

56 819 K_sequence listing
SEQUENCE LISTING

<110> Life science Inkubator GmbH
<120> VLP with a targeting peptide
<130> 56 819 K
<160> 59

<170> PatentIn version 3.5

<210> 1
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide

<400> 1

Cys Gly Asn Lys Arg Thr Arg Gly Cys
1 5

<210> 2
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide

<400> 2

Lys Cys Cys Tyr Ser Leu
1 5

<210> 3
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide

<400> 3

Cys Arg Glu Lys Ala
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<210> 4
<211> 15
<212> PRT
<213> Campylobacter spec.

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Asp Ser Leu Lys Ser Tyr Trp Tyr Leu Gln Lys Phe Ser Trp Arg
1 5 10 15

<210> 5
<211> 15
<212> PRT

56 819 K_sequence listing

<213> Campylobacter spec.

<400> 5

Lys Arg Pro Thr Met Arg Phe Arg Tyr Thr Trp Asn Pro Met Lys
1 5 10 15

<210> 6

<211> 31

<212> PRT

<213> Homo sapiens (human)

<400> 6

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<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed peptide

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Cys Met Gly Thr Ile Asn Thr Arg Thr Lys Lys Cys
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<211> 12

<212> PRT

<213> Artificial Sequence

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<223> Designed peptide

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<210> 9

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed peptide

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Leu Thr Val Ser Pro Trp Tyr
1 5

<210> 10

<211> 12

<212> PRT

56 819 K_sequence listing

<213> Artificial Sequence

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<223> Designed peptide

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Trp Asn Leu Pro Trp Tyr Tyr Ser Val Ser Pro Thr
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<210> 11

<211> 16

<212> PRT

<213> Artificial Sequence

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<223> Designed peptide

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Asn Gly Tyr Glu Ile Glu Trp Tyr Ser Trp Val Thr His Gly Met Tyr
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<210> 12

<211> 611

<212> PRT

<213> JC-Polyomavirus

<400> 12

Met Ala Pro Thr Lys Arg Lys Gly Glu Pro Lys Asp Pro Val Gln Val
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Pro Lys Leu Leu Ile Arg Gly Gly Val Glu Val Leu Glu Val Lys Thr
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Gly Val Asp Ser Ile Thr Glu Val Glu Cys Phe Leu Thr Pro Glu Met
35 40 45

Gly Asp Pro Asp Glu His Leu Arg Gly Phe Ser Lys Ser Ile Ser Ile
50 55 60

Ser Asp Thr Phe Glu Ser Asp Ser Pro Asn Arg Asp Met Leu Pro Cys
65 70 75 80

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

Cys Gly Asn Ile Leu Met Trp Glu Ala Val Thr Leu Lys Thr Glu Val
100 105 110

Ile Gly Val Thr Ser Leu Met Asn Val His Ser Asn Gly Gln Ala Thr
115 120 125

His Asp Asn Gly Ala Gly Lys Pro Val Gln Gly Thr Ser Phe His Phe
130 135 140

56 819 K_sequence listing

Phe Ser Val Gly Gly Glu Ala Leu Glu Leu Gln Gly Val Val Phe Asn
 145 150 155 160
 Tyr Arg Thr Lys Tyr Pro Asp Gly Thr Ile Phe Pro Lys Asn Ala Thr
 165 170 175
 Val Gln Ser Gln Val Met Asn Thr Glu His Lys Ala Tyr Leu Asp Lys
 180 185 190
 Asn Lys Ala Tyr Pro Val Glu Cys Trp Val Pro Asp Pro Thr Arg Asn
 195 200 205
 Glu Asn Thr Arg Tyr Phe Gly Thr Leu Thr Gly Gly Glu Asn Val Pro
 210 215 220
 Pro Val Leu His Ile Thr Asn Thr Ala Thr Thr Val Leu Leu Asp Glu
 225 230 235 240
 Phe Gly Val Gly Pro Leu Cys Lys Gly Asp Asn Leu Tyr Leu Ser Ala
 245 250 255
 Val Asp Val Cys Gly Met Phe Thr Asn Gly Ser Gln Gln Trp Arg Gly
 260 265 270
 Leu Ser Arg Tyr Phe Lys Val Gln Leu Arg Lys Arg Arg Val Lys Asn
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 Pro Tyr Pro Ile Ser Phe Leu Leu Thr Asp Leu Ile Asn Arg Arg Thr
 290 295 300
 Pro Arg Val Asp Gly Gln Pro Met Tyr Gly Met Asp Ala Gln Val Glu
 305 310 315 320
 Glu Val Arg Val Phe Glu Gly Thr Glu Glu Leu Pro Gly Asp Pro Asp
 325 330 335
 Met Met Arg Tyr Val Asp Lys Tyr Gly Gln Leu Gln Thr Lys Met Cys
 340 345 350
 Ile Thr Gly Asp Ala Leu Val Ala Leu Pro Glu Gly Glu Ser Val Arg
 355 360 365
 Ile Ala Asp Ile Val Pro Gly Ala Arg Pro Asn Ser Asp Asn Ala Ile
 370 375 380
 Asp Leu Lys Val Leu Asp Arg His Gly Asn Pro Val Leu Ala Asp Arg
 385 390 395 400
 Leu Phe His Ser Gly Glu His Pro Val Tyr Thr Val Arg Thr Val Glu
 405 410 415

56 819 K_sequence listing

Gly Leu Arg Val Thr Gly Thr Ala Asn His Pro Leu Leu Cys Leu Val
420 425 430

Asp Val Ala Gly Val Pro Thr Leu Leu Trp Lys Leu Ile Asp Glu Ile
435 440 445

Lys Pro Gly Asp Tyr Ala Val Ile Gln Arg Ser Ala Phe Ser Val Asp
450 455 460

Cys Ala Gly Phe Ala Arg Gly Lys Pro Glu Phe Ala Pro Thr Thr Tyr
465 470 475 480

Thr Val Gly Val Pro Gly Leu Val Arg Phe Leu Glu Ala His His Arg
485 490 495

Asp Pro Asp Ala Gln Ala Ile Ala Asp Glu Leu Thr Asp Gly Arg Phe
500 505 510

Tyr Tyr Ala Lys Val Ala Ser Val Thr Asp Ala Gly Val Gln Pro Val
515 520 525

Tyr Ser Leu Arg Val Asp Thr Ala Asp His Ala Phe Ile Thr Asn Gly
530 535 540

Phe Val Ser His Ala Thr Gly Leu Thr Gly Leu Asn Ser Gly Leu Thr
545 550 555 560

Thr Asn Pro Gly Val Ser Ala Trp Gln Val Asn Thr Ala Tyr Thr Ala
565 570 575

Gly Gln Leu Val Thr Tyr Asn Gly Lys Thr Tyr Lys Cys Leu Gln Pro
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His Thr Ser Leu Ala Gly Trp Glu Pro Ser Asn Val Pro Ala Leu Trp
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Gln Leu Gln
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<210> 13
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<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide

<400> 13

Arg Arg Arg Arg Ser Gly Cys Gly Asn Lys Arg Thr Arg Gly Cys Gly
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Ser Glu Glu Glu Glu
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56 819 K_sequence listing

<210> 14
 <211> 632
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed peptide

<400> 14

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

Gly Asp Pro Asp Glu His Leu Arg Gly Phe Ser Lys Ser Ile Ser Ile
50          55          60

Ser Asp Thr Phe Glu Ser Asp Ser Pro Asn Arg Asp Met Leu Pro Cys
65          70          75          80

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

Cys Gly Asn Ile Leu Met Trp Glu Ala Val Thr Leu Lys Thr Glu Val
100         105         110

Ile Gly Val Thr Ser Leu Met Asn Val His Ser Asn Gly Gln Ala Thr
115         120         125

His Arg Arg Arg Arg Ser Gly Cys Gly Asn Lys Arg Thr Arg Gly Cys
130         135         140

Gly Ser Glu Glu Glu Glu Gly Ala Gly Lys Pro Val Gln Gly Thr Ser
145         150         155         160

Phe His Phe Phe Ser Val Gly Gly Glu Ala Leu Glu Leu Gln Gly Val
165         170         175

Val Phe Asn Tyr Arg Thr Lys Tyr Pro Asp Gly Thr Ile Phe Pro Lys
180         185         190

Asn Ala Thr Val Gln Ser Gln Val Met Asn Thr Glu His Lys Ala Tyr
195         200         205

Leu Asp Lys Asn Lys Ala Tyr Pro Val Glu Cys Trp Val Pro Asp Pro
210         215         220
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56 819 K_sequence listing

Thr 225	Arg	Asn	Glu	Asn	Thr 230	Arg	Tyr	Phe	Gly	Thr 235	Leu	Thr	Gly	Gly	Glu 240
Asn	Val	Pro	Pro	Val 245	Leu	His	Ile	Thr	Asn 250	Thr	Ala	Thr	Thr	Val 255	Leu
Leu	Asp	Glu	Phe 260	Gly	Val	Gly	Pro	Leu 265	Cys	Lys	Gly	Asp	Asn 270	Leu	Tyr
Leu	Ser	Ala 275	Val	Asp	Val	Cys	Gly 280	Met	Phe	Thr	Asn	Arg 285	Ser	Gly	Ser
Gln	Gln 290	Trp	Arg	Gly	Leu	Ser 295	Arg	Tyr	Phe	Lys	Val 300	Gln	Leu	Arg	Lys
Arg 305	Arg	Val	Lys	Asn	Pro 310	Tyr	Pro	Ile	Ser	Phe 315	Leu	Leu	Thr	Asp	Leu 320
Ile	Asn	Arg	Arg	Thr 325	Pro	Arg	Val	Asp	Gly 330	Gln	Pro	Met	Tyr	Gly 335	Met
Asp	Ala	Gln	Val 340	Glu	Glu	Val	Arg	Val 345	Phe	Glu	Gly	Thr	Glu 350	Glu	Leu
Pro	Gly	Asp 355	Pro	Asp	Met	Met	Arg 360	Tyr	Val	Asp	Lys	Tyr 365	Gly	Gln	Leu
Gln	Thr 370	Lys	Met	Cys	Ile	Thr 375	Gly	Asp	Ala	Leu	Val 380	Ala	Leu	Pro	Glu
Gly 385	Glu	Ser	Val	Arg	Ile 390	Ala	Asp	Ile	Val	Pro 395	Gly	Ala	Arg	Pro	Asn 400
Ser	Asp	Asn	Ala	Ile 405	Asp	Leu	Lys	Val	Leu 410	Asp	Arg	His	Gly	Asn 415	Pro
Val	Leu	Ala	Asp 420	Arg	Leu	Phe	His	Ser 425	Gly	Glu	His	Pro	Val 430	Tyr	Thr
Val	Arg	Thr 435	Val	Glu	Gly	Leu	Arg 440	Val	Thr	Gly	Thr	Ala 445	Asn	His	Pro
Leu	Leu 450	Cys	Leu	Val	Asp	Val 455	Ala	Gly	Val	Pro	Thr 460	Leu	Leu	Trp	Lys
Leu 465	Ile	Asp	Glu	Ile	Lys 470	Pro	Gly	Asp	Tyr	Ala 475	Val	Ile	Gln	Arg	Ser 480
Ala	Phe	Ser	Val	Asp 485	Cys	Ala	Gly	Phe	Ala 490	Arg	Gly	Lys	Pro	Glu 495	Phe

56 819_K_sequence listing
Ala Pro Thr Thr Tyr Thr Val Gly Val Pro Gly Leu Val Arg Phe Leu
500 505 510
Glu Ala His His Arg Asp Pro Asp Ala Gln Ala Ile Ala Asp Glu Leu
515 520 525
Thr Asp Gly Arg Phe Tyr Tyr Ala Lys Val Ala Ser Val Thr Asp Ala
530 535 540
Gly Val Gln Pro Val Tyr Ser Leu Arg Val Asp Thr Ala Asp His Ala
545 550 555 560
Phe Ile Thr Asn Gly Phe Val Ser His Ala Thr Gly Leu Thr Gly Leu
565 570 575
Asn Ser Gly Leu Thr Thr Asn Pro Gly Val Ser Ala Trp Gln Val Asn
580 585 590
Thr Ala Tyr Thr Ala Gly Gln Leu Val Thr Tyr Asn Gly Lys Thr Tyr
595 600 605
Lys Cys Leu Gln Pro His Thr Ser Leu Ala Gly Trp Glu Pro Ser Asn
610 615 620
Val Pro Ala Leu Trp Gln Leu Gln
625 630

<210> 15
<211> 632
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide

<400> 15

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

56 819 K_sequence listing

Cys Gly Asn Ile Leu Met Trp Glu Ala Val Thr Leu Lys Thr Glu Val
 100 105 110
 Ile Gly Val Thr Ser Leu Met Asn Val His Ser Asn Gly Gln Ala Thr
 115 120 125
 His Asp Asn Gly Ala Gly Lys Pro Val Gln Gly Thr Ser Phe His Phe
 130 135 140
 Phe Ser Val Gly Gly Glu Ala Leu Glu Leu Gln Gly Val Val Phe Asn
 145 150 155 160
 Tyr Arg Thr Lys Tyr Pro Asp Gly Thr Ile Phe Pro Lys Asn Ala Thr
 165 170 175
 Val Gln Ser Gln Val Met Asn Thr Glu His Lys Ala Tyr Leu Asp Lys
 180 185 190
 Asn Lys Ala Tyr Pro Val Glu Cys Trp Val Pro Asp Pro Thr Arg Asn
 195 200 205
 Glu Asn Thr Arg Tyr Phe Gly Thr Leu Thr Gly Gly Glu Asn Val Pro
 210 215 220
 Pro Val Leu His Ile Thr Asn Thr Ala Thr Thr Val Leu Leu Asp Glu
 225 230 235 240
 Phe Gly Val Gly Pro Leu Cys Lys Gly Asp Asn Leu Tyr Leu Ser Ala
 245 250 255
 Val Asp Val Cys Gly Met Phe Thr Asn Arg Arg Arg Arg Ser Gly Cys
 260 265 270
 Gly Asn Lys Arg Thr Arg Gly Cys Gly Ser Glu Glu Glu Glu Gly Ser
 275 280 285
 Gln Gln Trp Arg Gly Leu Ser Arg Tyr Phe Lys Val Gln Leu Arg Lys
 290 295 300
 Arg Arg Val Lys Asn Pro Tyr Pro Ile Ser Phe Leu Leu Thr Asp Leu
 305 310 315 320
 Ile Asn Arg Arg Thr Pro Arg Val Asp Gly Gln Pro Met Tyr Gly Met
 325 330 335
 Asp Ala Gln Val Glu Glu Val Arg Val Phe Glu Gly Thr Glu Glu Leu
 340 345 350
 Pro Gly Asp Pro Asp Met Met Arg Tyr Val Asp Lys Tyr Gly Gln Leu
 355 360 365

56 819 K_sequence listing

Gln Thr Lys Met Cys Ile Thr Gly Asp Ala Leu Val Ala Leu Pro Glu
370 375 380

Gly Glu Ser Val Arg Ile Ala Asp Ile Val Pro Gly Ala Arg Pro Asn
385 390 395 400

Ser Asp Asn Ala Ile Asp Leu Lys Val Leu Asp Arg His Gly Asn Pro
405 410 415

Val Leu Ala Asp Arg Leu Phe His Ser Gly Glu His Pro Val Tyr Thr
420 425 430

Val Arg Thr Val Glu Gly Leu Arg Val Thr Gly Thr Ala Asn His Pro
435 440 445

Leu Leu Cys Leu Val Asp Val Ala Gly Val Pro Thr Leu Leu Trp Lys
450 455 460

Leu Ile Asp Glu Ile Lys Pro Gly Asp Tyr Ala Val Ile Gln Arg Ser
465 470 475 480

Ala Phe Ser Val Asp Cys Ala Gly Phe Ala Arg Gly Lys Pro Glu Phe
485 490 495

Ala Pro Thr Thr Tyr Thr Val Gly Val Pro Gly Leu Val Arg Phe Leu
500 505 510

Glu Ala His His Arg Asp Pro Asp Ala Gln Ala Ile Ala Asp Glu Leu
515 520 525

Thr Asp Gly Arg Phe Tyr Tyr Ala Lys Val Ala Ser Val Thr Asp Ala
530 535 540

Gly Val Gln Pro Val Tyr Ser Leu Arg Val Asp Thr Ala Asp His Ala
545 550 555 560

Phe Ile Thr Asn Gly Phe Val Ser His Ala Thr Gly Leu Thr Gly Leu
565 570 575

Asn Ser Gly Leu Thr Thr Asn Pro Gly Val Ser Ala Trp Gln Val Asn
580 585 590

Thr Ala Tyr Thr Ala Gly Gln Leu Val Thr Tyr Asn Gly Lys Thr Tyr
595 600 605

Lys Cys Leu Gln Pro His Thr Ser Leu Ala Gly Trp Glu Pro Ser Asn
610 615 620

Val Pro Ala Leu Trp Gln Leu Gln
625 630

56 819 K_sequence listing

<210> 16
 <211> 1065
 <212> DNA
 <213> JC-Polyomavirus

<400> 16
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 gagtgcttcc tcacccccga gatgggtgac cctgacgagc acctgagggg cttctccaag 180
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 ctgatcaacc gtcgtacccc tcgtgtggac ggccagcca tgtacggcat ggacgctcag 960
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<210> 17
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene sequence of designed peptide

<400> 17
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 gag 63

<210> 18
 <211> 1899
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene sequence of designed peptide

<400> 18

56 819 K_sequence listing

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gagtgtttcc tcacccccga gatgggtgac cctgacgagc acctgagggg cttctccaag	180
tccatctcca tctccgacac cttcgagtcc gactccccca accgtgacat gctgccctgc	240
tactccgtgg ctcgtatccc cctgcccac ctgaacgagg acctgacttg cggcaacatc	300
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cggctgtttc actccggcga gcatccgggtg tacacgggtgc gtacgggtcga aggtctgcgt	1320
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<210> 19
 <211> 1899
 <212> DNA

56 819 K_sequence listing

<213> Artificial Sequence

<220>

<223> Gene sequence of designed peptide

<400> 19

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gagtgtttcc tcacccccga gatgggtgac cctgacgagc acctgagggg cttctccaag	180
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gcccaagcta tcgccgacga gctgaccgac gggcggttct actacgcgaa agtcgccagt	1620
gtcaccgacg ccggcgtgca gccggtgtat agccttcgtg tcgacacggc agaccacgcg	1680
tttatcacga acgggttcgt cagccacgct actggcctca ccggtctgaa ctcaggcctc	1740
acgacaaaac ctggtgtatc cgcttggcag gtcaacacag cttatactgc gggacaattg	1800
gtcacatata acggcaagac gtataaatgt ttgcagcccc acacctcctt ggcaggatgg	1860

56 819 K_sequence listing
gaaccatcca acgttcctgc cttgtggcag cttcaatga

1899

<210> 20
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide

<400> 20

Arg Arg Arg Arg Ser Gly Cys
1 5

<210> 21
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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Cys Gly Ser Glu Glu Glu Glu
1 5

<210> 22
<211> 342
<212> PRT
<213> JC-Polyomavirus

<400> 22

Met Gly Ala Ala Leu Ala Leu Leu Gly Asp Leu Val Ala Thr Val Ser
1 5 10 15

Glu Ala Ala Ala Ala Thr Gly Phe Ser Val Ala Glu Ile Ala Ala Gly
20 25 30

Glu Ala Ala Ala Thr Ile Glu Val Glu Ile Ala Ser Leu Ala Thr Val
35 40 45

Glu Gly Ile Thr Ser Thr Ser Glu Ala Ile Ala Ala Ile Gly Leu Thr
50 55 60

Pro Glu Thr Tyr Ala Val Ile Thr Gly Ala Pro Gly Ala Val Ala Gly
65 70 75 80

Phe Ala Ala Leu Val Gln Thr Val Thr Gly Gly Ser Ala Ile Ala Gln
85 90 95

Leu Gly Tyr Arg Phe Phe Ala Asp Trp Asp His Lys Val Ser Thr Val
100 105 110

Gly Leu Phe Gln Gln Pro Ala Met Ala Leu Gln Leu Phe Asn Pro Glu
115 120 125

56 819 K_sequence listing

Asp Tyr Tyr Asp Ile Leu Phe Pro Gly Val Asn Ala Phe Val Asn Asn
130 135 140

Ile His Tyr Leu Asp Pro Arg His Trp Gly Pro Ser Leu Phe Ser Thr
145 150 155 160

Ile Ser Gln Ala Phe Trp Asn Leu Val Arg Asp Asp Leu Pro Ala Leu
165 170 175

Thr Ser Gln Glu Ile Gln Arg Arg Thr Gln Lys Leu Phe Val Glu Ser
180 185 190

Leu Ala Arg Phe Leu Glu Glu Thr Thr Trp Ala Ile Val Asn Ser Pro
195 200 205

Ala Asn Leu Tyr Asn Tyr Ile Ser Asp Tyr Tyr Ser Arg Leu Ser Pro
210 215 220

Val Arg Pro Ser Met Val Arg Gln Val Ala Gln Arg Glu Gly Thr Tyr
225 230 235 240

Ile Ser Phe Gly His Ser Tyr Thr Gln Ser Ile Asp Asp Ala Asp Ser
245 250 255

Ile Gln Glu Val Thr Gln Arg Leu Asp Leu Lys Thr Pro Asn Val Gln
260 265 270

Ser Gly Glu Phe Ile Glu Arg Ser Ile Ala Pro Gly Gly Ala Asn Gln
275 280 285

Arg Ser Pro Gln Trp Met Leu Pro Leu Leu Leu Gly Leu Tyr Gly Thr
290 295 300

Val Thr Pro Ala Leu Glu Ala Tyr Glu Asp Gly Pro Asn Lys Lys Lys
305 310 315 320

Arg Arg Lys Glu Gly Pro Arg Ala Ser Lys Thr Ser Tyr Lys Arg Arg
325 330 335

Ser Arg Ser Ser Arg Ser
340

<210> 23
<211> 225
<212> PRT
<213> JC-Polyomavirus
<400> 23

Met Ala Leu Gln Leu Phe Asn Pro Glu Asp Tyr Tyr Asp Ile Leu Phe
1 5 10 15

56 819 K_sequence listing

Pro Gly Val Asn Ala Phe Val Asn Asn Ile His Tyr Leu Asp Pro Arg
20 25 30

His Trp Gly Pro Ser Leu Phe Ser Thr Ile Ser Gln Ala Phe Trp Asn
35 40 45

Leu Val Arg Asp Asp Leu Pro Ala Leu Thr Ser Gln Glu Ile Gln Arg
50 55 60

Arg Thr Gln Lys Leu Phe Val Glu Ser Leu Ala Arg Phe Leu Glu Glu
65 70 75 80

Thr Thr Trp Ala Ile Val Asn Ser Pro Ala Asn Leu Tyr Asn Tyr Ile
85 90 95

Ser Asp Tyr Tyr Ser Arg Leu Ser Pro Val Arg Pro Ser Met Val Arg
100 105 110

Gln Val Ala Gln Arg Glu Gly Thr Tyr Ile Ser Phe Gly His Ser Tyr
115 120 125

Thr Gln Ser Ile Asp Asp Ala Asp Ser Ile Gln Glu Val Thr Gln Arg
130 135 140

Leu Asp Leu Lys Thr Pro Asn Val Gln Ser Gly Glu Phe Ile Glu Arg
145 150 155 160

Ser Ile Ala Pro Gly Gly Ala Asn Gln Arg Ser Ala Pro Gln Trp Met
165 170 175

Leu Pro Leu Leu Leu Gly Leu Tyr Gly Thr Val Thr Pro Ala Leu Glu
180 185 190

Ala Tyr Glu Asp Gly Pro Asn Lys Lys Lys Arg Arg Lys Glu Gly Pro
195 200 205

Arg Ala Ser Ser Lys Thr Ser Tyr Lys Arg Arg Ser Arg Ser Ser Arg
210 215 220

Ser
225

<210> 24
<211> 36
<212> PRT
<213> JC-Polyomavirus

<400> 24

Ser Gly Glu Phe Ile Glu Arg Ser Ile Ala Pro Gly Gly Ala Asn Gln
1 5 10 15

56 819 K_sequence listing
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Thr Val Thr Pro
 35

<210> 25
 <211> 51
 <212> PRT
 <213> Homo sapiens (human)
 <400> 25

Met Ala Arg Tyr Arg Cys Cys Arg Ser Gln Ser Arg Ser Arg Tyr Tyr
 1 5 10 15

Arg Gln Arg Gln Arg Ser Arg Arg Arg Arg Arg Ser Cys Gln Thr
 20 25 30

Arg Arg Arg Ala Met Arg Cys Cys Arg Pro Arg Tyr Arg Pro Arg Cys
 35 40 45

Arg Arg His
 50

<210> 26
 <211> 21
 <212> PRT
 <213> Homo sapiens (human)
 <400> 26

Ser Gln Ser Arg Ser Arg Tyr Tyr Arg Gln Arg Gln Arg Ser Arg Arg
 1 5 10 15

Arg Arg Arg Arg Ser
 20

<210> 27
 <211> 17
 <212> PRT
 <213> Human immunodeficiency virus (HIV)
 <400> 27

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Lys Arg Lys
 1 5 10 15

Gly

<210> 28
 <211> 16
 <212> PRT
 <213> Drosophila spec.
 <400> 28

56 819 K_sequence listing

Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
1 5 10 15

<210> 29
<211> 21
<212> PRT
<213> Human papillomavirus type 33 (HPV33)

<400> 29

Phe Ile Leu Arg Arg Arg Arg Lys Arg Phe Pro Tyr Phe Phe Thr Asp
1 5 10 15

Val Arg Val Ala Ala
20

<210> 30
<211> 21
<212> PRT
<213> Human papillomavirus type 33 (HPV33)

<400> 30

Asp Asp Leu Arg Arg Arg Arg Lys Arg Phe Pro Tyr Phe Phe Thr Asp
1 5 10 15

Val Arg Val Ala Ala
20

<210> 31
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide

<400> 31

Arg Gly Gly Arg Leu Ser Tyr Ser Arg Arg Arg Phe Ser Thr Ser Thr
1 5 10 15

Gly Arg

<210> 32
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide

<400> 32

Arg Arg Leu Ser Tyr Ser Arg Arg Arg Phe
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<210> 33
<211> 12

56 819 K_sequence listing

<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide

<400> 33

Pro Ile Arg Arg Arg Lys Lys Leu Arg Arg Leu Lys
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<210> 34
<211> 12
<212> PRT
<213> Artificial Sequence

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<400> 34

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<210> 35
<211> 15
<212> PRT
<213> Feline herpesvirus 1

<400> 35

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1 5 10 15

<210> 36
<211> 19
<212> PRT
<213> Brome mosaic virus

<400> 36

Lys Met Thr Arg Ala Gln Arg Arg Ala Ala Ala Arg Arg Asn Arg Trp
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Thr Ala Arg

<210> 37
<211> 13
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<213> Human T-cell lymphotropic virus

<400> 37

Thr Arg Arg Gln Arg Thr Arg Arg Ala Arg Arg Asn Arg
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<210> 38
<211> 13
<212> PRT
<213> Human immunodeficiency virus (HIV)

56 819 K_sequence listing

<400> 38

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln
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<210> 39

<211> 13

<212> PRT

<213> Human papillomavirus type 33 (HPV33)

<400> 39

Gly Arg Arg Arg Arg Arg Arg Arg Arg Arg Pro Pro Gln
1 5 10

<210> 40

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Gene sequence of designed peptide

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<210> 41

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Gene sequence of designed peptide

<400> 41

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<210> 42

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<212> DNA

<213> Artificial Sequence

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<223> Gene sequence of designed peptide

<400> 42

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catgacagta agagaattat gcagtgtctg cataaccatg agtgataaca ctgcccga 540

56 819 K_sequence listing

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56 819 K_sequence listing

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56 819 K_sequence listing

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56 819 K_sequence listing

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<220>
 <223> Gene sequence of designed peptide

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<210> 44
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<210> 45
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 <212> PRT
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56 819 K_sequence listing

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<210> 46

<211> 4

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Glu Arg Glu Arg
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<210> 47

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<212> PRT

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<400> 47

Glu Glu Arg Arg Glu Glu
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<210> 48

<211> 6

<212> PRT

<213> Artificial Sequence

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<210> 49

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Designed interaction region peptide

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<210> 50

<211> 6

<212> PRT

<213> Artificial Sequence

56 819 K_sequence listing

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<212> PRT

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Asp Asp Asp Arg Arg
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<223> Designed interaction region peptide

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Arg Arg Arg Arg Glu
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<210> 53

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