

LISTA DE SECUENCIAS

<110> Universitätsklinikum Hamburg-Eppendorf (UKE)

<120> Nucleasa efectora TAL para la inactivación específica del correceptor
del vih CCR5

<130> PAT 1473 PCT

<150> DE102014106327.9

<151> 2014-05-07

<160> 18

<170> BiSSAP 1.3

<210> 1

<211> 19

<212> ADN

<213> Homo sapiens

<400> 1

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<210> 2

<211> 19

<212> ADN

<213> Homo sapiens

<400> 2

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<210> 3

<211> 1071

<212> PRT

<213> Secuencia artificial

<220>

<223> CCR5-Uco-L

<400> 3

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Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
          20           25           30
Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr
          35           40           45
Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
          50           55           60
Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His
65           70           75           80
Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val
          85           90           95
Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala
          100          105          110
Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala
          115          120          125
Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp
          130          135          140
Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val
145          150          155          160
Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn
          165          170          175
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn His Gly Gly Lys
          180          185          190
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
          195          200          205
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
          210          215          220
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
225          230          235          240
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
          245          250          255
Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
          260          265          270
Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala

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275	280	285
Ser Asn His Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
290	295	300
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala		
305	310	315
Ile Ala Ser Asn His Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
325	330	335
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val		
340	345	350
Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val		
355	360	365
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu		
370	375	380
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
385	390	395
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
405	410	415
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala		
420	425	430
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
435	440	445
Leu Thr Pro Glu Gln Val Val Ala Ile Val Ser Asn Gly Gly Gly Lys		
450	455	460
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
465	470	475
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly		
485	490	495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
500	505	510
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His		
515	520	525
Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
530	535	540
Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
545	550	555
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
565	570	575
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala		
580	585	590

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
 595 600 605
 Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
 610 615 620
 Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
 625 630 635 640
 Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
 645 650 655
 Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu
 660 665 670
 Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
 675 680 685
 Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala
 690 695 700
 Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
 705 710 715 720
 Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
 725 730 735
 Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
 740 745 750
 His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly
 755 760 765
 Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
 770 775 780
 Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
 785 790 795 800
 Asn Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg
 805 810 815
 Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu
 820 825 830
 Ala Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu
 835 840 845
 Pro His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu
 850 855 860
 Arg Thr Ser His Arg Val Ala Gly Ser Gln Leu Val Lys Ser Glu Leu
 865 870 875 880
 Glu Glu Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr Val Pro His
 885 890 895
 Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr Gln Asp Arg

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900	905	910
Ile Leu Glu Met Lys Val Met Glu Phe Phe Met Lys Val Tyr Gly Tyr		
915	920	925
Arg Gly Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Ile Tyr		
930	935	940
Thr Val Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp Thr Lys Ala		
945	950	955
Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp Glu Met Gln		
965	970	975
Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile Asn Pro Asn		
980	985	990
Glu Trp Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe Lys Phe Leu		
995	1000	1005
Phe Val Ser Gly His Phe Lys Gly Asn Tyr Lys Ala Gln Leu Thr Arg		
1010	1015	1020
Leu Asn His Ile Thr Asn Cys Asn Gly Ala Val Leu Ser Val Glu Glu		
1025	1030	1035
Leu Leu Ile Gly Gly Glu Met Ile Lys Ala Gly Thr Leu Thr Leu Glu		
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Glu Val Arg Arg Lys Phe Asn Asn Gly Glu Ile Asn Phe Arg Ser		
1060	1065	1070

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<212> PRT

<213> Secuencia artificial

<220>

<223> CCR5-Uco-R

<400> 4

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
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Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
20 25 30
Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr
35 40 45
Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
50 55 60

Ala	Gln	His	His	Glu	Ala	Leu	Val	Gly	His	Gly	Phe	Thr	His	Ala	His
65					70					75					80
Ile	Val	Ala	Leu	Ser	Gln	His	Pro	Ala	Ala	Leu	Gly	Thr	Val	Ala	Val
				85						90					95
Lys	Tyr	Gln	Asp	Met	Ile	Ala	Ala	Leu	Pro	Glu	Ala	Thr	His	Glu	Ala
			100						105					110	
Ile	Val	Gly	Val	Gly	Lys	Gln	Trp	Ser	Gly	Ala	Arg	Ala	Leu	Glu	Ala
		115					120					125			
Leu	Leu	Thr	Val	Ala	Gly	Glu	Leu	Arg	Gly	Pro	Pro	Leu	Gln	Leu	Asp
		130					135				140				
Thr	Gly	Gln	Leu	Leu	Lys	Ile	Ala	Lys	Arg	Gly	Gly	Val	Thr	Ala	Val
145						150				155					160
Glu	Ala	Val	His	Ala	Trp	Arg	Asn	Ala	Leu	Thr	Gly	Ala	Pro	Leu	Asn
				165					170						175
Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys
			180						185					190	
Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala
		195						200				205			
His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly
		210					215				220				
Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys
225						230				235					240
Gln	Ala	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn
				245					250					255	
Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val
			260						265					270	
Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala
		275						280					285		
Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu
		290					295					300			
Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala
305					310					315					320
Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg
				325					330					335	
Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Glu	Gln	Val
			340						345				350		
Val	Ala	Ile	Ala	Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val
		355						360					365		
Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Glu

370	375	380
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
385	390	395
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
405	410	415
Pro Glu Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala		
420	425	430
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
435	440	445
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn His Gly Gly Lys		
450	455	460
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
465	470	475
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly		
485	490	495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
500	505	510
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His		
515	520	525
Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
530	535	540
Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
545	550	555
Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
565	570	575
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala		
580	585	590
Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
595	600	605
Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val		
610	615	620
Val Ala Ile Ala Ser Asn His Gly Gly Lys Gln Ala Leu Glu Thr Val		
625	630	635
Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu		
645	650	655
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
660	665	670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
675	680	685

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala
 690 695 700
 Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
 705 710 715 720
 Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
 725 730 735
 Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
 740 745 750
 His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly
 755 760 765
 Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
 770 775 780
 Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn
 785 790 795 800
 Gly Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg
 805 810 815
 Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu
 820 825 830
 Ala Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu
 835 840 845
 Pro His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu
 850 855 860
 Arg Thr Ser His Arg Val Ala Gly Ser Gln Leu Val Lys Ser Glu Leu
 865 870 875 880
 Glu Glu Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr Val Pro His
 885 890 895
 Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr Gln Asp Arg
 900 905 910
 Ile Leu Glu Met Lys Val Met Glu Phe Phe Met Lys Val Tyr Gly Tyr
 915 920 925
 Arg Gly Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Ile Tyr
 930 935 940
 Thr Val Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp Thr Lys Ala
 945 950 955 960
 Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp Glu Met Gln
 965 970 975
 Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile Asn Pro Asn
 980 985 990
 Glu Trp Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe Lys Phe Leu

- 9 -

995	1000	1005
Phe Val Ser Gly His Phe Lys Gly Asn Tyr Lys Ala Gln Leu Thr Arg		
1010	1015	1020
Leu Asn His Ile Thr Asn Cys Asn Gly Ala Val Leu Ser Val Glu Glu		
1025	1030	1035
Leu Leu Ile Gly Gly Glu Met Ile Lys Ala Gly Thr Leu Thr Leu Glu		
	1045	1050
Glu Val Arg Arg Lys Phe Asn Asn Gly Glu Ile Asn Phe Arg Ser		1055
	1060	1065
		1070

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<212> PRT

<213> Secuencia artificial

<220>

<223> Repetición de TALEN

<220>

<221> SITIO

<222> 4

<223> Xaa = cualquier aminoácido o E, Q, D o A

<220>

<221> SITIO

<222> 10

<223> Xaa = cualquier aminoácido o A o V

<220>

<221> SITIO

<222> 12..13

<223> Par de aminoácidos variable de la repetición (RVD)

<220>

<221> SITIO

<222> 32

<223> Xaa = cualquier aminoácido o A o D

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Leu Thr Pro Xaa Gln Val Val Ala Ile Xaa Ser Xaa Xaa Gly Gly Lys
 1 5 10 15
 Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Xaa
 20 25 30
 His Gly

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<220>
 <221> SITIO
 <222> 12..13
 <223> Par de aminoácidos variable de la repetición (RVD)

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 Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys
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 Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
 20 25 30
 His Gly

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 <223> Repetición de TALEN

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 <221> SITIO
 <222> 12..13

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Leu	Thr	Pro	Gln	Gln	Val	Val	Ala	Ile	Ala	Ser	Xaa	Xaa	Gly	Gly	Lys
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Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala
			20					25					30		
His	Gly														

<210> 8

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<223> Repetición de TALEN

<220>

<221> SITIO

<222> 12..13

<223> Par de aminoácidos variable de la repetición (RVD)

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Leu	Thr	Pro	Asp	Gln	Val	Val	Ala	Ile	Ala	Ser	Xaa	Xaa	Gly	Gly	Lys
1				5					10					15	
Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp
			20					25					30		
His	Gly														

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<223> Repetición de TALEN

- 12 -

<220>

<221> SITIO

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<223> Par de aminoácidos variable de la repetición (RVD)

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Leu	Thr	Pro	Ala	Gln	Val	Val	Ala	Ile	Ala	Ser	Xaa	Xaa	Gly	Gly	Lys
1				5				10						15	
Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp
			20				25						30		
His	Gly														

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<223> Repetición de TALEN

<220>

<221> SITIO

<222> 12..13

<223> Par de aminoácidos variable de la repetición (RVD)

<400> 10

Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Val	Ser	Xaa	Xaa	Gly	Gly	Lys
1				5				10						15	
Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala
			20				25						30		
His	Gly														

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<211> 1059

<212> ADN

<213> Homo sapiens

<220>

<223> ADN de hCCR5

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ttcatctttg gttttgtggg caacatgctg gtcactctca tcctgataaa ctgcaaaagg	180
ctgaagagca tgactgacat ctacctgctc aacctggcca tctctgacct gtttttcctt	240
cttactgtcc ctttctgggc tcactatgct gccgccagc gggactttgg aaatacaatg	300
tgtcaactct tgacagggct ctattttata ggcttcttct ctggaatctt cttcatcatc	360
ctcctgacaa tcgataggta cctggctgct gtccatgctg tgtttgcttt aaaagccagg	420
acggtcacct ttgggggtgg gacaagtgtg atcacttggg tgggtggctgt gtttgcgtct	480
ctcccaggaa tcacttttac cagatctcaa aaagaaggc ttcattacac ctgcagctct	540
cattttccat acagtcagta tcaattctgg aagaatttcc agacattaaa gatagtcac	600
ttggggctgg tcctgccgct gcttgtcatg gtcactctgct actcgggaat cctaaaaact	660
ctgcttcggt gtcgaaatga gaagaagagg cacagggctg tgaggcttat cttcaccatc	720
atgattgttt attttctctt ctgggctccc tacaacattg tccttctcct gaacaccttc	780
caggaattct ttggcctgaa taattgcagt agctctaaca ggttggaaca agctatgcag	840
gtgacagaga ctcttgggat gacgcactgc tgcacaaacc ccatcatcta tgcctttgtc	900
ggggagaagt tcagaaacta cctcttagtc ttcttccaaa agcacattgc caaacgcttc	960
tgcaaatgct gttctatttt ccagcaagag gctcccagc gagcaagctc agtttacacc	1020
cgatccactg gggagcagga aatatctgtg ggcttgtga	1059

<210> 12

<211> 198

<212> PRT

<213> Planomicrobium okeanokoites

<220>

<223> Dominio de escisión de FokI

<400> 12

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

<210> 13

- 15 -

<211> 1037

<212> PRT

<213> Secuencia artificial

<220>

<223> CCR5-Mco-L

<400> 13

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

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245																250																255															
Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val																																
260																265																270															
Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala																																
275																280																285															
Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu																																
290																295																300															
Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala																																
305																310																315															
Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg																																
325																330																335															
Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Glu	Gln	Val																																
340																345																350															
Val	Ala	Ile	Ala	Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val																																
355																360																365															
Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr	Pro	Glu																																
370																375																380															
Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala	Leu	Glu																																
385																390																395															
Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly	Leu	Thr																																
405																410																415															
Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly	Gly	Lys	Gln	Ala																																
420																425																430															
Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala	His	Gly																																
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Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	His	Asp	Gly	Gly	Lys																																
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Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys	Gln	Ala																																
465																470																475															
His	Gly	Leu	Thr	Pro	Glu	Gln	Val	Val	Ala	Ile	Ala	Ser	Asn	Ile	Gly																																
485																490																495															
Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val	Leu	Cys																																
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Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu	Pro	Val																																
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560																565																570															

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 565 570 575
 Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala
 580 585 590
 Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
 595 600 605
 Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val
 610 615 620
 Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
 625 630 635 640
 Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu
 645 650 655
 Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
 660 665 670
 Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr
 675 680 685
 Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
 690 695 700
 Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
 705 710 715 720
 Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
 725 730 735
 Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
 740 745 750
 His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly
 755 760 765
 Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp
 770 775 780
 Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys
 785 790 795 800
 Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His
 805 810 815
 Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr
 820 825 830
 Ser His Arg Val Ala Gly Ser Gln Leu Val Lys Ser Glu Leu Glu Glu
 835 840 845
 Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr Val Pro His Glu Tyr
 850 855 860
 Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr Gln Asp Arg Ile Leu

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865 870 875 880
 Glu Met Lys Val Met Glu Phe Phe Met Lys Val Tyr Gly Tyr Arg Gly
 885 890 895
 Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Ile Tyr Thr Val
 900 905 910
 Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp Thr Lys Ala Tyr Ser
 915 920 925
 Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp Glu Met Gln Arg Tyr
 930 935 940
 Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile Asn Pro Asn Glu Trp
 945 950 955 960
 Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe Lys Phe Leu Phe Val
 965 970 975
 Ser Gly His Phe Lys Gly Asn Tyr Lys Ala Gln Leu Thr Arg Leu Asn
 980 985 990
 His Ile Thr Asn Cys Asn Gly Ala Val Leu Ser Val Glu Glu Leu Leu
 995 1000 1005
 Ile Gly Gly Glu Met Ile Lys Ala Gly Thr Leu Thr Leu Glu Glu Val
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 Arg Arg Lys Phe Asn Asn Gly Glu Ile Asn Phe Arg Ser
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<211> 1037

<212> PRT

<213> Secuencia artificial

<220>

<223> CCR5-Mco-R

<400> 14

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 Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr
 35 40 45
 Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val
 50 55 60

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

370	375	380
Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu		
385	390	395
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
405	410	415
Pro Glu Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala		
420	425	430
Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly		
435	440	445
Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys		
450	455	460
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala		
465	470	475
His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly		
485	490	495
Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys		
500	505	510
Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn		
515	520	525
Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val		
530	535	540
Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala		
545	550	555
Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu		
565	570	575
Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala		
580	585	590
Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg		
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Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val		
610	615	620
Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val		
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Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu		
645	650	655
Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu		
660	665	670
Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr		
675	680	685

Pro Glu Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
 690 695 700
 Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly
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 Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys
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 Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala
 740 745 750
 His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Asn Gly Gly
 755 760 765
 Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu Ser Arg Pro Asp
 770 775 780
 Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val Ala Leu Ala Cys
 785 790 795 800
 Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys Gly Leu Pro His
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 Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile Pro Glu Arg Thr
 820 825 830
 Ser His Arg Val Ala Gly Ser Gln Leu Val Lys Ser Glu Leu Glu Glu
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 Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr Val Pro His Glu Tyr
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 Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr Gln Asp Arg Ile Leu
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 Glu Met Lys Val Met Glu Phe Phe Met Lys Val Tyr Gly Tyr Arg Gly
 885 890 895
 Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Ile Tyr Thr Val
 900 905 910
 Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp Thr Lys Ala Tyr Ser
 915 920 925
 Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp Glu Met Gln Arg Tyr
 930 935 940
 Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile Asn Pro Asn Glu Trp
 945 950 955 960
 Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe Lys Phe Leu Phe Val
 965 970 975
 Ser Gly His Phe Lys Gly Asn Tyr Lys Ala Gln Leu Thr Arg Leu Asn
 980 985 990
 His Ile Thr Asn Cys Asn Gly Ala Val Leu Ser Val Glu Glu Leu Leu

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Ile	Gly	Gly	Glu	Met	Ile	Lys	Ala	Gly	Thr	Leu	Thr	Leu	Glu	Glu	Val
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<212> ADN

<213> Homo sapiens

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18

<210> 16

<211> 18

<212> PRT

<213> Homo sapiens

<400> 16

Cys	Thr	Thr	Cys	Ala	Gly	Cys	Cys	Thr	Thr	Thr	Thr	Gly	Cys	Ala	Gly
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<211> 3788

<212> ARN

<213> Secuencia artificial

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<223> ARNm de CCR5-Uco-L

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120

ccagcagccg uagauuugag aacuuuggga uauucacagc agcagcagga aaagaucaag	180
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<211> 3788

<212> ARN

<213> Secuencia artificial

<220>

<223> ARNm de CCR5-Uco-R

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ugugccu <u>ucu</u>	aguugccagc	caucugu <u>ugu</u>	uugcc <u>cc</u> ucc	cccgu <u>g</u> ccu	ccuugac <u>ccu</u>	3300
ggaaggugcc	acuccc <u>acu</u> g	uccuuu <u>cc</u> ua	au <u>aaaa</u> ugag	gaaauug <u>cau</u>	cacaacacuc	3360
aacc <u>cu</u> aucu	cgguc <u>u</u> auuc	uuuugauuu <u>a</u>	uaagggauuu	ugccg <u>auu</u> uc	ggccuauugg	3420
uu <u>aaaaaa</u> aug	agcugauuu <u>a</u>	ac <u>aaaaaa</u> uuu	aacgcga <u>uu</u>	aa <u>u</u> ucugugg	aauguguguc	3480
agu <u>u</u> agggug	uggaaagucc	ccaggc <u>ucc</u>	cagcaggcag	aaguaug <u>caa</u>	agcaugcau <u>c</u>	3540
uca <u>uu</u> aguc	agcaaccagg	uguggaa <u>agu</u>	ccccaggc <u>uc</u>	cccagcaggc	agaaguaugc	3600
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ccc <u>u</u> aacucc	gcc <u>ca</u> guucc	gcc <u>ca</u> uucuc	cgcc <u>cc</u> augg	cugacua <u>uu</u>	uuuuuu <u>uuu</u>	3720
augcagaggc	cgaggcc <u>gcc</u>	ucugcc <u>c</u> ug	agcuauu <u>cca</u>	gaaguag <u>uga</u>	ggaggcuuuu	3780
uuggaggc						3788