

Untitled\_ST25FINAL  
SEQUENCE LISTING

<110> Zurko Research

<120> Uso de colagenasa G recombinante, colagenasa H recombinante y pz-peptidasa recombinante para el tratamiento de enfermedades que cursan con alteraciones del colágeno.

<130> Zurko 2281

<160> 8

<170> PatentIn version 3.5

<210> 1

<211> 1008

<212> PRT

<213> Artificial Sequence

<220>

<223> Colagenasa G

<400> 1

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Leu Ser Tyr Thr Glu Leu Thr Asn Leu Ile Lys Asn Ile Lys Trp Asn  
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Gln Ile Asn Gly Leu Phe Asn Tyr Ser Thr Gly Ser Gln Lys Phe Phe  
35 40 45

Gly Asp Lys Asn Arg Val Gln Ala Ile Ile Asn Ala Leu Gln Glu Ser  
50 55 60

Gly Arg Thr Tyr Thr Ala Asn Asp Met Lys Gly Ile Glu Thr Phe Thr  
65 70 75 80

Glu Val Leu Arg Ala Gly Phe Tyr Leu Gly Tyr Tyr Asn Asp Gly Leu  
85 90 95

Ser Tyr Leu Asn Asp Arg Asn Phe Gln Asp Lys Cys Ile Pro Ala Met  
100 105 110

Ile Ala Ile Gln Lys Asn Pro Asn Phe Lys Leu Gly Thr Ala Val Gln  
115 120 125

Asp Glu Val Ile Thr Ser Leu Gly Lys Leu Ile Gly Asn Ala Ser Ala  
130 135 140

Asn Ala Glu Val Val Asn Asn Cys Val Pro Val Leu Lys Gln Phe Arg  
145 150 155 160

Glu Asn Leu Asn Gln Tyr Ala Pro Asp Tyr Val Lys Gly Thr Ala Val  
165 170 175

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Asn Glu Leu Ile Lys Gly Ile Glu Phe Asp Phe Ser Gly Ala Ala Tyr  
 180 185 190  
 Glu Lys Asp Val Lys Thr Met Pro Trp Tyr Gly Lys Ile Asp Pro Phe  
 195 200 205  
 Ile Asn Glu Leu Lys Ala Leu Gly Leu Tyr Gly Asn Ile Thr Ser Ala  
 210 215 220  
 Thr Glu Trp Ala Ser Asp Val Gly Ile Tyr Tyr Leu Ser Lys Phe Gly  
 225 230 235 240  
 Leu Tyr Ser Thr Asn Arg Asn Asp Ile Val Gln Ser Leu Glu Lys Ala  
 245 250 255  
 Val Asp Met Tyr Lys Tyr Gly Lys Ile Ala Phe Val Ala Met Glu Arg  
 260 265 270  
 Ile Thr Trp Asp Tyr Asp Gly Ile Gly Ser Asn Gly Lys Lys Val Asp  
 275 280 285  
 His Asp Lys Phe Leu Asp Asp Ala Glu Lys His Tyr Leu Pro Lys Thr  
 290 295 300  
 Tyr Thr Phe Asp Asn Gly Thr Phe Ile Ile Arg Ala Gly Asp Lys Val  
 305 310 315 320  
 Ser Glu Glu Lys Ile Lys Arg Leu Tyr Trp Ala Ser Arg Glu Val Lys  
 325 330 335  
 Ser Gln Phe His Arg Val Val Gly Asn Asp Lys Ala Leu Glu Val Gly  
 340 345 350  
 Asn Ala Asp Asp Val Leu Thr Met Lys Ile Phe Asn Ser Pro Glu Glu  
 355 360 365  
 Tyr Lys Phe Asn Thr Asn Ile Asn Gly Val Ser Thr Asp Asn Gly Gly  
 370 375 380  
 Leu Tyr Ile Glu Pro Arg Gly Thr Phe Tyr Thr Tyr Glu Arg Thr Pro  
 385 390 395 400  
 Gln Gln Ser Ile Phe Ser Leu Glu Glu Leu Phe Arg His Glu Tyr Thr  
 405 410 415  
 His Tyr Leu Gln Ala Arg Tyr Leu Val Asp Gly Leu Trp Gly Gln Gly  
 420 425 430  
 Pro Phe Tyr Glu Lys Asn Arg Leu Thr Trp Phe Asp Glu Gly Thr Ala  
 435 440 445

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Glu Phe Phe Ala Gly Ser Thr Arg Thr Ser Gly Val Leu Pro Arg Lys  
 450 455 460  
 Ser Ile Leu Gly Tyr Leu Ala Lys Asp Lys Val Asp His Arg Tyr Ser  
 465 470 475 480  
 Leu Lys Lys Thr Leu Asn Ser Gly Tyr Asp Asp Ser Asp Trp Met Phe  
 485 490 495  
 Tyr Asn Tyr Gly Phe Ala Val Ala His Tyr Leu Tyr Glu Lys Asp Met  
 500 505 510  
 Pro Thr Phe Ile Lys Met Asn Lys Ala Ile Leu Asn Thr Asp Val Lys  
 515 520 525  
 Ser Tyr Asp Glu Ile Ile Lys Lys Leu Ser Asp Asp Ala Asn Lys Asn  
 530 535 540  
 Thr Glu Tyr Gln Asn His Ile Gln Glu Leu Ala Asp Lys Tyr Gln Gly  
 545 550 555  
 Ala Gly Ile Pro Leu Val Ser Asp Asp Tyr Leu Lys Asp His Gly Tyr  
 565 570 575  
 Lys Lys Ala Ser Glu Val Tyr Ser Glu Ile Ser Lys Ala Ala Ser Leu  
 580 585 590  
 Thr Asn Thr Ser Val Thr Ala Glu Lys Ser Gln Tyr Phe Asn Thr Phe  
 595 600 605  
 Thr Leu Arg Gly Thr Tyr Thr Gly Glu Thr Ser Lys Gly Glu Phe Lys  
 610 615 620  
 Asp Trp Asp Glu Met Ser Lys Lys Leu Asp Gly Thr Leu Glu Ser Leu  
 625 630 635 640  
 Ala Lys Asn Ser Trp Ser Gly Tyr Lys Thr Leu Thr Ala Tyr Phe Thr  
 645 650 655  
 Asn Tyr Arg Val Thr Ser Asp Asn Lys Val Gln Tyr Asp Val Val Phe  
 660 665 670  
 His Gly Val Leu Thr Asp Asn Ala Asp Ile Ser Asn Asn Lys Ala Pro  
 675 680 685  
 Ile Ala Lys Val Thr Gly Pro Ser Thr Gly Ala Val Gly Arg Asn Ile  
 690 695 700  
 Glu Phe Ser Gly Lys Asp Ser Lys Asp Glu Asp Gly Lys Ile Val Ser  
 705 710 715 720

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Tyr Asp Trp Asp Phe Gly Asp Gly Ala Thr Ser Arg Gly Lys Asn Ser  
725 730 735

Val His Ala Tyr Lys Lys Ala Gly Thr Tyr Asn Val Thr Leu Lys Val  
740 745 750

Thr Asp Asp Lys Gly Ala Thr Ala Thr Glu Ser Phe Thr Ile Glu Ile  
755 760 765

Lys Asn Glu Asp Thr Thr Thr Pro Ile Thr Lys Glu Met Glu Pro Asn  
770 775 780

Asp Asp Ile Lys Glu Ala Asn Gly Pro Ile Val Glu Gly Val Thr Val  
785 790 795 800

Lys Gly Asp Leu Asn Gly Ser Asp Asp Ala Asp Thr Phe Tyr Phe Asp  
805 810 815

Val Lys Glu Asp Gly Asp Val Thr Ile Glu Leu Pro Tyr Ser Gly Ser  
820 825 830

Ser Asn Phe Thr Trp Leu Val Tyr Lys Glu Gly Asp Asp Gln Asn His  
835 840 845

Ile Ala Ser Gly Ile Asp Lys Asn Asn Ser Lys Val Gly Thr Phe Lys  
850 855 860

Ser Thr Lys Gly Arg His Tyr Val Phe Ile Tyr Lys His Asp Ser Ala  
865 870 875 880

Ser Asn Ile Ser Tyr Ser Leu Asn Ile Lys Gly Leu Gly Asn Glu Lys  
885 890 895

Leu Lys Glu Lys Glu Asn Asn Asp Ser Ser Asp Lys Ala Thr Val Ile  
900 905 910

Pro Asn Phe Asn Thr Thr Met Gln Gly Ser Leu Leu Gly Asp Asp Ser  
915 920 925

Arg Asp Tyr Tyr Ser Phe Glu Val Lys Glu Glu Gly Glu Val Asn Ile  
930 935 940

Glu Leu Asp Lys Lys Asp Glu Phe Gly Val Thr Trp Thr Leu His Pro  
945 950 955 960

Glu Ser Asn Ile Asn Asp Arg Ile Thr Tyr Gly Gln Val Asp Gly Asn  
965 970 975

Lys Val Ser Asn Lys Val Lys Leu Arg Pro Gly Lys Tyr Tyr Leu Leu  
980 985 990

# Untitled\_ST25FINAL

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 <211> 981  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Colagenasa H

<400> 2

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Asn Tyr Tyr Asp Leu Val Asp Leu Leu Val Lys Thr Glu Ile Glu Asn  
 20 25 30

Leu Pro Asp Leu Phe Gln Tyr Ser Ser Asp Ala Lys Glu Phe Tyr Gly  
 35 40 45

Asn Lys Thr Arg Met Ser Phe Ile Met Asp Glu Ile Gly Arg Arg Ala  
 50 55 60

Pro Gln Tyr Thr Glu Ile Asp His Lys Gly Ile Pro Thr Leu Val Glu  
 65 70 75 80

Val Val Arg Ala Gly Phe Tyr Leu Gly Phe His Asn Lys Glu Leu Asn  
 85 90 95

Glu Ile Asn Lys Arg Ser Phe Lys Glu Arg Val Ile Pro Ser Ile Leu  
 100 105 110

Ala Ile Gln Lys Asn Pro Asn Phe Lys Leu Gly Thr Glu Val Gln Asp  
 115 120 125

Lys Ile Val Ser Ala Thr Gly Leu Leu Ala Gly Asn Glu Thr Ala Pro  
 130 135 140

Pro Glu Val Val Asn Asn Phe Thr Pro Ile Leu Gln Asp Cys Ile Lys  
 145 150 155 160

Asn Ile Asp Arg Tyr Ala Leu Asp Asp Leu Lys Ser Lys Ala Leu Phe  
 165 170 175

Asn Val Leu Ala Ala Pro Thr Tyr Asp Ile Thr Glu Tyr Leu Arg Ala  
 180 185 190

Thr Lys Glu Lys Pro Glu Asn Thr Pro Trp Tyr Gly Lys Ile Asp Gly  
 195 200 205

Phe Ile Asn Glu Leu Lys Lys Leu Ala Leu Tyr Gly Lys Ile Asn Asp  
 210 215 220

# Untitled\_ST25FINAL

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

# Untitled\_ST25FINAL

Phe Tyr Asn Tyr Ala Cys Met Phe Met Asp Tyr Met Tyr Asn Lys Asp  
 500 505 510  
 Met Gly Ile Leu Asn Lys Leu Asn Asp Leu Ala Lys Asn Asn Asp Val  
 515 520 525  
 Asp Gly Tyr Asp Asn Tyr Ile Arg Asp Leu Ser Ser Asn Tyr Ala Leu  
 530 535 540  
 Asn Asp Lys Tyr Gln Asp His Met Gln Glu Arg Ile Asp Asn Tyr Glu  
 545 550 555 560  
 Asn Leu Thr Val Pro Phe Val Ala Asp Asp Tyr Leu Val Arg His Ala  
 565 570 575  
 Tyr Lys Asn Pro Asn Glu Ile Tyr Ser Glu Ile Ser Glu Val Ala Lys  
 580 585 590  
 Leu Lys Asp Ala Lys Ser Glu Val Lys Lys Ser Gln Tyr Phe Ser Thr  
 595 600 605  
 Phe Thr Leu Arg Gly Ser Tyr Thr Gly Gly Ala Ser Lys Gly Lys Leu  
 610 615 620  
 Glu Asp Gln Lys Ala Met Asn Lys Phe Ile Asp Asp Ser Leu Lys Lys  
 625 630 635 640  
 Leu Asp Thr Tyr Ser Trp Ser Gly Tyr Lys Thr Leu Thr Ala Tyr Phe  
 645 650 655  
 Thr Asn Tyr Lys Val Asp Ser Ser Asn Arg Val Thr Tyr Asp Val Val  
 660 665 670  
 Phe His Gly Tyr Leu Pro Asn Glu Gly Asp Ser Lys Asn Ser Leu Pro  
 675 680 685  
 Tyr Gly Lys Ile Asn Gly Thr Tyr Lys Gly Thr Glu Lys Glu Lys Ile  
 690 695 700  
 Lys Phe Ser Ser Glu Gly Ser Phe Asp Pro Asp Gly Lys Ile Val Ser  
 705 710 715 720  
 Tyr Glu Trp Asp Phe Gly Asp Gly Asn Lys Ser Asn Glu Glu Asn Pro  
 725 730 735  
 Glu His Ser Tyr Asp Lys Val Gly Thr Tyr Thr Val Lys Leu Lys Val  
 740 745 750  
 Thr Asp Asp Lys Gly Glu Ser Ser Val Ser Thr Thr Thr Ala Glu Ile  
 755 760 765

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Lys Asp Leu Ser Glu Asn Lys Leu Pro Val Ile Tyr Met His Val Pro  
770 775 780

Lys Ser Gly Ala Leu Asn Gln Lys Val Val Phe Tyr Gly Lys Gly Thr  
785 790 795 800

Tyr Asp Pro Asp Gly Ser Ile Ala Gly Tyr Gln Trp Asp Phe Gly Asp  
805 810 815

Gly Ser Asp Phe Ser Ser Glu Gln Asn Pro Ser His Val Tyr Thr Lys  
820 825 830

Lys Gly Glu Tyr Thr Val Thr Leu Arg Val Met Asp Ser Ser Gly Gln  
835 840 845

Met Ser Glu Lys Thr Met Lys Ile Lys Ile Thr Asp Pro Val Tyr Pro  
850 855 860

Ile Gly Thr Glu Lys Glu Pro Asn Asn Ser Lys Glu Thr Ala Ser Gly  
865 870 875 880

Pro Ile Val Pro Gly Ile Pro Val Ser Gly Thr Ile Glu Asn Thr Ser  
885 890 895

Asp Gln Asp Tyr Phe Tyr Phe Asp Val Ile Thr Pro Gly Glu Val Lys  
900 905 910

Ile Asp Ile Asn Lys Leu Gly Tyr Gly Gly Ala Thr Trp Val Val Tyr  
915 920 925

Asp Glu Asn Asn Asn Ala Val Ser Tyr Ala Thr Asp Asp Gly Gln Asn  
930 935 940

Leu Ser Gly Lys Phe Lys Ala Asp Lys Pro Gly Arg Tyr Tyr Ile His  
945 950 955 960

Leu Tyr Met Phe Asn Gly Ser Tyr Met Pro Tyr Arg Ile Asn Ile Glu  
965 970 975

Gly Ser Val Gly Arg  
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<211> 3357  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Colagenasa G y péptido señal

<400> 3  
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# Untitled\_ST25FINAL

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aaattaagaa	atgctccaaa	tgaagagaat	agtaaaaagg	tagaagatag	taaaaatgat	240
aaggtagaac	atgtgaaaaa	tatagaagag	gcaaagggtg	agcaagttgc	acccgaagta	300
aaatctaaat	caactttaag	aagtgccttct	atagcgaata	ctaattctga	gaaatatgat	360
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tggaatcaaa	ttaatgggtt	atttaattat	agtacagggt	ctcaaaagtt	ctttggagat	480
aaaaatcgtg	tacaagctat	aattaatgct	ttacaagaaa	gtggaagaac	ttacactgca	540
aatgatatga	agggtataga	aactttcact	gagggtttta	gagctgggtt	ttatttaggg	600
tactataatg	atgggtttatc	ttattttaaat	gatagaaact	tccaagataa	atgtatacct	660
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cagtcacttg	aaaaggctgt	agatatgtat	aagtatggta	aaatagcctt	tgtagcaatg	1140
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acctttatta	taagagcagg	ggataaggta	tccgaagaaa	aaataaaaag	gctatattgg	1320
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> péptido señal colagenasa G

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aaattaagaa	atgctccaaa	tgaagagaat	agtaaaaagg	tagaagatag	taaaaatgat	240
aaggtagaac	atgtgaaaaa	tatagaagag	gcaaagggtg	agcaagttgc	acccgaagta	300
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<210> 5  
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<212> PRT

<213> Artificial Sequence

<220>

<223> péptido señal colagenasa G

<400> 5

Met Lys Lys Asn Ile Leu Lys Ile Leu Met Asp Ser Tyr Ser Lys Glu  
1 5 10 15

Ser Lys Ile Gln Thr Val Arg Arg Val Thr Ser Val Ser Leu Leu Ala  
20 25 30

Val Tyr Leu Thr Met Asn Thr Ser Ser Leu Val Leu Ala Lys Pro Ile  
35 40 45

Glu Asn Thr Asn Asp Thr Ser Ile Lys Asn Val Glu Lys Leu Arg Asn  
50 55 60

Ala Pro Asn Glu Glu Asn Ser Lys Lys Val Glu Asp Ser Lys Asn Asp  
65 70 75 80

Lys Val Glu His Val Lys Asn Ile Glu Glu Ala Lys Val Glu Gln Val  
85 90 95

Ala Pro Glu Val Lys Ser Lys Ser Thr Leu Arg Ser Ala Ser  
100 105 110

<210> 6

<211> 3066

<212> DNA

<213> Artificial Sequence

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<223> colagenasa H y péptido señal

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ttagtagatt tgcttgtaa gactgaaatt gagaatttac cagacctttt tcagtatagt	240
tcagatgcaa aagagttcta tggaaataaa actcgtatga gctttatcat ggatgaaatt	300
ggtagaaggg cacctcagta tacagagata gatcataaag gtattcctac tttagtagaa	360
gttgtaagag ctggatttta cttaggattc cataacaagg aattgaatga aataaacaag	420
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gaaacagcgc ctccagaagt tgtaaataat ttacaccaa tacttcaaga ctgtataaag	600
aatatagaca gatacgctct tgatgattta aagtcaaaag cattatttaa tgttttagct	660
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# Untitled\_ST25FINAL

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acaatgggta	tctacaacag	tcccgaagaa	tataaactca	atagtgttct	atacggatat	1260
gatactaata	atggtggtat	gtatatagag	ccagaaggaa	ctttcttcac	ctatgaaaga	1320
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