

SEQUENCE LISTING

<110> Max-Delbrueck-Centrum fuer Molekulare Medizin, et al.

<120> Method of detecting new immunogenic T cell epitopes and isolating new antigen-specific T cell receptors by means of an MHC cell library

<130> MDC15851PCT

<160> 71

<170> BiSSAP 1.3

<210> 1

<211> 9

<212> PRT

<213> Alphapapillomavirus 9

<220>

<223> HPV16 E5 epitope restricted to HLA-B*15:01

<400> 1

Ser Ala Phe Arg Cys Phe Ile Val Tyr
1 5

<210> 2

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 of TRA specific for E5 epitope

<400> 2

Cys Ala Glu Ser Glu Tyr Gly Asn Lys Leu Val Phe
1 5 10

<210> 3

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> variable region of TRA specific for E5 epitope, TRAV17

<400> 3

Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
1 5 10 15
Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
20 25 30
Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
35 40 45
Ile Asn Asn Leu Gln Trp Tyr Arg Gln Asn Ser Gly Arg Gly Leu Val

50		55		60											
His	Leu	Ile	Leu	Ile	Arg	Ser	Asn	Glu	Arg	Glu	Lys	His	Ser	Gly	Arg
65					70					75					80
Leu	Arg	Val	Thr	Leu	Asp	Thr	Ser	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Ile
				85					90					95	
Thr	Ala	Ser	Arg	Ala	Ala	Asp	Thr	Ala	Ser	Tyr	Phe	Cys	Ala	Glu	Ser
			100					105					110		
Glu	Tyr	Gly	Asn	Lys	Leu	Val	Phe	Gly	Ala	Gly	Thr	Ile	Leu	Arg	Val
		115					120					125			
Lys	Ser	Tyr													
130															

<210> 4

<211> 267

<212> PRT

<213> Artificial Sequence

<220>

<223> TRA specific for E5 epitope, optimized

<400> 4

Met	Glu	Thr	Leu	Leu	Gly	Val	Ser	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu
1				5					10					15	
Ala	Arg	Val	Asn	Ser	Gln	Gln	Gly	Glu	Glu	Asp	Pro	Gln	Ala	Leu	Ser
			20				25					30			
Ile	Gln	Glu	Gly	Glu	Asn	Ala	Thr	Met	Asn	Cys	Ser	Tyr	Lys	Thr	Ser
		35					40					45			
Ile	Asn	Asn	Leu	Gln	Trp	Tyr	Arg	Gln	Asn	Ser	Gly	Arg	Gly	Leu	Val
	50					55					60				
His	Leu	Ile	Leu	Ile	Arg	Ser	Asn	Glu	Arg	Glu	Lys	His	Ser	Gly	Arg
65					70					75					80
Leu	Arg	Val	Thr	Leu	Asp	Thr	Ser	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Ile
				85					90					95	
Thr	Ala	Ser	Arg	Ala	Ala	Asp	Thr	Ala	Ser	Tyr	Phe	Cys	Ala	Glu	Ser
			100					105					110		
Glu	Tyr	Gly	Asn	Lys	Leu	Val	Phe	Gly	Ala	Gly	Thr	Ile	Leu	Arg	Val
		115					120					125			
Lys	Ser	Tyr	Ile	Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln	Leu	Lys	Asp
	130				135						140				
Pro	Arg	Ser	Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser
145				150					155					160	
Gln	Ile	Asn	Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp
			165						170					175	
Lys	Thr	Val	Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala
		180					185						190		
Ile	Ala	Trp	Ser	Asn	Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp	Ile	Phe	Lys
		195					200					205			
Glu	Thr	Asn	Ala	Thr	Tyr	Pro	Ser	Ser	Asp	Val	Pro	Cys	Asp	Ala	Thr
	210					215					220				
Leu	Thr	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn	Phe	Gln	Asn
225					230					235					240
Leu	Ser	Val	Met	Gly	Leu	Arg	Ile	Leu	Leu	Lys	Val	Ala	Gly	Phe	
				245					250					255	

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

<210> 5
 <211> 804
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRA specific for E5 epitope, optimized

<400> 5
 atggaaacac tgctgggcgt gtccctcgtg atcctgtggc tgcagctggc tagagtgaac 60
 agccagcagg gcgaggaaga tcctcaggcc ctgagcatcc aggaaggcga gaacgccacc 120
 atgaactgca gctacaagac cagcatcaac aacctgcagt ggtacaggca gaatagcggc 180
 agaggactgg tgcacctgat cctgatccgg tccaacgaga gagagaagca ctccggcaga 240
 ctgagagtga ccctggacac ctccaagaag tccagctccc tgctgattac cgccagcaga 300
 gccgccgata ccgcctccta cttttgcgcc gagagcgagt acggcaacaa gctggtgttt 360
 ggccgccgaa ccatactgcg cgtgaagtcc tacatccaga accccgagcc cgccgtgtat 420
 cagctgaagg accccagaag ccaggacagc accctgtgcc tgttcaccga cttcgacagc 480
 cagatcaacg tgcccaagac catggaaagc ggcaccttca tcaccgataa gaccgtgctg 540
 gacatgaagg ccatggacag caagagcaac ggcgccattg cctggtccaa ccagaccagc 600
 ttcacatgcc aggacatctt caaagagaca aagccacct accccagcag cgacgtgccc 660
 tgtgatgcca ccctgaccga gaagtccttc gagacagaca tgaatctgaa cttccagaac 720
 ctgagcgtga tgggcctgag aatcctgctg ctgaaggtgg ccggcttcaa cctgctgatg 780
 accctgagac tgttgtccag ctga 804

<210> 6
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR3 of TRB specific for E5 epitope

<400> 6
 Cys Ala Ser Ser Tyr Arg Gln Gln Glu Thr Gln Tyr Phe
 1 5 10

<210> 7
 <211> 131
 <212> PRT
 <213> Artificial Sequence

<220>

<223> variable region of TRB specific for E5 epitope, TRBV6-5

<400> 7

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

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<210> 8
 <211> 304
 <212> PRT
 <213> Artificial Sequence

<220>

<223> TRB specific for E5 epitope, optimized

<400> 8

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

```

Leu	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	
Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	His	Gln	Gly	Val	Leu	Ser	Ala
			260					265					270		
Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val
		275					280					285			
Leu	Val	Ser	Gly	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Lys	Lys	Asn	Ser
	290					295					300				

<210> 9

<211> 915

<212> DNA

<213> Artificial Sequence

<220>

<223> TRB specific for E5 epitope, optimized

<400> 9

atgtctatcg gcctgctgtg ttgtgccgcc ctgtccctgc tgtgggccgg acctgtgaat	60
gctggcgtga cccagacccc caagttccag gtgctgaaaa ccggccagag catgaccctg	120
cagtgcgccc aggacatgaa ccacgagtac atgagctggt acagacagga ccccgcatg	180
ggcctgcggc tgatccacta ttctgtggga gccggcatca ccgaccaggg cgaagtgcgc	240
aatggctaca acgtgtccag aagcaccacc gaggacttcc cactgcggct gctgtctgcc	300
gccccatctc agaccagcgt gtacttctgc gccagcagct accggcagca ggaaaccag	360
tacttcggcc ctggcaccag actgctggtg ctggaagatc tgcggaacgt gaccccccc	420
aaggtgtccc tgttcgagcc tagcaaggcc gagatcgcca acaagcagaa agccaccctc	480
gtgtgcctgg ccagaggctt cttccccgac catgtggaac tgtcttggtg ggtcaacggc	540
aaagaggtgc acagcggcgt gtccaccgat cccaggcct acaaagagag caactacgc	600

tactgcctga gcagcaggct gcgggtgtcc gccaccttct ggcacaaccc ccggaaccac	660
ttcagatgcc aggtgcagtt ccacggcctg agcgaagagg acaagtggcc tgagggcagc	720
cccaagcccc tgacacagaa tatctctgcc gaagcctggg gcagagccga ctgtggcatt	780
accagcgcca gctaccatca gggcgtgctg agcgccacca tcctgtacga gatcctgctg	840
ggcaaggcca ccctgtacgc cgtgctggtg tcaggcctgg tgctgatggc catggtcaag	900
aagaagaaca gctga	915

<210> 10
 <211> 10
 <212> PRT
 <213> Cytomegalovirus

<220>
 <223> CMV pp65 epitope restricted to HLA-B*07:02

<400> 10
 Thr Pro Arg Val Thr Gly Gly Gly Ala Met
 1 5 10

<210> 11
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR3 of TRA specific for pp65 epitope

<400> 11
 Cys Ala Thr Val Ile Arg Met Asp Ser Ser Tyr Lys Leu Ile Phe
 1 5 10 15

<210> 12
 <211> 134
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> variable region of TRA specific for pp65 epitope, TRAV17

<400> 12
 Met Glu Thr Leu Leu Gly Val Ser Leu Val Ile Leu Trp Leu Gln Leu
 1 5 10 15
 Ala Arg Val Asn Ser Gln Gln Gly Glu Glu Asp Pro Gln Ala Leu Ser
 20 25 30
 Ile Gln Glu Gly Glu Asn Ala Thr Met Asn Cys Ser Tyr Lys Thr Ser
 35 40 45

Ile	Asn	Asn	Leu	Gln	Trp	Tyr	Arg	Gln	Asn	Ser	Gly	Arg	Gly	Leu	Val
	50					55					60				
His	Leu	Ile	Leu	Ile	Arg	Ser	Asn	Glu	Arg	Glu	Lys	His	Ser	Gly	Arg
65					70					75					80
Leu	Arg	Val	Thr	Leu	Asp	Thr	Ser	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Ile
				85					90					95	
Thr	Ala	Ser	Arg	Ala	Ala	Asp	Thr	Ala	Ser	Tyr	Phe	Cys	Ala	Thr	Val
			100					105					110		
Ile	Arg	Met	Asp	Ser	Ser	Tyr	Lys	Leu	Ile	Phe	Gly	Ser	Gly	Thr	Arg
		115					120					125			
Leu	Leu	Val	Arg	Pro	Asp										
	130														

<210> 13

<211> 270

<212> PRT

<213> Artificial Sequence

<220>

<223> TRA specific for pp65 epitope, optimized

<400> 13

Met	Glu	Thr	Leu	Leu	Gly	Val	Ser	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu
1			5					10						15	
Ala	Arg	Val	Asn	Ser	Gln	Gln	Gly	Glu	Glu	Asp	Pro	Gln	Ala	Leu	Ser
			20				25					30			
Ile	Gln	Glu	Gly	Glu	Asn	Ala	Thr	Met	Asn	Cys	Ser	Tyr	Lys	Thr	Ser
		35				40					45				
Ile	Asn	Asn	Leu	Gln	Trp	Tyr	Arg	Gln	Asn	Ser	Gly	Arg	Gly	Leu	Val
	50					55					60				
His	Leu	Ile	Leu	Ile	Arg	Ser	Asn	Glu	Arg	Glu	Lys	His	Ser	Gly	Arg
65					70					75					80
Leu	Arg	Val	Thr	Leu	Asp	Thr	Ser	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Ile
				85					90					95	
Thr	Ala	Ser	Arg	Ala	Ala	Asp	Thr	Ala	Ser	Tyr	Phe	Cys	Ala	Thr	Val
			100					105					110		
Ile	Arg	Met	Asp	Ser	Ser	Tyr	Lys	Leu	Ile	Phe	Gly	Ser	Gly	Thr	Arg
		115					120					125			
Leu	Leu	Val	Arg	Pro	Asp	Ile	Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln
	130					135				140					
Leu	Lys	Asp	Pro	Arg	Ser	Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp
145					150					155					160
Phe	Asp	Ser	Gln	Ile	Asn	Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe
				165					170					175	
Ile	Thr	Asp	Lys	Thr	Val	Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser
			180					185					190		
Asn	Gly	Ala	Ile	Ala	Trp	Ser	Asn	Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp
		195					200					205			
Ile	Phe	Lys	Glu	Thr	Asn	Ala	Thr	Tyr	Pro	Ser	Ser	Asp	Val	Pro	Cys
	210					215					220				
Asp	Ala	Thr	Leu	Thr	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn
225					230					235					240
Phe	Gln	Asn	Leu	Ser	Val	Met	Gly	Leu	Arg	Ile	Leu	Leu	Leu	Lys	Val

				245					250					255
Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser	
			260					265					270	

<210> 14
 <211> 813
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRA specific for pp65 epitope, optimized

<400> 14
 atggaaacac tgctgggcgt gtcactcgtg atcctgtggc tgcagctggc tagagtgaac 60
 agccagcagg gggaagagga ccctcaggcc ctgagcattc aggaaggcga gaacgccacc 120
 atgaactgca gctacaagac cagcatcaac aacctgcagt ggtacaggca gaactccggc 180
 agaggactgg tgcacctgat cctgatccgg tccaacgaga gagagaagca ctccggacgg 240
 ctgagagtga ccctggacac ctccaagaag tccagctccc tgctgattac cgccagcaga 300
 gccgccgata ccgcctccta cttttgcgcc accgtgatcc ggatggacag ctcctacaag 360
 ctgatctttg gcagcggcac cagactgctc gtgcggcccg atatccagaa ccctgagcct 420
 gccgtgtacc agctgaagga ccccagaagc caggacagca cactgtgcct gttcaccgac 480
 ttcgacagcc agatcaacgt gcccagacc atggaaagcg gcaccttcat caccgacaag 540
 acagtgctgg acatgaaggc catggacagc aagagcaacg gcgccattgc ctggtccaac 600
 cagaccagct tcacatgcca ggacatcttc aaagagacaa acgccaccta ccccagcagc 660
 gacgtgccct gtgatgccac cctgaccgag aagtccttcg agacagacat gaacctgaat 720
 ttccagaacc tgtccgtgat gggcctgaga atcctgctgc tgaaggtggc cggcttcaat 780
 ctgctgatga ccctgcggct gtggtccagc tga 813

<210> 15
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR3 of TRB specific for pp65 epitope

<400> 15
 Cys Ala Ser Ser Leu Ile Gly Val Ser Ser Tyr Asn Glu Gln Phe Phe
 1 5 10 15

<210> 16
 <211> 135
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> variable region of TRB specific for pp65 epitope, TRBV7-9

<400> 16
 Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1 5 10 15
 Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
 20 25 30
 Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
 35 40 45
 Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
 50 55 60
 Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
 65 70 75 80
 Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
 85 90 95
 Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
 100 105 110
 Ser Ser Leu Ile Gly Val Ser Ser Tyr Asn Glu Gln Phe Phe Gly Pro
 115 120 125
 Gly Thr Arg Leu Thr Val Leu
 130 135

<210> 17
 <211> 308
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TRB specific for pp65 epitope, optimized

<400> 17
 Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
 1 5 10 15
 Asp His Ala Asp Thr Gly Val Ser Gln Asp Pro Arg His Lys Ile Thr
 20 25 30
 Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
 35 40 45
 Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
 50 55 60
 Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
 65 70 75 80
 Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
 85 90 95
 Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala

aaagccaccc tcgtgtgcct ggccagaggc ttcttccccg accatgtgga actgtcttgg 540
 tgggtcaacg gcaaagaggt gcacagcgga gtgtccaccg acccccaggc ctacaaagag 600
 agcaactaca gctactgcct gagcagcaga ctgcgggtgt ccgccacctt ctggcacaac 660
 ccccggaacc acttcaggtg ccaggtgcag tttcacggcc tgagcgaaga ggacaagtgg 720
 cccgagggca gccctaagcc cgtgaccag aatatctctg ccgaagcctg gggcagagcc 780
 gactgtggca ttaccagcgc cagctacat cagggcgtgc tgagcgccac catcctgtac 840
 gagatcctgc tgggcaaggc caccctgtac gccgtgctgg tgtctggcct ggtgctgatg 900
 gccatggtca agaagaagaa cagctga 927

<210> 19
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Homsap TRAV38-2/DV8*01 F

<400> 19
 Cys Ala Tyr Arg Ser Trp Asn Tyr Gly Gln Asn Phe Val Phe
 1 5 10

<210> 20
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Homsap TRAV8-6*02 F

<400> 20
 Cys Ala Val Ser Glu Pro Ala Ala Gly Asn Lys Leu Thr Phe
 1 5 10

<210> 21
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Homsap TRAV26-2*01 F

<400> 21
 Cys Ile Leu Arg Gly Ala Gly Gly Thr Ser Tyr Gly Lys Leu Thr Phe
 1 5 10 15

<210> 22
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Homsap TRAV8-6*02 F

<400> 22
Cys Ala Val Ile Thr Asn Ala Gly Lys Ser Thr Phe
1 5 10

<210> 23
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Homsap TRAV25*01 F

<400> 23
Cys Ala Gly Pro Pro Ser Gly Thr Tyr Lys Tyr Ile Phe
1 5 10

<210> 24
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Homsap TRAV6*02 (F)

<400> 24
Cys Ala Leu Pro Met Glu Tyr Gly Asn Lys Leu Val Phe
1 5 10

<210> 25
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Homsap TRBV5-1*01 F

<400> 25
Cys Ala Ser Ser Ser Arg Gly His Gln Asn Thr Gly Glu Leu Phe Phe
1 5 10 15

<210> 26

<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Homsap TRBV12-3*01 F

<400> 26
Cys Ala Ser Ser Pro Glu Gly Glu Gly Val Thr Gly Glu Leu Phe Phe
1 5 10 15

<210> 27
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Homsap TRBV5-1*01 F

<400> 27
Cys Ala Ser Thr Leu Arg Gly Tyr Thr Glu Ala Phe Phe
1 5 10

<210> 28
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Homsap TRBV5-5*02 (F)

<400> 28
Cys Ala Ser Ser Pro Trp Ala Asp Ser Asn Gln Pro Gln His Phe
1 5 10 15

<210> 29
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Homsap TRBV20-1*01 F

<400> 29
Cys Ser Ala Gly Thr Ser Gly Gly Pro Ala Tyr Glu Gln Tyr Phe
1 5 10 15

<210> 30
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Homsap TRBV27*01 F

<400> 30

Cys	Ala	Ser	Ser	Ser	Pro	Leu	Ala	Asp	Asp	Tyr	Asn	Glu	Gln	Phe	Phe
1				5					10					15	

<210> 31

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Homsap TRBV6-2*01 F

<400> 31

Cys	Ala	Ser	Ser	His	Arg	Arg	Ala	His	Arg	Ala	Arg	Glu	Gln	Tyr	Phe
1				5					10					15	

<210> 32

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Homsap TRAV14/DV4*01 F

<400> 32

Cys	Ala	Met	Arg	Glu	Gly	Lys	Asp	Ser	Ser	Tyr	Lys	Leu	Ile	Phe
1				5					10					15

<210> 33

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Homsap TRAV8-1*01 F

<400> 33

Cys	Ala	Val	Asn	Arg	Gly	Gly	Ser	Asn	Tyr	Lys	Leu	Thr	Phe
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<210> 34

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Homsap TRAV3*01 F

<400> 34

Cys Ala Val Arg Asp Ile Gly Gly Phe Lys Thr Ile Phe
1 5 10

<210> 35

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Homsap TRAV1-2*01 F

<400> 35

Cys Ala Leu Asp Gly Gln Lys Leu Leu Phe
1 5 10

<210> 36

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Homsap TRAV4*01 F

<400> 36

Cys Leu Val Gly Gly Leu Arg Gly Asn Val Leu His Cys
1 5 10

<210> 37

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Homsap TRBV27*01 F

<400> 37

Cys Ala Ser Arg Leu Gly Gly Gly Asn Tyr Asn Glu Gln Phe Phe
1 5 10 15

<210> 38

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Homsap TRBV20-1*01 F

<400> 38

Cys Ser Ala Ser Pro Arg Asp Arg Lys Phe Ser Gly Asn Thr Ile Tyr

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ggcaaggcca ccctgtacgc cgtgctggtg tcaggcctgg tgctgatggc catggtcaag	900
aagaagaaca gcggcagcgg cgccaccaac tttagcctgc tgaaacaggc cggcgacgtg	960
gaagagaacc ccgggccccat ggaaacactg ctgggcgtgt ccctcgtgat cctgtggctg	1020
cagctggcta gagtgaacag ccagcagggc gaggaagatc ctcaggccct gagcatccag	1080
gaaggcgaga acgccacat gaactgcagc tacaagacca gcatcaacaa cctgcagtgg	1140
tacaggcaga atagcggcag aggactggtg cacctgatcc tgatccggtc caacgagaga	1200
gagaagcact ccggcagact gagagtgacc ctggacacct ccaagaagtc cagctccctg	1260
ctgattaccg ccagcagagc cgccgatacc gcctcctact tttgcgccga gagcgagtac	1320
ggcaacaagc tgggtgtttgg cgccggaacc atcctgcgcg tgaagtccta catccagaac	1380
cccgagcccc ccgtgtatca gctgaaggac ccagaagcc aggacagcac cctgtgcctg	1440
ttcaccgact tcgacagcca gatcaacgtg cccaagacca tggaaagcgg caccttcac	1500
accgataaga ccgtgctgga catgaaggcc atggacagca agagcaacgg cgccattgcc	1560
tggccaacc agaccagctt cacatgccag gacatcttca aagagacaaa cgccacctac	1620
cccagcagcg acgtgccctg tgatgccacc ctgaccgaga agtccttcga gacagacatg	1680
aatctgaact tccagaacct gagcgtgatg ggcctgagaa tcctgctgct gaaggtggcc	1740
ggcttcaacc tgctgatgac cctgagactg tggccagct ga	1782

<210> 41

<211> 1803

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR transgene cassette specific for the pp65 epitope

<400> 41

atgggaacat ctctgctgtg ttggatggcc ctgtgcctgc tgggagccga tcatgccgat	60
acaggcgtgt cccaggaccc ccggcacaag attaccaagc ggggccagaa cgtgaccttc	120
agatgcgacc ccatcagcga gcacaaccgg ctgtactggt acagacagac cctgggccag	180
ggacccgagt tcctgacctt cttccagaac gaggcccagc tggaagagag ccggctgctg	240
agcgacagat tcagcgccga aagacccaag ggcagcttca gcaccctgga aatccagcgg	300

accgagcagg gcgacagcgc catgtatctg tgtgccagca gcctgatcgg cgtgtccagc	360
tacaacgagc agttcttcgg ccctggcacc cggctgaccg tgctggaaga tctgagaaac	420
gtgaccccc ccaaggtgtc cctgttcgag cctagcaagg ccgagatcgc caacaagcag	480
aaagccaccc tcgtgtgcct ggccagaggc ttcttccccg accatgtgga actgtcttgg	540
tgggtcaacg gcaaagaggt gcacagcggg gtgtccaccg acccccaggc ctacaaagag	600
agcaactaca gctactgcct gagcagcaga ctgcgggtgt ccgccacctt ctggcacaaac	660
ccccggaacc acttcaggtg ccaggtgcag ttccacggcc tgagcgaaga ggacaagtgg	720
cccgagggca gccctaagcc cgtgaccag aatatctctg ccgaagcctg gggcagagcc	780
gactgtggca ttaccagcgc cagctaccat cagggcgtgc tgagcgccac catcctgtac	840
gagatcctgc tgggcaaggc caccctgtac gccgtgctgg tgtctggcct ggtgctgatg	900
gccatggtca agaagaagaa cagcggcagc ggcgccacca acttcagcct gctgaaacag	960
gccggcgacg tggaagagaa ccccgggccc atggaaacac tgctgggcgt gtcactcgtg	1020
atcctgtggc tgcagctggc tagagtgaac agccagcagg gggaagagga ccctcaggcc	1080
ctgagcattc aggaaggcga gaacgccacc atgaactgca gctacaagac cagcatcaac	1140
aacctgcagt ggtacaggca gaactccggc agaggactgg tgcacctgat cctgatccgg	1200
tccaacgaga gagagaagca ctccggacgg ctgagagtga ccctggacac ctccaagaag	1260
tccagctccc tgctgattac cgccagcaga gccgccgata ccgcctccta cttttgcgcc	1320
accgtgatcc ggatggacag ctctacaag ctgatctttg gcagcggcac cagactgctc	1380
gtgcggccccg atatccagaa ccctgagcct gccgtgtacc agctgaagga cccagaagc	1440
caggacagca cactgtgcct gttcaccgac ttcgacagcc agatcaacgt gccaagacc	1500
atggaaagcg gcaccttcat caccgacaag acagtgtctg acatgaaggc catggacagc	1560
aagagcaacg gcgccattgc ctggtccaac cagaccagct tcacatgcca ggacatcttc	1620
aaagagacaa acgccaccta ccccagcagc gacgtgccct gtgatgccac cctgaccgag	1680
aagtccttcg agacagacat gaacctgaat ttccagaacc tgtccgtgat gggcctgaga	1740
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tga	1803

<210> 42
<211> 12
<212> PRT
<213> Alphapapillomavirus 9

<220>
<223> potential epitope of E5

<400> 42
Leu Ile Arg Pro Leu Leu Leu Ser Val Ser Thr Tyr
1 5 10

<210> 43
<211> 13
<212> PRT
<213> Alphapapillomavirus 9

<220>
<223> potential epitope of E5

<400> 43
Leu Leu Ile Arg Pro Leu Leu Leu Ser Val Ser Thr Tyr
1 5 10

<210> 44
<211> 9
<212> PRT
<213> Alphapapillomavirus 9

<220>
<223> potential epitope of E5

<400> 44
Phe Leu Ile His Thr His Ala Arg Phe
1 5

<210> 45
<211> 10
<212> PRT
<213> Alphapapillomavirus 9

<220>
<223> potential epitope of E5

<400> 45
Ala Ser Ala Phe Arg Cys Phe Ile Val Tyr
1 5 10

<210> 46
<211> 10
<212> PRT
<213> Alphapapillomavirus 9

<220>

<223> potential epitope of E5

<400> 46

Leu Leu Trp Ile Thr Ala Ala Ser Ala Phe
1 5 10

<210> 47

<211> 13

<212> PRT

<213> Alphapapillomavirus 9

<220>

<223> epitope of E5

<400> 47

Ile Thr Ala Ala Ser Ala Phe Arg Cys Phe Ile Val Tyr
1 5 10

<210> 48

<211> 8

<212> PRT

<213> Alphapapillomavirus 9

<220>

<223> potential epitope of E5

<400> 48

Leu Leu Leu Ser Val Ser Thr Tyr
1 5

<210> 49

<211> 11

<212> PRT

<213> Alphapapillomavirus 9

<220>

<223> epitope of E5

<400> 49

Ala Ala Ser Ala Phe Arg Cys Phe Ile Val Tyr
1 5 10

<210> 50

<211> 14

<212> PRT

<213> Alphapapillomavirus 9

<220>

<223> potential epitope of E5

<400> 50

Ser Ala Phe Arg Cys Phe Ile Val Tyr Ile Ile Phe Val Tyr
1 5 10

<210> 51

<211> 14

<212> PRT

<213> Alphapapillomavirus 9

<220>

<223> epitope of E5

<400> 51

Trp Ile Thr Ala Ala Ser Ala Phe Arg Cys Phe Ile Val Tyr
1 5 10

<210> 52

<211> 12

<212> PRT

<213> Alphapapillomavirus 9

<220>

<223> epitope of E5

<400> 52

Thr Ala Ala Ser Ala Phe Arg Cys Phe Ile Val Tyr
1 5 10

<210> 53

<211> 11

<212> PRT

<213> Alphapapillomavirus 9

<220>

<223> potential epitope of E5

<400> 53

Leu Leu Leu Trp Ile Thr Ala Ala Ser Ala Phe
1 5 10

<210> 54

<211> 9

<212> PRT

<213> Alphapapillomavirus 9

<220>

<223> potential epitope of E5

<400> 54

Leu Leu Ala Cys Phe Leu Leu Cys Phe
1 5

<210> 55

<211> 8

<212> PRT
<213> Alphapapillomavirus 9

<220>
<223> potential epitope of E5

<400> 55
Trp Ile Thr Ala Ala Ser Ala Phe
1 5

<210> 56
<211> 8
<212> PRT
<213> Alphapapillomavirus 9

<220>
<223> potential epitope of E5

<400> 56
Leu Ile His Thr His Ala Arg Phe
1 5

<210> 57
<211> 13
<212> PRT
<213> Alphapapillomavirus 9

<220>
<223> epitope of E5

<400> 57
Leu Leu Trp Ile Thr Ala Ala Ser Ala Phe Arg Cys Phe
1 5 10

<210> 58
<211> 593
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR cassette specific for the E5 epitope

<400> 58
Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15
Gly Pro Val Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu
20 25 30
Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45
Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60
Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

Asn	Gly	Tyr	Asn	Val	Ser	Arg	Ser	Thr	Thr	Glu	Asp	Phe	Pro	Leu	Arg	85	90	95
Leu	Leu	Ser	Ala	Ala	Pro	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Ala	Ser	100	105	110
Ser	Tyr	Arg	Gln	Gln	Glu	Thr	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	Leu	115	120	125
Leu	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
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
Pro	Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	245	250	255
Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	His	Gln	Gly	Val	Leu	Ser	Ala	260	265	270
Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr	Leu	Tyr	Ala	Val	275	280	285
Leu	Val	Ser	Gly	Leu	Val	Leu	Met	Ala	Met	Val	Lys	Lys	Lys	Asn	Ser	290	295	300
Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	305	310	315
Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu	Thr	Leu	Leu	Gly	Val	Ser	Leu	Val	325	330	335
Ile	Leu	Trp	Leu	Gln	Leu	Ala	Arg	Val	Asn	Ser	Gln	Gln	Gly	Glu	Glu	340	345	350
Asp	Pro	Gln	Ala	Leu	Ser	Ile	Gln	Glu	Gly	Glu	Asn	Ala	Thr	Met	Asn	355	360	365
Cys	Ser	Tyr	Lys	Thr	Ser	Ile	Asn	Asn	Leu	Gln	Trp	Tyr	Arg	Gln	Asn	370	375	380
Ser	Gly	Arg	Gly	Leu	Val	His	Leu	Ile	Leu	Ile	Arg	Ser	Asn	Glu	Arg	385	390	395
Glu	Lys	His	Ser	Gly	Arg	Leu	Arg	Val	Thr	Leu	Asp	Thr	Ser	Lys	Lys	405	410	415
Ser	Ser	Ser	Leu	Leu	Ile	Thr	Ala	Ser	Arg	Ala	Ala	Asp	Thr	Ala	Ser	420	425	430
Tyr	Phe	Cys	Ala	Glu	Ser	Glu	Tyr	Gly	Asn	Lys	Leu	Val	Phe	Gly	Ala	435	440	445
Gly	Thr	Ile	Leu	Arg	Val	Lys	Ser	Tyr	Ile	Gln	Asn	Pro	Glu	Pro	Ala	450	455	460
Val	Tyr	Gln	Leu	Lys	Asp	Pro	Arg	Ser	Gln	Asp	Ser	Thr	Leu	Cys	Leu	465	470	475
Phe	Thr	Asp	Phe	Asp	Ser	Gln	Ile	Asn	Val	Pro	Lys	Thr	Met	Glu	Ser	485	490	495
Gly	Thr	Phe	Ile	Thr	Asp	Lys	Thr	Val	Leu	Asp	Met	Lys	Ala	Met	Asp			

			500				505				510						
Ser	Lys	Ser	Asn	Gly	Ala	Ile	Ala	Trp	Ser	Asn	Gln	Thr	Ser	Phe	Thr		
		515					520					525					
Cys	Gln	Asp	Ile	Phe	Lys	Glu	Thr	Asn	Ala	Thr	Tyr	Pro	Ser	Ser	Asp		
	530					535					540						
Val	Pro	Cys	Asp	Ala	Thr	Leu	Thr	Glu	Lys	Ser	Phe	Glu	Thr	Asp	Met		
545					550					555					560		
Asn	Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val	Met	Gly	Leu	Arg	Ile	Leu	Leu		
			565						570					575			
Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu	Met	Thr	Leu	Arg	Leu	Trp	Ser		
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Ser

<210> 59

<211> 600

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR cassette specific for the pp65 epitope

<400> 59

Met	Gly	Thr	Ser	Leu	Cys	Trp	Met	Ala	Leu	Cys	Leu	Leu	Gly	Ala			
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Asp	His	Ala	Asp	Thr	Gly	Val	Ser	Gln	Asp	Pro	Arg	His	Lys	Ile	Thr		
		20					25					30					
Lys	Arg	Gly	Gln	Asn	Val	Thr	Phe	Arg	Cys	Asp	Pro	Ile	Ser	Glu	His		
	35					40					45						
Asn	Arg	Leu	Tyr	Trp	Tyr	Arg	Gln	Thr	Leu	Gly	Gln	Gly	Pro	Glu	Phe		
	50				55				60								
Leu	Thr	Tyr	Phe	Gln	Asn	Glu	Ala	Gln	Leu	Glu	Lys	Ser	Arg	Leu	Leu		
65				70					75					80			
Ser	Asp	Arg	Phe	Ser	Ala	Glu	Arg	Pro	Lys	Gly	Ser	Phe	Ser	Thr	Leu		
			85					90					95				
Glu	Ile	Gln	Arg	Thr	Glu	Gln	Gly	Asp	Ser	Ala	Met	Tyr	Leu	Cys	Ala		
	100						105						110				
Ser	Ser	Leu	Ile	Gly	Val	Ser	Ser	Tyr	Asn	Glu	Gln	Phe	Phe	Gly	Pro		
	115					120						125					
Gly	Thr	Arg	Leu	Thr	Val	Leu	Glu	Asp	Leu	Arg	Asn	Val	Thr	Pro	Pro		
	130				135						140						
Lys	Val	Ser	Leu	Phe	Glu	Pro	Ser	Lys	Ala	Glu	Ile	Ala	Asn	Lys	Gln		
145				150					155					160			
Lys	Ala	Thr	Leu	Val	Cys	Leu	Ala	Arg	Gly	Phe	Phe	Pro	Asp	His	Val		
			165					170					175				
Glu	Leu	Ser	Trp	Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser		
	180						185						190				
Thr	Asp	Pro	Gln	Ala	Tyr	Lys	Glu	Ser	Asn	Tyr	Ser	Tyr	Cys	Leu	Ser		
	195					200						205					
Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	His	Asn	Pro	Arg	Asn	His		
	210				215						220						
Phe	Arg	Cys	Gln	Val	Gln	Phe	His	Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp		
225				230					235					240			

Pro	Glu	Gly	Ser	Pro	Lys	Pro	Val	Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala			
				245					250					255				
Trp	Gly	Arg	Ala	Asp	Cys	Gly	Ile	Thr	Ser	Ala	Ser	Tyr	His	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	Gly	Leu	Val	Leu	Met	Ala	Met	Val	Lys			
	290					295					300							
Lys	Lys	Asn	Ser	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln			
305				310					315						320			
Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu	Thr	Leu	Leu	Gly			
			325					330							335			
Val	Ser	Leu	Val	Ile	Leu	Trp	Leu	Gln	Leu	Ala	Arg	Val	Asn	Ser	Gln			
			340					345					350					
Gln	Gly	Glu	Glu	Asp	Pro	Gln	Ala	Leu	Ser	Ile	Gln	Glu	Gly	Glu	Asn			
		355					360					365						
Ala	Thr	Met	Asn	Cys	Ser	Tyr	Lys	Thr	Ser	Ile	Asn	Asn	Leu	Gln	Trp			
	370					375					380							
Tyr	Arg	Gln	Asn	Ser	Gly	Arg	Gly	Leu	Val	His	Leu	Ile	Leu	Ile	Arg			
385					390					395					400			
Ser	Asn	Glu	Arg	Glu	Lys	His	Ser	Gly	Arg	Leu	Arg	Val	Thr	Leu	Asp			
			405					410							415			
Thr	Ser	Lys	Lys	Ser	Ser	Ser	Leu	Leu	Ile	Thr	Ala	Ser	Arg	Ala	Ala			
		420						425					430					
Asp	Thr	Ala	Ser	Tyr	Phe	Cys	Ala	Thr	Val	Ile	Arg	Met	Asp	Ser	Ser			
	435					440					445							
Tyr	Lys	Leu	Ile	Phe	Gly	Ser	Gly	Thr	Arg	Leu	Leu	Val	Arg	Pro	Asp			
	450				455					460								
Ile	Gln	Asn	Pro	Glu	Pro	Ala	Val	Tyr	Gln	Leu	Lys	Asp	Pro	Arg	Ser			
465				470					475						480			
Gln	Asp	Ser	Thr	Leu	Cys	Leu	Phe	Thr	Asp	Phe	Asp	Ser	Gln	Ile	Asn			
			485					490						495				
Val	Pro	Lys	Thr	Met	Glu	Ser	Gly	Thr	Phe	Ile	Thr	Asp	Lys	Thr	Val			
		500						505					510					
Leu	Asp	Met	Lys	Ala	Met	Asp	Ser	Lys	Ser	Asn	Gly	Ala	Ile	Ala	Trp			
	515					520					525							
Ser	Asn	Gln	Thr	Ser	Phe	Thr	Cys	Gln	Asp	Ile	Phe	Lys	Glu	Thr	Asn			
	530				535					540								
Ala	Thr	Tyr	Pro	Ser	Ser	Asp	Val	Pro	Cys	Asp	Ala	Thr	Leu	Thr	Glu			
545				550					555						560			
Lys	Ser	Phe	Glu	Thr	Asp	Met	Asn	Leu	Asn	Phe	Gln	Asn	Leu	Ser	Val			
			565					570						575				
Met	Gly	Leu	Arg	Ile	Leu	Leu	Leu	Lys	Val	Ala	Gly	Phe	Asn	Leu	Leu			
		580					585						590					
Met	Thr	Leu	Arg	Leu	Trp	Ser	Ser											
	595					600												

<210> 60

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> variable region of TRA specific for E5 epitope, TRAV17

<400> 60

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agtcaacagg gagaagagga tcctcaggcc ttgagcatcc aggagggtga aaatgccacc      120
atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt      180
agaggccttg tccacctaatt ttttaatacgt tcaaatgaaa gagagaaaca cagtggaaga      240
ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg      300
gcagcagaca ctgcttctta cttctgtgcc gaatccgaat atggaaacaa actggtcttt      360
ggcgcaggaa ccattctgag agtcaagtcc tat                                     393
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<210> 61

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> variable region of TRB specific for E5 epitope, TRBV6-5

<400> 61

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gctgggtgtca ctgagacccc aaaattccag gtcctgaaga caggacagag catgacactg      120
cagtgtgccc aggatatgaa ccatgaatac atgtcctggt atcgacaaga cccaggcatg      180
gggctgaggc tgattcatta ctgagttggt gctgggtatca ctgaccaagg agaagtcccc      240
aatggctaca atgtctccag atcaaccaca gaggatttcc cgctcaggct gctgtcggct      300
gctccctccc agacatctgt gtacttctgt gccagcagtt accggcagca agagaccag      360
tacttcgggc caggcacgcg gtcctggtg ctc                                     393
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<210> 62

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> variable region of TRA specific for pp65 epitope, TRAV17

<400> 62

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atggaaactc tcctgggagt gtcattggtg attctatggc ttcaactggc tagggtgaac      60
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 atgaactgca gttacaaaac tagtataaac aatttacagt ggtatagaca aaattcaggt 180
 agaggccttg tccacctaatt tttataacgt tcaaataaaa gagagaaaca cagtgggaaga 240
 ttaagagtca cgcttgacac ttccaagaaa agcagttcct tgttgatcac ggcttcccgg 300
 gcagcagaca ctgcttctta cttctgtgct acggttatcc ggatggatag cagctataaa 360
 ttgatcttcg ggagtgggac cagactgctg gtcaggcctg at 402

<210> 63

<211> 405

<212> PRT

<213> Artificial Sequence

<220>

<223> variable region of TRB specific for pp65 epitope, TRBV7-9

<400> 63

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Gly	Ala	Thr	Cys	Ala	Cys	Gly	Cys	Ala	Gly	Ala	Thr	Ala	Cys	Thr	Gly	
			50					55				60				
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65						70				75					80	
Cys	Ala	Gly	Ala	Cys	Ala	Cys	Ala	Ala	Gly	Ala	Thr	Cys	Ala	Cys	Ala	
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Thr	Ala	Ala	Cys	Thr	Thr	Thr	Cys	Ala	Gly	Gly	Thr	Gly	Thr	Gly	Ala	
			115					120				125				
Thr	Cys	Cys	Ala	Ala	Thr	Thr	Cys	Thr	Gly	Ala	Ala	Cys	Ala	Cys		
			130				135			140						
Ala	Ala	Cys	Cys	Gly	Cys	Cys	Thr	Thr	Thr	Ala	Thr	Thr	Gly	Gly	Thr	
145						150				155					160	
Ala	Cys	Cys	Gly	Ala	Cys	Ala	Gly	Ala	Cys	Cys	Cys	Thr	Gly	Gly	Gly	
			165					170					175			
Gly	Cys	Ala	Gly	Gly	Gly	Cys	Cys	Cys	Ala	Gly	Ala	Gly	Thr	Thr	Thr	
			180					185					190			
Cys	Thr	Gly	Ala	Cys	Thr	Thr	Ala	Cys	Thr	Thr	Cys	Cys	Ala	Gly	Ala	
			195				200					205				
Ala	Thr	Gly	Ala	Ala	Gly	Cys	Thr	Cys	Ala	Ala	Cys	Thr	Ala	Gly	Ala	
			210			215					220					
Ala	Ala	Ala	Ala	Thr	Cys	Ala	Ala	Gly	Gly	Cys	Thr	Gly	Cys	Thr	Cys	
225					230					235					240	
Ala	Gly	Thr	Gly	Ala	Thr	Cys	Gly	Gly	Thr	Cys	Thr	Cys	Thr	Gly		

				245					250					255			
Cys	Ala	Gly	Ala	Gly	Ala	Gly	Gly	Cys	Cys	Thr	Ala	Ala	Gly	Gly	Gly		
			260					265					270				
Ala	Thr	Cys	Thr	Thr	Thr	Cys	Thr	Cys	Cys	Ala	Cys	Cys	Thr	Thr	Gly		
		275					280					285					
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Ala	Gly	Cys	Ala	Gly	Gly	Gly	Gly	Ala	Cys	Thr	Cys	Gly	Gly	Cys			
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Cys	Ala	Thr	Gly	Thr	Ala	Thr	Cys	Thr	Cys	Thr	Gly	Thr	Gly	Cys	Cys		
			325					330				335					
Ala	Gly	Cys	Ala	Gly	Cys	Thr	Thr	Ala	Ala	Thr	Ala	Gly	Gly	Gly	Gly		
		340					345					350					
Thr	Cys	Ala	Gly	Cys	Thr	Cys	Cys	Thr	Ala	Cys	Ala	Ala	Thr	Gly	Ala		
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<223> CDR1 of TRA specific for E5 epitope

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Thr Ser Ile Asn Asn

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5

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<212> PRT

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5

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<223> CDR2 of TRB specific for pp65 epitope

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Phe Gln Asn Glu Ala Gln

1

5