

LISTADO DE SECUENCIAS

<110> Kyoto University
TAKEDA PHARMACEUTICAL COMPANY LIMITED

<120> Banco celular maestro de células T

<130> 093085

<150> JP 2019-212718

<151> 2019-11-25

<160> 7

<170> PatentIn versión 3.5

<210> 1

<211> 629

<212> PRT

<213> Secuencia artificial

<220>

<223> Vgamma9 Vdelta2 TCR

<220>

<221> PÉPTIDO

<222> (1)..(315)

<223> receptor gamma de células T

<220>

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<222> (316)..(337)

<223> P2A

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<222> (338)..(629)

<223> receptor delta de células T

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

Cys	Val	Tyr	Gly	Ala	Gly	His	Leu	Glu	Gln	Pro	Gln	Ile	Ser	Ser	Thr
			20					25					30		

Lys Thr Leu Ser Lys Thr Ala Arg Leu Glu Cys Val Val Ser Gly Ile
35 40 45

Thr Ile Ser Ala Thr Ser Val Tyr Trp Tyr Arg Glu Arg Pro Gly Glu
50 55 60

Val Ile Gln Phe Leu Val Ser Ile Ser Tyr Asp Gly Thr Val Arg Lys
65 70 75 80

Glu Ser Gly Ile Pro Ser Gly Lys Phe Glu Val Asp Arg Ile Pro Glu
85 90 95

Thr Ser Thr Ser Thr Leu Thr Ile His Asn Val Glu Lys Gln Asp Ile
100 105 110

Ala Thr Tyr Tyr Cys Ala Leu Trp Glu Ala Gln Gln Glu Leu Gly Lys
115 120 125

Lys Ile Lys Val Phe Gly Pro Gly Thr Lys Leu Ile Ile Thr Asp Lys
130 135 140

Gln Leu Asp Ala Asp Val Ser Pro Lys Pro Thr Ile Phe Leu Pro Ser
145 150 155 160

Ile Ala Glu Thr Lys Leu Gln Lys Ala Gly Thr Tyr Leu Cys Leu Leu
165 170 175

Glu Lys Phe Phe Pro Asp Val Ile Lys Ile His Trp Glu Glu Lys Lys
180 185 190

Ser Asn Thr Ile Leu Gly Ser Gln Glu Gly Asn Thr Met Lys Thr Asn
195 200 205

Asp Thr Tyr Met Lys Phe Ser Trp Leu Thr Val Pro Glu Lys Ser Leu
210 215 220

Asp Lys Glu His Arg Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly
225 230 235 240

Val Asp Gln Glu Ile Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr
245 250 255

Met Asp Pro Lys Asp Asn Cys Ser Lys Asp Ala Asn Asp Thr Leu Leu
260 265 270

Leu Gln Leu Thr Asn Thr Ser Ala Tyr Tyr Met Tyr Leu Leu Leu Leu
275 280 285

Leu Lys Ser Val Val Tyr Phe Ala Ile Ile Thr Cys Cys Leu Leu Arg
290 295 300

Arg Thr Ala Phe Cys Cys Asn Gly Glu Lys Ser Gly Ser Gly Ala Thr
305 310 315 320

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
325 330 335

Pro Met Glu Arg Ile Ser Ser Leu Ile His Leu Ser Leu Phe Trp Ala
340 345 350

Gly Val Met Ser Ala Ile Glu Leu Val Pro Glu His Gln Thr Val Pro
355 360 365

Val Ser Ile Gly Val Pro Ala Thr Leu Arg Cys Ser Met Lys Gly Glu
370 375 380

Ala Ile Gly Asn Tyr Tyr Ile Asn Trp Tyr Arg Lys Thr Gln Gly Asn
385 390 395 400

Thr Met Thr Phe Ile Tyr Arg Glu Lys Asp Ile Tyr Gly Pro Gly Phe
405 410 415

Lys Asp Asn Phe Gln Gly Asp Ile Asp Ile Ala Lys Asn Leu Ala Val
420 425 430

Leu Lys Ile Leu Ala Pro Ser Glu Arg Asp Glu Gly Ser Tyr Tyr Cys
435 440 445

Ala Cys Asp Thr Leu Gly Met Gly Gly Glu Tyr Thr Asp Lys Leu Ile
450 455 460

Phe Gly Lys Gly Thr Arg Val Thr Val Glu Pro Arg Ser Gln Pro His
465 470 475 480

Thr Lys Pro Ser Val Phe Val Met Lys Asn Gly Thr Asn Val Ala Cys
485 490 495

Leu Val Lys Glu Phe Tyr Pro Lys Asp Ile Arg Ile Asn Leu Val Ser
500 505 510

Ser Lys Lys Ile Thr Glu Phe Asp Pro Ala Ile Val Ile Ser Pro Ser
515 520 525

Gly Lys Tyr Asn Ala Val Lys Leu Gly Lys Tyr Glu Asp Ser Asn Ser
530 535 540

Val Thr Cys Ser Val Gln His Asp Asn Lys Thr Val His Ser Thr Asp
545 550 555 560

Phe Glu Val Lys Thr Asp Ser Thr Asp His Val Lys Pro Lys Glu Thr
565 570 575

Glu Asn Thr Lys Gln Pro Ser Lys Ser Cys His Lys Pro Lys Ala Ile
580 585 590

Val His Thr Glu Lys Val Asn Met Met Ser Leu Thr Val Leu Gly Leu
595 600 605

Arg Met Leu Phe Ala Lys Thr Val Ala Val Asn Phe Leu Leu Thr Ala
610 615 620

Lys Leu Phe Phe Leu
625

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<212> PRT
<213> Secuencia artificial

<220>
<223> CD19-CAR(CD8-CD28-4-1BB-CD3z)

<220>
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<223> secuencia líder de cadena pesada de inmunoglobulina

<220>
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<223> región variable de cadena ligera de anticuerpo anti-CD19

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<223> Enlazador de péptido

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<223> región variable de cadena pesada de anticuerpo anti-CD19

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<223> secuencia derivada de CD8

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<222> (345)..(385)
<223> región de dominio intracelular de CD28

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<222> (386)..(432)
<223> región de dominio intracelular de 4-1BB

<220>
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<222> (433)..(544)
<223> región de dominio intracelular de CD3 zeta

<400> 2

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Ala His Ser Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala
20 25 30

Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile
35 40 45

Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys
50 55 60

Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn
85 90 95

Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr
100 105 110

Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Lys
130 135 140

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
145 150 155 160

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
165 170 175

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
180 185 190

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
195 200 205

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
210 215 220

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
225 230 235 240

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
245 250 255

Val Thr Val Ser Ser Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr
260 265 270

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
275 280 285

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
290 295 300

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
305 310 315 320

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
325 330 335

Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu
340 345 350

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
355 360 365

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
370 375 380

Ser Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile

<222> (1)..(19)
 <223> secuencia líder de cadena pesada de inmunoglobulina

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 <223> región variable de cadena ligera de anticuerpo anti-BCMA

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 <222> (131)..(148)
 <223> Enlazador de péptido

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 <223> secuencia derivada de CD8

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 <223> región de dominio intracelular de CD28

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 <221> PÉPTIDO
 <222> (393)..(439)
 <223> región de dominio intracelular de 4-1BB

 <220>
 <221> PÉPTIDO
 <222> (440)..(551)
 <223> región de dominio intracelular de CD3 zeta

 <400> 3

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15

Ala His Ser Asp Ile Val Leu Thr Gln Ser Pro Pro Ser Leu Ala Met
 20 25 30

Ser Leu Gly Lys Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val
 35 40 45

Thr Ile Leu Gly Ser His Leu Ile His Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Pro Pro Thr Leu Leu Ile Gln Leu Ala Ser Asn Val Gln Thr Gly
65 70 75 80

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

Thr Ile Asp Pro Val Glu Glu Asp Asp Val Ala Val Tyr Tyr Cys Leu
100 105 110

Gln Ser Arg Thr Ile Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125

Ile Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
130 135 140

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

Lys Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr
165 170 175

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

Leu Lys Trp Met Gly Trp Ile Asn Thr Glu Thr Arg Glu Pro Ala Tyr
195 200 205

Ala Tyr Asp Phe Arg Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala
210 215 220

Ser Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala
225 230 235 240

Thr Tyr Phe Cys Ala Leu Asp Tyr Ser Tyr Ala Met Asp Tyr Trp Gly
245 250 255

Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ala Ala Phe Val Pro Val
260 265 270

Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
275 280 285

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
290 295 300

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
305 310 315 320

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
325 330 335

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg
340 345 350

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
355 360 365

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
370 375 380

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Phe Ser Val Val Lys Arg Gly
385 390 395 400

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
405 410 415

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
420 425 430

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
435 440 445

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
450 455 460

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
465 470 475 480

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
485 490 495

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
500 505 510

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
515 520 525

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
530 535 540

Met Gln Ala Leu Pro Pro Arg
545 550

<210> 4

<211> 584

<212> PRT

<213> Secuencia artificial

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<222> (23)..(126)

<223> región variable de cadena ligera de anticuerpo anti-CD19

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<221> PÉPTIDO
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 <223> Enlazador de péptido

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 <220>
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 <223> región de dominio intracelular de CD3 zeta

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Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15

Ala His Ser Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala
 20 25 30

Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile
 35 40 45

Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys
 50 55 60

Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg
 65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn
85 90 95

Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr
100 105 110

Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys
130 135 140

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
145 150 155 160

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
165 170 175

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
180 185 190

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
195 200 205

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
210 215 220

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
225 230 235 240

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
245 250 255

Val Thr Val Ser Ser Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr
260 265 270

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser

275

280

285

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
 290 295 300

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
 305 310 315 320

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
 325 330 335

Thr Leu Tyr Cys Asn His Arg Asn Arg Ser Lys Arg Ser Arg Leu Leu
 340 345 350

His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg
 355 360 365

Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg
 370 375 380

Ser His Thr Asn Asn Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp
 385 390 395 400

Thr Val Ile Val Gly Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly
 405 410 415

Leu Ala Gly Pro Ala Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp
 420 425 430

His Thr Pro His Tyr Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser
 435 440 445

Cys Ser Asp Val Met Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro
 450 455 460

Leu Pro Thr Ala Ala Ser Gly Lys Arg Val Lys Phe Ser Arg Ser Ala
 465 470 475 480

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
485 490 495

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
500 505 510

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
515 520 525

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
530 535 540

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
545 550 555 560

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
565 570 575

His Met Gln Ala Leu Pro Pro Arg
580

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 <222> (262)..(344)
 <223> secuencia derivada de CD8

 <220>
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 <222> (345)..(391)
 <223> región de dominio intracelular de 4-1BB

 <220>
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 <222> (392)..(503)
 <223> región de dominio intracelular de CD3 zeta

 <400> 5

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15

Ala His Ser Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala
 20 25 30

Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile
 35 40 45

Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys
 50 55 60

Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg
 65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn
 85 90 95

Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr

100

105

110

Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys
 130 135 140

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
 145 150 155 160

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
 165 170 175

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
 180 185 190

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
 195 200 205

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
 210 215 220

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
 225 230 235 240

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
 245 250 255

Val Thr Val Ser Ser Phe Val Pro Val Phe Leu Pro Ala Lys Pro Thr
 260 265 270

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
 275 280 285

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
 290 295 300

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
305 310 315 320

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
325 330 335

Thr Leu Tyr Cys Asn His Arg Asn Arg Phe Ser Val Val Lys Arg Gly
340 345 350

Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val
355 360 365

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
370 375 380

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
385 390 395 400

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
405 410 415

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
420 425 430

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
435 440 445

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
450 455 460

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
465 470 475 480

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
485 490 495

Met Gln Ala Leu Pro Pro Arg

500

<210> 6
<211> 87
<212> PRT
<213> Homo sapiens

<400> 6

His Thr Asn Asn Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr
1 5 10 15

Val Ile Val Gly Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu
20 25 30

Ala Gly Pro Ala Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp His
35 40 45

Thr Pro His Tyr Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys
50 55 60

Ser Asp Val Met Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu
65 70 75 80

Pro Thr Ala Ala Ser Gly Lys
85

<210> 7
<211> 400
<212> PRT
<213> Homo sapiens

<220>
<221> SEÑAL
<222> (1)..(23)
<223> secuencia líder de IL-2 humana

<220>
<221> PÉPTIDO
<222> (24)..(137)
<223> IL-15 humana

<220>
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<222> (138)..(161)
<223> Enlazador de péptido

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<222> (162)..(400)
<223> IL-15Ra humana

<400> 7

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

Val Thr Asn Ser Ala Thr Ser Asn Trp Val Asn Val Ile Ser Asp Leu
20 25 30

Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu
35 40 45

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

Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala
65 70 75 80

Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser
85 90 95

Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
100 105 110

Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His
115 120 125

Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Ser Leu Gln Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp
165 170 175

Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys
180 185 190

Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys
195 200 205

Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu
210 215 220

Lys Cys Ile Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro
225 230 235 240

Ser Thr Val Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser
245 250 255

Pro Ser Gly Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr
260 265 270

Ala Ala Thr Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser
275 280 285

Lys Ser Pro Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser
290 295 300

His Gly Thr Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala
305 310 315 320

Ser Ala Ser His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp
325 330 335

Thr Thr Val Ala Ile Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser
340 345 350

Ala Val Ser Leu Leu Ala Cys Tyr Leu Lys Ser Arg Gln Thr Pro Pro
355 360 365

Leu Ala Ser Val Glu Met Glu Ala Met Glu Ala Leu Pro Val Thr Trp
370 375 380

Gly Thr Ser Ser Arg Asp Glu Asp Leu Glu Asn Cys Ser His His Leu
385 390 395 400