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<220>
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		Ser	Gln
		Glu	Ile
		His	Ala
		Arg	Phe
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			Arg
			Arg

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<400> 6

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<220>
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<400> 8

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Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe
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Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val Asn
35 40 45

Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe Thr
50 55 60

Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu His
65 70 75 80

Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp Phe
85 90 95

His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp Asn
100 105 110

Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu Lys
115 120 125

Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser Lys
130 135 140

Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile Lys
145 150 155 160

Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr Tyr
165 170 175

His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr Ser
180 185 190

Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu Met
195 200 205

Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe Val
210 215 220

Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr Pro
225 230 235 240

Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu Pro
245 250 255

Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr Leu
260 265 270

Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser Gly
275 280 285

Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro Arg
290 295 300

Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala Val

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Asp Cys Ala Leu	Asp Pro Leu Ser	Glu Thr Lys Cys Thr	Leu Lys Ser			
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Phe Thr Val Glu	Lys Gly Ile Tyr	Gln Thr Ser Asn Phe	Arg Val Gln			
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Pro Thr Glu Ser	Ile Val Arg Phe	Pro Asn Ile Thr	Asn Leu Cys Pro			
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Phe Gly Glu Val	Phe Asn Ala Thr	Arg Phe Ala Ser	Val Tyr Ala Trp			
	370		375			380
Asn Arg Lys Arg	Ile Ser Asn Cys Val	Ala Asp Tyr Ser	Val Leu Tyr			
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Asn Ser Ala Ser	Phe Ser Thr Phe	Lys Cys Tyr Gly	Val Ser Pro Thr			
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Lys Leu Asn Asp	Leu Cys Phe Thr	Asn Val Tyr Ala	Asp Ser Phe Val			
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Ile Arg Gly Asp	Glu Val Arg Gln	Ile Ala Pro Gly	Gln Thr Gly Lys			
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Ile Ala Asp Tyr	Asn Tyr Lys Leu	Pro Asp Asp Phe	Thr Gly Cys Val			
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Ile Ala Trp Asn	Ser Asn Asn Leu	Asp Ser Lys Val	Gly Gly Asn Tyr			
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Asn Tyr Leu Tyr	Arg Leu Phe Arg	Lys Ser Asn Leu	Lys Pro Phe Glu			
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Arg Asp Ile Ser	Thr Glu Ile Tyr	Gln Ala Gly Ser	Thr Pro Cys Asn			
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Gly Val Glu Gly	Phe Asn Cys Tyr	Phe Pro Leu Gln	Ser Tyr Gly Phe			
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Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu
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Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys Lys
545 550 555 560

Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn Gly
565 570 575

Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu Pro
580 585 590

Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val Arg
595 600 605

Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe Gly
610 615 620

Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val Ala
625 630 635 640

Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile His
645 650 655

Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser Asn
660 665 670

Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val Asn
675 680 685

Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser
690 695 700

Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala Ser
705 710 715 720

Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser Val
725 730 735

Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile Ser

740

745

750

Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val Asp
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Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe Asn
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Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser Phe
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Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe
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Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp Leu
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Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn Ser
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Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr
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Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu
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Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
1010 1015 1020

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr
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Lys Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe
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Pro Gln Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr
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Val Pro Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys
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His Asp Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser
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Asn Gly Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro
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Gln Ile Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp
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Val Val Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln

1160

1165

1170

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 1190 1195 1200

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<210> 12
 <211> 235
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> Dominio de unión al receptor de pico del tPA

<400> 12

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Ala	Val	Phe	Val	Ser	Ala	Ser	Gln	Glu	Ile	His	Ala	Arg	Phe	Arg	Arg
			20					25					30		

Pro	Asn	Ile	Thr	Asn	Leu	Cys	Pro	Phe	Gly	Glu	Val	Phe	Asn	Ala	Thr
		35					40					45			

Arg	Phe	Ala	Ser	Val	Tyr	Ala	Trp	Asn	Arg	Lys	Arg	Ile	Ser	Asn	Cys
	50					55					60				

Val	Ala	Asp	Tyr	Ser	Val	Leu	Tyr	Asn	Ser	Ala	Ser	Phe	Ser	Thr	Phe
65					70				75						80

Lys	Cys	Tyr	Gly	Val	Ser	Pro	Thr	Lys	Leu	Asn	Asp	Leu	Cys	Phe	Thr
				85					90					95	

Asn	Val	Tyr	Ala	Asp	Ser	Phe	Val	Ile	Arg	Gly	Asp	Glu	Val	Arg	Gln
			100					105					110		

Ile Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu
115 120 125

Pro Asp Asp Phe Thr Gly Cys Val Ile Ala Trp Asn Ser Asn Asn Leu
130 135 140

Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg
145 150 155 160

Lys Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr
165 170 175

Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr
180 185 190

Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr
195 200 205

Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu His Ala Pro
210 215 220

Ala Thr Val Cys Gly Pro Lys Lys Ser Thr Asn
225 230 235

<210> 13
<211> 708
<212> ADN
<213> Secuencia artificial

<220>
<223> que codifica el dominio de unión al receptor de proteína de pico del SARS-CoV2 con tPA

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gacagcttcg tgatccgtgg agatgaagtg cggcagattg cacctggaca gacaggcaag 360

atgccgact acaactacaa gctgcccgcac gacttcaccg gctgtgtgat tgcctggaac	420
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cagcccacaa atggcgtggg ctaccagcct tacagagtgg tgggtgctgag cttcgagctg	660
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<210> 14
 <211> 1304
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> proteína de prefusión de pico del tPA

<400> 14

Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Val	Leu	Leu	Leu	Cys	Gly
1				5					10					15	

Ala	Val	Phe	Val	Ser	Ala	Ser	Gln	Glu	Ile	His	Ala	Arg	Phe	Arg	Arg
			20					25					30		

Phe	Val	Phe	Leu	Val	Leu	Leu	Pro	Leu	Val	Ser	Ser	Gln	Cys	Val	Asn
			35				40					45			

Leu	Thr	Thr	Arg	Thr	Gln	Leu	Pro	Pro	Ala	Tyr	Thr	Asn	Ser	Phe	Thr
	50					55					60				

Arg	Gly	Val	Tyr	Tyr	Pro	Asp	Lys	Val	Phe	Arg	Ser	Ser	Val	Leu	His
65					70					75				80	

Ser	Thr	Gln	Asp	Leu	Phe	Leu	Pro	Phe	Phe	Ser	Asn	Val	Thr	Trp	Phe
			85					90						95	

His	Ala	Ile	His	Val	Ser	Gly	Thr	Asn	Gly	Thr	Lys	Arg	Phe	Asp	Asn
			100					105					110		

Pro	Val	Leu	Pro	Phe	Asn	Asp	Gly	Val	Tyr	Phe	Ala	Ser	Thr	Glu	Lys
		115					120					125			

Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser Lys
130 135 140

Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile Lys
145 150 155 160

Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr Tyr
165 170 175

His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr Ser
180 185 190

Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu Met
195 200 205

Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe Val
210 215 220

Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr Pro
225 230 235 240

Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu Pro
245 250 255

Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr Leu
260 265 270

Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser Gly
275 280 285

Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro Arg
290 295 300

Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala Val
305 310 315 320

Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys Ser
325 330 335

Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val Gln

340

345

350

Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys Pro
 355 360 365

Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala Trp
 370 375 380

Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr
 385 390 395 400

Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro Thr
 405 410 415

Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe Val
 420 425 430

Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Lys
 435 440 445

Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys Val
 450 455 460

Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr
 465 470 475 480

Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe Glu
 485 490 495

Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn
 500 505 510

Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe
 515 520 525

Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu
 530 535 540

Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys Lys
 545 550 555 560

Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn Gly
565 570 575

Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu Pro
580 585 590

Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val Arg
595 600 605

Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe Gly
610 615 620

Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val Ala
625 630 635 640

Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile His
645 650 655

Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser Asn
660 665 670

Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val Asn
675 680 685

Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser
690 695 700

Tyr Gln Thr Gln Thr Asn Ser Pro Gly Ser Ala Ser Ser Val Ala Ser
705 710 715 720

Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser Val
725 730 735

Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile Ser
740 745 750

Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val Asp
755 760 765

Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu Leu

770

775

780

Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr Gly
 785 790 795 800

Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln Val
 805 810 815

Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe Asn
 820 825 830

Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser Phe
 835 840 845

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

Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp Leu
 865 870 875 880

Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu
 885 890 895

Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly Thr
 900 905 910

Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro
 915 920 925

Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln
 930 935 940

Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn Ser
 945 950 955 960

Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala Leu
 965 970 975

Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr
 980 985 990

Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu
995 1000 1005

Asn Asp Ile Leu Ser Arg Leu Asp Pro Pro Glu Ala Glu Val Gln
1010 1015 1020

Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr
1025 1030 1035

Val Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala
1040 1045 1050

Asn Leu Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser
1055 1060 1065

Lys Arg Val Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe
1070 1075 1080

Pro Gln Ser Ala Pro His Gly Val Val Phe Leu His Val Thr Tyr
1085 1090 1095

Val Pro Ala Gln Glu Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys
1100 1105 1110

His Asp Gly Lys Ala His Phe Pro Arg Glu Gly Val Phe Val Ser
1115 1120 1125

Asn Gly Thr His Trp Phe Val Thr Gln Arg Asn Phe Tyr Glu Pro
1130 1135 1140

Gln Ile Ile Thr Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp
1145 1150 1155

Val Val Ile Gly Ile Val Asn Asn Thr Val Tyr Asp Pro Leu Gln
1160 1165 1170

Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys
1175 1180 1185

Asn His Thr Ser Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile

1190

1195

1200

Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn
1205 1210 1215

Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu
1220 1225 1230

Leu Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile Trp
1235 1240 1245

Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile
1250 1255 1260

Met Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys
1265 1270 1275

Cys Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu
1280 1285 1290

Pro Val Leu Lys Gly Val Lys Leu His Tyr Thr
1295 1300

<210> 15

<211> 3918

<212> ADN

<213> Secuencia artificial

<220>

<223> que codifica la proteína de prefusión de pico del SARS-CoV2 con tPA

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<210> 16
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Péptido por ELISpot

<400> 16

Met	Phe	Val	Phe	Leu	Val	Leu	Leu	Pro	Leu	Val	Ser	Ser	Gln	Cys
1				5					10					15

<210> 17
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Péptido por ELISpot

<400> 17

Leu	Val	Leu	Leu	Pro	Leu	Val	Ser	Ser	Gln	Cys	Val	Asn	Leu	Thr
1				5					10					15

<210> 18
<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Péptido por ELISpot

<400> 18

Pro	Leu	Val	Ser	Ser	Gln	Cys	Val	Asn	Leu	Thr	Thr	Arg	Thr	Gln
1				5					10					15

<210> 19

<211> 15
<212> PRT
<213> Secuencia artificial

<220>
<223> Péptido por ELISpot

<400> 19

Met	Phe	Val	Phe	Leu	Val	Leu	Leu	Pro	Leu	Val	Ser	Ser	Gln	Cys
1				5					10					15

<210> 20
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