

SEQUENCE LISTING

<110> AZURRX SAS

<120> MOLECULE PROTEIQUE HYBRIDE APTE A INHIBER AU MOINS UN
ANTIBIOTIQUE ET COMPOSITION PHARMACEUTIQUE LA COMPORTANT

<130> AZR1 PCT

<150> FR1459935

<151> 2014-10-16

<160> 44

<170> PatentIn version 3.5

<210> 1

<211> 263

<212> PRT

<213> Escherichia coli

<400> 1

His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly
1				5					10					15	

Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu
			20					25					30		

Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Val	Ser	Thr	Phe	Lys
		35					40					45			

Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu
	50						55				60				

Gln	Leu	Gly	Arg	Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr
65					70					75					80

Ser	Pro	Val	Thr	Glu	Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu
				85					90					95	

Leu	Cys	Ser	Ala	Ala	Ile	Thr	Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu
			100					105						110	

Leu	Leu	Thr	Thr	Ile	Gly	Gly	Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His
		115					120					125			

Asn	Met	Gly	Asp	His	Val	Thr	Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu
	130						135				140				

Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala Ala
 145 150 155 160

Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
 165 170 175

Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala
 180 185 190

Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp
 195 200 205

Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu
 210 215 220

Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly
 225 230 235 240

Ser Gln Ala Thr Met Asp Glu Arg Asp Arg Gln Ile Ala Glu Ile Gly
 245 250 255

Ala Ser Leu Ile Lys His Trp
 260

<210> 2
 <211> 263
 <212> PRT
 <213> Escherichia coli

<400> 2

Gln Thr Ser Ala Val Gln Gln Lys Leu Ala Ala Leu Glu Lys Ser Ser
 1 5 10 15

Gly Gly Arg Leu Gly Val Ala Leu Ile Asp Thr Ala Asp Asn Thr Gln
 20 25 30

Val Leu Tyr Arg Gly Asp Glu Arg Phe Pro Met Cys Ser Thr Ser Lys
 35 40 45

Val Met Ala Ala Ala Val Leu Lys Gln Ser Glu Thr Gln Lys Gln
 50 55 60

Leu Leu Asn Gln Pro Val Glu Ile Lys Pro Ala Asp Leu Val Asn Tyr
 65 70 75 80

Asn Pro Ile Ala Glu Lys His Val Asn Gly Thr Met Thr Leu Ala Glu
85 90 95

Leu Ser Ala Ala Ala Leu Gln Tyr Ser Asp Asn Thr Ala Met Asn Lys
100 105 110

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

Ala Ile Gly Asp Glu Thr Phe Arg Leu Asp Arg Thr Glu Pro Thr Leu
130 135 140

Asn Thr Ala Ile Pro Gly Asp Pro Arg Asp Thr Thr Thr Pro Arg Ala
145 150 155 160

Met Ala Gln Thr Leu Arg Gln Leu Thr Leu Gly His Ala Leu Gly Glu
165 170 175

Thr Gln Arg Ala Gln Leu Val Thr Trp Leu Lys Gly Asn Thr Thr Gly
180 185 190

Ala Ala Ser Ile Arg Ala Gly Leu Pro Thr Ser Trp Thr Ala Gly Asp
195 200 205

Lys Thr Gly Ser Gly Gly Tyr Gly Thr Thr Asn Asp Ile Ala Val Ile
210 215 220

Trp Pro Gln Gly Arg Ala Pro Leu Val Leu Val Thr Tyr Phe Thr Gln
225 230 235 240

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

Arg Ile Ile Ala Glu Gly Leu
260

<210> 3

<211> 257

<212> PRT

<213> Staphylococcus aureus

<400> 3

Lys Glu Leu Asn Asp Leu Glu Lys Lys Tyr Asn Ala His Ile Gly Val
1 5 10 15

Tyr Ala Leu Asp Thr Lys Ser Gly Lys Glu Val Lys Phe Asn Ser Asp
 20 25 30

Lys Arg Phe Ala Tyr Ala Ser Thr Ser Lys Ala Ile Asn Ser Ala Ile
 35 40 45

Leu Leu Glu Gln Val Pro Tyr Asn Lys Leu Asn Lys Lys Val His Ile
 50 55 60

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

Gly Lys Asp Ile Thr Leu Lys Ala Leu Ile Glu Ala Ser Met Thr Tyr
 85 90 95

Ser Asp Asn Thr Ala Asn Asn Lys Ile Ile Lys Glu Ile Gly Gly Ile
 100 105 110

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

Pro Val Arg Tyr Glu Ile Glu Leu Asn Tyr Tyr Ser Pro Lys Ser Lys
 130 135 140

Lys Asp Thr Ser Thr Pro Ala Ala Phe Gly Lys Thr Leu Asn Lys Leu
 145 150 155 160

Ile Ala Asn Gly Lys Leu Ser Lys Glu Asn Lys Lys Phe Leu Leu Asp
 165 170 175

Leu Met Leu Asn Asn Lys Ser Gly Asp Thr Leu Ile Lys Asp Gly Val
 180 185 190

Pro Lys Asp Tyr Lys Val Ala Asp Lys Ser Gly Gln Ala Ile Thr Tyr
 195 200 205

Ala Ser Arg Asn Asp Val Ala Phe Val Tyr Pro Lys Gly Gln Ser Glu
 210 215 220

Pro Ile Val Leu Val Ile Phe Thr Asn Lys Asp Asn Lys Ser Asp Lys
 225 230 235 240

Pro Asn Asp Lys Leu Ile Ser Glu Thr Ala Lys Ser Val Met Lys Glu
 245 250 255

Phe

<210> 4

<211> 199

<212> PRT

<213> Escherichia coli

<400> 4

Met	Ser	Asn	Ala	Lys	Thr	Lys	Leu	Gly	Ile	Thr	Lys	Tyr	Ser	Ile	Val
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Thr	Asn	Ser	Asn	Asp	Ser	Val	Thr	Leu	Arg	Leu	Met	Thr	Glu	His	Asp
			20					25					30		

Leu	Ala	Met	Leu	Tyr	Glu	Trp	Leu	Asn	Arg	Ser	His	Ile	Val	Glu	Trp
		35					40					45			

Trp	Gly	Gly	Glu	Glu	Ala	Arg	Pro	Thr	Leu	Ala	Asp	Val	Gln	Glu	Gln
	50					55					60				

Tyr	Leu	Pro	Ser	Val	Leu	Ala	Gln	Glu	Ser	Val	Thr	Pro	Tyr	Ile	Ala
65					70					75					80

Met	Leu	Asn	Gly	Glu	Pro	Ile	Gly	Tyr	Ala	Gln	Ser	Tyr	Val	Ala	Leu
				85					90					95	

Gly	Ser	Gly	Asp	Gly	Arg	Trp	Glu	Glu	Glu	Thr	Asp	Pro	Gly	Val	Arg
			100					105					110		

Gly	Ile	Asp	Gln	Leu	Leu	Ala	Asn	Ala	Ser	Gln	Leu	Gly	Lys	Gly	Leu
		115					120					125			

Gly	Thr	Lys	Leu	Val	Arg	Ala	Leu	Val	Glu	Leu	Leu	Phe	Asn	Asp	Pro
	130					135					140				

Glu	Val	Thr	Lys	Ile	Gln	Thr	Asp	Pro	Ser	Pro	Ser	Asn	Leu	Arg	Ala
145					150					155					160

Ile	Arg	Cys	Tyr	Glu	Lys	Ala	Gly	Phe	Glu	Arg	Gln	Gly	Thr	Val	Thr
				165					170					175	

Thr	Pro	Tyr	Gly	Pro	Ala	Val	Tyr	Met	Val	Gln	Thr	Arg	Gln	Ala	Phe
			180					185					190		

Glu Arg Thr Arg Ser Asp Ala
195

<210> 5

<211> 419

<212> PRT

<213> Escherichia coli

<400> 5

Met Arg Phe Glu Glu Trp Val Lys Asp Lys His Ile Pro Phe Lys Leu
1 5 10 15

Asn His Pro Asp Asp Asn Tyr Asp Asp Phe Lys Pro Leu Arg Lys Ile
20 25 30

Ile Gly Asp Thr Arg Val Val Ala Leu Gly Glu Asn Ser His Phe Ile
35 40 45

Lys Glu Phe Phe Leu Leu Arg His Thr Leu Leu Arg Phe Phe Ile Glu
50 55 60

Asp Leu Gly Phe Thr Thr Phe Ala Phe Glu Phe Gly Phe Ala Glu Gly
65 70 75 80

Gln Ile Ile Asn Asn Trp Ile His Gly Gln Gly Thr Asp Asp Glu Ile
85 90 95

Gly Arg Phe Leu Lys His Phe Tyr Tyr Pro Glu Glu Leu Lys Thr Thr
100 105 110

Phe Leu Trp Leu Arg Glu Tyr Asn Lys Ala Ala Lys Glu Lys Ile Thr
115 120 125

Phe Leu Gly Ile Asp Ile Pro Arg Asn Gly Gly Ser Tyr Leu Pro Asn
130 135 140

Met Glu Ile Val His Asp Phe Phe Arg Thr Ala Asp Lys Glu Ala Leu
145 150 155 160

His Ile Ile Asp Asp Ala Phe Asn Ile Ala Lys Lys Ile Asp Tyr Phe
165 170 175

Ser Thr Ser Gln Ala Ala Leu Asn Leu His Glu Leu Thr Asp Ser Glu
180 185 190

Lys Cys Arg Leu Thr Ser Gln Leu Ala Arg Val Lys Val Arg Leu Glu
 195 200 205

Ala Met Ala Pro Ile His Ile Glu Lys Tyr Gly Ile Asp Lys Tyr Glu
 210 215 220

Thr Ile Leu His Tyr Ala Asn Gly Met Ile Tyr Leu Asp Tyr Asn Ile
 225 230 235 240

Gln Ala Met Ser Gly Phe Ile Ser Gly Gly Gly Met Gln Gly Asp Met
 245 250 255

Gly Ala Lys Asp Lys Tyr Met Ala Asp Ser Val Leu Trp His Leu Lys
 260 265 270

Asn Pro Gln Ser Glu Gln Lys Val Ile Val Val Ala His Asn Ala His
 275 280 285

Ile Gln Lys Thr Pro Ile Leu Tyr Asp Gly Phe Leu Ser Cys Leu Pro
 290 295 300

Met Gly Gln Arg Leu Lys Asn Ala Ile Gly Asp Asp Tyr Met Ser Leu
 305 310 315 320

Gly Ile Thr Ser Tyr Ser Gly His Thr Ala Ala Leu Tyr Pro Glu Val
 325 330 335

Asp Thr Lys Tyr Gly Phe Arg Val Asp Asn Phe Gln Leu Gln Glu Pro
 340 345 350

Asn Glu Gly Ser Val Glu Lys Ala Ile Ser Gly Cys Gly Val Thr Asn
 355 360 365

Ser Phe Val Phe Phe Arg Asn Ile Pro Glu Asp Leu Gln Ser Ile Pro
 370 375 380

Asn Met Ile Arg Phe Asp Ser Ile Tyr Met Lys Ala Glu Leu Glu Lys
 385 390 395 400

Ala Phe Asp Gly Ile Phe Gln Ile Glu Lys Ser Ser Val Ser Glu Val
 405 410 415

Val Tyr Glu

<210> 6
 <211> 388
 <212> PRT
 <213> Bacteroides fragilis

<400> 6

Met Thr Met Arg Ile Asp Thr Asp Lys Gln Met Asn Leu Leu Ser Asp
 1 5 10 15

Lys Asn Val Ala Ile Ile Gly Gly Gly Pro Val Gly Leu Thr Met Ala
 20 25 30

Lys Leu Leu Gln Gln Asn Gly Ile Asp Val Ser Val Tyr Glu Arg Asp
 35 40 45

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

Gly Ser Gly Gln Glu Ala Met Lys Lys Ala Gly Leu Leu Gln Thr Tyr
 65 70 75 80

Tyr Asp Leu Ala Leu Pro Met Gly Val Asn Ile Ala Asp Lys Lys Gly
 85 90 95

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

Pro Glu Ile Asn Arg Asn Asp Leu Arg Ala Ile Leu Leu Asn Ser Leu
 115 120 125

Glu Asn Asp Thr Val Ile Trp Asp Arg Lys Leu Val Met Leu Glu Pro
 130 135 140

Gly Lys Lys Lys Trp Thr Leu Thr Phe Glu Asn Lys Pro Ser Glu Thr
 145 150 155 160

Ala Asp Leu Val Ile Leu Ala Asn Gly Gly Met Ser Lys Val Arg Lys
 165 170 175

Phe Val Thr Asp Thr Glu Val Glu Glu Thr Gly Thr Phe Asn Ile Gln
 180 185 190

Ala Asp Ile His Gln Pro Glu Ile Asn Cys Pro Gly Phe Phe Gln Leu
 195 200 205

Cys Asn Gly Asn Arg Leu Met Ala Ser His Gln Gly Asn Leu Leu Phe
 210 215 220

Ala Asn Pro Asn Asn Asn Gly Ala Leu His Phe Gly Ile Ser Phe Lys
 225 230 235 240

Thr Pro Asp Glu Trp Lys Asn Gln Thr Gln Val Asp Phe Gln Asn Arg
 245 250 255

Asn Ser Val Val Asp Phe Leu Leu Lys Glu Phe Ser Asp Trp Asp Glu
 260 265 270

Arg Tyr Lys Glu Leu Ile His Thr Thr Leu Ser Phe Val Gly Leu Ala
 275 280 285

Thr Arg Ile Phe Pro Leu Glu Lys Pro Trp Lys Ser Lys Arg Pro Leu
 290 295 300

Pro Ile Thr Met Ile Gly Asp Ala Ala His Leu Met Pro Pro Phe Ala
 305 310 315 320

Gly Gln Gly Val Asn Ser Gly Leu Val Asp Ala Leu Ile Leu Ser Asp
 325 330 335

Asn Leu Ala Asp Gly Lys Phe Asn Ser Ile Glu Glu Ala Val Lys Asn
 340 345 350

Tyr Glu Gln Gln Met Phe Met Tyr Gly Lys Glu Ala Gln Glu Glu Ser
 355 360 365

Thr Gln Asn Glu Ile Glu Met Phe Lys Pro Asp Phe Thr Phe Gln Gln
 370 375 380

Leu Leu Asn Val
 385

<210> 7

<211> 267

<212> PRT

<213> Enterococcus faecium

<400> 7

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

Ser Asp Glu Arg Ile Thr Ala Cys Met Met Tyr Gly Ser Phe Thr Lys
 20 25 30

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

His Ser Ile Thr Ser Asn Phe Asp Ser Ser Asn Trp Leu Phe Asp Val
 50 55 60

Ala Pro Tyr Leu Met Leu Tyr Lys Asn Glu Tyr Gly Thr Glu Val Val
 65 70 75 80

Ile Phe Asp Asn Leu Ile Arg Gly Glu Phe His Phe Leu Ser Glu Lys
 85 90 95

Asp Met Asn Ile Ile Pro Ser Phe Lys Asp Ser Gly Tyr Ile Pro Asp
 100 105 110

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

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

Ala Asn Phe Leu Leu Cys Asn Phe Ser Asn Leu Trp Leu Met Gly Ile
 145 150 155 160

Asn Val Leu Lys Arg Gly Glu Tyr Ala Arg Ser Leu Glu Leu Leu Ser
 165 170 175

Gln Leu Gln Lys Asn Thr Leu Gln Leu Ile Arg Met Ala Glu Lys Asn
 180 185 190

Ala Asp Asn Trp Leu Asn Met Ser Lys Asn Leu Glu Lys Glu Ile Ser
 195 200 205

Leu Glu Asn Tyr Lys Lys Phe Ala Lys Thr Thr Ala Arg Leu Asp Lys
 210 215 220

Val Glu Leu Phe Glu Ala Tyr Lys Asn Ser Leu Leu Leu Val Met Asp
 225 230 235 240

Leu Gln Ser His Leu Ile Glu Gln Tyr Asn Leu Lys Val Thr His Asp

245

250

255

Ile Leu Glu Arg Leu Leu Asn Tyr Ile Ser Glu
 260 265

<210> 8

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion 1 TEM36-6G-CTXM16

<400> 8

His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
 1 5 10 15

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
 20 25 30

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Val Ser Thr Phe Lys
 35 40 45

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu
 50 55 60

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
 65 70 75 80

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
 85 90 95

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
 100 105 110

Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
 115 120 125

Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
 130 135 140

Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala Ala
 145 150 155 160

Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
 165 170 175

Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala
 180 185 190

Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp
 195 200 205

Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu
 210 215 220

Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly
 225 230 235 240

Ser Gln Ala Thr Met Asp Glu Arg Asp Arg Gln Ile Ala Glu Ile Gly
 245 250 255

Ala Ser Leu Ile Lys His Trp Gly Gly Gly Gly Gly Gly Gln Thr Ser
 260 265 270

Ala Val Gln Gln Lys Leu Ala Ala Leu Glu Lys Ser Ser Gly Gly Arg
 275 280 285

Leu Gly Val Ala Leu Ile Asp Thr Ala Asp Asn Thr Gln Val Leu Tyr
 290 295 300

Arg Gly Asp Glu Arg Phe Pro Met Cys Ser Thr Ser Lys Val Met Ala
 305 310 315 320

Ala Ala Ala Val Leu Lys Gln Ser Glu Thr Gln Lys Gln Leu Leu Asn
 325 330 335

Gln Pro Val Glu Ile Lys Pro Ala Asp Leu Val Asn Tyr Asn Pro Ile
 340 345 350

Ala Glu Lys His Val Asn Gly Thr Met Thr Leu Ala Glu Leu Ser Ala
 355 360 365

Ala Ala Leu Gln Tyr Ser Asp Asn Thr Ala Met Asn Lys Leu Ile Ala
 370 375 380

Gln Leu Gly Gly Pro Gly Gly Val Thr Ala Phe Ala Arg Ala Ile Gly
 385 390 395 400

Asp Glu Thr Phe Arg Leu Asp Arg Thr Glu Pro Thr Leu Asn Thr Ala

405

410

415

Ile Pro Gly Asp Pro Arg Asp Thr Thr Thr Pro Arg Ala Met Ala Gln
 420 425 430

Thr Leu Arg Gln Leu Thr Leu Gly His Ala Leu Gly Glu Thr Gln Arg
 435 440 445

Ala Gln Leu Val Thr Trp Leu Lys Gly Asn Thr Thr Gly Ala Ala Ser
 450 455 460

Ile Arg Ala Gly Leu Pro Thr Ser Trp Thr Ala Gly Asp Lys Thr Gly
 465 470 475 480

Ser Gly Gly Tyr Gly Thr Thr Asn Asp Ile Ala Val Ile Trp Pro Gln
 485 490 495

Gly Arg Ala Pro Leu Val Leu Val Thr Tyr Phe Thr Gln Pro Gln Gln
 500 505 510

Asn Ala Glu Ser Arg Arg Asp Val Leu Ala Ser Ala Ala Arg Ile Ile
 515 520 525

Ala Glu Gly Leu
 530

<210> 9

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion 2 CTXM16-6G-TEM36

<400> 9

Gln Thr Ser Ala Val Gln Gln Lys Leu Ala Ala Leu Glu Lys Ser Ser
 1 5 10 15

Gly Gly Arg Leu Gly Val Ala Leu Ile Asp Thr Ala Asp Asn Thr Gln
 20 25 30

Val Leu Tyr Arg Gly Asp Glu Arg Phe Pro Met Cys Ser Thr Ser Lys
 35 40 45

Val Met Ala Ala Ala Ala Val Leu Lys Gln Ser Glu Thr Gln Lys Gln
 50 55 60

Leu Leu Asn Gln Pro Val Glu Ile Lys Pro Ala Asp Leu Val Asn Tyr
65 70 75 80

Asn Pro Ile Ala Glu Lys His Val Asn Gly Thr Met Thr Leu Ala Glu
85 90 95

Leu Ser Ala Ala Ala Leu Gln Tyr Ser Asp Asn Thr Ala Met Asn Lys
100 105 110

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

Ala Ile Gly Asp Glu Thr Phe Arg Leu Asp Arg Thr Glu Pro Thr Leu
130 135 140

Asn Thr Ala Ile Pro Gly Asp Pro Arg Asp Thr Thr Thr Pro Arg Ala
145 150 155 160

Met Ala Gln Thr Leu Arg Gln Leu Thr Leu Gly His Ala Leu Gly Glu
165 170 175

Thr Gln Arg Ala Gln Leu Val Thr Trp Leu Lys Gly Asn Thr Thr Gly
180 185 190

Ala Ala Ser Ile Arg Ala Gly Leu Pro Thr Ser Trp Thr Ala Gly Asp
195 200 205

Lys Thr Gly Ser Gly Gly Tyr Gly Thr Thr Asn Asp Ile Ala Val Ile
210 215 220

Trp Pro Gln Gly Arg Ala Pro Leu Val Leu Val Thr Tyr Phe Thr Gln
225 230 235 240

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

Arg Ile Ile Ala Glu Gly Leu Gly Gly Gly Gly Gly His Pro Glu
260 265 270

Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val
275 280 285

Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe

290

295

300

Arg Pro Glu Glu Arg Phe Pro Met Val Ser Thr Phe Lys Val Leu Leu
 305 310 315 320

Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu Gly
 325 330 335

Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val
 340 345 350

Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser
 355 360 365

Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr
 370 375 380

Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly
 385 390 395 400

Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala
 405 410 415

Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala Ala Met Ala Thr
 420 425 430

Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg
 435 440 445

Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu
 450 455 460

Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly
 465 470 475 480

Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp
 485 490 495

Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala
 500 505 510

Thr Met Asp Glu Arg Asp Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu
 515 520 525

Ile Lys His Trp
530

<210> 10
<211> 537
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion 3 TEM36-G(EAAAK)2-CTXM16

<400> 10

His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
1 5 10 15

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
20 25 30

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Val Ser Thr Phe Lys
35 40 45

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu
50 55 60

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
65 70 75 80

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
85 90 95

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
100 105 110

Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
115 120 125

Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
130 135 140

Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala Ala
145 150 155 160

Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
165 170 175

Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala

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

Thr Leu Asn Thr Ala Ile Pro Gly Asp Pro Arg Asp Thr Thr Thr Pro
 420 425 430

Arg Ala Met Ala Gln Thr Leu Arg Gln Leu Thr Leu Gly His Ala Leu
 435 440 445

Gly Glu Thr Gln Arg Ala Gln Leu Val Thr Trp Leu Lys Gly Asn Thr
 450 455 460

Thr Gly Ala Ala Ser Ile Arg Ala Gly Leu Pro Thr Ser Trp Thr Ala
 465 470 475 480

Gly Asp Lys Thr Gly Ser Gly Gly Tyr Gly Thr Thr Asn Asp Ile Ala
 485 490 495

Val Ile Trp Pro Gln Gly Arg Ala Pro Leu Val Leu Val Thr Tyr Phe
 500 505 510

Thr Gln Pro Gln Gln Asn Ala Glu Ser Arg Arg Asp Val Leu Ala Ser
 515 520 525

Ala Ala Arg Ile Ile Ala Glu Gly Leu
 530 535

<210> 11
 <211> 4158
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> vecteur et sequence clonnee TEM36

<400> 11
 acattgcctg aattggtttg ccccggaaga ttggggaaac ttggatctga ttaccttagc 60
 tgcaggtacc actgagcgtc agaccccgta gaaaagatca aaggatcttc ttgagatcct 120
 ttttttctgc gcgtaatctg ctgcttgcaa acaaaaaaac caccgctacc agcgggtggtt 180
 tgtttgtcgg atcaagagct accaactctt tttccgaagg taactggctt cagcagagcg 240
 cagataccaa atactgttct tctagtgtag ccgtagttag gccaccactt caagaactct 300
 gtagcaccgc ctacatacct cgctctgcta atcctgttac cagtggctgc tgccagtggc 360
 gataagtcgt gtcttaccgg gttggactca agacgatagt taccggataa ggcgcagcgg 420
 tcgggctgaa cgggggggttc gtgcacacag cccagcttgg agcgaacgac ctacaccgaa 480
 ctgagatacc tacagcgtga gctatgagaa agcgccacgc ttcccgaagg gagaaaggcg 540

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 <211> 900
 <212> DNA
 <213> Escherichia coli

<400> 12
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<210> 13
 <211> 1680
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion 1 TEM36-G6-CTXM16

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<210> 14

<211> 1634

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion 2 CTXM16-G6-TEM36

<400> 14

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tgaggggcgg ccgc                                           1634

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<210> 15
<211> 1648
<212> DNA

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<213> Artificial Sequence

<220>

<223> fusion 3 TEM36-G(EAAAK)2-CTXM16

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1648

<210> 16

<211> 870

<212> DNA

<213> Escherichia coli

<400> 16

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acaccaggt attgtatcgt	
gggatgaac gcttcccgat gtgctctaca tctaaagtta	240
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<210> 17

<211> 627

<212> DNA

<213> Escherichia coli

<400> 17

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gcgattcgct gctatgagaa agcgggcttc gagcgccagg gcaactgtcac cacgccgtat      540
ggtccagctg ttacatgggt ccagacgcgc caggcgtttg agcgtaccgg tagcgacgcg      600
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<210> 18
<211> 1416
<212> DNA
<213> Artificial Sequence

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<220>
<223> fusion 5 AAC-H6-CTXM16

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<210> 19

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<212> DNA

<213> Escherichia coli

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cgtgaactgt gtagtgcagc gattaccatg agcgataaca cggccgcaaa tctgctgctg      1620
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cgtggcagtc gcggtattat cgcagcgctg ggcccggatg gtaaaccgag tcgtattgtg      1980
gttatctaca ccacgggcag ccaggcgacc atggatgaac gtgatcgcca gattgcagaa      2040
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<213> Artificial Sequence

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<400> 21

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Thr Asn Ser Asn Asp Ser Val Thr Leu Arg Leu Met Thr Glu His Asp
              20              25              30

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Leu Ala Met Leu Tyr Glu Trp Leu Asn Arg Ser His Ile Val Glu Trp
              35              40              45

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Trp Gly Gly Glu Glu Ala Arg Pro Thr Leu Ala Asp Val Gln Glu Gln
50              55              60

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Tyr Leu Pro Ser Val Leu Ala Gln Glu Ser Val Thr Pro Tyr Ile Ala
65              70              75              80

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Met Leu Asn Gly Glu Pro Ile Gly Tyr Ala Gln Ser Tyr Val Ala Leu
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Gly Ser Gly Asp Gly Arg Trp Glu Glu Glu Thr Asp Pro Gly Val Arg
100              105              110

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Gly Ile Asp Gln Leu Leu Ala Asn Ala Ser Gln Leu Gly Lys Gly Leu
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Gly Thr Lys Leu Val Arg Ala Leu Val Glu Leu Leu Phe Asn Asp Pro
 130 135 140

Glu Val Thr Lys Ile Gln Thr Asp Pro Ser Pro Ser Asn Leu Arg Ala
 145 150 155 160

Ile Arg Cys Tyr Glu Lys Ala Gly Phe Glu Arg Gln Gly Thr Val Thr
 165 170 175

Thr Pro Tyr Gly Pro Ala Val Tyr Met Val Gln Thr Arg Gln Ala Phe
 180 185 190

Glu Arg Thr Arg Ser Asp Ala His His His His His His Gln Thr Ser
 195 200 205

Ala Val Gln Gln Lys Leu Ala Ala Leu Glu Lys Ser Ser Gly Gly Arg
 210 215 220

Leu Gly Val Ala Leu Ile Asp Thr Ala Asp Asn Thr Gln Val Leu Tyr
 225 230 235 240

Arg Gly Asp Glu Arg Phe Pro Met Cys Ser Thr Ser Lys Val Met Ala
 245 250 255

Ala Ala Ala Val Leu Lys Gln Ser Glu Thr Gln Lys Gln Leu Leu Asn
 260 265 270

Gln Pro Val Glu Ile Lys Pro Ala Asp Leu Val Asn Tyr Asn Pro Ile
 275 280 285

Ala Glu Lys His Val Asn Gly Thr Met Thr Leu Ala Glu Leu Ser Ala
 290 295 300

Ala Ala Leu Gln Tyr Ser Asp Asn Thr Ala Met Asn Lys Leu Ile Ala
 305 310 315 320

Gln Leu Gly Gly Pro Gly Gly Val Thr Ala Phe Ala Arg Ala Ile Gly
 325 330 335

Asp Glu Thr Phe Arg Leu Asp Arg Thr Glu Pro Thr Leu Asn Thr Ala

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Ile	Pro	Gly	Asp	Pro	Arg	Asp	Thr	Thr	Thr	Pro	Arg	Ala	Met	Ala	Gln		
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Thr	Leu	Arg	Gln	Leu	Thr	Leu	Gly	His	Ala	Leu	Gly	Glu	Thr	Gln	Arg		
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Ala	Gln	Leu	Val	Thr	Trp	Leu	Lys	Gly	Asn	Thr	Thr	Gly	Ala	Ala	Ser		
385					390					395					400		
Ile	Arg	Ala	Gly	Leu	Pro	Thr	Ser	Trp	Thr	Ala	Gly	Asp	Lys	Thr	Gly		
				405					410					415			
Ser	Gly	Gly	Tyr	Gly	Thr	Thr	Asn	Asp	Ile	Ala	Val	Ile	Trp	Pro	Gln		
			420					425					430				
Gly	Arg	Ala	Pro	Leu	Val	Leu	Val	Thr	Tyr	Phe	Thr	Gln	Pro	Gln	Gln		
		435					440					445					
Asn	Ala	Glu	Ser	Arg	Arg	Asp	Val	Leu	Ala	Ser	Ala	Ala	Arg	Ile	Ile		
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			20					25					30				
Ile	Gly	Asp	Thr	Arg	Val	Val	Ala	Leu	Gly	Glu	Asn	Ser	His	Phe	Ile		
		35					40					45					
Lys	Glu	Phe	Phe	Leu	Leu	Arg	His	Thr	Leu	Leu	Arg	Phe	Phe	Ile	Glu		
	50					55					60						

Asp Leu Gly Phe Thr Thr Phe Ala Phe Glu Phe Gly Phe Ala Glu Gly
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Gln Ile Ile Asn Asn Trp Ile His Gly Gln Gly Thr Asp Asp Glu Ile
85 90 95

Gly Arg Phe Leu Lys His Phe Tyr Tyr Pro Glu Glu Leu Lys Thr Thr
100 105 110

Phe Leu Trp Leu Arg Glu Tyr Asn Lys Ala Ala Lys Glu Lys Ile Thr
115 120 125

Phe Leu Gly Ile Asp Ile Pro Arg Asn Gly Gly Ser Tyr Leu Pro Asn
130 135 140

Met Glu Ile Val His Asp Phe Phe Arg Thr Ala Asp Lys Glu Ala Leu
145 150 155 160

His Ile Ile Asp Asp Ala Phe Asn Ile Ala Lys Lys Ile Asp Tyr Phe
165 170 175

Ser Thr Ser Gln Ala Ala Leu Asn Leu His Glu Leu Thr Asp Ser Glu
180 185 190

Lys Cys Arg Leu Thr Ser Gln Leu Ala Arg Val Lys Val Arg Leu Glu
195 200 205

Ala Met Ala Pro Ile His Ile Glu Lys Tyr Gly Ile Asp Lys Tyr Glu
210 215 220

Thr Ile Leu His Tyr Ala Asn Gly Met Ile Tyr Leu Asp Tyr Asn Ile
225 230 235 240

Gln Ala Met Ser Gly Phe Ile Ser Gly Gly Gly Met Gln Gly Asp Met
245 250 255

Gly Ala Lys Asp Lys Tyr Met Ala Asp Ser Val Leu Trp His Leu Lys
260 265 270

Asn Pro Gln Ser Glu Gln Lys Val Ile Val Val Ala His Asn Ala His
275 280 285

Ile Gln Lys Thr Pro Ile Leu Tyr Asp Gly Phe Leu Ser Cys Leu Pro

290

295

300

Met Gly Gln Arg Leu Lys Asn Ala Ile Gly Asp Asp Tyr Met Ser Leu
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Gly Ile Thr Ser Tyr Ser Gly His Thr Ala Ala Leu Tyr Pro Glu Val
 325 330 335

Asp Thr Lys Tyr Gly Phe Arg Val Asp Asn Phe Gln Leu Gln Glu Pro
 340 345 350

Asn Glu Gly Ser Val Glu Lys Ala Ile Ser Gly Cys Gly Val Thr Asn
 355 360 365

Ser Phe Val Phe Phe Arg Asn Ile Pro Glu Asp Leu Gln Ser Ile Pro
 370 375 380

Asn Met Ile Arg Phe Asp Ser Ile Tyr Met Lys Ala Glu Leu Glu Lys
 385 390 395 400

Ala Phe Asp Gly Ile Phe Gln Ile Glu Lys Ser Ser Val Ser Glu Val
 405 410 415

Val Tyr Glu His His His His His His His Pro Glu Thr Leu Val Lys
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Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu
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Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu
 450 455 460

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

Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His
 485 490 495

Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His
 500 505 510

Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr
 515 520 525

Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly
 530 535 540

Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr
 545 550 555 560

Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp
 565 570 575

Glu Arg Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys
 580 585 590

Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile
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Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala
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Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg
 625 630 635 640

Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser
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