

eolf-seql
SEQUENCE LISTING

<110> Oslo universitetssykehus HF

<120> T-Cell Receptors which Recognise Frameshift Mutants of TGFBR1I

<130> 27.18.123119/01

<150> GB 1608052.5

<151> 2016-05-09

<160> 82

<170> PatentIn version 3.5

<210> 1

<211> 9

<212> PRT

<213> Homo sapiens

<400> 1

Arg Leu Ser Ser Cys Val Pro Val Ala
1 5

<210> 2

<211> 5

<212> PRT

<213> Homo sapiens

<400> 2

Asp Ser Val Asn Asn
1 5

<210> 3

<211> 5

<212> PRT

<213> Homo sapiens

<400> 3

Ile Pro Ser Gly Thr
1 5

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<210> 4
 <211> 11
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 <213> Homo sapiens

<400> 4

Cys Ala Val Asn Ala Gly Asn Met Leu Thr Phe
 1 5 10

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

<400> 5

Met Asp His Glu Asn
 1 5

<210> 6
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 6

Ser Tyr Asp Val Lys Met
 1 5

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

<400> 7

Cys Ala Ser Ser Ser Gly Val Thr Gly Glu Leu Phe Phe
 1 5 10

<210> 8
 <211> 127
 <212> PRT
 <213> Homo sapiens

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<400> 8

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

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

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly
100 105 110

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro
115 120 125

<210> 9

<211> 141

<212> PRT

<213> Homo sapiens

<400> 9

His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
1 5 10 15

Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
20 25 30

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Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr
35 40 45

Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
50 55 60

Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65 70 75 80

Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
85 90 95

Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
100 105 110

Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
115 120 125

Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
130 135 140

<210> 10
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-modified Radium-1 alpha-chain constant region

<400> 10

His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
1 5 10 15

Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
20 25 30

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Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys
35 40 45

Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
50 55 60

Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
65 70 75 80

Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
85 90 95

Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
100 105 110

Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
115 120 125

Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
130 135 140

<210> 11
<211> 268
<212> PRT
<213> Homo sapiens

<400> 11

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile

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

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly
100 105 110

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His
115 120 125

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
130 135 140

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
145 150 155 160

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

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
180 185 190

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
195 200 205

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
210 215 220

Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln
225 230 235 240

Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly

245 eolf-seql 250 255

Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 12
<211> 268
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-modified Radium-1 alpha-chain

<400> 12

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

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

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly
100 105 110

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His
115 120 125

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Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
130 135 140

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
145 150 155 160

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val
165 170 175

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
180 185 190

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
195 200 205

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
210 215 220

Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln
225 230 235 240

Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly
245 250 255

Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
260 265

<210> 13
<211> 131
<212> PRT
<213> Homo sapiens

<400> 13

Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val
1 5 10 15

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

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
35 40 45

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
85 90 95

Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu
115 120 125

Thr Val Leu
130

<210> 14
<211> 179
<212> PRT
<213> Homo sapiens

<400> 14

Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
1 5 10 15

Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
20 25 30

Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn

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35

40

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Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys
50 55 60

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
65 70 75 80

Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
85 90 95

Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
100 105 110

Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
115 120 125

Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser
130 135 140

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
145 150 155 160

Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
165 170 175

Ser Arg Gly

<210> 15

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Cysteine-modified Radium-1 beta-chain constant region

<400> 15

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Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
1 5 10 15

Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
20 25 30

Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
35 40 45

Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys
50 55 60

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
65 70 75 80

Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
85 90 95

Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
100 105 110

Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
115 120 125

Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser
130 135 140

Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala
145 150 155 160

Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp
165 170 175

Ser Arg Gly

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<210> 16
 <211> 310
 <212> PRT
 <213> Homo sapiens

<400> 16

Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val
 1 5 10 15

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

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
 35 40 45

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
 50 55 60

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
 65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
 85 90 95

Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met Tyr Leu Cys Ala Ser
 100 105 110

Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu
 115 120 125

Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val
 130 135 140

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
 145 150 155 160

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Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly
260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
275 280 285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
290 295 300

Arg Lys Asp Ser Arg Gly
305 310

<210> 17
<211> 310
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-modified Radium-1 beta-chain

eolf-seql

<400> 17

Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val
1 5 10 15

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

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
35 40 45

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
85 90 95

Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu
115 120 125

Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val
130 135 140

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
145 150 155 160

Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln
180 185 190

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Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly
260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
275 280 285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
290 295 300

Arg Lys Asp Ser Arg Gly
305 310

<210> 18
<211> 26
<212> PRT
<213> picornavirus

<400> 18

Arg Ala Lys Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
1 5 10 15

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
20 25

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<210> 19
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Double Myc-tag

<400> 19

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Glu Gln Lys Leu Ile Ser
 1 5 10 15

Glu Glu Asp Leu
 20

<210> 20
 <211> 147
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Radium-1 alpha-chain variable region with double Myc-tag

<400> 20

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
 1 5 10 15

Cys Cys Val Arg Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Glu Gln
 20 25 30

Lys Leu Ile Ser Glu Glu Asp Leu Gly Ile Gln Val Glu Gln Ser Pro
 35 40 45

Pro Asp Leu Ile Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn
 50 55 60

Phe Ser Asp Ser Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp
 65 70 75 80

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Gly Gln Leu Ile Asn Leu Phe Tyr Ile Pro Ser Gly Thr Lys Gln Asn
85 90 95

Gly Arg Leu Ser Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu
100 105 110

Tyr Ile Ser Ser Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala
115 120 125

Val Asn Ala Gly Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met
130 135 140

Val Lys Pro
145

<210> 21
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> Radium-1 alpha-chain with double Myc-tag

<400> 21

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Glu Gln
20 25 30

Lys Leu Ile Ser Glu Glu Asp Leu Gly Ile Gln Val Glu Gln Ser Pro
35 40 45

Pro Asp Leu Ile Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn
50 55 60

Phe Ser Asp Ser Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp

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65		70		75		80									
Gly	Gln	Leu	Ile	Asn	Leu	Phe	Tyr	Ile	Pro	Ser	Gly	Thr	Lys	Gln	Asn
				85					90					95	
Gly	Arg	Leu	Ser	Ala	Thr	Thr	Val	Ala	Thr	Glu	Arg	Tyr	Ser	Leu	Leu
			100					105					110		
Tyr	Ile	Ser	Ser	Ser	Gln	Thr	Thr	Asp	Ser	Gly	Val	Tyr	Phe	Cys	Ala
		115					120					125			
Val	Asn	Ala	Gly	Asn	Met	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Met
	130					135					140				
Val	Lys	Pro	His	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg
145					150					155					160
Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp
				165					170					175	
Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr
			180					185					190		
Asp	Lys	Thr	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser
		195					200					205			
Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe
	210					215					220				
Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser
225					230					235					240
Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn
				245					250					255	
Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu

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260

265

270

Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
275 280 285

<210> 22

<211> 288

<212> PRT

<213> Artificial Sequence

<220>

<223> Cysteine-modified Radium-1 alpha-chain with double Myc-tag

<400> 22

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Glu Gln
20 25 30

Lys Leu Ile Ser Glu Glu Asp Leu Gly Ile Gln Val Glu Gln Ser Pro
35 40 45

Pro Asp Leu Ile Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn
50 55 60

Phe Ser Asp Ser Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp
65 70 75 80

Gly Gln Leu Ile Asn Leu Phe Tyr Ile Pro Ser Gly Thr Lys Gln Asn
85 90 95

Gly Arg Leu Ser Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu
100 105 110

Tyr Ile Ser Ser Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala
115 120 125

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Val Asn Ala Gly Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met
 130 135 140

Val Lys Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg
 145 150 155 160

Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp
 165 170 175

Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr
 180 185 190

Asp Lys Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser
 195 200 205

Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe
 210 215 220

Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser
 225 230 235 240

Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn
 245 250 255

Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu
 260 265 270

Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 275 280 285

<210> 23
 <211> 136
 <212> PRT
 <213> Mus musculus
 <400> 23

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Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser
1 5 10 15

Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn
20 25 30

Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr Val
35 40 45

Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp
50 55 60

Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn
65 70 75 80

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

Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val
100 105 110

Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu
115 120 125

Met Thr Leu Arg Leu Trp Ser Ser
130 135

<210> 24

<211> 136

<212> PRT

<213> Artificial Sequence

<220>

<223> Cysteine-modified murinised Radium-1 alpha chain constant region

<400> 24

Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser
1 5 10 15

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Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn
20 25 30

Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Cys Val
35 40 45

Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp
50 55 60

Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn
65 70 75 80

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

Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val
100 105 110

Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu
115 120 125

Met Thr Leu Arg Leu Trp Ser Ser
130 135

<210> 25
<211> 263
<212> PRT
<213> Artificial Sequence

<220>
<223> Radium-1 alpha-chain with murinised constant region

<400> 25

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

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Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

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

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly
100 105 110

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro Ile
115 120 125

Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln
130 135 140

Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn Val
145 150 155 160

Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr Val Leu
165 170 175

Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser
180 185 190

Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala
195 200 205

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Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu Lys
210 215 220

Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val Met
225 230 235 240

Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met
245 250 255

Thr Leu Arg Leu Trp Ser Ser
260

<210> 26

<211> 263

<212> PRT

<213> Artificial Sequence

<220>

<223> Radium-1 alpha-chain with cysteine-modified murinised constant region

<400> 26

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

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

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser

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85

90

95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly
 100 105 110

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro Ile
 115 120 125

Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln
 130 135 140

Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn Val
 145 150 155 160

Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Cys Val Leu
 165 170 175

Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser
 180 185 190

Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala
 195 200 205

Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu Lys
 210 215 220

Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val Met
 225 230 235 240

Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met
 245 250 255

Thr Leu Arg Leu Trp Ser Ser
 260

<210> 27

eolf-seql

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> Radium-1 alpha chain with double Myc-tag and murinised constant region

<400> 27

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Glu Gln
20 25 30

Lys Leu Ile Ser Glu Glu Asp Leu Gly Ile Gln Val Glu Gln Ser Pro
35 40 45

Pro Asp Leu Ile Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn
50 55 60

Phe Ser Asp Ser Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp
65 70 75 80

Gly Gln Leu Ile Asn Leu Phe Tyr Ile Pro Ser Gly Thr Lys Gln Asn
85 90 95

Gly Arg Leu Ser Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu
100 105 110

Tyr Ile Ser Ser Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala
115 120 125

Val Asn Ala Gly Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met
130 135 140

Val Lys Pro Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp
145 150 155 160

eolf-seql

Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser
165 170 175

Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp
180 185 190

Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala
195 200 205

Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys
210 215 220

Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr
225 230 235 240

Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn
245 250 255

Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
260 265 270

Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
275 280

<210> 28
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> Radium-1 alpha-chain with double Myc-tag and cysteine-modified
murinised constant region

<400> 28

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

eolf-seql

Cys	Cys	Val	Arg	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Glu	Gln			
			20					25					30					
Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Gly	Ile	Gln	Val	Glu	Gln	Ser	Pro			
		35					40					45						
Pro	Asp	Leu	Ile	Leu	Gln	Glu	Gly	Ala	Asn	Ser	Thr	Leu	Arg	Cys	Asn			
	50					55					60							
Phe	Ser	Asp	Ser	Val	Asn	Asn	Leu	Gln	Trp	Phe	His	Gln	Asn	Pro	Trp			
65					70					75					80			
Gly	Gln	Leu	Ile	Asn	Leu	Phe	Tyr	Ile	Pro	Ser	Gly	Thr	Lys	Gln	Asn			
				85					90					95				
Gly	Arg	Leu	Ser	Ala	Thr	Thr	Val	Ala	Thr	Glu	Arg	Tyr	Ser	Leu	Leu			
			100					105					110					
Tyr	Ile	Ser	Ser	Ser	Gln	Thr	Thr	Asp	Ser	Gly	Val	Tyr	Phe	Cys	Ala			
		115					120					125						
Val	Asn	Ala	Gly	Asn	Met	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Met			
	130					135					140							
Val	Lys	Pro	Ile	Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln	Leu	Lys	Asp			
145					150					155					160			
Pro	Arg	Ser	Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser			
				165					170					175				
Gln	Ile	Asn	Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp			
			180					185					190					
Lys	Cys	Val	Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala			
		195					200					205						

eolf-seql

Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys
 210 215 220

Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr
 225 230 235 240

Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn
 245 250 255

Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
 260 265 270

Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 275 280

<210> 29
 <211> 125
 <212> PRT
 <213> Mus musculus

<400> 29

Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
 1 5 10 15

Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu
 20 25 30

Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
 35 40 45

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Ala Tyr Lys
 50 55 60

Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
 65 70 75 80

eolf-seql

Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe
85 90 95

His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro
100 105 110

Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala
115 120 125

<210> 30

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Cysteine-modified murinised Radium-1 beta-chain constant region

<400> 30

Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu Phe Glu Pro
1 5 10 15

Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu
20 25 30

Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
35 40 45

Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Ala Tyr Lys
50 55 60

Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
65 70 75 80

Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe
85 90 95

His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro
100 105 110

eolf-seql

Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala
115 120 125

<210> 31
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> Radium-1 beta-chain with murinised constant region

<400> 31

Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val
1 5 10 15

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

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
35 40 45

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
85 90 95

Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu
115 120 125

eolf-seq1

Thr Val Leu Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu
130 135 140

Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu
145 150 155 160

Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
180 185 190

Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg
195 200 205

Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln
210 215 220

Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser
225 230 235 240

Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala
245 250 255

<210> 32

<211> 256

<212> PRT

<213> Artificial Sequence

<220>

<223> Radium-1 beta-chain with cysteine-modified murinised constant region

<400> 32

Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val
1 5 10 15

Gly Leu Val Asp Val Lys Val Thr Gln Ser Ser Arg Tyr Leu Val Lys

eolf-seql

20

25

30

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
35 40 45

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
85 90 95

Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu
115 120 125

Thr Val Leu Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser Leu
130 135 140

Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu
145 150 155 160

Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln
180 185 190

Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg
195 200 205

Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln

eolf-seql

210

215

220

Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser
225 230 235 240

Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala
245 250 255

<210> 33

<211> 604

<212> PRT

<213> Artificial Sequence

<220>

<223> Radium-1 scTCR with 2A linker

<400> 33

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

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

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly
100 105 110

eolf-seql

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His
115 120 125

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
130 135 140

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
145 150 155 160

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

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
180 185 190

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
195 200 205

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
210 215 220

Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln
225 230 235 240

Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly
245 250 255

Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser Arg Ala Lys Arg
260 265 270

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
275 280 285

Glu Glu Asn Pro Gly Pro Met Gly Ile Arg Leu Leu Cys Arg Val Ala
290 295 300

eolf-seql

Phe Cys Phe Leu Ala Val Gly Leu Val Asp Val Lys Val Thr Gln Ser
305 310 315 320

Ser Arg Tyr Leu Val Lys Arg Thr Gly Glu Lys Val Phe Leu Glu Cys
325 330 335

Val Gln Asp Met Asp His Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro
340 345 350

Gly Leu Gly Leu Arg Leu Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys
355 360 365

Glu Lys Gly Asp Ile Pro Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys
370 375 380

Glu Arg Phe Ser Leu Ile Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser
385 390 395 400

Met Tyr Leu Cys Ala Ser Ser Ser Gly Val Thr Gly Glu Leu Phe Phe
405 410 415

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

Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His
435 440 445

Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp
450 455 460

His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly
465 470 475 480

Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp
485 490 495

eolf-seql

Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp
500 505 510

Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu
515 520 525

Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln
530 535 540

Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser
545 550 555 560

Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile
565 570 575

Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val
580 585 590

Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly
595 600

<210> 34
<211> 604
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-modified Radium-1 scTCR with 2A linker

<400> 34

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser

eolf-seql

35

40

45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
 50 55 60

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

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
 85 90 95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly
 100 105 110

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His
 115 120 125

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
 130 135 140

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
 145 150 155 160

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val
 165 170 175

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
 180 185 190

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
 195 200 205

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
 210 215 220

Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln

eolf-seql

420

425

430

Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His
435 440 445

Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp
450 455 460

His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly
465 470 475 480

Val Cys Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp
485 490 495

Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp
500 505 510

Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu
515 520 525

Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln
530 535 540

Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser
545 550 555 560

Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile
565 570 575

Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val
580 585 590

Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly
595 600

<210> 35

eolf-seql

<211> 624

<212> PRT

<213> Artificial Sequence

<220>

<223> Double Myc-tagged Radium-1 scTCR with 2A linker

<400> 35

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Glu Gln
20 25 30

Lys Leu Ile Ser Glu Glu Asp Leu Gly Ile Gln Val Glu Gln Ser Pro
35 40 45

Pro Asp Leu Ile Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn
50 55 60

Phe Ser Asp Ser Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp
65 70 75 80

Gly Gln Leu Ile Asn Leu Phe Tyr Ile Pro Ser Gly Thr Lys Gln Asn
85 90 95

Gly Arg Leu Ser Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu
100 105 110

Tyr Ile Ser Ser Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala
115 120 125

Val Asn Ala Gly Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met
130 135 140

Val Lys Pro His Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg
145 150 155 160

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Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp
165 170 175

Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr
180 185 190

Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser
195 200 205

Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe
210 215 220

Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser
225 230 235 240

Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn
245 250 255

Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu
260 265 270

Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
275 280 285

Arg Ala Lys Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
290 295 300

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ile Arg Leu Leu
305 310 315 320

Cys Arg Val Ala Phe Cys Phe Leu Ala Val Gly Leu Val Asp Val Lys
325 330 335

Val Thr Gln Ser Ser Arg Tyr Leu Val Lys Arg Thr Gly Glu Lys Val
340 345 350

eolf-seql

Phe Leu Glu Cys Val Gln Asp Met Asp His Glu Asn Met Phe Trp Tyr
 355 360 365

Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Ile Tyr Phe Ser Tyr Asp
 370 375 380

Val Lys Met Lys Glu Lys Gly Asp Ile Pro Glu Gly Tyr Ser Val Ser
 385 390 395 400

Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile Leu Glu Ser Ala Ser Thr
 405 410 415

Asn Gln Thr Ser Met Tyr Leu Cys Ala Ser Ser Ser Gly Val Thr Gly
 420 425 430

Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val Leu Glu Asp Leu
 435 440 445

Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala
 450 455 460

Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly
 465 470 475 480

Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu
 485 490 495

Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro
 500 505 510

Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser
 515 520 525

Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln
 530 535 540

eolf-seql

Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys
545 550 555 560

Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys
565 570 575

Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile
580 585 590

Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val
595 600 605

Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly
610 615 620

<210> 36

<211> 624

<212> PRT

<213> Artificial Sequence

<220>

<223> Double Myc-tagged cysteine-modified Radium-1 scTCR with 2A linker

<400> 36

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Glu Gln
20 25 30

Lys Leu Ile Ser Glu Glu Asp Leu Gly Ile Gln Val Glu Gln Ser Pro
35 40 45

Pro Asp Leu Ile Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn
50 55 60

Phe Ser Asp Ser Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp

eolf-seql

65		70		75		80									
Gly	Gln	Leu	Ile	Asn	Leu	Phe	Tyr	Ile	Pro	Ser	Gly	Thr	Lys	Gln	Asn
				85					90					95	
Gly	Arg	Leu	Ser	Ala	Thr	Thr	Val	Ala	Thr	Glu	Arg	Tyr	Ser	Leu	Leu
			100					105					110		
Tyr	Ile	Ser	Ser	Ser	Gln	Thr	Thr	Asp	Ser	Gly	Val	Tyr	Phe	Cys	Ala
		115					120					125			
Val	Asn	Ala	Gly	Asn	Met	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Met
	130					135					140				
Val	Lys	Pro	His	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg
145					150					155					160
Asp	Ser	Lys	Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp
				165					170					175	
Ser	Gln	Thr	Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr
			180					185					190		
Asp	Lys	Cys	Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser
		195					200					205			
Ala	Val	Ala	Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe
	210					215					220				
Asn	Asn	Ser	Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser
225					230					235					240
Ser	Cys	Asp	Val	Lys	Leu	Val	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Thr	Asn
				245					250					255	
Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu	Leu	Leu

eolf-seq1

260

265

270

Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
275 280 285

Arg Ala Lys Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
290 295 300

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ile Arg Leu Leu
305 310 315 320

Cys Arg Val Ala Phe Cys Phe Leu Ala Val Gly Leu Val Asp Val Lys
325 330 335

Val Thr Gln Ser Ser Arg Tyr Leu Val Lys Arg Thr Gly Glu Lys Val
340 345 350

Phe Leu Glu Cys Val Gln Asp Met Asp His Glu Asn Met Phe Trp Tyr
355 360 365

Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Ile Tyr Phe Ser Tyr Asp
370 375 380

Val Lys Met Lys Glu Lys Gly Asp Ile Pro Glu Gly Tyr Ser Val Ser
385 390 395 400

Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile Leu Glu Ser Ala Ser Thr
405 410 415

Asn Gln Thr Ser Met Tyr Leu Cys Ala Ser Ser Ser Gly Val Thr Gly
420 425 430

Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val Leu Glu Asp Leu
435 440 445

Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala

eolf-seql

450

455

460

Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly
 465 470 475 480

Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu
 485 490 495

Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro
 500 505 510

Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser
 515 520 525

Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln
 530 535 540

Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys
 545 550 555 560

Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys
 565 570 575

Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile
 580 585 590

Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val
 595 600 605

Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly
 610 615 620

<210> 37

<211> 545

<212> PRT

<213> Artificial Sequence

eolf-seql

<220>

<223> Radium-1 scTCR with murinised constant regions and 2A linker

<400> 37

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

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

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly
100 105 110

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro Ile
115 120 125

Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln
130 135 140

Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn Val
145 150 155 160

Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr Val Leu
165 170 175

eolf-seql

Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser
180 185 190

Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala
195 200 205

Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu Lys
210 215 220

Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val Met
225 230 235 240

Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met
245 250 255

Thr Leu Arg Leu Trp Ser Ser Arg Ala Lys Arg Gly Ser Gly Ala Thr
260 265 270

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
275 280 285

Pro Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala
290 295 300

Val Gly Leu Val Asp Val Lys Val Thr Gln Ser Ser Arg Tyr Leu Val
305 310 315 320

Lys Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp
325 330 335

His Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg
340 345 350

Leu Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile
355 360 365

eolf-seql

Pro Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu
370 375 380

Ile Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met Tyr Leu Cys Ala
385 390 395 400

Ser Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg
405 410 415

Leu Thr Val Leu Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser
420 425 430

Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr
435 440 445

Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser
450 455 460

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
465 470 475 480

Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu
485 490 495

Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys
500 505 510

Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly
515 520 525

Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg
530 535 540

Ala
545

eolf-seql

<210> 38
 <211> 545
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Radium-1 scTCR with cysteine-modified murinised constant regions
 and 2A linker

<400> 38

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
 1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
 20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
 35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
 50 55 60

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

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
 85 90 95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly
 100 105 110

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro Ile
 115 120 125

Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln
 130 135 140

eolf-seql

Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser Gln Ile Asn Val
145 150 155 160

Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Cys Val Leu
165 170 175

Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser
180 185 190

Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala
195 200 205

Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr Leu Thr Glu Lys
210 215 220

Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn Leu Ser Val Met
225 230 235 240

Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met
245 250 255

Thr Leu Arg Leu Trp Ser Ser Arg Ala Lys Arg Gly Ser Gly Ala Thr
260 265 270

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
275 280 285

Pro Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala
290 295 300

Val Gly Leu Val Asp Val Lys Val Thr Gln Ser Ser Arg Tyr Leu Val
305 310 315 320

Lys Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp
325 330 335

eolf-seq1

His Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg
340 345 350

Leu Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile
355 360 365

Pro Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu
370 375 380

Ile Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met Tyr Leu Cys Ala
385 390 395 400

Ser Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg
405 410 415

Leu Thr Val Leu Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser
420 425 430

Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr
435 440 445

Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser
450 455 460

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro
465 470 475 480

Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu
485 490 495

Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys
500 505 510

Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly
515 520 525

eolf-seql

Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg
530 535 540

Ala
545

<210> 39
<211> 565
<212> PRT
<213> Artificial Sequence

<220>
<223> Double Myc-tagged Radium-1 scTCR with murinised constant regions

<400> 39

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Glu Gln
20 25 30

Lys Leu Ile Ser Glu Glu Asp Leu Gly Ile Gln Val Glu Gln Ser Pro
35 40 45

Pro Asp Leu Ile Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn
50 55 60

Phe Ser Asp Ser Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp
65 70 75 80

Gly Gln Leu Ile Asn Leu Phe Tyr Ile Pro Ser Gly Thr Lys Gln Asn
85 90 95

Gly Arg Leu Ser Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu
100 105 110

Tyr Ile Ser Ser Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala
115 120 125

eolf-seql

Val Asn Ala Gly Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met
130 135 140

Val Lys Pro Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp
145 150 155 160

Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser
165 170 175

Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp
180 185 190

Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala
195 200 205

Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys
210 215 220

Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr
225 230 235 240

Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn
245 250 255

Leu Ser Val Met Gly Leu Arg Ile Leu Leu Lys Val Ala Gly Phe
260 265 270

Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser Arg Ala Lys Arg Gly
275 280 285

Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu
290 295 300

Glu Asn Pro Gly Pro Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe
305 310 315 320

eolf-seql

Cys Phe Leu Ala Val Gly Leu Val Asp Val Lys Val Thr Gln Ser Ser
325 330 335

Arg Tyr Leu Val Lys Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val
340 345 350

Gln Asp Met Asp His Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly
355 360 365

Leu Gly Leu Arg Leu Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu
370 375 380

Lys Gly Asp Ile Pro Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu
385 390 395 400

Arg Phe Ser Leu Ile Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met
405 410 415

Tyr Leu Cys Ala Ser Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly
420 425 430

Glu Gly Ser Arg Leu Thr Val Leu Glu Asp Leu Arg Asn Val Thr Pro
435 440 445

Pro Lys Val Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys
450 455 460

Gln Lys Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His
465 470 475 480

Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val
485 490 495

Ser Thr Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu
500 505 510

eolf-seql

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn
515 520 525

His Phe Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys
530 535 540

Trp Pro Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu
545 550 555 560

Ala Trp Gly Arg Ala
565

<210> 40
<211> 565
<212> PRT
<213> Artificial Sequence

<220>
<223> Double Myc-tagged Radium-1 scTCR with cysteine-modified murinised
constant regions and 2A linker

<400> 40

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Glu Gln
20 25 30

Lys Leu Ile Ser Glu Glu Asp Leu Gly Ile Gln Val Glu Gln Ser Pro
35 40 45

Pro Asp Leu Ile Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn
50 55 60

Phe Ser Asp Ser Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp
65 70 75 80

eolf-seql

Gly Gln Leu Ile Asn Leu Phe Tyr Ile Pro Ser Gly Thr Lys Gln Asn
85 90 95

Gly Arg Leu Ser Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu
100 105 110

Tyr Ile Ser Ser Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala
115 120 125

Val Asn Ala Gly Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met
130 135 140

Val Lys Pro Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp
145 150 155 160

Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe Asp Ser
165 170 175

Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp
180 185 190

Lys Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala
195 200 205

Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys
210 215 220

Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp Ala Thr
225 230 235 240

Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe Gln Asn
245 250 255

Leu Ser Val Met Gly Leu Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
260 265 270

eolf-seql

Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser Arg Ala Lys Arg Gly
 275 280 285

Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu
 290 295 300

Glu Asn Pro Gly Pro Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe
 305 310 315 320

Cys Phe Leu Ala Val Gly Leu Val Asp Val Lys Val Thr Gln Ser Ser
 325 330 335

Arg Tyr Leu Val Lys Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val
 340 345 350

Gln Asp Met Asp His Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly
 355 360 365

Leu Gly Leu Arg Leu Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu
 370 375 380

Lys Gly Asp Ile Pro Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu
 385 390 395 400

Arg Phe Ser Leu Ile Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met
 405 410 415

Tyr Leu Cys Ala Ser Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly
 420 425 430

Glu Gly Ser Arg Leu Thr Val Leu Glu Asp Leu Arg Asn Val Thr Pro
 435 440 445

Pro Lys Val Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys
 450 455 460

eolf-seql

Gln Lys Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His
465 470 475 480

Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val
485 490 495

Cys Thr Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu
500 505 510

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn
515 520 525

His Phe Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys
530 535 540

Trp Pro Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu
545 550 555 560

Ala Trp Gly Arg Ala
565

<210> 41
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> Encodes SEQ ID NO: 33

<400> 41
atgaagagga tattgggagc tctgctgggg ctcttgagtg cccagggttg ctgtgtgaga 60
ggaatacaag tggagcagag tcctccagac ctgattctcc aggagggagc caattccacg 120
ctgcggtgca atttttctga ctctgtgaac aatttgcagt ggtttcatca aaacccttgg 180
ggacagctca tcaacctgtt ttacattccc tcagggacaa aacagaatgg aagattaagc 240
gccacgactg tcgctacgga acgctacagc ttattgtaca tttcctcttc ccagaccaca 300

eolf-seq1

gactcaggcg tttatcttctg tgctgtgaat gcaggcaaca tgctcacctt tggaggggga	360
acaagggttaa tgggtcaaacc ccatatccag aaccctgacc ctgccgtgta ccagctgaga	420
gactctaaat ccagtgacaa gtctgtctgc ctattcaccg attttgattc tcaaacaaat	480
gtgtcacaaa gtaaggattc tgatgtgtat atcacagaca aaactgtgct agacatgagg	540
tctatggact tcaagagcaa cagtgtgtg gcctggagca acaaatctga ctttgcatgt	600
gcaaacgcct tcaacaacag cattattcca gaagacacct tcttccccag cccagaaagt	660
tcctgtgatg tcaagctggg cgagaaaagc ttgaaacag atacgaacct aaactttcaa	720
aacctgtcag tgattggggt ccgaatcctc ctctaaaag tggccgggtt taatctgctc	780
atgacgctgc ggctgtgggc cagcagagcc aagagaggca gcggcgccac caacttcagc	840
ctgctgaagc aggccggcga cgtggaagag aaccctggac caatgggaat caggctcctc	900
tgctgtgtgg ccttttgttt cctggctgta ggcctcgtag atgtgaaagt aaccagagc	960
tcgagatatc tagtcaaaag gacgggagag aaagtttttc tggaatgtgt ccaggatatg	1020
gaccatgaaa atatgttctg gtatcgacaa gaccaggtc tggggctacg gctgatctat	1080
ttctcatatg atgttaaaat gaaagaaaaa ggagatattc ctgaggggta cagtgtctct	1140
agagagaaga aggagcgctt ctccctgatt ctggagtccg ccagcaccaa ccagacatct	1200
atgtacctct gtgccagcag ttctggagtc accggggagc tgttttttgg agaaggctct	1260
aggctgaccg tactggagga cctgaaaaac gtgtttccac ccgaggctgc tgtgtttgag	1320
ccatcagaag cagagatctc ccacaccaa aaggccacac tgggtgtgcct ggccacaggc	1380
ttctaccccg accacgtgga gctgagctgg tgggtgaatg ggaaggaggt gcacagtggg	1440
gtcagcacag acccgagcc cctcaaggag cagcccgccc tcaatgactc cagatactgc	1500
ctgagcagcc gcctgagggt ctgggccacc ttctggcaga accccgcaa ccacttccgc	1560
tgtcaagtcc agttctacgg gctctcgag aatgacgagt ggaccagga tagggccaaa	1620
cctgtcacc agatcgtcag cgccgaggcc tggggtagag cagactgtgg cttcacctcc	1680
gagtcctacc agcaaggggt cctgtctgcc accatcctct atgagatctt gctagggaag	1740

eolf-seql

gccaccttgt atgccgtgct ggtcagtgcc ctcgtgctga tggccatggg caagagaaag 1800
gattccagag gctag 1815

<210> 42
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> Encodes SEQ ID NO: 34

<400> 42
atgaagagga tattgggagc tctgctgggg ctcttgagtg cccaggtttg ctgtgtgaga 60
ggaatacaag tggagcagag tcctccagac ctgattctcc aggagggagc caattccacg 120
ctgcggtgca atttttctga ctctgtgaac aatttgcagt ggtttcatca aaacccttgg 180
ggacagctca tcaacctgtt ttacattccc tcagggacaa aacagaatgg aagattaagc 240
gccacgactg tcgctacgga acgctacagc ttattgtaca tttcctcttc ccagaccaca 300
gactcaggcg tttatttctg tgctgtgaat gcaggcaaca tgctcacctt tggaggggga 360
acaagggttaa tgggtcaaacc ccatatccag aaccctgacc ctgccgtgta ccagctgaga 420
gactctaaat ccagtgacaa gtctgtctgc ctattcaccg attttgattc tcaaacaaat 480
gtgtcacaaa gtaaggattc tgatgtgtat atcacagaca aatgcgtgct agacatgagg 540
tctatggact tcaagagcaa cagtgtgtg gcctggagca acaaatctga ctttgcatgt 600
gcaaacgcct tcaacaacag cattattcca gaagacacct tcttccccag cccagaaagt 660
tcctgtgatg tcaagctggg cgagaaaagc tttgaaacag atacgaacct aaactttcaa 720
aacctgtcag tgattggggt ccgaatcctc ctcttaaaag tggccggggt taatctgctc 780
atgacgctgc ggctgtgggc cagcagagcc aagagaggca gcggcgccac caacttcagc 840
ctgctgaagc aggccggcga cgtggaagag aaccctggac caatgggaat caggctcctc 900
tgtcgtgtgg ctttttgttt cctggctgta ggctcgtag atgtgaaagt aaccagagc 960
tcgagatatc tagtcaaaag gacgggagag aaagtttttc tggaatgtgt ccaggatatg 1020

eolf-seq1

gaccatgaaa atatgttctg gtatcgacaa gaccaggtc tggggctacg gctgatctat	1080
ttctcatatg atgttaaaat gaaagaaaaa ggagatattc ctgaggggta cagtgtctct	1140
agagagaaga aggagcgctt ctccctgatt ctggagtcg ccagcaccaa ccagacatct	1200
atgtacctct gtgccagcag ttctggagtc accggggagc tgttttttgg agaaggctct	1260
aggctgaccg tactggagga cctgaaaaac gtgttccac ccgaggtcgc tgtgtttgag	1320
ccatcagaag cagagatctc ccacacccaa aaggccacac tgggtgtgcct ggccacaggc	1380
ttctaccccg accacgtgga gctgagctgg tgggtgaatg ggaaggaggt gcacagtggg	1440
gtctgtacag acccgagcc cctcaaggag cagcccgccc tcaatgactc cagatactgc	1500
ctgagcagcc gcctgagggt ctcgccacc ttctggcaga accccgcaa ccacttccgc	1560
tgtcaagtcc agttctacgg gctctcggag aatgacgagt ggaccagga tagggccaaa	1620
cctgtcacc agatcgtcag cgccgaggcc tggggtagag cagactgtgg cttcacctcc	1680
gagtcttacc agcaaggggt cctgtctgcc accatcctct atgagatctt gctaggaag	1740
gccaccttgt atgccgtgct ggtcagtgcc ctctgtctga tggccatggt caagagaaag	1800
gattccagag gctag	1815

<210> 43

<211> 1875

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 35

<400> 43

atgaagagga tattgggagc tctgctgggg ctcttgagtg cccaggtttg ctgtgtgaga	60
gagcagaagc tgatcagcga ggaggacctg gagcagaagc tgatcagcga ggaggacctg	120
ggaatacaag tggagcagag tcctccagac ctgattctcc aggagggagc caattccacg	180
ctgcggtgca atttttctga ctctgtgaac aatttgaggt ggtttcatca aaaccttgg	240
ggacagctca tcaacctgtt ttacattccc tcagggacaa aacagaatgg aagattaagc	300

eolf-seq1

gccacgactg tcgctacgga acgctacagc ttattgtaca tttcctcttc ccagaccaca	360
gactcaggcg tttatttctg tgctgtgaat gcaggcaaca tgctcacctt tggaggggga	420
acaagggttaa tgggtcaaacc ccatatccag aaccctgacc ctgccgtgta ccagctgaga	480
gactctaaat ccagtgacaa gtctgtctgc ctattcaccg attttgattc tcaaacaaat	540
gtgtcacaaa gtaaggattc tgatgtgtat atcacagaca aaactgtgct agacatgagg	600
tctatggact tcaagagcaa cagtgtgtg gcctggagca acaaatctga ctttgcattg	660
gcaaacgcct tcaacaacag cattattcca gaagacacct tcttccccag cccagaaagt	720
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aacctgtcag tgattggggt ccgaatcctc ctctaaaaag tggccggggt taatctgtc	840
atgacgctgc ggctgtggc cagcagagcc aagagaggca gcggcgccac caacttcagc	900
ctgctgaagc aggccggcga cgtggaagag aaccctggac caatgggaat caggctcctc	960
tgctgtgtgg ctttttgtt cctggctgta ggctcgtag atgtgaaagt aaccagagc	1020
tccagatatc tagtcaaaag gacgggagag aaagtttttc tggaatgtgt ccaggatatg	1080
gacatgaaa atatgttctg gtatcgacaa gaccaggtc tggggctacg gctgatctat	1140
ttctcatatg atgttaaaat gaaagaaaaa ggagatattc ctgaggggta cagtgtctct	1200
agagagaaga aggagcgctt ctccctgatt ctggagtcgc ccagcaccaa ccagacatct	1260
atgtacctct gtgccagcag ttctggagtc accggggagc tggttttttg agaaggctct	1320
aggctgaccg tactggagga cctgaaaaac gtgttccac ccgaggctgc tgtgtttgag	1380
ccatcagaag cagagatctc ccacacccaa aaggccacac tgggtgtcct ggccacaggc	1440
ttctaccccg accacgtgga gctgagctgg tgggtgaatg ggaaggaggc gcacagtggg	1500
gtcagcacag acccgagcc cctcaaggag cagcccgccc tcaatgactc cagatactgc	1560
ctgagcagcc gcctgagggt ctcggccacc ttctggcaga accccgcaa ccacttccgc	1620
tgtcaagtcc agttctacgg gctctcggag aatgacgagt ggaccagga tagggccaaa	1680
cctgtcacc cagatcgtcag cgccgaggcc tggggtagag cagactgtgg cttcacctcc	1740

eolf-seql

gagtcttacc agcaaggggt cctgtctgcc accatcctct atgagatctt gctaggggaag 1800
gccaccttgt atgccgtgct ggtcagtgcc ctctgtctga tggccatggt caagagaaaag 1860
gattccagag gctag 1875

<210> 44
<211> 1875
<212> DNA
<213> Artificial Sequence

<220>
<223> Encodes SEQ ID NO: 36

<400> 44
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gagcagaagc tgatcagcga ggaggacctg gagcagaagc tgatcagcga ggaggacctg 120
ggaatacaag tggagcagag tcctccagac ctgattctcc aggagggagc caattccacg 180
ctgcggtgca atttttctga ctctgtgaac aatttgagtg ggtttcatca aaacccttgg 240
ggacagctca tcaacctgtt ttacattccc tcagggacaa aacagaatgg aagattaagc 300
gccacgactg tcgctacgga acgctacagc ttattgtaca tttcctcttc ccagaccaca 360
gactcaggcg tttatttctg tgctgtgaat gcaggcaaca tgctcacctt tggaggggga 420
acaagggttaa tgggtcaaacc ccatatccag aaccctgacc ctgccgtgta ccagctgaga 480
gactctaaat ccagtgacaa gtctgtctgc ctattcaccg attttgattc tcaaacaat 540
gtgtcacaaa gtaaggattc tgatgtgtat atcacagaca aatgcgtgct agacatgagg 600
tctatggact tcaagagcaa cagtgtgtg gcctggagca acaaatctga ctttgcatgt 660
gcaaacgcct tcaacaacag cattattcca gaagacacct tcttccccag cccagaaaagt 720
tcctgtgatg tcaagctggg cgagaaaagc ttgaaacag atacgaacct aaactttcaa 780
aacctgtcag tgattgggtt ccgaatcctc ctctaaaag tggccgggtt taatctgctc 840
atgacgctgc ggctgtggtc cagcagagcc aagagaggca gcggcgccac caacttcagc 900
ctgctgaagc aggccggcga cgtggaagag aaccctggac caatgggaat caggctcctc 960

eolf-seq1

tgtcgtgtgg ccttttgttt cctggctgta ggcttcgtag atgtgaaagt aaccagagc	1020
tcgagatatc tagtcaaaag gacgggagag aaagtttttc tggaatgtgt ccaggatatg	1080
gaccatgaaa atatgttctg gtatcgacaa gaccaggtc tggggctacg gctgatctat	1140
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agagagaaga aggagcgctt ctccctgatt ctggagtccg ccagcaccaa ccagacatct	1260
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aggctgaccg tactggagga cctgaaaaac gtgttccac ccgaggtcgc tgtgtttgag	1380
ccatcagaag cagagatctc ccacaccaa aaggccacac tgggtgtcct ggccacaggc	1440
ttctaccccg accacgtgga gctgagctgg tgggtgaatg ggaaggaggt gcacagtggg	1500
gtctgtacag acccgcagcc cctcaaggag cagcccgcc tcaatgactc cagatactgc	1560
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cctgtcacc agatcgtcag cgccgaggcc tggggtagag cagactgtgg cttcacctcc	1740
gagtcttacc agcaaggggt cctgtctgcc accatcctct atgagatctt gctaggggaag	1800
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gattccagag gctag	1875

<210> 45
 <211> 1638
 <212> DNA
 <213> Artificial Sequence

<220>
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ctgcggtgca atttttctga ctctgtgaac aatttgcagt ggtttcatca aaaccttgg	180

eolf-seq1

ggacagctca tcaacctgtt ttacattccc tcagggacaa aacagaatgg aagattaagc	240
gccacgactg tcgctacgga acgctacagc ttattgtaca tttcctcttc ccagaccaca	300
gactcaggcg tttattttctg tgctgtgaat gcaggcaaca tgctcacctt tggaggggga	360
acaaggttaa tgggtcaaacc catccagaac ccagaacctg ctgtgtacca gttaaaagat	420
cctcgggtctc aggacagcac cctctgcctg ttcaccgact ttgactccca aatcaatgtg	480
ccgaaaacca tggaatctgg aacgttcatc actgacaaaa ctgtgctgga catgaaagct	540
atggattcca agagcaatgg ggccattgcc tggagcaacc agacaagctt cacctgccaa	600
gatatcttca aagagaccaa cgccacctac cccagttcag acgttccctg tgatgccacg	660
ttgactgaga aaagctttga aacagatatg aacctaaact ttcaaaacct gtcagttatg	720
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caggcctaca aggagagcaa ttatagctac tgcctgagca gccgcctgag ggtctctgct	1500
accttctggc acaatcctcg aaaccacttc cgctgccaaag tgcagttcca tgggctttca	1560
gaggaggaca agtggccaga gggctcacc aaacctgtca cacagaacat cagtgcagag	1620

eolf-seql

gcctggggcc gagcatag

1638

<210> 46

<211> 1638

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 38

<400> 46

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ctgcggtgca atttttctga ctctgtgaac aatttgcagt ggtttcatca aaacccttgg	180
ggacagctca tcaacctgtt ttacattccc tcaggggacaa aacagaatgg aagattaagc	240
gccacgactg tcgctacgga acgctacagc ttattgtaca tttcctcttc ccagaccaca	300
gactcaggcg tttatctctg tgctgtgaat gcaggcaaca tgctcacctt tggaggggga	360
acaagggttaa tgggtcaaacc catccagaac ccagaacctg ctgtgtacca gttaaaagat	420
cctcgggtctc aggacagcac cctctgcctg ttcaccgact ttgactccca aatcaatgtg	480
ccgaaaacca tggaatctgg aacgttcatc actgacaaat gcgtgctgga catgaaagct	540
atggattcca agagcaatgg ggccattgcc tggagcaacc agacaagctt cacctgccaa	600
gatatcttca aagagaccaa cgccacctac cccagttcag acgttccctg tgatgccacg	660
ttgactgaga aaagctttga aacagatatg aacctaaact ttcaaaacct gtcagttatg	720
ggactccgaa tcctcctgct gaaagtagcc ggatttaacc tgctcatgac gctgaggctg	780
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aaaaggacgg gagagaaaagt ttttctggaa tgtgtccagg atatggacca tgaaaatatg	1020
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eolf-seql

aaaatgaaag aaaaaggaga tattcctgag gggtagctg tctctagaga gaagaaggag	1140
cgcttctccc tgattctgga gtccgccagc accaaccaga catctatgta cctctgtgcc	1200
agcagttctg gagtcaccgg ggagctgttt tttggagaag gctctaggct gaccgtactg	1260
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accttctggc acaatcctcg aaaccacttc cgctgccaag tgcagttcca tgggctttca	1560
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gcctggggcc gagcatag	1638

<210> 47
 <211> 1698
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes SEQ ID NO: 39

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ctgcggtgca atttttctga ctctgtgaac aatttgagtg ggtttcatca aaacccttgg	240
ggacagctca tcaacctgtt ttacattccc tcagggacaa aacagaatgg aagattaagc	300
gccacgactg tcgctacgga acgctacagc ttattgtaca tttcctcttc ccagaccaca	360
gactcaggcg tttatttctg tgctgtgaat gcaggcaaca tgctcacctt tggaggggga	420
acaagggttaa tgggtcaaacc catccagaac ccagaacctg ctgtgtacca gttaaaagat	480
cctcgggtctc aggacagcac cctctgcctg ttcaccgact ttgactccca aatcaatgtg	540

eolf-seq1

ccgaaaacca tggaatctgg aacgttcac	actgacaaaa ctgtgctgga catgaaagct	600
atggattcca agagcaatgg ggccattgcc	tggagcaacc agacaagctt cacctgccaa	660
gatatcttca aagagaccaa cgccacctac	cccagttcag acgttccctg tgatgccacg	720
ttgactgaga aaagctttga aacagatatg	aacctaaact ttcaaaacct gtcagttatg	780
ggactccgaa tcctcctgct gaaagtagcc	ggatttaacc tgctcatgac gctgaggctg	840
tgggtccagta gagccaagag aggcagcggc	gccaccaact tcagcctgct gaagcaggcc	900
ggcgacgtgg aagagaaccc tggaccaatg	ggaatcaggc tcctctgtcg tgtggccttt	960
tgtttcctgg ctgtaggcct cgtagatgtg	aaagtaaccc agagctcgag atatctagtc	1020
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caggcctaca aggagagcaa ttatagctac	tgccctgagca gccgcctgag ggtctctgct	1560
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<210> 48

<211> 1698

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 40

eolf-seql

<400> 48

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ggaatacaag tggagcagag tcctccagac ctgattctcc aggagggagc caattccacg	180
ctgcggtgca atttttctga ctctgtgaac aatttgagtg ggtttcatca aaacccttgg	240
ggacagctca tcaacctgtt ttacattccc tcagggacaa aacagaatgg aagattaagc	300
gccacgactg tcgctacgga acgctacagc ttattgtaca tttcctcttc ccagaccaca	360
gactcaggcg tttatctctg tgctgtgaat gcaggcaaca tgctcacctt tggaggggga	420
acaagggttaa tgggtcaaacc catccagaac ccagaacctg ctgtgtacca gttaaaagat	480
cctcgggtctc aggacagcac cctctgcctg ttcaccgact ttgactccca aatcaatgtg	540
ccgaaaacca tgggaatctgg aacgttcatc actgacaaat gcgtgctgga catgaaagct	600
atggattcca agagcaatgg ggccattgcc tggagcaacc agacaagctt cacctgccaa	660
gatatcttca aagagaccaa cgccacctac cccagttcag acgttccctg tgatgccacg	720
ttgactgaga aaagctttga aacagatatg aacctaaact ttcaaaacct gtcagttatg	780
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cgcttctccc tgattctgga gtccgccagc accaaccaga catctatgta cctctgtgcc	1260
agcagttctg gagtcaccgg ggagctgttt tttggagaag gctctaggct gaccgtactg	1320
gaggatctga gaaatgtgac tccacccaag gtctccttgt ttgagccatc aaaagcagag	1380

eolf-seql

attgcaaaca aacaaaaggc taccctcgtg tgcttggcca ggggcttctt ccctgaccac 1440
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 caggcctaca aggagagcaa ttatagctac tgcctgagca gccgcctgag ggtctctgct 1560
 accttctggc acaatcctcg aaaccacttc cgctgccaag tgcagttcca tgggctttca 1620
 gaggaggaca agtggccaga gggctcacc aaacctgtca cacagaacat cagtgcagag 1680
 gcctggggcc gagcatag 1698

<210> 49
 <211> 23
 <212> PRT
 <213> Homo sapiens

<400> 49

Ser Leu Val Arg Leu Ser Ser Cys Val Pro Val Ala Leu Met Ser Ala
 1 5 10 15

Met Thr Thr Ser Ser Ser Gln
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<210> 50
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 50

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
 1 5 10 15

Cys Cys Val Arg
 20

<210> 51
 <211> 16
 <212> PRT
 <213> Homo sapiens

eolf-seql

<400> 51

Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val
1 5 10 15

<210> 52

<211> 8

<212> PRT

<213> picornavirus

<220>

<221> X

<222> (2)..(2)

<223> Val or Ile

<220>

<221> X

<222> (4)..(4)

<223> Any amino acid

<400> 52

Asp Xaa Glu Xaa Asn Pro Gly Pro
1 5

<210> 53

<211> 10

<212> DNA

<213> Homo sapiens

<400> 53

aataaa

10

<210> 54

<211> 9

<212> PRT

<213> Homo sapiens

<400> 54

Ile Leu Ala Lys Phe Leu His Trp Leu
1 5

eolf-seql

<210> 55
<211> 19
<212> PRT
<213> Homo sapiens

<400> 55

Lys Ser Leu Val Arg Leu Ser Ser Cys Val Pro Val Ala Leu Met Ser
1 5 10 15

Ala Met Thr

<210> 56
<211> 10
<212> PRT
<213> Homo sapiens

<400> 56

Glu Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5 10

<210> 57
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Site-directed mutagenesis forward primer

<400> 57
gaggaccaga cccagaaggc ggagctcgtg gagac 35

<210> 58
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Site-directed mutagenesis reverse primer

<400> 58
gtctccacga gctccgcctt ctgggtctgg tcctc 35

eolf-seql

<210> 59
<211> 15
<212> PRT
<213> Escherichia coli

<400> 59

Gly	Gly	Leu	Asn	Asp	Ile	Phe	Glu	Ala	Gln	Lys	Ile	Glu	Trp	His
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<210> 60
<211> 95
<212> PRT
<213> Homo sapiens

<400> 60

His	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys
1				5					10					15	

Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr
			20					25					30		

Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Thr
		35					40					45			

Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala
	50					55					60				

Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser
65					70					75					80

Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys
				85					90					95

<210> 61
<211> 95
<212> PRT
<213> Artificial Sequence

eolf-seql

<220>

<223> Cysteine-modified truncated Radium-1 alpha-chain constant region

<400> 61

His	Ile	Gln	Asn	Pro	Asp	Pro	Ala	Val	Tyr	Gln	Leu	Arg	Asp	Ser	Lys
1				5					10					15	

Ser	Ser	Asp	Lys	Ser	Val	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Thr
			20					25					30		

Asn	Val	Ser	Gln	Ser	Lys	Asp	Ser	Asp	Val	Tyr	Ile	Thr	Asp	Lys	Cys
		35					40					45			

Val	Leu	Asp	Met	Arg	Ser	Met	Asp	Phe	Lys	Ser	Asn	Ser	Ala	Val	Ala
	50					55					60				

Trp	Ser	Asn	Lys	Ser	Asp	Phe	Ala	Cys	Ala	Asn	Ala	Phe	Asn	Asn	Ser
65					70					75					80

Ile	Ile	Pro	Glu	Asp	Thr	Phe	Phe	Pro	Ser	Pro	Glu	Ser	Ser	Cys
				85					90					95

<210> 62

<211> 131

<212> PRT

<213> Homo sapiens

<400> 62

Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val	Phe	Glu	Pro
1				5					10					15	

Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu	Val	Cys	Leu
			20					25					30		

Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp	Trp	Val	Asn
		35					40					45			

eolf-seql

Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys
50 55 60

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
65 70 75 80

Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
85 90 95

Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
100 105 110

Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
115 120 125

Ala Asp Cys
130

<210> 63

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> Cysteine-modified truncated Radium-1 beta-chain constant region

<400> 63

Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro
1 5 10 15

Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu
20 25 30

Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn
35 40 45

Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys

eolf-seql

50

55

60

Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu
65 70 75 80

Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys
85 90 95

Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp
100 105 110

Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg
115 120 125

Ala Asp Cys
130

<210> 64
<211> 222
<212> PRT
<213> Homo sapiens

<400> 64

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

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

eolf-seql

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly
100 105 110

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His
115 120 125

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
130 135 140

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
145 150 155 160

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

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
180 185 190

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
195 200 205

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
210 215 220

<210> 65

<211> 222

<212> PRT

<213> Artificial Sequence

<220>

<223> Cysteine-modified truncated Radium-1 alpha-chain

<400> 65

eolf-seql

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

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

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly
100 105 110

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His
115 120 125

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
130 135 140

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
145 150 155 160

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val
165 170 175

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
180 185 190

eolf-seql

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
 195 200 205

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
 210 215 220

<210> 66
 <211> 262
 <212> PRT
 <213> Homo sapiens
 <400> 66

Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val
 1 5 10 15

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

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
 35 40 45

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
 50 55 60

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
 65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
 85 90 95

Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met Tyr Leu Cys Ala Ser
 100 105 110

Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu
 115 120 125

Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val

eolf-seql

130

135

140

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
145 150 155 160

Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys
260

<210> 67

<211> 262

<212> PRT

<213> Artificial Sequence

<220>

<223> Cysteine-modified truncated Radium-1 beta-chain

<400> 67

Met Gly Ile Arg Leu Leu Cys Arg Val Ala Phe Cys Phe Leu Ala Val
1 5 10 15

eolf-seql

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

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
35 40 45

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
50 55 60

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
85 90 95

Leu Glu Ser Ala Ser Thr Asn Gln Thr Ser Met Tyr Leu Cys Ala Ser
100 105 110

Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu
115 120 125

Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val
130 135 140

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
145 150 155 160

Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln
180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
195 200 205

eolf-seql

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
245 250 255

Trp Gly Arg Ala Asp Cys
260

<210> 68

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

<223> Soluble cysteine-modified Radium-1 scTCR with 2A linker

<400> 68

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

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

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser

eolf-seql

85

90

95

Ser Gln Thr Thr Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly
 100 105 110

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His
 115 120 125

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
 130 135 140

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
 145 150 155 160

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val
 165 170 175

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
 180 185 190

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
 195 200 205

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Arg Ala
 210 215 220

Lys Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
 225 230 235 240

Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ile Arg Leu Leu Cys Arg
 245 250 255

Val Ala Phe Cys Phe Leu Ala Val Gly Leu Val Asp Val Lys Val Thr
 260 265 270

Gln Ser Ser Arg Tyr Leu Val Lys Arg Thr Gly Glu Lys Val Phe Leu

eolf-seql

275

280

285

Glu Cys Val Gln Asp Met Asp His Glu Asn Met Phe Trp Tyr Arg Gln
 290 295 300

Asp Pro Gly Leu Gly Leu Arg Leu Ile Tyr Phe Ser Tyr Asp Val Lys
 305 310 315 320

Met Lys Glu Lys Gly Asp Ile Pro Glu Gly Tyr Ser Val Ser Arg Glu
 325 330 335

Lys Lys Glu Arg Phe Ser Leu Ile Leu Glu Ser Ala Ser Thr Asn Gln
 340 345 350

Thr Ser Met Tyr Leu Cys Ala Ser Ser Ser Gly Val Thr Gly Glu Leu
 355 360 365

Phe Phe Gly Glu Gly Ser Arg Leu Thr Val Leu Glu Asp Leu Lys Asn
 370 375 380

Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile
 385 390 395 400

Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr
 405 410 415

Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His
 420 425 430

Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu
 435 440 445

Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr
 450 455 460

Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr

eolf-seql

Asn Met Leu Thr Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His
 115 120 125

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser
 130 135 140

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn
 145 150 155 160

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val
 165 170 175

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp
 180 185 190

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
 195 200 205

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Arg Ala
 210 215 220

Lys Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
 225 230 235 240

Asp Val Glu Glu Asn Pro Gly Pro Met Gly Ile Arg Leu Leu Cys Arg
 245 250 255

Val Ala Phe Cys Phe Leu Ala Val Gly Leu Val Asp Val Lys Val Thr
 260 265 270

Gln Ser Ser Arg Tyr Leu Val Lys Arg Thr Gly Glu Lys Val Phe Leu
 275 280 285

Glu Cys Val Gln Asp Met Asp His Glu Asn Met Phe Trp Tyr Arg Gln
 290 295 300

eolf-seql

Asp Pro Gly Leu Gly Leu Arg Leu Ile Tyr Phe Ser Tyr Asp Val Lys
305 310 315 320

Met Lys Glu Lys Gly Asp Ile Pro Glu Gly Tyr Ser Val Ser Arg Glu
325 330 335

Lys Lys Glu Arg Phe Ser Leu Ile Leu Glu Ser Ala Ser Thr Asn Gln
340 345 350

Thr Ser Met Tyr Leu Cys Ala Ser Ser Ser Gly Val Thr Gly Glu Leu
355 360 365

Phe Phe Gly Glu Gly Ser Arg Leu Thr Val Leu Glu Asp Leu Lys Asn
370 375 380

Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile
385 390 395 400

Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr
405 410 415

Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His
420 425 430

Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu
435 440 445

Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr
450 455 460

Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr
465 470 475 480

Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val
485 490 495

eolf-seql

Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Gly
 500 505 510

Gly His His His His His His
 515

<210> 70
 <211> 1530
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes SEQ ID NO: 69

<400> 70
 atgaagagga tattgggagc tctgctgggg ctcttgagtg cccagggttg ctgtgtgaga 60
 ggaatacaag tggagcagag tcctccagac ctgattctcc aggaggagc caattccacg 120
 ctgcggtgca atttttctga ctctgtgaac aatttgagc ggtttcatca aaacccttgg 180
 ggacagctca tcaacctgtt ttacattccc tcagggacaa aacagaatgg aagattaagc 240
 gccacgactg tcgctacgga acgctacagc ttattgtaca tttcctcttc ccagaccaca 300
 gactcaggcg tttatctctg tgctgtgaat gcaggcaaca tgctcacctt tggaggggga 360
 acaagggttaa tgggtcaaacc ccatatccag aaccctgacc ctgccgtgta ccagctgaga 420
 gactctaaat ccagtgacaa gtctgtctgc ctattcaccg attttgattc tcaaacaat 480
 gtgtcacaaa gtaaggattc tgatgtgtat atcacagaca aatgcgtgct agacatgagg 540
 tctatggact tcaagagcaa cagtgtgtg gcctggagca acaaatctga ctttgcatgt 600
 gcaaacgcct tcaacaacag cattattcca gaagacacct tcttccccag cccagaaagt 660
 tcctgtagag ccaagagagg cagcggcgcc accaacttca gcctgctgaa gcaggccggc 720
 gacgtggaag agaaccctgg accaatggga atcaggctcc tctgtcgtgt ggccttttgt 780
 ttcctggctg taggcctcgt agatgtgaaa gtaaccacaga gctcgagata tctagtcaaa 840
 aggacgggag agaaagtttt tctggaatgt gtccaggata tggacatga aaatatgttc 900

eolf-seql

tggtatcgac aagacccagg tctggggcta cggctgatct atttctcata tgatgttaaa	960
atgaaagaaa aaggagatat tcctgagggg tacagtgtct ctagagagaa gaaggagcgc	1020
ttctccctga ttctggagtc cgccagcacc aaccagacat ctatgtacct ctgtgccagc	1080
agttctggag tcaccgggga gctgtttttt ggagaaggct ctaggctgac cgtactggag	1140
gacctgaaaa acgtgttccc acccgaggtc gctgtgtttg agccatcaga agcagagatc	1200
tcccacaccc aaaaggccac actggtgtgc ctggccacag gcttctaccc cgaccacgtg	1260
gagctgagct ggtgggtgaa tgggaaggag gtgcacagtg gggctctgtac agacccgcag	1320
cccctcaagg agcagcccg cctcaatgac tccagatact gcctgagcag ccgcctgagg	1380
gtctcggcca ctttctggca gaacccccgc aaccacttcc gctgtcaagt ccagttctac	1440
gggctctcgg agaatgacga gtggaccag gatagggcca aacctgtcac ccagatcgtc	1500
agcgccgagg cctggggtag agcagactgt	1530

<210> 71
 <211> 1557
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes SEQ ID NO: 69

<400> 71	
atgaagagga tattgggagc tctgctgggg ctcttgagtg cccaggtttg ctgtgtgaga	60
ggaatacaag tggagcagag tcctccagac ctgattctcc aggaggagc caattccacg	120
ctgcggtgca atttttctga ctctgtgaac aatttgagc ggtttcatca aaacccttgg	180
ggacagctca tcaacctgtt ttacattccc tcagggacaa aacagaatgg aagattaagc	240
gccacgactg tcgctacgga acgctacagc ttattgtaca tttcctcttc ccagaccaca	300
gactcaggcg tttatctctg tgctgtgaat gcaggcaaca tgctcacctt tggaggggga	360
acaagggttaa tgggtcaaacc ccatatccag aaccctgacc ctgccgtgta ccagctgaga	420
gactctaaat ccagtgacaa gtctgtctgc ctattcaccg attttgattc tcaaacaat	480

eolf-seql

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gtgtcacaaa gtaaggattc tgatgtgtat atcacagaca aatgcgtgct agacatgagg      540
tctatggact tcaagagcaa cagtgtgtg gcctggagca acaaatctga ctttgcattgt      600
gcaaacgcct tcaacaacag cattattcca gaagacacct tcttccccag cccagaaagt      660
tcctgtagag ccaagagagg cagcggcgcc accaacttca gcctgctgaa gcaggccggc      720
gacgtggaag agaaccctgg accaatggga atcaggctcc tctgtcgtgt ggccttttgt      780
ttcctggctg taggcctcgt agatgtgaaa gtaaccagga gctcgagata tctagtcaaa      840
aggacgggag agaaagtttt tctggaatgt gtccaggata tggacatga aaatatgttc      900
tggtatcgac aagaccagg tctggggcta cggctgatct atttctcata tgatgttaaa      960
atgaaagaaa aaggagatat tcctgagggg tacagtgtct ctagagagaa gaaggagcgc     1020
ttctccctga ttctggagtc cgccagcacc aaccagacat ctatgtacct ctgtgccagc     1080
agttctggag tcaccgggga gctgtttttt ggagaaggct ctaggctgac cgtactggag     1140
gacctgaaaa acgtgttccc acccgaggct gctgtgtttg agccatcaga agcagagatc     1200
tcccacaccc aaaaggccac actggtgtgc ctggccacag gcttctaccc cgaccacgtg     1260
gagctgagct ggtgggtgaa tgggaaggag gtgcacagtg gggctctgtac agaccgcag      1320
cccctcaagg agcagcccgc cctcaatgac tccagatact gcctgagcag ccgcctgagg      1380
gtctcggcca ctttctggca gaacccccgc aaccacttcc gctgtcaagt ccagttctac      1440
gggctctcgg agaatgacga gtggaccag gatagggcca aacctgtcac ccagatcgtc      1500
agcgccgagg cctggggtag agcagactgt ggtggcggtc atcaccatca ccatcac        1557

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<210> 72
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 72

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

eolf-seql

Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser Val Asn Asn Leu
20 25 30

Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile Asn Leu Phe Tyr
35 40 45

Ile Pro Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser Ala Thr Thr Val
50 55 60

Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser Ser Gln Thr Thr
65 70 75 80

Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly Asn Met Leu Thr
85 90 95

Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro
100 105

<210> 73
<211> 202
<212> PRT
<213> Homo sapiens

<400> 73

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

Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser Val Asn Asn Leu
20 25 30

Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile Asn Leu Phe Tyr
35 40 45

Ile Pro Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser Ala Thr Thr Val
50 55 60

eolf-seq1

Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser Ser Gln Thr Thr
65 70 75 80

Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly Asn Met Leu Thr
85 90 95

Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His Ile Gln Asn Pro
100 105 110

Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser
115 120 125

Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser
130 135 140

Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg
145 150 155 160

Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser
165 170 175

Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp
180 185 190

Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
195 200

<210> 74
<211> 202
<212> PRT
<213> Artificial Sequence

<220>
<223> Mature truncated cysteine-modified Radium-1 alpha-chain

<400> 74

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

eolf-seql

Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser Val Asn Asn Leu
20 25 30

Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile Asn Leu Phe Tyr
35 40 45

Ile Pro Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser Ala Thr Thr Val
50 55 60

Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser Ser Gln Thr Thr
65 70 75 80

Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly Asn Met Leu Thr
85 90 95

Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His Ile Gln Asn Pro
100 105 110

Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser
115 120 125

Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser
130 135 140

Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val Leu Asp Met Arg
145 150 155 160

Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser
165 170 175

Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp
180 185 190

Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
195 200

eolf-seql

<210> 75
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 75

Gly Leu Val Asp Val Lys Val Thr Gln Ser Ser Arg Tyr Leu Val Lys
 1 5 10 15

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
 20 25 30

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
 35 40 45

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
 50 55 60

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
 65 70 75 80

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

Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu
 100 105 110

Thr Val Leu
 115

<210> 76
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 76

eolf-seql

Gly Leu Val Asp Val Lys Val Thr Gln Ser Ser Arg Tyr Leu Val Lys
1 5 10 15

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
20 25 30

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
35 40 45

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
50 55 60

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
65 70 75 80

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

Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu
100 105 110

Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val
115 120 125

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
130 135 140

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

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

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
180 185 190

eolf-seql

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
195 200 205

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
210 215 220

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
225 230 235 240

Trp Gly Arg Ala Asp Cys
245

<210> 77

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> Mature truncated cysteine-modified Radium-1 beta-chain

<400> 77

Gly Leu Val Asp Val Lys Val Thr Gln Ser Ser Arg Tyr Leu Val Lys
1 5 10 15

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
20 25 30

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
35 40 45

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
50 55 60

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
65 70 75 80

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

eolf-seql

Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu
100 105 110

Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val
115 120 125

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
130 135 140

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

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln
165 170 175

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
180 185 190

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
195 200 205

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
210 215 220

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
225 230 235 240

Trp Gly Arg Ala Asp Cys
245

<210> 78
<211> 211
<212> PRT
<213> Artificial Sequence

<220>

eolf-seql

<223> Mature truncated cysteine-modified Radium-1 alpha-chain with linker and His-tag

<400> 78

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

Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser Val Asn Asn Leu
20 25 30

Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile Asn Leu Phe Tyr
35 40 45

Ile Pro Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser Ala Thr Thr Val
50 55 60

Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser Ser Gln Thr Thr
65 70 75 80

Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly Asn Met Leu Thr
85 90 95

Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His Ile Gln Asn Pro
100 105 110

Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser
115 120 125

Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser
130 135 140

Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val Leu Asp Met Arg
145 150 155 160

Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser
165 170 175

eolf-seql

Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp
 180 185 190

Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Gly Gly Gly His His His
 195 200 205

His His His
 210

<210> 79

<211> 255

<212> PRT

<213> Artificial Sequence

<220>

<223> Mature truncated cysteine-modified Radium-1 beta-chain with
 linker and His-tag

<400> 79

Gly Leu Val Asp Val Lys Val Thr Gln Ser Ser Arg Tyr Leu Val Lys
 1 5 10 15

Arg Thr Gly Glu Lys Val Phe Leu Glu Cys Val Gln Asp Met Asp His
 20 25 30

Glu Asn Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu
 35 40 45

Ile Tyr Phe Ser Tyr Asp Val Lys Met Lys Glu Lys Gly Asp Ile Pro
 50 55 60

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Arg Phe Ser Leu Ile
 65 70 75 80

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

eolf-seql

Ser Ser Gly Val Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu
100 105 110

Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val
115 120 125

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
130 135 140

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

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro Gln
165 170 175

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
180 185 190

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
195 200 205

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
210 215 220

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
225 230 235 240

Trp Gly Arg Ala Asp Cys Gly Gly Gly His His His His His His
245 250 255

<210> 80

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> MART-1 26-35 peptide analogue

eolf-seql

<400> 80

Glu Leu Ala Gly Ile Gly Ile Leu Thr Val
1 5 10

<210> 81

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Mature truncated Radium-1 alpha-chain with 2A peptide-derived residues at C-terminus

<400> 81

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

Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser Val Asn Asn Leu
20 25 30

Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile Asn Leu Phe Tyr
35 40 45

Ile Pro Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser Ala Thr Thr Val
50 55 60

Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser Ser Gln Thr Thr
65 70 75 80

Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly Asn Met Leu Thr
85 90 95

Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His Ile Gln Asn Pro
100 105 110

Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser
115 120 125

eolf-seql

Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser
130 135 140

Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg
145 150 155 160

Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser
165 170 175

Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp
180 185 190

Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Arg Ala Lys Arg Gly Ser
195 200 205

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
210 215 220

Asn Pro Gly
225

<210> 82
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Mature truncated cysteine-modified Radium-1 alpha-chain with 2A
peptide-derived residues at C-terminus

<400> 82

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

Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser Val Asn Asn Leu
20 25 30

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Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile Asn Leu Phe Tyr
 35 40 45

Ile Pro Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser Ala Thr Thr Val
 50 55 60

Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser Ser Gln Thr Thr
 65 70 75 80

Asp Ser Gly Val Tyr Phe Cys Ala Val Asn Ala Gly Asn Met Leu Thr
 85 90 95

Phe Gly Gly Gly Thr Arg Leu Met Val Lys Pro His Ile Gln Asn Pro
 100 105 110

Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser
 115 120 125

Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser
 130 135 140

Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Cys Val Leu Asp Met Arg
 145 150 155 160

Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser
 165 170 175

Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp
 180 185 190

Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Arg Ala Lys Arg Gly Ser
 195 200 205

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
 210 215 220

Asn Pro Gly
225

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