcccttg tggtcaccaa agctggctac 420
tactacatct actccaaggt gcagctgggc ggtgtgggct gcccgctggg cctggccagc 480
accatcaccc acggcctcta caagcgcaca ccccgctacc ccgaggagct ggagctgttg 540
gtcagccagc agtcaccctg cggacgggcc accagcagct cccgggtctg gtgggacagc 600
agcttcctgg gtggtgtggt acacctggag gctggggagg aggtggtcgt ccgtgtgctg 660
gatgaacgcc tggttcgact gcgtgatggt acccggtctt acttcggggc tttcatggtg 720
tga                                                              723
```

<210> 52
<211> 240
<212> PRT
<213> Homo sapiens

<220>
<223> a full length hLIGHT

<400> 52
```
Met Glu Glu Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln
 1               5                  10                  15
Thr Asp Ile Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser
            20                  25                  30
Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly
```

```
        35                  40                  45
Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
    50                  55                  60
Leu Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp
65                  70                  75                  80
Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala
                85                  90                  95
His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu
            100                 105                 110
Leu Trp Glu Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr
        115                 120                 125
His Asp Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr
    130                 135                 140
Ser Lys Val Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser
145                 150                 155                 160
Thr Ile Thr His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu
                165                 170                 175
Leu Glu Leu Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser
            180                 185                 190
Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His
        195                 200                 205
Leu Glu Ala Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu
    210                 215                 220
Val Arg Leu Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
225                 230                 235                 240
```

<210> 53
<211> 630
<212> DNA
<213> Homo sapiens

<220>
<223> a soluble FLAG-tagged hLIGHT (240 aa)

<400> 53
```
atgcctggga agatggtcgt gatccttgga gcctcaaata tactttggat aatgtttgca 60
gcttctcaag ctgactacaa ggacgacgat gacaagtacg taggagagat ggtcacccgc 120
ctgcctgacg gacctgcagg ctcctgggag cagctgatac aagagcgaag gtctcacgag 180
gtcaacccag cagcgcatct cacaggggcc aactccagct tgaccggcag cgggggccg 240
ctgttatggg agactcagct gggcctggcc ttcctgaggg gcctcagcta ccacgatggg 300
gcccttgtgg tcaccaaagc tggctactac tacatctact ccaaggtgca gctgggcggt 360
gtgggctgcc cgctgggcct ggccagcacc atcacccacg gcctctacaa gcgcacaccc 420
cgctaccccg aggagctgga gctgttggtc agccagcagt caccctgcgg acgggccacc 480
agcagctccc gggtctggtg ggacagcagc ttcctgggtg gtgtggtaca cctggaggct 540
ggggaggagg tggtcgtccg tgtgctggat gaacgcctgg ttcgactgcg tgatggtacc 600
cggtcttact tcggggcttt catggtgtga                                  630
```

<210> 54
<211> 183
<212> PRT
<213> Homo sapiens

<220>
<223> a soluble FLAG-tagged hLIGHT (183 aa)

<400> 54
```
Asp Tyr Lys Asp Asp Asp Asp Lys Gly Glu Met Val Thr Arg Leu Pro
 1               5                  10                  15
Asp Gly Pro Ala Gly Ser Trp Glu Gln Leu Ile Gln Glu Arg Arg Ser
            20                  25                  30
```

```
His Glu Val Asn Pro Ala Ala His Leu Thr Gly Ala Asn Ser Ser Leu
        35                  40                  45
Thr Gly Ser Gly Gly Pro Leu Leu Trp Glu Thr Gln Leu Gly Leu Ala
    50                  55                  60
Phe Leu Arg Gly Leu Ser Tyr His Asp Gly Ala Leu Val Val Thr Lys
65                  70                  75                  80
Ala Gly Tyr Tyr Tyr Ile Tyr Ser Lys Val Gln Leu Gly Gly Val Gly
                85                  90                  95
Cys Pro Leu Gly Leu Ala Ser Thr Ile Thr His Gly Leu Tyr Lys Arg
            100                 105                 110
Thr Pro Arg Tyr Pro Glu Glu Leu Glu Leu Leu Val Ser Gln Gln Ser
        115                 120                 125
Pro Cys Gly Arg Ala Thr Ser Ser Ser Arg Val Trp Trp Asp Ser Ser
    130                 135                 140
Phe Leu Gly Gly Val Val His Leu Glu Ala Gly Glu Glu Val Val Val
145                 150                 155                 160
Arg Val Leu Asp Glu Arg Leu Val Arg Leu Arg Asp Gly Thr Arg Ser
                165                 170                 175
Tyr Phe Gly Ala Phe Met Val
            180
```

<210> 55
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer RACEUPS5'

<400> 55
ctaatacgac tcactatagg gc 22

<210> 56
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer IgG1p

<400> 56
tcttgtccac cttggtgttg ctgggcttgt g 31

<210> 57
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer HK5

<400> 57
aggcacacaa cagaggcagt tccagatttc 30

<210> 58
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> primer M13F

<400> 58
gtaaaacgac ggccagtg 18

<210> 59
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> primer M13R

<400> 59
caggaaacag ctatgac 17

<210> 60
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer E63HF85

<400> 60
agagagagag gtcgaccacc atgaaacacc tgtggttctt c 41

<210> 61
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer E63HR38

<400> 61
gagagagaga gctagctgag gagacggtga ccagggt 37

<210> 62
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> primer E63LF84

<400> 62
agagagagag atctctcacc atgtcgccat cacaactcat tg 42

<210> 63
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer E63LR43

<400> 63
agagagagag cgtacgtttg atctccacct tggtccctcc 40

<210> 64

<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer HH-2

<400> 64
gctggagggc acggtcacca cgctg 25

<210> 65
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer HK-2

<400> 65
gttgaagctc tttgtgacgg gcgagc 26

<210> 66
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer F23HF86

<400> 66
agagagagag gtcgaccacc atggacctcc tgcacaagaa c 41

<210> 67
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> primer F23HR55

<400> 67
agagagagag gctagctgag gagacggtga ccgt 34

<210> 68
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> primer F23LF36

<400> 68
agagagagag atctctcacc atggacatga gggtccccgc tc 42

<210> 69
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer F23LR43

<400> 69
agagagagag cgtacgtttg atctccacct tggtccctcc 40

<210> 70
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer E1HFSalI

<400> 70
agagagagag gtcgaccacc atggagttgg ggctgtgctg g 41

<210> 71
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer E1HRNheI

<400> 71
agagagagag gctagctgag gagacggtga ccagggc 37

<210> 72
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer F19HFSalI

<400> 72
agagagagag gtcgaccacc atgaaacacc tgtggttctt c 41

<210> 73
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer F19HRNheI

<400> 73
agagagagag gctagctgag gagacggtga ccgtggt 37

<210> 74
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> primer E1KF2+3BglII

<400> 74
agagagagag atctctcacc atggaaaccc cagcgcagct tc 42

<210> 75
<211> 40

<212> DNA
<213> Artificial Sequence

<220>
<223> primer E1KR2BsiWI

<400> 75
agagagagag cgtacgtttg atctccagct tggtcccctg 40

<210> 76
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer E1KR3BsiWI

<400> 76
agagagagag cgtacgtttg atttccacct tggtcccttg 40

<210> 77
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer F19KR1+2BsiWI

<400> 77
agagagagag cgtacgtttg atctccacct tggtccctcc 40

<210> 78
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer F19KR3BsiWI

<400> 78
agagagagag cgtacgtttg atctccagct tggtcccctg 40

<210> 79
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> primer F19KF1+2+3BglII

<400> 79
agagagagag atctctcacc atggacatga gggtccccgc tc 42

<210> 80
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer

<400> 80
gtaggagaga tggtcacccg cct 23

<210> 81
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 81
ggaacgcgaa ttcccacgtg tcagacccat gtccaat 37

<210> 82
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<223> E1 kappa light chain variable region #1 (E1 kappa(A))

<400> 82
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1   5   10   15
Leu Pro Gly Ala Arg Cys Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser
            20   25   30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
        35   40   45
Gln Gly Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
    50   55   60
Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val
65   70   75   80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
                85   90   95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
            100   105   110
Phe Asn Ser Tyr Arg Thr Leu Leu Ala Arg Gly Pro Ser Trp Arg Ser
        115   120   125

<210> 83
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<223> Amino acid sequence of cDNA of E1 kappa light chain
      variable region #3 (E1 kappa(C))

<400> 83
Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1   5   10   15
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
            20   25   30
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Tyr Arg Ala Ser Gln Ser
        35   40   45
Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50   55   60
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro
65   70   75   80

```
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
            100                 105                 110
Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125
```

<210> 84
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of E1 light chain variable region #1 (E1 kappa(A))

<400> 84
```
Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
 1               5                  10
```

<210> 85
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of E1 light chain variable region #3 (E1 kappa(C))

<400> 85
```
Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
 1               5                  10
```

<210> 86
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of E1 light chain variable region #1 (E1 kappa(A))

<400> 86
```
Asp Ala Ser Ser Leu Glu Ser
 1               5
```

<210> 87
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of E1 light chain variable region #3 (E1 kappa(C))

<400> 87
```
Gly Ala Ser Asn Arg Ala Thr
 1               5
```

<210> 88

<211> 8
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of E1 light chain variable region #1 (E1 kappa(A))

<400> 88
Gln Gln Phe Asn Ser Tyr Arg Thr
1 5

<210> 89
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of E1 light chain variable region #3 (E1 kappa(C))

<400> 89
Gln Gln Tyr Gly Ser Ser Pro Trp Thr
1 5

<210> 90
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<223> F19 kappa light chain variable region #1 (F19 kappa(A))

<400> 90
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15
Val Pro Gly Ala Arg Cys Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser
20 25 30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Val Ser
35 40 45
Gln Gly Ile Ser Ser Tyr Leu Asn Trp Tyr Arg Gln Lys Pro Gly Lys
50 55 60
Val Pro Lys Leu Leu Ile Tyr Ser Ala Ser Asn Leu Gln Ser Gly Val
65 70 75 80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95
Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Gly Gln Arg
100 105 110
Thr Tyr Asn Ala Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
115 120 125
Lys

<210> 91
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<223> F19 kappa light chain variable region #3 (F19 kappa(C))

<400> 91
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1   5   10   15
Leu Pro Gly Ala Arg Cys Val Ile Trp Met Thr Gln Ser Pro Ser Leu
            20   25   30
Leu Ser Ala Ser Thr Gly Asp Arg Val Thr Ile Ser Cys Arg Met Ser
        35   40   45
Gln Gly Ile Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
    50   55   60
Ala Pro Glu Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
65   70   75   80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
                85   90   95
Ile Ser Cys Leu Gln Ser Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
            100   105   110
Tyr Tyr Ser Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
        115   120   125
Lys

<210> 92
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<223> Amino acid sequence of cDNA of F19 kappa light chain
      variable region #4 (F19 kappa(D))

<400> 92
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1   5   10   15
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20   25   30
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly
        35   40   45
Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
    50   55   60
Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
65   70   75   80
Arg Phe Ser Gly Ser Gly Pro Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85   90   95
Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser
            100   105   110
Asn Trp His Pro Val Arg Pro Arg Asp Gln Gly Gly Asp Ser
        115   120   125

<210> 93
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of F19 light chain variable region #1 (F19 kappa(A))

<400> 93
Arg Val Ser Gln Gly Ile Ser Ser Tyr Leu Asn
 1   5   10

<210> 94
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of F19 light chain variable region #3 (F19 kappa(C))

<400> 94
Arg Met Ser Gln Gly Ile Ser Ser Tyr Leu Ala
 1   5   10

<210> 95
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> CDR1 of F19 light chain variable region #4 (F19 kappa(D))

<400> 95
Arg Ala Ser Gln Gly Val Ser Ser Tyr Leu Ala
 1   5   10

<210> 96
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of F19 light chain variable region #1 (F19 kappa(A))

<400> 96
Ser Ala Ser Asn Leu Gln Ser
 1   5

<210> 97
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of F19 light chain variable region #3 (F19 kappa(C))

<400> 97
Ala Ala Ser Thr Leu Gln Ser
 1   5

<210> 98
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> CDR2 of F19 light chain variable region #4 (F19 kappa(D))

<400> 98
Asp Ala Ser Asn Arg Ala Thr
 1   5

<210> 99
<211> 8
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of F19 light chain variable region #1 (F19 kappa(A))

<400> 99
Gln Arg Thr Asn Ala Pro Pro Thr
 1   5

<210> 100
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of F19 light chain variable region #3 (F19 kappa(C))

<400> 100
Gln Gln Tyr Tyr Ser Phe Pro Tyr Thr
 1   5

<210> 101
<211> 8
<212> PRT
<213> Homo sapiens

<220>
<223> CDR3 of F19 light chain variable region #4 (F19 kappa(D))

<400> 101
Gln Gln Arg Ser Asn Trp His Pro
 1   5

<210> 102
<211> 386
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of E1 kappa light chain variable region #1 (E1 kappa(A))

<400> 102
atggacatga gggtccccgc tcagctcctg gggcttctgc tgctctggct cccaggtgcc 60
agatgtgcca tccagttgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccgggc aagtcagggc attagcagtg ctttagcctg gtatcagcag 180
aaaccaggga aagctcctaa gctcctgatc tatgatgcct ccagtttgga aagtggggtc 240
ccatcaaggt tcagcggcag tggatctggg acagatttca ctctcaccat cagcagcctg 300
cagcctgaag attttgcaac ttattactgt caacagttta atagttaccg tacacttttg 360
gccaggggac caagctggag atcaaa   386

<210> 103
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of E1 kappa light chain variable region #3 (E1 kappa(C))

<400> 103
atggaaaccc cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctaca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 180
cctggccagg ctcccaggct cctcatctat ggtgcatcca acagggccac tggcatccca 240
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 300
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgtg gacgttcggc 360
caagggacca aggtggaaat caaa 384

<210> 104
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of F19 kappa light chain variable region #1 (F19 kappa(A))

<400> 104
atggacatga gggtccccgc tcagctcctg gggctcctac tgctctgggt cccaggtgcc 60
agatgtgaca tccagttgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 120
gtcaccatca cttgccgggt gagtcagggc attagcagtt atttaaattg gtatcggcag 180
aaaccaggga aagttcctaa gctcctgatc tatagtgcat ccaatttgca atctggagtc 240
ccatctcggt tcagtggcag tggatctggg acagatttca ctctcactat cagcagcctg 300
cagcctgaag atgttgcaac ttattacggt caacggactt acaatgcccc tcccactttc 360
ggcggaggga ccaaggtgga gatcaaa 387

<210> 105
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of F19 kappa chain variable region #3 (F19 kappa(C))

<400> 105
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ccatcaaggt tcagtggcag tggatctggg acagatttca ctctcaccat cagctgcctg 300
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<211> 380
<212> DNA
<213> Homo sapiens

<220>
<223> cDNA of F19 kappa chain variable region #4 (F19 kappa(D))

<400> 106

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gaccaaggtg gagattcaaa                                             380
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