

LISTADO DE SECUENCIAS

<110> KITE PHARMA, INC.
 Bedoya, Felipe

<120> GENERACIÓN ALTEARNATIVA DE CÉLULAS T HUMANAS ALOGENEICAS

<130> 125400-1426

<140> 17/940,186
 <141> 2022-09-08

<150> 63/242,909
 <151> 2021-09-10

<160> 91

<170> PatentIn versión 3.5

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 <223> 4-1BB secuencia de ácido nucleico del dominio coestimulador

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<223> CD28 secuencia de ácido nucleico del dominio coestimulador

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<223> CD28(YMFM) secuencia de ácido nucleico del dominio coestimulador

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Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Phe Met Thr
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Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
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Pro Arg Asp Phe Ala Ala Tyr Arg Ser
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Val Thr Leu
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20 25 30

Gln Ile Pro Ala Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro
35 40 45

Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro
50 55 60

Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala
65 70 75 80

Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg
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Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu
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catcgtcccc cgcctcctgg acaccgtgtt cagcaccagc ctcagaagag gcctcctgct 240
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Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser Pro
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<223> OX40 secuencia de ácido nucleico del dominio coestimulador

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Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
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Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
 20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
 35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
 50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
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Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
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cgggaccctg agatgggggg aaagccgaga aggaagaacc ctgaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcgagggcc tacagtgaga ttgggatgaa aggcgagcgc 240

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			20					25					30		
Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys
		35					40					45			
Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys
	50					55					60				
Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg
65					70					75					80
Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala
				85					90					95	
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gaactgcaga	aagataagat	ggcggaggcc	tacagtgaga	ttgggatgaa	aggcgagcgc	240
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Ser Leu Val Ile Thr Leu Tyr Cys
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 <223> Secuencia de aminoácidos del dominio bisagra CD8 alfa (CD8a)

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Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
 1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
 20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
 35 40 45

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 gacttcgcct gtgat 135

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Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
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 Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
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<223> Bisagra/enlazador

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Gly Gly Ser Gly Gly
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Cys Pro Pro Cys
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<223> Región de bisagra Ig

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Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys
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Ser Pro Asn Met Val Pro His Ala His His Ala Gln
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<400> 51

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Gly Cys Gly Gly Thr Gly Gly Thr Gly Gly Gly Thr Cys Gly Gly Gly
 20 25 30

Thr Gly Gly Cys Gly Gly Cys Gly Gly Ala Thr Cys Thr
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 <223> CD3epsilon

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 secuencia de ácido nucleico

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accgcctaca tgcagctgaa cagcctgacc agcgaggaca gcgccgtgta cttctgcaag	360
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gaggacctgg ccgtgtatta ctgccagaac gactacagct accccctgac cttcggagcc	780
ggcaccaagc tggaactgaa gtccggaacc acgacgccag cgccgcgacc accaacaccg	840
gcgcccacca tcgcgtcgca gccctgtcc ctgcgccag aggcgtgccg gccagcggcg	900
gggggcgcag tgcacacgag ggggctggac ttcgcctgtg atatctacat ctgggcgccc	960
ttggccggga cttgtggggt ctttctcctg tcaactggta tcacccttta ctgcacaaaa	1020
agaaaaaac agaggagtcg gagaaatgat gaggagctgg agacaagagc ccacagagta	1080
gctactgaag aaaggggccg gaagccccac caaattccag cttcaacccc tcagaatcca	1140
gcaacttccc aacatcctcc tccaccacct ggtcatcgtt ccaggcacc tagtcatcgt	1200
ccccgcctc ctggacaccg tgttcagcac cagcctcaga agaggcctcc tgctccgtcg	1260
ggcacacaag ttcaccagca gaaaggcccg cccctcccca gacctcgagt tcagccaaaa	1320
cctccccatg gggcagcaga aaactcattg tccccttcct ctaatatcga tagagtgaag	1380
ttcagcagga gcgcagacgc cccgcgtac aagcagggcc agaaccagct ctataacgag	1440
ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct	1500
gagatggggg gaaagccgag aaggaagaac cctcaggaag gcctgtacaa tgaactgcag	1560
aaagataaga tggcggaggc ctacagtgag attgggatga aaggcgagcg ccggaggggc	1620
aaggggcacg atggccttta ccagggtctc agtacagcca ccaaggacac ctacgacgcc	1680
cttcacatgc aggcctgcc ccctcgc	1707

<210> 70
 <211> 569
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Tn-MUC1 CAR
 secuencia de aminoácidos

<400> 70

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

Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu
 245 250 255
 Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Ser Gly Thr Thr Thr
 260 265 270
 Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
 275 280 285
 Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
 290 295 300
 His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
 305 310 315 320
 Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
 325 330 335
 Tyr Cys Thr Lys Arg Lys Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu
 340 345 350
 Leu Glu Thr Arg Ala His Arg Val Ala Thr Glu Glu Arg Gly Arg Lys
 355 360 365
 Pro His Gln Ile Pro Ala Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln
 370 375 380
 His Pro Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg
 385 390 395 400
 Pro Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro
 405 410 415
 Pro Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu
 420 425 430
 Pro Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn
 435 440 445
 Ser Leu Ser Pro Ser Ser Asn Ile Asp Arg Val Lys Phe Ser Arg Ser
 450 455 460
 Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu
 465 470 475 480
 Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
 485 490 495
 Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
 500 505 510
 Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
 515 520 525
 Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
 530 535 540

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
 545 550 555 560

Leu His Met Gln Ala Leu Pro Pro Arg
 565

<210> 71
 <211> 485
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Mesotelina CAR
 secuencia de aminoácidos (M5)

<400> 71

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
 20 25 30

Glu Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

Thr Phe Thr Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
 50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
 65 70 75 80

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
 85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr
 100 105 110

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

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met
 145 150 155 160

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
 165 170 175

Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Tyr Tyr Leu Ser Trp Tyr
 180 185 190

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Thr Ala Ser
 195 200 205

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Ile Leu Gln Asn Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
 210                               215                     220

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
225                               230                     235                     240

Thr Tyr Tyr Cys Leu Gln Thr Tyr Thr Thr Pro Asp Phe Gly Pro Gly
                               245                     250                     255

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
                               260                     265                     270

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
 275                               280                     285

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
 290                               295                     300

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
305                               310                     315                     320

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

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
 340                               345                     350

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu
 355                               360                     365

Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
 370                               375                     380

Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                               390                     395                     400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
 405                               410                     415

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
 420                               425                     430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
 435                               440                     445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
 450                               455                     460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
465                               470                     475                     480

Ala Leu Pro Pro Arg
                               485

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<210> 72
<211> 485
<212> PRT

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<213> Secuencia Artificial

<220>

<223> Mesotelina CAR

secuencia de aminoácidos (M11)

<400> 72

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val
20 25 30

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
35 40 45

Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
50 55 60

Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn
65 70 75 80

Tyr Ala Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
85 90 95

Ile Ser Thr Ala Tyr Met Glu Leu Arg Arg Leu Arg Ser Asp Asp Thr
100 105 110

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

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Arg Met
145 150 155 160

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
165 170 175

Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Tyr Tyr Leu Ser Trp Tyr
180 185 190

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Thr Ala Ser
195 200 205

Ile Leu Gln Asn Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
210 215 220

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
225 230 235 240

Thr Tyr Tyr Cys Leu Gln Thr Tyr Thr Thr Pro Asp Phe Gly Pro Gly
245 250 255

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
260 265 270

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

<210> 73
 <211> 237
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Dominio de unión específico de PSMA humanizado
 secuencia de aminoácidos

<400> 73

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

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

<210> 74

<211> 711

<212> ADN

<213> Secuencia Artificial

<220>

<223> Dominio de unión específico de PSMA humanizado
 secuencia de ácido nucleico

<400> 74

gagggtccagc tgggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata cacattcact gaatacacca tccactgggt gaggcaggcc 120

cctggaaagg gccttgagtg gattggaaac attaataccta acaatggtgg tactacctac 180

aaccagaagt tcgaggacag agtcacaatc actgtagaca agtccaccag cacagcctac 240
atggagctca gcagcctgag atctgaggat actgcagtct attactgtgc agctgggttg 300
aactttgact actggggcca aggcaccacg gtcaccgtct cctcaggagg cggaggatct 360
ggcggcggag gaagttctgg cggaggcagc gacattcaga tgaccagtc tcccagcacc 420
ctgtccgcat cagtaggaga cagggtcacc atcacttgca aggccagtca ggatgtgggt 480
actgctgtag actggtatca acagaaacca gggcaagctc ctaaactact gatttactgg 540
gcatccaccc ggcacactgg agtccctgat cgcttcagcg gcagtggatc tgggacagat 600
ttcactctca ccatcagcag actgcagcct gaagactttg cagtttatta ctgtcagcaa 660
tataacagct atcctctcac gttcggccag gggaccaagg tggatatcaa a 711

<210> 75
<211> 241
<212> PRT
<213> Secuencia Artificial

<220>
<223> Dominio de unión específico de Mesotelina
secuencia de aminoácidos

<400> 75

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

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145 150 155 160

Ser Gln Ser Ile Arg Tyr Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Leu Leu Ile Tyr Thr Ala Ser Ile Leu Gln Asn Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu
210 215 220

Gln Thr Tyr Thr Thr Pro Asp Phe Gly Pro Gly Thr Lys Val Glu Ile
225 230 235 240

Lys

<210> 76

<211> 201

<212> PRT

<213> Secuencia Artificial

<220>

<223> Receptor negativo dominante TGFPRII

secuencia de aminoácidos
(TGFbRII-DN)

<400> 76

Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu
1 5 10 15

Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val
20 25 30

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
35 40 45

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
50 55 60

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
65 70 75 80

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
85 90 95

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
100 105 110

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
115 120 125

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
 130 135 140

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu
 145 150 155 160

Leu Leu Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu
 165 170 175

Gly Val Ala Ile Ser Val Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn
 180 185 190

Arg Gln Gln Lys Leu Ser Ser Ser Gly
 195 200

<210> 77
 <211> 603
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Receptor negativo dominante TGFPRII

secuencia de ácido nucleico
 (TGFbRII-DN)

<400> 77
 atgggtcggg ggctgctcag gggcctgtgg ccgctgcaca tcgtcctgtg gacgcgtatc 60
 gccagcacga tcccaccgca cgttcagaag tcggttaata acgacatgat agtcactgac 120
 aacaacggtg cagtcaagtt tccacaactg tgtaaat ttt gtgatgtgag attttccacc 180
 tgtgacaacc agaaatcctg catgagcaac tgcagcatca cctccatctg tgagaagcca 240
 caggaagtct gtgtggctgt atggagaaaag aatgacgaga acataacact agagacagtt 300
 tgccatgacc ccaagctccc ctaccatgac tttattctg agatgctgc ttctccaaag 360
 tgcattatga aggaaaaaaaa aaagcctggt gagactttct tcatgtgttc ctgtagctct 420
 gatgagtgc atgacaacat catcttctca gaagaatata acaccagcaa tcctgacttg 480
 ttgctagtca tatttcaagt gacaggcatc agcctcctgc caccactggg agttgccata 540
 tctgtcatca tcatcttcta ctgctaccgc gtaaccggc agcagaagct gagttcatcc 600
 gga 603

<210> 78
 <211> 238
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> PD1-CTM-CD28 receptor secuencia de aminoácidos

<400> 78

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Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1          5          10          15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
          20          25          30

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

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
          50          55          60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65          70          75          80

Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
          85          90          95

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
          100          105          110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
          115          120          125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
          130          135          140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145          150          155          160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Phe Trp Val Leu Val Val
          165          170          175

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
          180          185          190

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
          195          200          205

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
          210          215          220

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
225          230          235

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<210> 79

<211> 714

<212> ADN

<213> Secuencia Artificial

<220>

<223> PD1-CTM-CD28 receptor secuencia de ácido nucleico

<400> 79

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atgcagatcc cacaggcgcc ctggccagtc gtctgggcgg tgctacaact gggctggcgg      60
ccaggatggt tcttagactc cccagacagg ccctggaacc cccccacctt ctccccagcc      120
ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg      180
gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc      240
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg      300
cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc      360
tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca      420
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcaccc      480
aggccagccg gccagttcca aaccctggtg ttttgggtgc tgggtggtgg tgggtggagtc      540
ctggcttgct atagcttgct agtaacagtg gcctttatta ttttctgggt gaggagtaag      600
aggagcaggc tcctgcacag tgactacatg aacatgactc cccgccgccc cgggcccacc      660
cgcaagcatt accagcccta tgccccacca cgcgacttcg cagcctatcg ctcc          714

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<210> 80
 <211> 232
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> PD1-PTM-CD28 receptor secuencia de aminoácidos
 <400> 80

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Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1              5              10              15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
                20              25              30

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

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
          50              55              60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65              70              75              80

Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
          85              90              95

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
          100             105             110

Ala Arg Arg Asn Asp Ser Gly Thr Val Leu Cys Gly Ala Ile Ser Leu
          115             120             125

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Ala Pro Lys Leu Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
 130 135 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
 145 150 155 160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly
 165 170 175

Leu Leu Gly Ser Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Arg
 180 185 190

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
 195 200 205

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
 210 215 220

Arg Asp Phe Ala Ala Val Arg Ser
 225 230

<210> 81
 <211> 696
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> PD1-PTM-CD28 receptor secuencia de ácido nucleico

<400> 81
 atgcagatcc cacaggcgcc ctggccagtc gtctgggcgg tgctacaact gggctggcgg 60
 ccaggatggt tcttagactc ccagacagc ccttggaacc ccccccactt ctccccagcc 120
 ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg 180
 gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc 240
 gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg 300
 cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc 360
 tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca 420
 gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcacc 480
 aggccagccg gccagttcca aaccctggtg gttggtgtcg tgggcggcct gctgggcagc 540
 ctggtgctgc tagtctgggt cctggccgtc atcaggagta agaggagcag gctcctgcac 600
 agtgactaca tgaacatgac tccccgccgc ccggggccca cccgcaagca ttaccagccc 660
 tatgccccac cagcgcactt cgcagcctat cgctcc 696

<210> 82
 <211> 232

<212> PRT

<213> Secuencia Artificial

<220>

<223> PD1A132L_PTM-CD28 receptor
secuencia de aminoácidos

<400> 82

Met	Gln	Ile	Pro	Gln	Ala	Pro	Trp	Pro	Val	Val	Trp	Ala	Val	Leu	Gln
1				5					10					15	

Leu	Gly	Trp	Arg	Pro	Gly	Trp	Phe	Leu	Asp	Ser	Pro	Asp	Arg	Pro	Trp
			20					25					30		

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

Asn	Ala	Thr	Phe	Thr	Cys	Ser	Phe	Ser	Asn	Thr	Ser	Glu	Ser	Phe	Val
	50					55					60				

Leu	Asn	Trp	Tyr	Arg	Met	Ser	Pro	Ser	Asn	Gln	Thr	Asp	Lys	Leu	Ala
65					70					75					80

Ala	Phe	Pro	Glu	Asp	Arg	Ser	Gln	Pro	Gly	Gln	Asp	Cys	Arg	Phe	Arg
				85					90					95	

Val	Thr	Gln	Leu	Pro	Asn	Gly	Arg	Asp	Phe	His	Met	Ser	Val	Val	Arg
			100					105					110		

Ala	Arg	Arg	Asn	Asp	Ser	Gly	Thr	Val	Leu	Cys	Gly	Ala	Ile	Ser	Leu
			115				120					125			

Ala	Pro	Lys	Leu	Gln	Ile	Lys	Glu	Ser	Leu	Arg	Ala	Glu	Leu	Arg	Val
	130					135					140				

Thr	Glu	Arg	Arg	Ala	Glu	Val	Pro	Thr	Ala	His	Pro	Ser	Pro	Ser	Pro
145					150					155					160

Arg	Pro	Ala	Gly	Gln	Phe	Gln	Thr	Leu	Val	Val	Gly	Val	Val	Gly	Gly
				165					170					175	

Leu	Leu	Gly	Ser	Leu	Val	Leu	Leu	Val	Trp	Val	Leu	Ala	Val	Ile	Arg
			180					185					190		

Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro
		195					200					205			

Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro
		210				215					220				

Arg	Asp	Phe	Ala	Ala	Val	Arg	Ser
225					230		

<210> 83

<211> 693

<212> ADN

<213> Secuencia Artificial

<220>

<223> PD1A132L_PTM-CD28 receptor
secuencia de ácido nucleico

<400> 83

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atgcagatcc cacaggcgcc ctggccagtc gtctgggcgg tgctacaact gggctggcgg      60
ccaggatggt tcttagactc cccagacagg ccctggaacc cccccacctt ctccccagcc      120
ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg      180
gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc      240
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg      300
cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc      360
tacctctgtg gggccatctc cctggccccc aagctgcaga tcaaagagag cctgcgggca      420
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcacc      480
aggccagccg gccagttcca aaccctgggt gttggtgtcg tgggcggcct gctgggcagc      540
ctggtgctgc tagtctgggt cctggccgtc atcaggagta agaggagcag gtcctgcac      600
agtgactaca tgaacatgac tccccgccgc cccgggcccga cccgcaagca ttaccagccc      660
tatgccccac cacgcgactt cgcagcctat cgc                                693

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<210> 84

<211> 237

<212> PRT

<213> Secuencia Artificial

<220>

<223> PD-1-4-1BB receptor
secuencia de aminoácidos
(PD1-BB)

<400> 84

```

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1              5              10             15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
20              25             30

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

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
50              55             60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65              70             75             80

```

Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
85 90 95

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
100 105 110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
115 120 125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
130 135 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145 150 155 160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Ile Tyr Ile Trp Ala Pro
165 170 175

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
180 185 190

Tyr Cys Lys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
195 200 205

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
210 215 220

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
225 230 235

<210> 85
<211> 711
<212> ADN
<213> Secuencia Artificial

<220>
<223> PD-1-4-1BB receptor
secuencia de ácido nucleico
(PD1-BB)

<400> 85
atgcagatcc cacagggcgcc ctggccagtc gtctggggcgg tgctacaact gggctggcgg 60
ccaggatggt tcttagactc cccagacagg ccctggaacc ccccccacctt ctccccagcc 120
ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg 180
gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc 240
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg 300
cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc 360
tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca 420
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcacc 480

```

aggccagccg gccagttcca aaccctgggt atctacatct gggcgccctt ggccgggact      540
tgtgggggtcc ttctcctgtc actggttatc accctttact gcaaaaaacg gggcagaaag      600
aaactcctgt atatattcaa acaaccattt atgagaccag tacaaactac tcaagaggaa      660
gatggctgta gctgccgatt tccagaagaa gaagaaggag gatgtgaact g                  711

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<210> 86

<211> 237

<212> PRT

<213> Secuencia Artificial

<220>

<223> PD1A132L_4-1BB receptor secuencia de aminoácidos
(PD1*BB)

<400> 86

```

Met Gln Ile Pro Gln Ala Pro Trp Pro Val Val Trp Ala Val Leu Gln
1                               5                10                15

Leu Gly Trp Arg Pro Gly Trp Phe Leu Asp Ser Pro Asp Arg Pro Trp
                20                25                30

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

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
                50                55                60

Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
65                70                75                80

Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg
                85                90                95

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
                100               105               110

Ala Arg Arg Asn Asp Ser Gly Thr Val Leu Cys Gly Ala Ile Ser Leu
                115               120               125

Ala Pro Lys Leu Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
                130               135               140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145               150               155               160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Ile Tyr Ile Trp Ala Pro
                165               170               175

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
                180               185               190

Val Cys Lys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
                195               200               205

```


Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys
35 40 45

Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys
50 55 60

Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg
65 70 75 80

Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr
85 90 95

Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro
100 105 110

Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu Leu Ala Ala
115 120 125

Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ser Leu Met Leu Met
130 135 140

Val Tyr Ile Arg Ala Ala Arg His Leu Cys Pro Pro Leu Pro Thr Pro
145 150 155 160

Cys Ala Ser Ser Ala Ile Glu Phe Pro Gly Gly Lys Glu Thr Trp Gln
165 170 175

Trp Ile Asn Pro Val Asp Phe Gln Glu Glu Ala Ser Leu Gln Glu Ala
180 185 190

Leu Val Val Glu Met Ser Trp Asp Lys Gly Glu Arg Thr Glu Pro Leu
195 200 205

Glu Lys Thr Glu Leu Pro Glu Gly Ala Pro Glu Leu Ala Leu Asp Thr
210 215 220

Glu Leu Ser Leu Glu Asp Gly Asp Arg Cys Lys Ala Lys Met
225 230 235

<210> 89

<211> 714

<212> ADN

<213> Secuencia Artificial

<220>

<223> TGFβR-IL12Rβ1 receptor secuencia de ácido nucleico

<400> 89

atggaggcgg cggtcgctgc tccgcgtccc cggctgctcc tcctcgtgct ggcggcggcg 60

gcggcggcgg cggcggcgct gctcccgggg gcgacggcgt tacagtgttt ctgccacctc 120

tgtacaaaag acaatttttac ttgtgtgaca gatgggctct gctttgtctc tgtcacagag 180

accacagaca aagttataca caacagcatg tgtatagctg aaattgactt aattcctcga 240

gataggccgt ttgtatgtgc accctcttca aaaactgggt ctgtgactac aacatattgc 300

```

tgcaatcagg accattgcaa taaaatagaa cttccaacta ctgtaaagtc atcacctggc      360
cttggtcctg tggaactggc agctgtcatt gctggaccag tgtgcttcgt ctgcatctca      420
ctcatgttga tggctctatat cagggccgca cggcacctgt gcccgccgct gcccacaccc      480
tgtgccagct ccgccattga gttccctgga gggaaggaga cttggcagtg gatcaaccca      540
gtggacttcc aggaagaggc atccctgcag gaggccctgg tggtagagat gtcctggggac      600
aaaggcgaga ggactgagcc tctcgagaag acagagctac ctgaggggtgc ccctgagctg      660
gccctggata cagagttgtc cttggaggat ggagacaggt gcaaggccaa gatg          714

```

<210> 90

<211> 403

<212> PRT

<213> Secuencia Artificial

<220>

<223> TGFβR-IL12Rβ2 receptor secuencia de aminoácidos

<400> 90

```

Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu
1           5           10           15

Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val
20           25           30

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
35           40           45

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
50           55           60

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
65           70           75           80

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
85           90           95

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
100          105          110

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
115          120          125

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
130          135          140

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu
145          150          155          160

Leu Leu Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu
165          170          175

```

Gly Val Ala Ile Ser Val Ile Ile Ile Phe Tyr Gln Gln Lys Val Phe
 180 185 190
 Val Leu Leu Ala Ala Leu Arg Pro Gln Trp Cys Ser Arg Glu Ile Pro
 195 200 205
 Asp Pro Ala Asn Ser Thr Cys Ala Lys Lys Tyr Pro Ile Ala Glu Glu
 210 215 220
 Lys Thr Gln Leu Pro Leu Asp Arg Leu Leu Ile Asp Trp Pro Thr Pro
 225 230 235 240
 Glu Asp Pro Glu Pro Leu Val Ile Ser Glu Val Leu His Gln Val Thr
 245 250 255
 Pro Val Phe Arg His Pro Pro Cys Ser Asn Trp Pro Gln Arg Glu Lys
 260 265 270
 Gly Ile Gln Gly His Gln Ala Ser Glu Lys Asp Met Met His Ser Ala
 275 280 285
 Ser Ser Pro Pro Pro Pro Arg Ala Leu Gln Ala Glu Ser Arg Gln Leu
 290 295 300
 Val Asp Leu Tyr Lys Val Leu Glu Ser Arg Gly Ser Asp Pro Lys Pro
 305 310 315 320
 Glu Asn Pro Ala Cys Pro Trp Thr Val Leu Pro Ala Gly Asp Leu Pro
 325 330 335
 Thr His Asp Gly Tyr Leu Pro Ser Asn Ile Asp Asp Leu Pro Ser His
 340 345 350
 Glu Ala Pro Leu Ala Asp Ser Leu Glu Glu Leu Glu Pro Gln His Ile
 355 360 365
 Ser Leu Ser Val Phe Pro Ser Ser Ser Leu His Pro Leu Thr Phe Ser
 370 375 380
 Cys Gly Asp Lys Leu Thr Leu Asp Gln Leu Lys Met Arg Cys Asp Ser
 385 390 395 400
 Leu Met Leu

<210> 91
 <211> 1209
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> TGFβR-IL12Rβ2 receptor secuencia de ácido nucleico

<400> 91
 atgggtcggg ggctgctcag gggcctgtgg ccgctgcaca tcgtcctgtg gacgcgtatc 60
 gccagcacga tcccaccgca cgttcagaag tcggttaata acgacatgat agtcactgac 120

aacaacggtg cagtcaagtt tccacaactg tgtaaatTTT gtgatgtgag attttccacc	180
tgTgacaacc agaaatcctg catgagcaac tgcagcatca cctccatctg tgagaagcca	240
caggaagtct gtgtggctgt atggagaaaag aatgacgaga acataaact agagacagtt	300
tgccatgacc ccaagctccc ctacatgac ttTattctgg aagatgtctg ttctccaaag	360
tgcattatga aggaaaaaaaa aaagcctggt gagactttct tcatgtgttc ctgtagctct	420
gatgagtga atgacaacat catcttctca gaagaatata acaccagcaa tcctgacttg	480
ttgctagtca tatttcaagt gacaggcatc agcctcctgc caccactggg agttgccata	540
tctgtcatca tcatcttcta ccagcaaaag gtgtttgttc tcctagcagc cctcagacct	600
cagtgggtga gcagagaaat tccagatcca gcaaatagca cttgcgctaa gaaatatccc	660
attgcagagg agaagacaca gctgcccttg gacaggctcc tgatagactg gcccacgcct	720
gaagatcctg aaccgctggt catcagtga gtccttcac aagtgacccc agttttcaga	780
catccccct gctccaactg gccacaaag gaaaaaggaa tccaaggtca tcaggcctct	840
gagaaagaca tgatgcacag tgcctcaagc ccaccacctc caagagctct ccaagctgag	900
agcagacaac tggTggatct gtacaaggTg ctggagagca ggggctccga cccaaagcca	960
gaaaaccag cctgtccctg gacggtgctc ccagcaggTg accttcccac ccatgatggc	1020
tacttaccct ccaacataga tgacctcccc tcacatgagg cacctctcgc tgactctctg	1080
gaagaactgg agcctcagca catctccctt tctgttttcc cctcaagttc tcttcacca	1140
ctcaccttct cctgtggTga taagctgact ctggatcagt taaagatgag gtgtgactcc	1200
ctcatgctc	1209