

P778PC00.ST25
SEQUENCE LISTING

<110> Universitat de Girona

<120> A method for specific detection of Salmonella spp

<130> P778PC00

<160> 7

<170> PatentIn version 3.3

<210> 1

<211> 1824

<212> DNA

<213> Salmonella enterica

<220>

<221> CDS

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ggt	aaa	act	acc	ctg	gtt	gat	aag	ctg	ctc	cag	caa	tcc	ggt	acg	ttc		
Gly	Lys	Thr	Thr	Leu	Val	Asp	Lys	Leu	Leu	Gln	Gln	Ser	Gly	Thr	Phe		96
			20					25					30				

gac	gcg	cgt	gcc	gaa	act	caa	gag	cga	gtg	atg	gac	tcc	aac	gat	ttg		
Asp	Ala	Arg	Ala	Glu	Thr	Gln	Glu	Arg	Val	Met	Asp	Ser	Asn	Asp	Leu		144
		35					40					45					

gag	aaa	gag	cgt	ggt	att	act	atc	ctc	gct	aaa	aac	acc	gct	att	aaa		
Glu	Lys	Glu	Arg	Gly	Ile	Thr	Ile	Leu	Ala	Lys	Asn	Thr	Ala	Ile	Lys		192
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Trp	Asn	Asp	Tyr	Arg	Ile	Asn	Ile	Val	Asp	Thr	Pro	Gly	His	Ala	Asp		240
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ttc	ggt	ggt	gaa	gta	gag	cgc	gtc	atg	tcc	atg	gtt	gac	tct	gtg	ctg		
Phe	Gly	Gly	Glu	Val	Glu	Arg	Val	Met	Ser	Met	Val	Asp	Ser	Val	Leu		288
			85						90					95			

ctg	gtg	gtt	gac	gca	ttt	gac	ggc	ccg	atg	ccg	caa	acg	cgc	ttc	gtg		
Leu	Val	Val	Asp	Ala	Phe	Asp	Gly	Pro	Met	Pro	Gln	Thr	Arg	Phe	Val		336
			100					105					110				

acc	aaa	aaa	gcc	ttt	gct	cat	ggc	ctg	aaa	ccc	att	gtg	gtt	atc	aac		
Thr	Lys	Lys	Ala	Phe	Ala	His	Gly	Leu	Lys	Pro	Ile	Val	Val	Ile	Asn		384
		115					120					125					

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Phe	Asp	Leu	Phe	Val	Asn	Leu	Asp	Ala	Thr	Asp	Glu	Gln	Leu	Asp	Phe		480
145				150						155					160		

ccg	atc	atc	tac	gct	tcg	gcg	ctg	aac	ggt	atc	gcg	ggt	ctg	gac	cac		
Pro	Ile	Ile	Tyr	Ala	Ser	Ala	Leu	Asn	Gly	Ile	Ala	Gly	Leu	Asp	His		528
			165						170					175			

gaa	gat	atg	gcg	gaa	gac	atg	acc	ccg	cta	tat	cag	gcg	att	gtt	gat		
Glu	Asp	Met	Ala	Glu	Asp	Met	Thr	Pro	Leu	Tyr	Gln	Ala	Ile	Val	Asp		576

Side

P778PC00.ST25																
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atc Ile	tcc Ser 210	cag Gln	ctg Leu	gac Asp	tac Tyr	aac Asn 215	aac Asn	tat Tyr	gtt Val	ggc Gly	gtt Val 220	atc Ile	ggc Gly	att Ile	ggc Gly	672
cgt Arg 225	atc Ile	aaa Lys	cgc Arg	ggc Gly	aaa Lys 230	gtg Val	aag Lys	ccg Pro	aac Asn	cag Gln 235	cag Gln	gtc Val	act Thr	atc Ile	atc Ile 240	720
gat Asp	agt Ser	gaa Glu	ggg Gly	aaa Lys 245	acc Thr	cgt Arg	aac Asn	gcg Ala	aaa Lys 250	gta Val	ggc Gly	aaa Lys	gtg Val	ctg Leu 255	acg Thr	768
cat His	ctg Leu	ggc Gly	ctg Leu 260	gag Glu	cgt Arg	atc Ile	gac Asp	agc Ser 265	aac Asn	atc Ile	gcc Ala	gaa Glu	gcg Ala 270	ggc Gly	gat Asp	816
atc Ile	att Ile	gcg Ala 275	atc Ile	acc Thr	ggc Gly	ctg Leu	ggc Gly 280	gag Glu	ctg Leu	aac Asn	att Ile	tcc Ser 285	gac Asp	acc Thr	atc Ile	864
tgc Cys	gac Asp 290	ccg Pro	cag Gln	aac Asn	gtt Val	gaa Glu 295	gcg Ala	ctg Leu	ccg Pro	gcg Ala	ctg Leu 300	tcc Ser	gtt Val	gat Asp	gag Glu	912
ccg Pro 305	acc Thr	gtg Val	tct Ser	atg Met	ttc Phe 310	ttc Phe	tgc Cys	gtt Val	aac Asn	acc Thr 315	tgc Ser	ccg Pro	ttc Phe	tgc Cys	ggc Gly 320	960
aaa Lys	gaa Glu	ggc Gly	aag Lys	ttt Phe 325	gtg Val	act Thr	tct Ser	cgt Arg	cag Gln 330	att Ile	ctt Leu	gac Asp	cgt Arg	ctg Leu 335	aac Asn	1008
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ggc Gly	aaa Lys	ggc Gly 435	cg Arg	gta Val	cgt Arg	ctc Leu	gac Asp 440	tac Tyr	gtg Val	atc Ile	cca Pro	agc Ser 445	cgt Arg	ggg Gly	ctg Leu	1344
att Ile	ggc Gly 450	ttc Phe	cgt Arg	tca Ser	gaa Glu	ttc Phe 455	atg Met	acc Thr	atg Met	act Thr	tcc Ser 460	ggc Gly	acg Thr	ggc Gly	ctg Leu	1392

Side

P778PC00.ST25

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ggc Gly	cag Gln	cgt Arg	cag Gln	aac Asn 485	ggc Gly	gta Val	ctg Leu	atc Ile	tcc Ser 490	aac Asn	ggt Gly	cag Gln	ggt Gly	aaa Lys 495	gcg Ala	1488
gtg Val	gcg Ala	ttt Phe	gcg Ala 500	ctg Leu	ttc Phe	ggt Gly	ttg Leu	cag Gln 505	gat Asp	cgc Arg	ggt Gly	aag Lys	ctg Leu 510	ttc Phe	ctg Leu	1536
ggt Gly	cac His	ggc Gly 515	gcg Ala	gaa Glu	gtt Val	tat Tyr	gaa Glu 520	ggc Gly	cag Gln	att Ile	att Ile	ggt Gly 525	att Ile	cac His	agt Ser	1584
cgc Arg	tcc Ser 530	aac Asn	gac Asp	ctg Leu	acg Thr	gta Val 535	aac Asn	tgc Cys	ctg Leu	acc Thr	ggt Gly 540	aag Lys	aaa Lys	ctg Leu	acc Thr	1632
aac Asn 545	atg Met	cgt Arg	gcg Ala	tcc Ser	ggt Gly 550	acg Thr	gat Asp	gaa Glu	gcg Ala	gtg Val 555	att Ile	ctg Leu	gtt Val	ccg Pro	cca Pro 560	1680
att Ile	aaa Lys	atg Met	agc Ser	ctt Leu 565	gag Glu	caa Gln	gcg Ala	ctg Leu	gag Glu 570	ttc Phe	att Ile	gat Asp	gac Asp	gac Asp 575	gaa Glu	1728
ctg Leu	gta Val	gaa Glu	gtc Val 580	acc Thr	cca Pro	acc Thr	tct Ser	atc Ile 585	cgt Arg	atc Ile	cgt Arg	aaa Lys	cgt Arg 590	cac His	ctg Leu	1776
acg Thr	gaa Glu	aac Asn 595	gat Asp	cgc Arg	cgc Arg	cgt Arg	gcg Ala 600	aac Asn	cgt Arg	ggt Gly	cag Gln	aaa Lys 605	gaa Glu	gag Glu	taa	1824

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Asp Ala Arg Ala Glu Thr Gln Glu Arg Val Met Asp Ser Asn Asp Leu
 35 40 45

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

Trp Asn Asp Tyr Arg Ile Asn Ile Val Asp Thr Pro Gly His Ala Asp
 65 70 75 80

Phe Gly Gly Glu Val Glu Arg Val Met Ser Met Val Asp Ser Val Leu
 85 90 95

Side

P778PC00.ST25

Leu Val Val Asp Ala Phe Asp Gly Pro Met Pro Gln Thr Arg Phe Val
 100 105 110
 Thr Lys Lys Ala Phe Ala His Gly Leu Lys Pro Ile Val Val Ile Asn
 115 120 125
 Lys Val Asp Arg Pro Gly Ala Arg Pro Asp Trp Val Val Asp Gln Val
 130 135 140
 Phe Asp Leu Phe Val Asn Leu Asp Ala Thr Asp Glu Gln Leu Asp Phe
 145 150 155 160
 Pro Ile Ile Tyr Ala Ser Ala Leu Asn Gly Ile Ala Gly Leu Asp His
 165 170 175
 Glu Asp Met Ala Glu Asp Met Thr Pro Leu Tyr Gln Ala Ile Val Asp
 180 185 190
 His Val Pro Ala Pro Asp Val Asp Leu Asp Gly Pro Leu Gln Met Gln
 195 200 205
 Ile Ser Gln Leu Asp Tyr Asn Asn Tyr Val Gly Val Ile Gly Ile Gly
 210 215 220
 Arg Ile Lys Arg Gly Lys Val Lys Pro Asn Gln Gln Val Thr Ile Ile
 225 230 235 240
 Asp Ser Glu Gly Lys Thr Arg Asn Ala Lys Val Gly Lys Val Leu Thr
 245 250 255
 His Leu Gly Leu Glu Arg Ile Asp Ser Asn Ile Ala Glu Ala Gly Asp
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 Ile Ile Ala Ile Thr Gly Leu Gly Glu Leu Asn Ile Ser Asp Thr Ile
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 Cys Asp Pro Gln Asn Val Glu Ala Leu Pro Ala Leu Ser Val Asp Glu
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 Pro Thr Val Ser Met Phe Phe Cys Val Asn Thr Ser Pro Phe Cys Gly
 305 310 315 320
 Lys Glu Gly Lys Phe Val Thr Ser Arg Gln Ile Leu Asp Arg Leu Asn
 325 330 335
 Lys Glu Leu Val His Asn Val Ala Leu Arg Val Glu Glu Thr Glu Asp
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 Ala Asp Ala Phe Arg Val Ser Gly Arg Gly Glu Leu His Leu Ser Val
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 Leu Ile Glu Asn Met Arg Arg Glu Gly Phe Glu Leu Ala Val Ser Arg
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370

375

380

Pro Lys Val Ile Phe Arg Glu Ile Asp Gly Arg Lys Gln Glu Pro Tyr
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Glu Asn Val Thr Leu Asp Val Glu Glu Gln His Gln Gly Ser Val Met
 405 410 415

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

Gly Lys Gly Arg Val Arg Leu Asp Tyr Val Ile Pro Ser Arg Gly Leu
 435 440 445

Ile Gly Phe Arg Ser Glu Phe Met Thr Met Thr Ser Gly Thr Gly Leu
 450 455 460

Leu Tyr Ser Thr Phe Ser His Tyr Asp Asp Ile Arg Pro Gly Glu Val
 465 470 475 480

Gly Gln Arg Gln Asn Gly Val Leu Ile Ser Asn Gly Gln Gly Lys Ala
 485 490 495

Val Ala Phe Ala Leu Phe Gly Leu Gln Asp Arg Gly Lys Leu Phe Leu
 500 505 510

Gly His Gly Ala Glu Val Tyr Glu Gly Gln Ile Ile Gly Ile His Ser
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Arg Ser Asn Asp Leu Thr Val Asn Cys Leu Thr Gly Lys Lys Leu Thr
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Asn Met Arg Ala Ser Gly Thr Asp Glu Ala Val Ile Leu Val Pro Pro
 545 550 555 560

Ile Lys Met Ser Leu Glu Gln Ala Leu Glu Phe Ile Asp Asp Asp Glu
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