

LISTADO DE SECUENCIAS

<110> Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA)

<120> Uso de flagelinas del género *Marinobacter* como adyuvantes vacunales

<130> CO-03251

<160> 33

<170> PatentIn version 3.5

<210> 1

<211> 1566

<212> DNA

<213> *Marinobacter algicola* (DG893)

<220>

<221> Flagelina F

<222> (1)..(1566)

<220>

<221> característica

<222> (1525)..(1545)

<223> Región que codifica para una cola de histidinas

<220>

<221> característica

<222> (1553)..(1563)

<223> Región que codifica para la secuencia KDEL

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gccaaggacg acgcccgcgg actggccatc tccgagcgat tcacatcgca gatcaaaggt	180
ctcaaccagg ccattcgaaa cgccaatgac ggtatttccc tggtcagac cgccgaaggc	240
gccctggggc aatccggaaa catcctgcag cgcacccggg aactcgccgt acagtccgcc	300
aacgctacca actccgcac tgacaggaag gccctgcagt ctgaagtaaa ccagctaaaa	360
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accttcagg ctcagaagtt ccaggctggc gccaacgaaa accagagcat cgccgtttcc	480
atcgaaggtg cccgaaccgc cgacctagca aacaacacgc tcgacgctgc caacgcaacc	540
ctgaaccagg gcaccggttc aacaacggca gcgatgcga cgttaccgcg aaaaaacacg	600
atcgccacgc agaattctac catttccagc tcgctggaca gccaggtggt gccattaca	660
gcaggtgaca cagcgggaaga catcgccgca gccatcaacg acattggtgc cagcaggggt	720
gtgaacgcaa cggcaagaac atcggcgacc ctgagcaaca ccgctaccac gccaatcgcc	780

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gccgggggaat tgacactgga ctctccggtt agcttcgcgg cgacgtctga cgccaccctg     1140
gccgcaggca gcgttctgaa cagtgcacag aataccgccg ccggctccac acctgaagaa     1200
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gagtcgacca ttgccaacct gagtacgacc tctgagaacc tttcggccgc gcgttcgcga     1380
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caggctggct tgtcgggtatt ggcccaggcc aacgcaagac cgcagcaggt tctgcagctg     1500
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ctgtaa                                                                    566

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<210> 2
<211> 521
<212> PRT
<213> Marinobacter algicola (DG893)

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<220>
<221> Flagelina F
<222> (1)..(521)

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<220>
<221> CARACTERÍSTICA
<222> (509)..(515)
<223> Cola de histidinas

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<220>
<221> CARACTERÍSTICA
<222> (518)..(521)
<223> Secuencia KDEL

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Asn Leu Asn Thr Ser Gln Glu Asp Ser Asn Val Ala Leu Gln Arg Leu
          20           25           30

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Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Leu
          35           40           45

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Val	Gln	Ser	Ala	Asn	Ala	Thr	Asn	Ser	Ala	Ser	Asp	Arg	Lys	Ala	Leu		
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Gln	Ser	Glu	Val	Asn	Gln	Leu	Lys	Gly	Glu	Leu	Glu	Arg	Ile	Ala	Thr		
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Thr	Thr	Glu	Phe	Asn	Gly	Leu	Lys	Leu	Leu	Asp	Gly	Thr	Phe	Gln	Ala		
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Gln	Lys	Phe	Gln	Ala	Gly	Ala	Asn	Glu	Asn	Gln	Ser	Ile	Ala	Val	Ser		
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Ala	Thr	Leu	Pro	Ala	Gln	Asn	Thr	Ile	Ala	Thr	Gln	Asn	Leu	Thr	Ile		
	195						200					205					
Ser	Ser	Ser	Leu	Asp	Ser	Gln	Val	Val	Pro	Ile	Thr	Ala	Gly	Asp	Thr		
	210					215					220						
Ala	Glu	Asp	Ile	Ala	Ala	Ala	Ile	Asn	Asp	Ile	Gly	Ala	Thr	Thr	Gly		
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Val	Asn	Ala	Thr	Ala	Arg	Thr	Ser	Ala	Thr	Leu	Ser	Asn	Thr	Ala	Thr		
			245						250					255			
Thr	Pro	Ile	Ala	Val	Pro	Gln	Thr	Val	Ser	Leu	Thr	Leu	Ser	Asn	Gly		
		260					265							270			
Ser	Ser	Ser	Ala	Thr	Ile	Ser	Ala	Gln	Ile	Thr	Asp	Ala	Asn	Asp	Leu		
		275					280					285					
Ser	Ala	Ile	Ala	Arg	Glu	Val	Asn	Ala	Ala	Ser	Gly	Lys	Thr	Gly	Ile		
	290					295					300						
Thr	Ala	Glu	Val	Ala	Asn	Asp	Gly	Ser	Ile	Thr	Leu	Ile	Gln	Glu	Gln		
305					310					315					320		
Gly	Lys	Asp	Ile	Thr	Ile	Glu	Asp	Phe	Thr	Ala	Ala	Gly	Ser	Gln	Gln		
			325						330					335			
Leu	Ala	Val	Gln	Gly	Ser	Gly	Asp	Pro	Ser	Ala	Ile	Glu	Leu	Thr	Asn		
			340					345					350				
Gly	Gly	Ala	Asn	Ala	Thr	Arg	Ile	Ala	Gly	Glu	Leu	Thr	Leu	Asp	Ser		
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Ser Val Ser Phe Ala Ala Thr Ser Asp Ala Thr Leu Ala Ala Gly Ser
370 375 380

Val Leu Asn Ser Ala Gln Asn Thr Ala Ala Gly Ser Thr Pro Glu Glu
385 390 395 400

Val Ala Gly Ile Asp Ile Ser Thr Val Asp Gly Ala Thr Ser Ala Leu
405 410 415

Ala Val Val Asp Ala Ala Leu Glu Thr Ile Ser Gly Ile Arg Ala Asp
420 425 430

Leu Gly Ala Ala Gln Asn Arg Leu Glu Ser Thr Ile Ala Asn Leu Ser
435 440 445

Thr Thr Ser Glu Asn Leu Ser Ala Ala Arg Ser Arg Ile Arg Asp Ala
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Asp Phe Ala Ala Glu Ser Ala Glu Leu Ala Arg Thr Gln Val Leu Gln
465 470 475 480

Gln Ala Gly Leu Ser Val Leu Ala Gln Ala Asn Ala Arg Pro Gln Gln
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Val Leu Gln Leu Leu Gln Gly Ala Cys Gly Ser Arg His His His His
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His His His Ala Arg Lys Asp Glu Leu
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<212> DNA
<213> Marinobacter algicola (DG893)

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<221> Flagelina FR
<222> (1)..(1557)

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<222> (1516)..(1536)
<223> Región que codifica para una cola de histidinas

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<222> (1543)..(1554)
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caagagcttg atcgtattgc cgggtaccacc cagtttaacg gcctcaacct tctggatggc 420
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actgtcagtc agggcacggg ttctgttgca gtcgcggccg ctgatgtggc aaccgttgcc 600
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<210> 4
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<212> PRT
<213> Marinobacter algicola (DG893)

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<223> Cola de histidinas

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<222> (514)..(518)

<223> Secuencia KDEL

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Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Leu
 35 40 45

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 50 55 60

Gln Arg Asn Ala Asn Asp Gly Ile Ser Leu Ala Gln Thr Ala Glu Gly
 65 70 75 80

Ala Leu Glu Glu Thr Thr Asn Ile Leu Gln Arg Ile Arg Glu Leu Ser
 85 90 95

Val Gln Ser Ala Asn Ser Thr Asn Ser Ser Ser Asp Arg Ser Ala Leu
 100 105 110

Gln Gly Glu Val Asn Gln Leu Lys Gln Glu Leu Asp Arg Ile Ala Gly
 115 120 125

Thr Thr Gln Phe Asn Gly Leu Asn Leu Leu Asp Gly Ser Phe Thr Ala
 130 135 140

Gln Ser Phe Gln Val Gly Ala Asn Ala Asn Gln Thr Ile Ser Val Ser
 145 150 155 160

Val Thr Gly Ala Arg Gly Ala Asp Leu Gly Asn Asn Thr Val Ser Gly
 165 170 175

Glu Ser Asp Thr Thr Val Ser Gln Gly Thr Gly Ser Val Ala Val Ala
 180 185 190

Ala Ala Asp Val Ala Thr Val Ala Asn Asn Thr Ile Ala Thr Gln Asn
 195 200 205

Ile Thr Val Ser Gly Thr Glu Gly Ser Glu Val Ile Gly Ile Thr Gln
 210 215 220

Gly Asp Thr Ala Glu Ala Ile Ala Ala Ala Val Asn Ala Glu Thr Gly
 225 230 235 240

Thr Thr Gly Val Thr Ala Thr Ala Ser Thr Thr Ala Thr Leu Ala Gly
 245 250 255

Leu Ser Asp Asp Gly Thr Val Ser Phe Thr Leu Gly Ser Gly Gly Asp
 260 265 270

Thr Ala Thr Ile Ser Ala Ala Val Thr Thr Thr Asp Leu Gly Ala Leu
 275 280 285

Ala Lys Ala Ile Asn Asp Thr Ser Gly Thr Thr Gly Val Thr Ala Glu
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 Ala Asn Gly Gly Glu Ile Thr Leu Thr Gln Ala Asp Gly Lys Asp Ile
 305 310 315 320
 Arg Leu Gln Asp Phe Ala Asn Ser Gly Asn Ala Thr Gly Thr Ala Thr
 325 330 335
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 340 345 350
 Thr Asp Ser Thr Ile Ala Ser Gly Ser Val Glu Phe Ala Ser Ser Gly
 355 360 365
 Ala Phe Ser Val Ser Ser Ser Val Ala Glu Thr Ala Gly Ser Ile Leu
 370 375 380
 Asn Val Ala Ala Asp Thr Val Val Gly Ser Asn Leu Gln Ser Val Ser
 385 390 395 400
 Ser Ile Asp Ile Gly Thr Val Ala Gly Ala Asn Ser Ala Ile Glu Ile
 405 410 415
 Ala Asp Ala Ala Leu Glu Gln Ile Ser Gly Ile Arg Ala Asp Leu Gly
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 Ala Ala Gln Asn Arg Phe Glu Ser Thr Ile Ala Asn Leu Ser Thr Thr
 435 440 445
 Ala Glu Asn Leu Ser Ala Ala Asn Ser Arg Ile Leu Asp Ala Asp Phe
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 Ala Ser Glu Thr Ala Lys Leu Ser Lys Ala Gln Val Leu Gln Gln Ala
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 Gly Ile Ser Val Leu Ala Gln Ala Asn Ala Arg Pro Gln Gln Val Leu
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<210> 5
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 <212> DNA
 <213> *Marinobacter algicola* (DG893)

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<223> Epítopo DUD

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<222> (1597)..(1671)

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<222> (1678)..(1752)

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<223> Epítopo DUD

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<210> 6
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<213> Marinobacter algicola (DG893)

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<222> (1)..(626)

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<222> (587)..(611)

<223> Epítopo DUD

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<223> Cola de histidinas

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<222> (624)..(627)

<223> Secuencia KDEL

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			20					25					30		

Ser	Ser	Gly	Leu	Arg	Ile	Asn	Ser	Ala	Lys	Asp	Asp	Ala	Ala	Gly	Leu
		35					40					45			

Ala	Ile	Ser	Glu	Arg	Phe	Thr	Ser	Gln	Ile	Lys	Gly	Leu	Asn	Gln	Ala
	50					55					60				

Ile	Arg	Asn	Ala	Asn	Asp	Gly	Ile	Ser	Leu	Ala	Gln	Thr	Ala	Glu	Gly
65					70					75					80

Ala	Leu	Gly	Glu	Ser	Gly	Asn	Ile	Leu	Gln	Arg	Ile	Arg	Glu	Leu	Ala
				85					90					95	

Val	Gln	Ser	Asn	Ala	Thr	Asn	Ser	Ala	Ser	Asp	Arg	Lys	Ala	Leu	Gln
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Ser	Glu	Val	Asn	Gln	Leu	Lys	Gly	Glu	Leu	Glu	Arg	Ile	Ala	Thr	Thr
		115					120					125			

Thr	Glu	Phe	Asn	Gly	Leu	Lys	Leu	Leu	Asp	Gly	Thr	Phe	Gln	Ala	Gln
	130					135					140				

Lys	Phe	Gln	Ala	Gly	Ala	Asn	Glu	Asn	Gln	Ser	Ile	Ala	Val	Ser	Ile
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Glu	Gly	Ala	Arg	Thr	Ala	Asp	Leu	Ala	Asn	Asn	Thr	Leu	Asp	Ala	Ala
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Asn	Ala	Thr	Leu	Asn	Gln	Gly	Thr	Gly	Ser	Thr	Thr	Ala	Ala	Asn	Ala
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Thr	Leu	Pro	Ala	Gln	Asn	Thr	Ile	Ala	Thr	Gln	Asn	Leu	Thr	Ile	Ser
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		210				215					220				

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 245 250 255
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 260 265 270
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 Ala Ile Ala Arg Glu Val Asn Ala Ala Ser Gly Lys Thr Gly Ile Thr
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 Ala Glu Val Ala Asn Asp Gly Ser Ile Thr Leu Ile Gln Glu Gln Gly
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 Gly Ala Ala Gln Asn Arg Leu Glu Ser Thr Ile Ala Asn Leu Ser Thr
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 450 455 460
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 465 470 475 480
 Ala Gly Leu Ser Val Leu Ala Gln Ala Asn Ala Arg Pro Gln Gln Val
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 Leu Gln Leu Leu Gln Gly Ala Cys His Pro Thr Glu Pro Tyr Thr Thr
 500 505 510
 Val Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn
 515 520 525
 Leu Gly Thr His Pro Thr Glu Pro Tyr Thr Thr Val Thr Thr Gln Asn
 530 535 540

Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu Ala Ser His Pro
545 550 555 560

Thr Glu Pro Tyr Thr Thr Val Thr Thr Gln Asn Thr Ala Ser Gln Thr
565 570 575

Met Ser Ala Ile Glu Asn Leu Leu Glu His Pro Thr Glu Pro Tyr Thr
580 585 590

Thr Val Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu
595 600 605

Asn Leu His His His His His His His His His His Ser Arg Lys Asp
610 615 620

Glu Leu
625

<210> 7
<211> 1875
<212> DNA
<213> Marinobacter algicola (DG893)

<220>
<221> Flagelina FR4DUD
<222> (1)..(1875)

<220>
<221> característica
<222> (1507)..(1581)
<223> Epítipo DUD

<220>
<221> característica
<222> (1588)..(1662)
<223> Epítipo DUD

<220>
<221> característica
<222> (1669)..(1743)
<223> Epítipo DUD

<220>
<221> característica
<222> (1750)..(1824)
<223> Epítipo DUD

<220>
<221> característica
<222> (1825)..(1854)
<223> Secuencia que codifica para una cola de histidinas

<220>
<221> característica
<222> (1861)..(1872)
<223> Secuencia que codifica para la secuencia KDEL

<400> 7
atggctctcg gtattaacac taacgttgcg tctactgtcag ctcagaacca gctgaacaaa 60
tcccaggagc tttctaacca agctctggag cgtctgtctt ccggtctgcg catcaactcc 120
gccaaggacg atgctgctgg ccttgcaatt tcgacccgtt ttcagtccca gatctctggt 180
ctgaatgttg cccagcgtaa cgccaacgac ggtatttccc tggctcagac tgctgaagggt 240
gctctggaag aaaccaccaa catcctgcag cgcacccgtg agctgtctgt tcagtcggcc 300
aactctacca actcttcttc cgaccgctct gcacttcagg gcgaagtaaa ccagctgaag 360
caagagcttg atcgtattgc cgggtaccacc cagttaaagc gcctcaacct tctggatggc 420
agcttcactg cccagtcatt ccaggttggt gccaacgcta accagaccat ctcggtctct 480
gtaactggcg ctctgtggtgc cgaccttggt aacaacaccg tatccggtga aagtgatacc 540
actgtcagtc agggcacggg ttctgttgca gtcgcggccg ctgatgtggc aaccgttgcc 600
aacaatacga ttgctacaca gaacatcacc gtttctggaa ctgaaggctc tgaggtcac 660
ggattatccc agggcgatac tgcagaagcg attgcggtctg ctgttaacgc tgaaaccggc 720
acgactggtg taacggctac ggcacccacc acggcaaccc tcgctggtct gtctgacgat 780
ggtagcggtt cctttacgct tggcagtggt ggcgacacag cgaccatctc cgcagcggt 840
acgaccactg acctgggtgc gctggccaaa gcgatcaacg atacctcagg caccactggt 900
gttagcgctg aagcaaacgg tggcgaaatc aactgaccc aggtgatggg caaagacatc 960
cgtctgcagg actttgccaa ctcaggtaac gcgaccggt 1020
ggtagcccat cagcggttac tttgaccgct ggcagcactg acagcacgat tgcttctggc 1080
tctgttgaat tcgcctcttc cgggtgcattc tcagtaagct cctctgtcgc agagactgcc 1140
ggtagcattc tgaacgtcgc agccgacacc gtggttggtt ccaacctcca gtcagtgtct 1200
tctatcgaca tcggtactgt tgcgggcgct aacagcgcaa tcgagattgc agatgcggct 1260
ctggagcaga tcagtgggat ccgcgccgat ctgggtgctg ccagaaccg gttcgagtct 1320
acgatcgcca acctgagcac aactgccgaa aacctgtcgg ccgctaacag ccggattctg 1380
gatgcagact tcgcatctga aactgctaag ctgtccaagg cgcaggttct ccagcaagct 1440
ggtagctctg tactggcaca ggcgaaatgc cgtccacagc aggttctgtc cctcctgcag 1500
caattccatc cgactgagcc ttacacgaca gtcactactc agaactgc ttcacaaaca 1560
atgtcggcta ttgaaaattt aggtacccat ccgactgagc cttacacgac agtcactact 1620
cagaacactg cttcacaac aatgtcggct attgaaaatt tagctagcca tccgactgag 1680
ccttacacga cagtcactac tcagaacact gcttcacaaa caatgtcggc tattgaaaat 1740

ttactcgagc atccgactga gccttacacg acagtcacta ctcagaacac tgcttcacaa 1800
 acaatgtcgg ctattgaaaa ttacacccat caccatcacc atcaccatca ccattctaga 1860
 aaagatgaac tgtaa 1875

<210> 8
 <211> 624
 <212> PRT
 <213> Marinobacter algicola (DG893)

<220>
 <221> Flagelina FR4DUD
 <222> (1)..(624)

<220>
 <221> CARACTERÍSTICA
 <222> (503)..(527)
 <223> Epítipo DUD

<220>
 <221> CARACTERÍSTICA
 <222> (530)..(554)
 <223> Epítipo DUD

<220>
 <221> CARACTERÍSTICA
 <222> (557)..(581)
 <223> Epítipo DUD

<220>
 <221> CARACTERÍSTICA
 <222> (584)..(608)
 <223> Epítipo DUD

<220>
 <221> CARACTERÍSTICA
 <222> (609)..(618)
 <223> Cola de histidinas

<220>
 <221> CARACTERÍSTICA
 <222> (621)..(624)
 <223> Secuencia KDEL

<400> 8

Met Ala Leu Gly Ile Asn Thr Asn Val Ala Ser Leu Ser Ala Gln Asn
 1 5 10 15
 Gln Leu Asn Lys Ser Gln Glu Leu Ser Asn Gln Ala Leu Glu Arg Leu
 20 25 30
 Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Leu
 35 40 45
 Ala Ile Ser Thr Arg Phe Gln Ser Gln Ile Ser Gly Leu Asn Val Ala
 50 55 60

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

Ala Phe Ser Val Ser Ser Ser Val Ala Glu Thr Ala Gly Ser Ile Leu
 370 375 380
 Asn Val Ala Ala Asp Thr Val Val Gly Ser Asn Leu Gln Ser Val Ser
 385 390 395 400
 Ser Ile Asp Ile Gly Thr Val Ala Gly Ala Asn Ser Ala Ile Glu Ile
 405 410 415
 Ala Asp Ala Ala Leu Glu Gln Ile Ser Gly Ile Arg Ala Asp Leu Gly
 420 425 430
 Ala Ala Gln Asn Arg Phe Glu Ser Thr Ile Ala Asn Leu Ser Thr Thr
 435 440 445
 Ala Glu Asn Leu Ser Ala Ala Asn Ser Arg Ile Leu Asp Ala Asp Phe
 450 455 460
 Ala Ser Glu Thr Ala Lys Leu Ser Lys Ala Gln Val Leu Gln Gln Ala
 465 470 475 480
 Gly Ile Ser Val Leu Ala Gln Ala Asn Ala Arg Pro Gln Gln Val Leu
 485 490 495
 Ser Leu Leu Gln Gln Phe His Pro Thr Glu Pro Tyr Thr Thr Val Thr
 500 505 510
 Thr Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu Gly
 515 520 525
 Thr His Pro Thr Glu Pro Tyr Thr Thr Val Thr Thr Gln Asn Thr Ala
 530 535 540
 Ser Gln Thr Met Ser Ala Ile Glu Asn Leu Ala Ser His Pro Thr Glu
 545 550 555 560
 Pro Tyr Thr Thr Val Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser
 565 570 575
 Ala Ile Glu Asn Leu Leu Glu His Pro Thr Glu Pro Tyr Thr Thr Val
 580 585 590
 Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu
 595 600 605
 His His His His His His His His His His Ser Arg Lys Asp Glu Leu
 610 615 620

<210> 9
 <211> 1893
 <212> DNA
 <213> Salmonella typhimurium

<220>
 <221> Flagelina STF4DUD
 <222> (1)..(1893)
 <220>

<221> característica
 <222> (1525)..(1599)
 <223> Epítopo DUD

<220>
 <221> característica
 <222> (1606)..(1680)
 <223> Epítopo DUD

<220>
 <221> característica
 <222> (1686)..(1761)
 <223> Epítopo DUD

<220>
 <221> característica
 <222> (1768)..(1842)
 <223> Epítopo DUD

<220>
 <221> característica
 <222> (1843)..(1872)
 <223> Secuencia que codifica para una cola de histidinas

<220>
 <221> característica
 <222> (1889)..(1890)
 <223> Secuencia que codifica para la secuencia KDEL

<400> 9
 atggcacaag taatcaacac taacagtctg tcgctgctga cccagaataa cctgaacaaa 60
 tcccagtcg cactgggcac cgctatcgag cgtctgtctt ctggctctgcg tatcaacagc 120
 gcgaaagacg atgcggcagg tcaggcgatt gctaaccggt tcaccgcgaa catcaaaggt 180
 ctgactcagg ctccccgtaa cgctaacgac ggtatctcca ttgcgcagac cactgaaggc 240
 gcgctgaacg aaatcaacaa caacctgcag cgtgtgcgtg aactggcggt tcagtctgct 300
 aacagcacca actcccagtc tgacctcgac tccatccagg ctgaaatcac ccagcgcctg 360
 aacgaaatcg accgtgtatc cggccagact cagttcaacg gcgtgaaagt cctggcgcag 420
 gacaacaccc tgaccatcca ggttggcgcc aacgacggtg aaactatcga tatcgatctg 480
 aagcagatca actctcagac cctgggtctg gactcactga acgtgcagaa agcgtatgat 540
 gtgaaagata cagcagtaac aacgaaagct tatgccaata atggtactac actggatgta 600
 tcgggtcttg atgatgcagc tattaaagcg gctacgggtg gtacgaatgg tacggcttct 660
 gtaaccggtg gtgcggttaa atttgacgca gataataaca agtactttgt tactattggt 720
 ggctttactg gtgctgatgc cgccaaaaat ggcgattatg aagttaacgt tgctactgac 780
 ggtacagtaa cccttgcggc tggcgcaact aagaccacaa tgctgctgg tgcgacaact 840
 aaaacagaag tacaggagtt aaaagataca ccggcagttg tttcagcaga tgctaaaaat 900

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gccttaattg ctggcggcgt tgacgctacc gatgctaattg gcgctgagtt ggtcaaaatg      960
tcttataaccg ataaaaatgg taagacaatt gaaggcgggtt atgcgcttaa agctggcgat      1020
aagtattacg ccgcagatta cgatgaagcg acaggagcaa ttaaagctaa aaccacaagt      1080
tatactgctg ctgacggcac taccaaaaca gcggctaacc aactgggtgg cgtagacggt      1140
aaaaccgaag tcgttactat cgacggtaaa acctacaatg ccagcaaagc cgctgggtcat      1200
gatttcaaag cacaaccaga gctggcggaa gcagccgcta aaaccaccga aaacccgctg      1260
cagaaaattg atgccgcgct ggcgaggtg gatgcgctgc gctctgatct ggggtgcggta      1320
caaaaccgtt tcaactctgc taccaccaac ctgggcaata ccgtaaaca tctgtctgaa      1380
gcgcgtagcc gtatcgaaga ttccgactac gcgaccgaag tttccaacat gtctcgcgcg      1440
cagattctgc agcaggccgg tacttccgtt ctggcgcagg ctaaccaggt cccgcagaac      1500
gtgctgtctc tgttacgtga attccatccg actgagcctt acacgacagt cactactcag      1560
aacactgctt cacaacaat gtcggctatt gaaaatttag gtacccatcc gactgagcct      1620
tacacgacag tcaactactca gaacactgct tcacaaaca tgtcggctat tgaaaattta      1680
gctagccatc cgactgagcc ttacacgaca gtcactactc agaacactgc ttcacaaaca      1740
atgtcggcta ttgaaaattt actcgagcat ccgactgagc cttacacgac agtcactact      1800
cagaacactg cttcacaac aatgtcggct attgaaaatt tacaccatca ccatcaccat      1860
caccatcacc attctagaaa agatgaactg taa                                     1893

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<210> 10
<211> 630
<212> PRT
<213> Salmonella typhimurium

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<220>
<221> Flagelina STF4DUD
<222> (1)..(630)

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<220>
<221> CARACTERÍSTICA
<222> (509)..(533)
<223> Epítipo DUD

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<220>
<221> CARACTERÍSTICA
<222> (536)..(560)
<223> Epítipo DUD

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<220>
<221> CARACTERÍSTICA
<222> (563)..(587)
<223> Epítipo DUD

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<220>
 <221> CARACTERÍSTICA
 <222> (590)..(614)
 <223> Epítipo DUD

<220>
 <221> CARACTERÍSTICA
 <222> (615)..(624)
 <223> Cola de histidinas

<220>
 <221> CARACTERÍSTICA
 <222> (627)..(630)
 <223> Secuencia KDEL

<400> 10

Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln Asn
 1 5 10 15

Asn Leu Asn Lys Ser Gln Ser Ala Leu Gly Thr Ala Ile Glu Arg Leu
 20 25 30

Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln
 35 40 45

Ala Ile Ala Asn Arg Phe Thr Ala Asn Ile Lys Gly Leu Thr Gln Ala
 50 55 60

Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly
 65 70 75 80

Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ala
 85 90 95

Val Gln Ser Ala Asn Ser Thr Asn Ser Gln Ser Asp Leu Asp Ser Ile
 100 105 110

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

Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ala Gln Asp Asn Thr Leu
 130 135 140

Thr Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Asp Ile Asp Leu
 145 150 155 160

Lys Gln Ile Asn Ser Gln Thr Leu Gly Leu Asp Ser Leu Asn Val Gln
 165 170 175

Lys Ala Tyr Asp Val Lys Asp Thr Ala Val Thr Thr Lys Ala Tyr Ala
 180 185 190

Asn Asn Gly Thr Thr Leu Asp Val Ser Gly Leu Asp Asp Ala Ala Ile
 195 200 205

Lys Ala Ala Thr Gly Gly Thr Asn Gly Thr Ala Ser Val Thr Gly Gly
 210 215 220

Ala	Val	Lys	Phe	Asp	Ala	Asp	Asn	Asn	Lys	Tyr	Phe	Val	Thr	Ile	Gly	225	230	235	240
Gly	Phe	Thr	Gly	Ala	Asp	Ala	Ala	Lys	Asn	Gly	Asp	Tyr	Glu	Val	Asn	245	250	255	
Val	Ala	Thr	Asp	Gly	Thr	Val	Thr	Leu	Ala	Ala	Gly	Ala	Thr	Lys	Thr	260	265	270	
Thr	Met	Pro	Ala	Gly	Ala	Thr	Thr	Lys	Thr	Glu	Val	Gln	Glu	Leu	Lys	275	280	285	
Asp	Thr	Pro	Ala	Val	Val	Ser	Ala	Asp	Ala	Lys	Asn	Ala	Leu	Ile	Ala	290	295	300	
Gly	Gly	Val	Asp	Ala	Thr	Asp	Ala	Asn	Gly	Ala	Glu	Leu	Val	Lys	Met	305	310	315	320
Ser	Tyr	Thr	Asp	Lys	Asn	Gly	Lys	Thr	Ile	Glu	Gly	Gly	Tyr	Ala	Leu	325	330	335	
Lys	Ala	Gly	Asp	Lys	Tyr	Tyr	Ala	Ala	Asp	Tyr	Asp	Glu	Ala	Thr	Gly	340	345	350	
Ala	Ile	Lys	Ala	Lys	Thr	Thr	Ser	Tyr	Thr	Ala	Ala	Asp	Gly	Thr	Thr	355	360	365	
Lys	Thr	Ala	Ala	Asn	Gln	Leu	Gly	Gly	Val	Asp	Gly	Lys	Thr	Glu	Val	370	375	380	
Val	Thr	Ile	Asp	Gly	Lys	Thr	Tyr	Asn	Ala	Ser	Lys	Ala	Ala	Gly	His	385	390	395	400
Asp	Phe	Lys	Ala	Gln	Pro	Glu	Leu	Ala	Glu	Ala	Ala	Ala	Lys	Thr	Thr	405	410	415	
Glu	Asn	Pro	Leu	Gln	Lys	Ile	Asp	Ala	Ala	Leu	Ala	Gln	Val	Asp	Ala	420	425	430	
Leu	Arg	Ser	Asp	Leu	Gly	Ala	Val	Gln	Asn	Arg	Phe	Asn	Ser	Ala	Ile	435	440	445	
Thr	Asn	Leu	Gly	Asn	Thr	Val	Asn	Asn	Leu	Ser	Glu	Ala	Arg	Ser	Arg	450	455	460	
Ile	Glu	Asp	Ser	Asp	Tyr	Ala	Thr	Glu	Val	Ser	Asn	Met	Ser	Arg	Ala	465	470	475	480
Gln	Ile	Leu	Gln	Gln	Ala	Gly	Thr	Ser	Val	Leu	Ala	Gln	Ala	Asn	Gln	485	490	495	
Val	Pro	Gln	Asn	Val	Leu	Ser	Leu	Leu	Arg	Glu	Phe	His	Pro	Thr	Glu	500	505	510	
Pro	Tyr	Thr	Thr	Val	Thr	Thr	Gln	Asn	Thr	Ala	Ser	Gln	Thr	Met	Ser	515	520	525	
Ala	Ile	Glu	Asn	Leu	Gly	Thr	His	Pro	Thr	Glu	Pro	Tyr	Thr	Thr	Val	530	535	540	

Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu
545 550 555 560

Ala Ser His Pro Thr Glu Pro Tyr Thr Thr Val Thr Thr Gln Asn Thr
565 570 575

Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu Leu Glu His Pro Thr
580 585 590

Glu Pro Tyr Thr Thr Val Thr Thr Gln Asn Thr Ala Ser Gln Thr Met
595 600 605

Ser Ala Ile Glu Asn Leu His His His His His His His His His His
610 615 620

Ser Arg Lys Asp Glu Leu
625 630

<210> 11
<211> 29
<212> DNA
<213> Salmonella typhimurium

<220>
<221> característica
<223> Cebador 5' de la flagelina STF

<400> 11
gccggatcca tggcacaagt aatcaacac

29

<210> 12
<211> 27
<212> DNA
<213> Salmonella typhimurium

<220>
<221> característica
<223> Cebador 3' de la flagelina STF

<400> 12
gcggaattca cgtaacagag acagcac

27

<210> 13
<211> 13
<212> PRT
<213> Virus de la peste porcina africana (PPA)

<220>
<221> CARACTERÍSTICA
<222> (1)..(13)
<223> Dominio de unión de la proteína p54 a la dineína DCL8

<400> 13

Tyr Thr Thr Val Thr Thr Gln Asn Thr Ala Ser Gln Thr
1 5 10

<210> 14

<211> 25
 <212> PRT
 <213> Virus de la peste porcina africana (PPA)

<220>
 <221> CARACTERÍSTICA
 <222> (1)..(25)
 <223> Péptido modificado de la zona de unión de la proteína p54 a dineína (DUD modificado)

<220>
 <221> CARACTERÍSTICA
 <222> (1)..(5)
 <223> Secuencia de aminoácidos añadidos en el extremo 5´

<220>
 <221> CARACTERÍSTICA
 <222> (19)..(5)
 <223> Secuencia de aminoácidos añadidos en el extremo 3´

<400> 14

His	Pro	Thr	Glu	Pro	Tyr	Thr	Thr	Val	Thr	Thr	Gln	Asn	Thr	Ala	Ser
1				5					10					15	

Gln	Thr	Met	Ser	Ala	Ile	Glu	Asn	Leu
			20					25

<210> 15
 <211> 495
 <212> PRT
 <213> Salmonella typhimurium

<220>
 <221> Flagelina STF
 <222> (1)..(495)

<400> 15

Met	Ala	Gln	Val	Ile	Asn	Thr	Asn	Ser	Leu	Ser	Leu	Leu	Thr	Gln	Asn
1				5					10					15	

Asn	Leu	Asn	Lys	Ser	Gln	Ser	Ala	Leu	Gly	Thr	Ala	Ile	Glu	Arg	Leu
			20					25					30		

Ser	Ser	Gly	Leu	Arg	Ile	Asn	Ser	Ala	Lys	Asp	Asp	Ala	Ala	Gly	Gln
		35					40					45			

Ala	Ile	Ala	Asn	Arg	Phe	Thr	Ala	Asn	Ile	Lys	Gly	Leu	Thr	Gln	Ala
	50					55					60				

Ser	Arg	Asn	Ala	Asn	Asp	Gly	Ile	Ser	Ile	Ala	Gln	Thr	Thr	Glu	Gly
65				70					75					80	

Ala	Leu	Asn	Glu	Ile	Asn	Asn	Asn	Leu	Gln	Arg	Val	Arg	Glu	Leu	Ala
				85				90						95	

Val	Gln	Ser	Ala	Asn	Ser	Thr	Asn	Ser	Gln	Ser	Asp	Leu	Asp	Ser	Ile
			100					105					110		

Gln Ala Glu Ile Thr Gln Arg Leu Asn Glu Ile Asp Arg Val Ser Gly
 115 120 125
 Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ala Gln Asp Asn Thr Leu
 130 135 140
 Thr Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Asp Ile Asp Leu
 145 150 155 160
 Lys Gln Ile Asn Ser Gln Thr Leu Gly Leu Asp Thr Leu Asn Val Gln
 165 170 175
 Gln Lys Tyr Lys Val Ser Asp Thr Ala Ala Thr Val Thr Gly Tyr Ala
 180 185 190
 Asp Thr Thr Ile Ala Leu Asp Asn Ser Thr Phe Lys Ala Ser Ala Thr
 195 200 205
 Gly Leu Gly Gly Thr Asp Gln Lys Ile Asp Gly Asp Leu Lys Phe Asp
 210 215 220
 Asp Thr Thr Gly Lys Tyr Tyr Ala Lys Val Thr Val Thr Gly Gly Thr
 225 230 235 240
 Gly Lys Asp Gly Tyr Tyr Glu Val Ser Val Asp Lys Thr Asn Gly Glu
 245 250 255
 Val Thr Leu Ala Gly Gly Ala Thr Ser Pro Leu Thr Gly Gly Leu Pro
 260 265 270
 Ala Thr Ala Thr Glu Asp Val Lys Asn Val Gln Val Ala Asn Ala Asp
 275 280 285
 Leu Thr Glu Ala Lys Ala Ala Leu Thr Ala Ala Gly Val Thr Gly Thr
 290 295 300
 Ala Ser Val Val Lys Met Ser Tyr Thr Asp Asn Asn Gly Lys Thr Ile
 305 310 315 320
 Asp Gly Gly Leu Ala Val Lys Val Gly Asp Asp Tyr Tyr Ser Ala Thr
 325 330 335
 Gln Asn Lys Asp Gly Ser Ile Ser Ile Asn Thr Thr Lys Tyr Thr Ala
 340 345 350
 Asp Asp Gly Thr Ser Lys Thr Ala Leu Asn Lys Leu Gly Gly Ala Asp
 355 360 365
 Gly Lys Thr Glu Val Val Ser Ile Gly Gly Lys Thr Tyr Ala Ala Ser
 370 375 380
 Lys Ala Glu Gly His Asn Phe Lys Ala Gln Pro Asp Leu Ala Glu Ala
 385 390 395 400

Phe Asn Ser Ala Ile Thr Asn Leu Gly Asn Thr Val Asn Asn Leu Thr
435 440 445

Ser Ala Arg Ser Arg Ile Glu Asp Ser Asp Tyr Ala Thr Glu Val Ser
450 455 460

Asn Met Ser Arg Ala Gln Ile Leu Gln Gln Ala Gly Thr Ser Val Leu
465 470 475 480

Ala Gln Ala Asn Gln Val Pro Gln Asn Val Leu Ser Leu Leu Arg
485 490 495

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<210> 16
<211> 15
<212> PRT
<213> Marinobacter algicola (DG893)
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<220>
<221> Secuencia de interacción de la flagelina FR con TLR5
<222> (1)..(15)
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<400> 16

Asn Ile Leu Gln Arg Ile Arg Glu Leu Ser Val Gln Ser Ala Asn
1 5 10 15

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<210> 17
<211> 15
<212> PRT
<213> Marinobacter algicola (DG893)
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<220>
<221> Secuencia de interacción de la flagelina F con TLR5
<222> (1)..(15)
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<400> 17

Asn Ile Leu Gln Arg Ile Arg Glu Leu Ala Val Gln Ser Ala Asn
1 5 10 15

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<210> 18
<211> 17
<212> PRT
<213> Marinobacter algicola (DG893)
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<220>
<221> Secuencia ampliada de interacción de la flagelina F con TLR5
<222> (1)..(17)
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<400> 18

Asn Ile Leu Gln Arg Ile Arg Glu Leu Ala Val Gln Ser Ala Asn Ala
1 5 10 15

Thr

<210> 19
 <211> 1512
 <212> DNA
 <213> *Marinobacter algicola* (DG893)

<220>
 <221> Flagelina F
 <222> (1)..(1512)

<400> 19
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 gccaaaggacg acgccgccgg actggccatc tccgagcgat tcacatcgca gatcaaaggt 180
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 gcggcattgg aaaccatcag tggcattcgt gccgatctgg gcgccgcgca gaatcgactc 1320
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caggctggct tgtcgggtatt ggcccaggcc aacgcaagac cgcagcaggt tctgcagctg      1500
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<210> 20
<211> 503
<212> PRT
<213> Marinobacter algicola (DG893)

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<220>
<221> Flagelina F
<222> (1)..(503)

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<400> 20

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

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Ser Ser Ser Leu Asp Ser Gln Val Val Pro Ile Thr Ala Gly Asp Thr
 210 215 220
 Ala Glu Asp Ile Ala Ala Ala Ile Asn Asp Ile Gly Ala Thr Thr Gly
 225 230 235 240
 Val Asn Ala Thr Ala Arg Thr Ser Ala Thr Leu Ser Asn Thr Ala Thr
 245 250 255
 Thr Pro Ile Ala Val Pro Gln Thr Val Ser Leu Thr Leu Ser Asn Gly
 260 265 270
 Ser Ser Ser Ala Thr Ile Ser Ala Gln Ile Thr Asp Ala Asn Asp Leu
 275 280 285
 Ser Ala Ile Ala Arg Glu Val Asn Ala Ala Ser Gly Lys Thr Gly Ile
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 Thr Ala Glu Val Ala Asn Asp Gly Ser Ile Thr Leu Ile Gln Glu Gln
 305 310 315 320
 Gly Lys Asp Ile Thr Ile Glu Asp Phe Thr Ala Ala Gly Ser Gln Gln
 325 330 335
 Leu Ala Val Gln Gly Ser Gly Asp Pro Ser Ala Ile Glu Leu Thr Asn
 340 345 350
 Gly Gly Ala Asn Ala Thr Arg Ile Ala Gly Glu Leu Thr Leu Asp Ser
 355 360 365
 Ser Val Ser Phe Ala Ala Thr Ser Asp Ala Thr Leu Ala Ala Gly Ser
 370 375 380
 Val Leu Asn Ser Ala Gln Asn Thr Ala Ala Gly Ser Thr Pro Glu Glu
 385 390 395 400
 Val Ala Gly Ile Asp Ile Ser Thr Val Asp Gly Ala Thr Ser Ala Leu
 405 410 415
 Ala Val Val Asp Ala Ala Leu Glu Thr Ile Ser Gly Ile Arg Ala Asp
 420 425 430
 Leu Gly Ala Ala Gln Asn Arg Leu Glu Ser Thr Ile Ala Asn Leu Ser
 435 440 445
 Thr Thr Ser Glu Asn Leu Ser Ala Ala Arg Ser Arg Ile Arg Asp Ala
 450 455 460
 Asp Phe Ala Ala Glu Ser Ala Glu Leu Ala Arg Thr Gln Val Leu Gln
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 Gln Ala Gly Leu Ser Val Leu Ala Gln Ala Asn Ala Arg Pro Gln Gln
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 Val Leu Gln Leu Leu Gln Gly
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<210> 21

<211> 1503

<212> DNA

<213> Marinobacter algicola (DG893)

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<221> Flagelina FR

<222> (1) . . (1503)

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gctctggaag	aaaccaccaa	catcctgcag	cgcattccgtg	agctgtctgt	tcagtcggcc	300
aactctacca	actcttcttc	cgaccgctct	gcacttcagg	gcgaagtaaa	ccagctgaag	360
caagagcttg	atcgatttgc	cggtaccacc	cagtttaacg	gcctcaacct	tctggatggc	420
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actgtcagtc	aggggcacggg	ttctgttgca	gtcgcgggccg	ctgatgtggc	aaccgttgcc	600
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cgtctgcagg	actttgccaa	ctcaggtaac	gcgaccggta	ccgccacgct	gcagggcagc	1020
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gatgcagact	tcgcatctga	aactgctaag	ctgtccaagg	cgcaggttct	ccagcaagct	1440
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taa						1503

<210> 22
 <211> 500
 <212> PRT
 <213> *Marinobacter algicola* (DG893)

<220>
 <221> Flagelina FR
 <222> (1)..(500)

<400> 22

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

Leu Ser Asp Asp Gly Thr Val Ser Phe Thr Leu Gly Ser Gly Gly Asp
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 Thr Ala Thr Ile Ser Ala Ala Val Thr Thr Thr Asp Leu Gly Ala Leu
 275 280 285
 Ala Lys Ala Ile Asn Asp Thr Ser Gly Thr Thr Gly Val Thr Ala Glu
 290 295 300
 Ala Asn Gly Gly Glu Ile Thr Leu Thr Gln Ala Asp Gly Lys Asp Ile
 305 310 315 320
 Arg Leu Gln Asp Phe Ala Asn Ser Gly Asn Ala Thr Gly Thr Ala Thr
 325 330 335
 Leu Gln Gly Ser Gly Asp Pro Ser Ala Val Thr Leu Thr Ala Gly Ser
 340 345 350
 Thr Asp Ser Thr Ile Ala Ser Gly Ser Val Glu Phe Ala Ser Ser Gly
 355 360 365
 Ala Phe Ser Val Ser Ser Ser Val Ala Glu Thr Ala Gly Ser Ile Leu
 370 375 380
 Asn Val Ala Ala Asp Thr Val Val Gly Ser Asn Leu Gln Ser Val Ser
 385 390 395 400
 Ser Ile Asp Ile Gly Thr Val Ala Gly Ala Asn Ser Ala Ile Glu Ile
 405 410 415
 Ala Asp Ala Ala Leu Glu Gln Ile Ser Gly Ile Arg Ala Asp Leu Gly
 420 425 430
 Ala Ala Gln Asn Arg Phe Glu Ser Thr Ile Ala Asn Leu Ser Thr Thr
 435 440 445
 Ala Glu Asn Leu Ser Ala Ala Asn Ser Arg Ile Leu Asp Ala Asp Phe
 450 455 460
 Ala Ser Glu Thr Ala Lys Leu Ser Lys Ala Gln Val Leu Gln Gln Ala
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 Ser Leu Leu Gln
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<210> 23
 <211> 1836
 <212> DNA
 <213> *Marinobacter algicola* (DG893)

<220>
 <221> Flagelina F4DUD
 <222> (1)..(1836)

<220>

<221> característica
 <222> (1516)..(1590)
 <223> Epítopo DUD

<220>
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 <222> (1597)..(1671)
 <223> Epítopo DUD

<220>
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 <222> (1678)..(1752)
 <223> Epítopo DUD

<220>
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 <222> (1759)..(1833)
 <223> Epítopo DUD

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<210> 24
<211> 610
<212> PRT
<213> Marinobacter algicola (DG893)

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<220>
<221> Flagelina F4DUD
<222> (1)..(610)

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<220>
<221> CARACTERÍSTICA
<222> (506)..(530)
<223> Epítipo DUD

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<220>
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<222> (533)..(557)
<223> Epítipo DUD

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<220>
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<222> (560)..(584)
<223> Epítipo DUD

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<220>
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<222> (587)..(610)
<223> Epítipo DUD

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<400> 24

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1           5           10           15

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Ser	Ser	Gly 35	Leu	Arg	Ile	Asn 40	Ser	Ala	Lys	Asp	Asp	Ala 45	Ala	Gly	Leu
Ala	Ile 50	Ser	Glu	Arg	Phe	Thr 55	Ser	Gln	Ile	Lys	Gly 60	Leu	Asn	Gln	Ala
Ile 65	Arg	Asn	Ala	Asn	Asp 70	Gly	Ile	Ser	Leu	Ala 75	Gln	Thr	Ala	Glu	Gly 80
Ala	Leu	Gly	Glu	Ser 85	Gly	Asn	Ile	Leu	Gln 90	Arg	Ile	Arg	Glu	Leu 95	Ala
Val	Gln	Ser	Asn 100	Ala	Thr	Asn	Ser 105	Ala	Ser	Asp	Arg	Lys 110	Ala	Leu	Gln
Ser	Glu 115	Val	Asn	Gln	Leu	Lys	Gly 120	Glu	Leu	Glu	Arg	Ile 125	Ala	Thr	Thr
Thr	Glu 130	Phe	Asn	Gly	Leu	Lys 135	Leu	Leu	Asp	Gly	Thr 140	Phe	Gln	Ala	Gln
Lys 145	Phe	Gln	Ala	Gly	Ala 150	Asn	Glu	Asn	Gln	Ser 155	Ile	Ala	Val	Ser	Ile 160
Glu	Gly	Ala	Arg	Thr 165	Ala	Asp	Leu	Ala 170	Asn	Asn	Thr	Leu	Asp	Ala 175	Ala
Asn	Ala	Thr	Leu 180	Asn	Gln	Gly	Thr	Gly 185	Ser	Thr	Thr	Ala 190	Ala	Asn	Ala
Thr	Leu 195	Pro	Ala	Gln	Asn	Thr	Ile 200	Ala	Thr	Gln	Asn	Leu 205	Thr	Ile	Ser
Ser 210	Ser	Leu	Asp	Ser	Gln	Val 215	Val	Pro	Ile	Thr	Ala 220	Gly	Asp	Thr	Ala
Glu 225	Asp	Ile	Ala	Ala	Ala 230	Ile	Asn	Asp	Ile	Gly 235	Ala	Thr	Thr	Gly	Val 240
Asn	Ala	Thr	Ala	Arg 245	Thr	Ser	Ala	Thr	Leu 250	Ser	Asn	Thr	Ala	Thr 255	Thr
Pro	Ile	Ala	Val 260	Pro	Gln	Thr	Val	Ser 265	Leu	Thr	Leu	Ser	Asn 270	Gly	Ser
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Ala 290	Ile	Ala	Arg	Glu	Val	Asn 295	Ala	Ala	Ser	Gly	Lys 300	Thr	Gly	Ile	Thr
Ala 305	Glu	Val	Ala	Asn	Asp 310	Gly	Ser	Ile	Thr	Leu 315	Ile	Gln	Glu	Gln	Gly 320
Lys	Asp	Ile	Thr	Ile 325	Glu	Asp	Phe	Thr 330	Ala	Ala	Gly	Ser	Gln	Gln 335	Leu

Ala Val Gln Gly Ser Gly Asp Pro Ser Ala Ile Glu Leu Thr Asn Gly
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 Gly Ala Asn Ala Thr Arg Ile Ala Gly Glu Leu Thr Leu Asp Ser Ser
 355 360 365
 Val Ser Phe Ala Ala Thr Ser Asp Ala Thr Leu Ala Ala Gly Ser Val
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 Leu Asn Ser Ala Gln Asn Thr Ala Ala Gly Ser Thr Pro Glu Glu Val
 385 390 395 400
 Ala Gly Ile Asp Ile Ser Thr Val Asp Gly Ala Thr Ser Ala Leu Ala
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 Gly Ala Ala Gln Asn Arg Leu Glu Ser Thr Ile Ala Asn Leu Ser Thr
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 Thr Ser Glu Asn Leu Ser Ala Ala Arg Ser Arg Ile Arg Asp Ala Asp
 450 455 460
 Phe Ala Ala Glu Ser Ala Glu Leu Ala Arg Thr Gln Val Leu Gln Gln
 465 470 475 480
 Ala Gly Leu Ser Val Leu Ala Gln Ala Asn Ala Arg Pro Gln Gln Val
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 Leu Gln Leu Leu Gln Gly Ala Cys His Pro Thr Glu Pro Tyr Thr Thr
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 Val Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn
 515 520 525
 Leu Gly Thr His Pro Thr Glu Pro Tyr Thr Thr Val Thr Thr Gln Asn
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 565 570 575
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 580 585 590
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 Asn Leu
 610

<210> 25

<211> 1827

<212> DNA

<213> *Marinobacter algicola* (DG893)

<220>
 <221> Flagelina FR4DUD
 <222> (1)..(1827)

<220>
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 <222> (1507)..(1581)
 <223> Epítopo DUD

<220>
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 <222> (1588)..(1662)
 <223> Epítopo DUD

<220>
 <221> característica
 <222> (1669)..(1743)
 <223> Epítopo DUD

<220>
 <221> característica
 <222> (1750)..(1824)
 <223> Epítopo DUD

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ggtagcattc tgaacgtcgc agccgacacc gtggttggtt ccaacctcca gtcagtgtct 1200
tctatcgaca tcggtactgt tgccggcgct aacagcgcaa tcgagattgc agatgcggct 1260
ctggagcaga tcagtgggtat ccgcgccgat ctgggtgctg cccagaaccg gttcgagtct 1320
acgatcgcca acctgagcac aactgccgaa aacctgtcgg ccgctaacag ccggattctg 1380
gatgcagact tcgcatctga aactgctaag ctgtccaagg cgcaggttct ccagcaagct 1440
ggatatctctg tactggcaca ggccaatgcc cgtccacagc aggttctgtc cctcctgcag 1500
caattccatc cgactgagcc ttacacgaca gtcactactc agaactgc ttcacaaaca 1560
atgtcggcta ttgaaaattt aggtacccat ccgactgagc cttacacgac agtcactact 1620
cagaacactg cttcacaac aatgtcggct attgaaaatt tagctagcca tccgactgag 1680
ccttacacga cagtcactac tcagaacact gtttcacaaa caatgtcggc tattgaaaat 1740
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acaatgtcgg ctattgaaaa ttataa 1827

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<210> 26
<211> 608
<212> PRT
<213> Marinobacter algicola (DG893)

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<220>
<221> Flagelina FR4DUD
<222> (1)..(608)

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<220>
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<222> (503)..(527)
<223> Epítipo DUD

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<220>
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<222> (530)..(554)
<223> Epítipo DUD

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<220>
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<222> (557)..(581)
<223> Epítipo DUD

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<220>
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<222> (584)..(608)
<223> Epítipo DUD

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<400> 26

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			20					25					30			
Ser	Ser	Gly	Leu	Arg	Ile	Asn	Ser	Ala	Lys	Asp	Asp	Ala	Ala	Gly	Leu	
		35					40					45				
Ala	Ile	Ser	Thr	Arg	Phe	Gln	Ser	Gln	Ile	Ser	Gly	Leu	Asn	Val	Ala	
	50					55					60					
Gln	Arg	Asn	Ala	Asn	Asp	Gly	Ile	Ser	Leu	Ala	Gln	Thr	Ala	Glu	Gly	
65					70					75					80	
Ala	Leu	Glu	Glu	Thr	Thr	Asn	Ile	Leu	Gln	Arg	Ile	Arg	Glu	Leu	Ser	
				85					90					95		
Val	Gln	Ser	Ala	Asn	Ser	Thr	Asn	Ser	Ser	Ser	Asp	Arg	Ser	Ala	Leu	
			100					105					110			
Gln	Gly	Glu	Val	Asn	Gln	Leu	Lys	Gln	Glu	Leu	Asp	Arg	Ile	Ala	Gly	
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Thr	Thr	Gln	Phe	Asn	Gly	Leu	Asn	Leu	Leu	Asp	Gly	Ser	Phe	Thr	Ala	
	130					135					140					
Gln	Ser	Phe	Gln	Val	Gly	Ala	Asn	Ala	Asn	Gln	Thr	Ile	Ser	Val	Ser	
145					150					155					160	
Val	Thr	Gly	Ala	Arg	Gly	Ala	Asp	Leu	Gly	Asn	Asn	Thr	Val	Ser	Gly	
				165					170					175		
Glu	Ser	Asp	Thr	Thr	Val	Ser	Gln	Gly	Thr	Gly	Ser	Val	Ala	Val	Ala	
			180					185					190			
Ala	Ala	Asp	Val	Ala	Thr	Val	Ala	Asn	Asn	Thr	Ile	Ala	Thr	Gln	Asn	
		195					200					205				
Ile	Thr	Val	Ser	Gly	Thr	Glu	Gly	Ser	Glu	Val	Ile	Gly	Ile	Thr	Gln	
	210					215					220					
Gly	Asp	Thr	Ala	Glu	Ala	Ile	Ala	Ala	Ala	Val	Asn	Ala	Glu	Thr	Gly	
225					230					235					240	
Thr	Thr	Gly	Val	Thr	Ala	Thr	Ala	Ser	Thr	Thr	Ala	Thr	Leu	Ala	Gly	
				245					250					255		
Leu	Ser	Asp	Asp	Gly	Thr	Val	Ser	Phe	Thr	Leu	Gly	Ser	Gly	Gly	Asp	
			260					265					270			
Thr	Ala	Thr	Ile	Ser	Ala	Ala	Val	Thr	Thr	Thr	Asp	Leu	Gly	Ala	Leu	
		275					280					285				
Ala	Lys	Ala	Ile	Asn	Asp	Thr	Ser	Gly	Thr	Thr	Gly	Val	Thr	Ala	Glu	
	290					295					300					

Ala Asn Gly Gly Glu Ile Thr Leu Thr Gln Ala Asp Gly Lys Asp Ile
 305 310 315 320
 Arg Leu Gln Asp Phe Ala Asn Ser Gly Asn Ala Thr Gly Thr Ala Thr
 325 330 335
 Leu Gln Gly Ser Gly Asp Pro Ser Ala Val Thr Leu Thr Ala Gly Ser
 340 345 350
 Thr Asp Ser Thr Ile Ala Ser Gly Ser Val Glu Phe Ala Ser Ser Gly
 355 360 365
 Ala Phe Ser Val Ser Ser Ser Val Ala Glu Thr Ala Gly Ser Ile Leu
 370 375 380
 Asn Val Ala Ala Asp Thr Val Val Gly Ser Asn Leu Gln Ser Val Ser
 385 390 395 400
 Ser Ile Asp Ile Gly Thr Val Ala Gly Ala Asn Ser Ala Ile Glu Ile
 405 410 415
 Ala Asp Ala Ala Leu Glu Gln Ile Ser Gly Ile Arg Ala Asp Leu Gly
 420 425 430
 Ala Ala Gln Asn Arg Phe Glu Ser Thr Ile Ala Asn Leu Ser Thr Thr
 435 440 445
 Ala Glu Asn Leu Ser Ala Ala Asn Ser Arg Ile Leu Asp Ala Asp Phe
 450 455 460
 Ala Ser Glu Thr Ala Lys Leu Ser Lys Ala Gln Val Leu Gln Gln Ala
 465 470 475 480
 Gly Ile Ser Val Leu Ala Gln Ala Asn Ala Arg Pro Gln Gln Val Leu
 485 490 495
 Ser Leu Leu Gln Gln Phe His Pro Thr Glu Pro Tyr Thr Thr Val Thr
 500 505 510
 Thr Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu Gly
 515 520 525
 Thr His Pro Thr Glu Pro Tyr Thr Thr Val Thr Thr Gln Asn Thr Ala
 530 535 540
 Ser Gln Thr Met Ser Ala Ile Glu Asn Leu Ala Ser His Pro Thr Glu
 545 550 555 560
 Pro Tyr Thr Thr Val Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser
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 Thr Thr Gln Asn Thr Ala Ser Gln Thr Met Ser Ala Ile Glu Asn Leu
 595 600 605

<211> 24
 <212> PRT
 <213> Influenza A virus

<220>
 <221> CARACTERÍSTICA
 <222> (1)..(24)
 <223> Péptido M2-2009

<400> 27

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Cys Arg Cys Ser Asp Ser Ser Asp
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<210> 28
 <211> 1854
 <212> DNA
 <213> Marinobacter algicola (DG893)

<220>
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 <222> (1)..(1854)

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 <222> (1538)..(1584)
 <223> Epítipo M2-2009

<220>
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 <222> (1585)..(1655)
 <223> Epítipo M2-2009

<220>
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 <222> (1656)..(1728)
 <223> Epítipo M2-2009

<220>
 <221> característica
 <222> (1729)..(1800)
 <223> Epítipo M2-2009

<220>
 <221> característica
 <222> (1807)..(1825)
 <223> Secuencia que codifica para una cola de histidinas

<220>
 <221> característica
 <222> (1835)..(1846)
 <223> Secuencia que codifica para la secuencia KDEL

<400> 28

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aactccgcca	aggacgatgc	tgctggcctt	gcaatttcga	cccgttttca	gtcccagatc	180
tctggtctga	atgttgccca	gcgtaacgcc	aacgacggta	tttccctggc	tcagactgct	240
gaaggtgctc	tggaagaaac	caccaacatac	ctgcagcgca	tccgtgagct	gtctgttcag	300
tcggccaaact	ctaccaactc	ttcttccgac	cgctctgcac	ttcagggcga	agtaaaccag	360
ctgaagcaag	agcttgatcg	tattgccggc	accaccagc	ttaacggcct	caaccttctg	420
gatggcagct	tactgcccc	gtcattccag	gttggtgcca	acgctaacca	gaccatctcg	480
gtctctgtaa	ctggcgctcg	tggtgccgac	cttggtaaca	acaccgtatc	cggtgaaagt	540
gataccactg	tcagtcaggg	cacgggttct	gttgcagtcg	cggccgctga	tgtggcaacc	600
gttgccaaca	atacgattgc	tacacagaac	atcaccgttt	ctggaactga	aggctctgag	660
gtcatcggtg	ttaccaggg	cgatactgca	gaagcgattg	cggctgctgt	taacgctgaa	720
accggcacga	ctggtgtaac	ggctacggca	tccaccacgg	caaccctcgc	tggtctgtct	780
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gcggtaacga	ccactgacct	gggtgcgctg	gccaaagcga	tcaacgatac	ctcaggcacc	900
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attctggatg	cagacttcgc	atctgaaact	gctaagctgt	ccaaggcgca	ggttctccag	1440
caagctggta	tctctgtact	ggcacaggcg	aatgcccgtc	cacagcaggt	tctgtccctc	1500
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tgcagatgca	gcgattcaag	tgatatgagt	cttctaaccg	aggctcgaaac	gcctaccaga	1620
agcgaatggg	agtgcagatg	cagcgattca	agtgatatga	gtcttctaac	cgaggtcgaa	1680
acgcctacca	gaagcgaatg	ggagtgcaga	tgcagcgatt	caagtgatat	gagtcttcta	1740
accgaggtcg	aaacgcctac	cagaagcgaa	tgggagtgca	gatgcagcga	ttcaagtgat	1800
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<210> 29
 <211> 617
 <212> PRT
 <213> Marinobacter algicola (DG893)

<220>
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 <222> (1)..(617)

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 <223> Epítipo M2-2009

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 <223> Epítipo M2-2009

<220>
 <221> CARACTERÍSTICA
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 <223> Epítipo M2-2009

<220>
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 <222> (577)..(600)
 <223> Epítipo M2-2009

<220>
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 <222> (612)..(615)
 <223> Secuencia KDEL

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Arg Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala
 35 40 45

Gly Leu Ala Ile Ser Thr Arg Phe Gln Ser Gln Ile Ser Gly Leu Asn
 50 55 60

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

Glu Gly Ala Leu Glu Glu Thr Thr Asn Ile Leu Gln Arg Ile Arg Glu
 85 90 95

Leu Ser Val Gln Ser Ala Asn Ser Thr Asn Ser Ser Ser Asp Arg Ser
 100 105 110

Ala Leu Gln Gly Glu Val Asn Gln Leu Lys Gln Glu Leu Asp Arg Ile
 115 120 125
 Ala Gly Thr Thr Gln Phe Asn Gly Leu Asn Leu Leu Asp Gly Ser Phe
 130 135 140
 Thr Ala Gln Ser Phe Gln Val Gly Ala Asn Ala Asn Gln Thr Ile Ser
 145 150 155 160
 Val Ser Val Thr Gly Ala Arg Gly Ala Asp Leu Gly Asn Asn Thr Val
 165 170 175
 Ser Gly Glu Ser Asp Thr Thr Val Ser Gln Gly Thr Gly Ser Val Ala
 180 185 190
 Val Ala Ala Ala Asp Val Ala Thr Val Ala Asn Asn Thr Ile Ala Thr
 195 200 205
 Gln Asn Ile Thr Val Ser Gly Thr Glu Gly Ser Glu Val Ile Gly Ile
 210 215 220
 Thr Gln Gly Asp Thr Ala Glu Ala Ile Ala Ala Ala Val Asn Ala Glu
 225 230 235 240
 Thr Gly Thr Thr Gly Val Thr Ala Thr Ala Ser Thr Thr Ala Thr Leu
 245 250 255
 Ala Gly Leu Ser Asp Asp Gly Thr Val Ser Phe Thr Leu Gly Ser Gly
 260 265 270
 Gly Asp Thr Ala Thr Ile Ser Ala Ala Val Thr Thr Thr Asp Leu Gly
 275 280 285
 Ala Leu Ala Lys Ala Ile Asn Asp Thr Ser Gly Thr Thr Gly Val Thr
 290 295 300
 Ala Glu Ala Asn Gly Gly Glu Ile Thr Leu Thr Gln Ala Asp Gly Lys
 305 310 315 320
 Asp Ile Arg Leu Gln Asp Phe Ala Asn Ser Gly Asn Ala Thr Gly Thr
 325 330 335
 Ala Thr Leu Gln Gly Ser Gly Asp Pro Ser Ala Val Thr Leu Thr Ala
 340 345 350
 Gly Ser Thr Asp Ser Thr Ile Ala Ser Gly Ser Val Glu Phe Ala Ser
 355 360 365
 Ser Gly Ala Phe Ser Val Ser Ser Ser Val Ala Glu Thr Ala Gly Ser
 370 375 380
 Ile Leu Asn Val Ala Ala Asp Thr Val Val Gly Ser Asn Leu Gln Ser
 385 390 395 400
 Val Ser Ser Ile Asp Ile Gly Thr Val Ala Gly Ala Asn Ser Ala Ile
 405 410 415
 Glu Ile Ala Asp Ala Ala Leu Glu Gln Ile Ser Gly Ile Arg Ala Asp

420	425	430
Leu Gly Ala Ala Gln Asn Arg Phe Glu Ser Thr Ile Ala Asn Leu Ser		
435	440	445
Thr Thr Ala Glu Asn Leu Ser Ala Ala Asn Ser Arg Ile Leu Asp Ala		
450	455	460
Asp Phe Ala Ser Glu Thr Ala Lys Leu Ser Lys Ala Gln Val Leu Gln		
465	470	475
Gln Ala Gly Ile Ser Val Leu Ala Gln Ala Asn Ala Arg Pro Gln Gln		
485	490	495
Val Leu Ser Leu Leu Gln Gln Phe Met Ser Leu Leu Thr Glu Val Glu		
500	505	510
Thr Pro Thr Arg Ser Glu Trp Glu Cys Arg Cys Ser Asp Ser Ser Asp		
515	520	525
Met Ser Leu Leu Thr Glu Val Glu Thr Pro Thr Arg Ser Glu Trp Glu		
530	535	540
Cys Arg Cys Ser Asp Ser Ser Asp Met Ser Leu Leu Thr Glu Val Glu		
545	550	555
Thr Pro Thr Arg Ser Glu Trp Glu Cys Arg Cys Ser Asp Ser Ser Asp		
565	570	575
Met Ser Leu Leu Thr Glu Val Glu Thr Pro Thr Arg Ser Glu Trp Glu		
580	585	590
Cys Arg Cys Ser Asp Ser Ser Asp Ser Arg His His His His His His		
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His Ala Arg Lys Asp Glu Leu Lys Leu		
610	615	

<210> 30
 <211> 1815
 <212> DNA
 <213> Marinobacter algicola (DG893)

<220>
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 <222> (1)..(1815)

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 <223> Epítipo M2-2009

<220>
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 <223> Epítipo M2-2009

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 <223> Epítopo M2-2009

<220>
 <221> característica
 <222> (1729)..(1800)
 <223> Epítopo M2-2009

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 aactccgcca aggacgatgc tgctggcctt gcaatttcga cccgttttca gtcccagatc 180
 tctgggtctga atgttgccca gcgtaacgcc aacgacggta tttccctggc tcagactgct 240
 gaaggtgctc tggaagaaac caccaacatc ctgcagcgca tccgtgagct gtctgttcag 300
 tcggccaact ctaccaactc ttcttccgac cgctctgcac ttcagggcga agtaaaccag 360
 ctgaagcaag agcttgatcg tattgccggc accaccagc ttaacggcct caaccttctg 420
 gatggcagct tcaactgcca gtcattccag gttggtgcca acgctaacca gaccatctcg 480
 gtctctgtaa ctggcgctcg tgggtccgac cttggtaaca acaccgtatc cggtgaaagt 540
 gataccactg tcagtcaggg cacgggttct gttgcagtcg cggccgctga tgtggcaacc 600
 gttgccaaaca atacgattgc tacacagaac atcaccgttt ctggaactga aggctctgag 660
 gtcacgcgta ttaccaggg cgatactgca gaagcgattg cggctgctgt taacgctgaa 720
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 gacgatggta cggtttcctt tacgcttggc agtgggtggcg acacagcgac catctccgca 840
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 tctggctctg ttgaattcgc ctcttccggc gcattctcag taagctcctc tgtcgcagag 1140
 actgccggta gcattctgaa cgtcgcagcc gacaccgtgg ttggttccaa cctccagtca 1200
 gtgtcttcta tcgacatcgg tactgttgcg ggcgctaaca gcgcaatcga gattgcagat 1260
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 gagtctacga tcgccaacct gagcacaact gccgaaaacc tgtcggccgc taacagccgg 1380
 attctggatg cagacttcgc atctgaaact gctaagctgt ccaaggcgca ggttctccag 1440
 caagctggta tctctgtact ggcacaggcg aatgcccgtc cacagcaggt tctgtccctc 1500

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ctgcagcaat tcatgagtct tctaaccgag gtcgaaacgc ctaccagaag cgaatgggag      1560
tgcagatgca gcgattcaag tgatatgagt cttctaaccg aggtcgaac gcctaccaga      1620
agcgaatggg agtgcagatg cagcgattca agtgatatga gtcttctaac cgaggtcgaa      1680
acgcctacca gaagcgaatg ggagtgcaga tgcagcgatt caagtgatat gagtcttcta      1740
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<210> 31
<211> 604
<212> PRT
<213> Marinobacter algicola (DG893)

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<220>
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<220>
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<223> Epítipo M2-2009

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<223> Epítipo M2-2009

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<220>
<221> CARACTERÍSTICA
<222> (577)..(600)
<223> Epítipo M2-2009

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<400> 31

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Gln Asn Gln Leu Asn Lys Ser Gln Glu Leu Ser Asn Gln Ala Leu Glu
              20              25              30

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Arg Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala
              35              40              45

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Gly Leu Ala Ile Ser Thr Arg Phe Gln Ser Gln Ile Ser Gly Leu Asn
50              55              60

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Val	Ala	Gln	Arg	Asn	Ala	Asn	Asp	Gly	Ile	Ser	Leu	Ala	Gln	Thr	Ala	
65					70					75					80	
Glu	Gly	Ala	Leu	Glu	Glu	Thr	Thr	Asn	Ile	Leu	Gln	Arg	Ile	Arg	Glu	
				85					90					95		
Leu	Ser	Val	Gln	Ser	Ala	Asn	Ser	Thr	Asn	Ser	Ser	Ser	Asp	Arg	Ser	
			100					105					110			
Ala	Leu	Gln	Gly	Glu	Val	Asn	Gln	Leu	Lys	Gln	Glu	Leu	Asp	Arg	Ile	
		115					120					125				
Ala	Gly	Thr	Thr	Gln	Phe	Asn	Gly	Leu	Asn	Leu	Leu	Asp	Gly	Ser	Phe	
	130					135					140					
Thr	Ala	Gln	Ser	Phe	Gln	Val	Gly	Ala	Asn	Ala	Asn	Gln	Thr	Ile	Ser	
145					150					155					160	
Val	Ser	Val	Thr	Gly	Ala	Arg	Gly	Ala	Asp	Leu	Gly	Asn	Asn	Thr	Val	
				165					170					175		
Ser	Gly	Glu	Ser	Asp	Thr	Thr	Val	Ser	Gln	Gly	Thr	Gly	Ser	Val	Ala	
			180					185					190			
Val	Ala	Ala	Ala	Asp	Val	Ala	Thr	Val	Ala	Asn	Asn	Thr	Ile	Ala	Thr	
		195					200					205				
Gln	Asn	Ile	Thr	Val	Ser	Gly	Thr	Glu	Gly	Ser	Glu	Val	Ile	Gly	Ile	
	210					215					220					
Thr	Gln	Gly	Asp	Thr	Ala	Glu	Ala	Ile	Ala	Ala	Ala	Val	Asn	Ala	Glu	
225					230					235					240	
Thr	Gly	Thr	Thr	Gly	Val	Thr	Ala	Thr	Ala	Ser	Thr	Thr	Ala	Thr	Leu	
				245					250					255		
Ala	Gly	Leu	Ser	Asp	Asp	Gly	Thr	Val	Ser	Phe	Thr	Leu	Gly	Ser	Gly	
			260					265					270			
Gly	Asp	Thr	Ala	Thr	Ile	Ser	Ala	Ala	Val	Thr	Thr	Thr	Asp	Leu	Gly	
	275						280					285				
Ala	Leu	Ala	Lys	Ala	Ile	Asn	Asp	Thr	Ser	Gly	Thr	Thr	Gly	Val	Thr	
	290					295					300					
Ala	Glu	Ala	Asn	Gly	Gly	Glu	Ile	Thr	Leu	Thr	Gln	Ala	Asp	Gly	Lys	
305				310						315					320	
Asp	Ile	Arg	Leu	Gln	Asp	Phe	Ala	Asn	Ser	Gly	Asn	Ala	Thr	Gly	Thr	
				325					330					335		
Ala	Thr	Leu	Gln	Gly	Ser	Gly	Asp	Pro	Ser	Ala	Val	Thr	Leu	Thr	Ala	
			340					345					350			
Gly	Ser	Thr	Asp	Ser	Thr	Ile	Ala	Ser	Gly	Ser	Val	Glu	Phe	Ala	Ser	
		355					360					365				
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 Val Ser Ser Ile Asp Ile Gly Thr Val Ala Gly Ala Asn Ser Ala Ile
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 Glu Ile Ala Asp Ala Ala Leu Glu Gln Ile Ser Gly Ile Arg Ala Asp
 420 425 430
 Leu Gly Ala Ala Gln Asn Arg Phe Glu Ser Thr Ile Ala Asn Leu Ser
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 Asp Phe Ala Ser Glu Thr Ala Lys Leu Ser Lys Ala Gln Val Leu Gln
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 Gln Ala Gly Ile Ser Val Leu Ala Gln Ala Asn Ala Arg Pro Gln Gln
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 Thr Pro Thr Arg Ser Glu Trp Glu Cys Arg Cys Ser Asp Ser Ser Asp
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 Met Ser Leu Leu Thr Glu Val Glu Thr Pro Thr Arg Ser Glu Trp Glu
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 Cys Arg Cys Ser Asp Ser Ser Asp Met Ser Leu Leu Thr Glu Val Glu
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Ser	Ala	Gln	Asn	Gln	Leu	Asn	Lys	Ser	Gln	Glu	Leu	Ser	Asn	Gln	Ala	50	55	60	
Leu	Glu	Arg	Leu	Ser	Ser	Gly	Leu	Arg	Ile	Asn	Ser	Ala	Lys	Asp	Asp	65	70	75	80
Ala	Ala	Gly	Leu	Ala	Ile	Ser	Thr	Arg	Phe	Gln	Ser	Gln	Ile	Ser	Gly	85	90	95	
Leu	Asn	Val	Ala	Gln	Arg	Asn	Ala	Asn	Asp	Gly	Ile	Ser	Leu	Ala	Gln	100	105	110	
Thr	Ala	Glu	Gly	Ala	Leu	Glu	Glu	Thr	Thr	Asn	Ile	Leu	Gln	Arg	Ile	115	120	125	
Arg	Glu	Leu	Ser	Val	Gln	Ser	Ala	Asn	Ser	Thr	Asn	Ser	Ser	Ser	Asp	130	135	140	
Arg	Ser	Ala	Leu	Gln	Gly	Glu	Val	Asn	Gln	Leu	Lys	Gln	Glu	Leu	Asp	145	150	155	160
Arg	Ile	Ala	Gly	Thr	Thr	Gln	Phe	Asn	Gly	Leu	Asn	Leu	Leu	Asp	Gly	165	170	175	

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 195 200 205
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 Val Ala Val Ala Ala Ala Asp Val Ala Thr Val Ala Asn Asn Thr Ile
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 Ala Glu Thr Gly Thr Thr Gly Val Thr Ala Thr Ala Ser Thr Thr Ala
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Leu Ser Thr Thr Ala Glu Asn Leu Ser Ala Ala Asn Ser Arg Ile Leu
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 His His Ala Arg Lys Asp Glu Leu Lys Leu
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