

SEQ Prot 20236_ST25.txt
SEQUENCE LISTING

<110> Medizinische Hochschule Hannover (MHH)
École polytechnique fédérale de Lausanne (EPFL)
<120> Enzymes having alpha2,9 endosialidase activity
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<170> PatentIn version 3.5
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<212> DNA
<213> Enterobacteria phage phi92

<220>
<221> gene
<222> (1)..(2757)

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SEQ Prot 20236_ST25.txt

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 <212> PRT
 <213> Enterobacteria phage phi92

<220>
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 <222> (1)..(918)

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SEQ Prot 20236_ST25.txt

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 Trp Arg Asp Glu Gly Asp Pro Arg Gly Trp Gly Ala Val Gly Asp Gly
 65 70 75 80
 Ala Thr Asp Asp Thr Asn Ala Ile Thr Gln Leu Leu Ala Ala Met Pro
 85 90 95
 Asp Gly Trp Ile Ile Asp Gly Arg Asn Leu Thr Phe Lys Val Thr Thr
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 Leu Pro Asp Ile Ser Lys Phe Lys Asn Ala Ala Phe Val Tyr Glu Arg
 115 120 125
 Ile Val Gly Gln Pro Leu Thr Tyr Val Ser Glu Gly Phe Phe Asp Gly
 130 135 140
 Asn Leu Thr Lys Ile Thr Asp Thr Pro Phe Tyr Asn Ala Trp Thr Gln
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 Asp Lys Thr Phe Val Tyr Asp Asn Val Ile Tyr Ala Pro Phe Met Ala
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 Gly Val Cys Gly Asn Arg Leu Tyr Ala Val Ile Glu Thr Arg Tyr Leu
 225 230 235 240
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 Tyr Tyr Arg Arg Pro Thr Gly Gly Ile Thr Ile Ser Ser Gly Ser Thr
 260 265 270
 Thr Ala Thr Ile Val Leu Lys Lys His Gly Leu Lys Val Gly Asp Ala
 275 280 285
 Val Asn Phe Ser Asn Ser Gly Ala Thr Gly Val Ser Gly Asn Met Thr
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SEQ Prot 20236_ST25.txt

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 340 345 350
 Ala Tyr Ser Thr Asn Ala Asp Leu Cys Val Thr Glu Thr His Ser Phe
 355 360 365
 Thr Val Ile Asp Asp Asp Asn Tyr Thr Phe Ala Val Gly Tyr His Asn
 370 375 380
 Gly Asp Ile Ser Pro Arg Arg Leu Gly Ile Leu Tyr Phe Asn Asn Ala
 385 390 395 400
 Tyr Ser Asp Pro Ser Ser Phe Thr Arg Arg Thr Ile Ser Gln Glu Tyr
 405 410 415
 Ala Asp Asn Ala Ala Glu Pro Cys Ile Lys Tyr Tyr Asp Gly Ile Leu
 420 425 430
 Tyr Leu Thr Thr Arg Gly Thr Ser Thr Ser Ala Ala Gly Ser Thr Leu
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 Ala Met Ser Ala Asp Leu Gly Glu Asn Trp Asn Tyr Leu Arg Phe Pro
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 Asn Asn Val His His Thr Asn Leu Pro Phe Ala Lys Val Gly Asp Tyr
 465 470 475 480
 Leu Tyr Ile Phe Gly Thr Glu Arg Ser Phe Gly Glu Trp Glu Gly Gln
 485 490 495
 Glu Leu Asp Asn Arg Tyr Lys Gly Thr Tyr Pro Arg Thr Phe Met Cys
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 Lys Ile Asn Val Ser Ser Trp Pro Val Ser Leu Ser Asn Val Gln Trp
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 Phe Asn Ile Thr Asp Gln Ile Tyr Gln Gly His Ile Val Asn Ser Ala
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 Cys Gly Val Gly Ser Val Cys Val Lys Asp Gly Trp Leu Tyr Tyr Ile
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SEQ Prot 20236_ST25.txt

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 Ser Ala Val Arg Val Lys Leu Asp Gly Asp Tyr Gly Val Ile Ala Lys
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 Gly Glu Thr Pro Tyr Thr Thr Asp Gly Ser Leu Leu Gln Leu Tyr Gly
 690 695 700
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 Leu Gly Gly Ala Ser Asn Arg Trp Ser Glu Val Tyr Ala Ser Thr Gly
 740 745 750
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 Glu Asp Ile Leu Leu Lys Ala Trp Glu Asp Ile His Val Ile Ser Tyr
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 Gln Trp Leu Ser Ala Val Ala Glu Lys Gly Asp Ser Ala Arg Ile His
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SEQ Prot 20236_ST25.txt

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Pro Ala Gly Ser Arg Trp Gly Ile Arg Ala Asp Gln Met Phe Phe Ile
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<213> Enterobacteria phage K1F

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SEQ Prot 20236_ST25.txt

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<222> (1)..(1064)

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Arg Phe Leu Asn Pro Thr Met Ile Glu Met Leu Val Asp Gln Ser Gly
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Phe Asp Ile Val Arg Ile His Arg Gln Thr Gly Thr Asp Leu Val Val
65 70 75 80

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

Ala Lys Asp Ser Glu Asp Glu Ala Arg Arg Ile Ala Glu Ser Ile Arg
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Ala Ala Gly Leu Ile Gly Tyr Met Thr Arg Arg Ser Phe Glu Lys Gly
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Tyr Asn Val Thr Thr Trp Ser Glu Val Leu Leu Trp Glu Glu Asp Gly
165 170 175

Asp Tyr Tyr Arg Trp Asp Gly Thr Leu Pro Lys Asn Val Pro Ala Gly
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Ser Thr Pro Glu Thr Ser Gly Gly Ile Gly Leu Gly Ala Trp Val Ser
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SEQ Prot 20236_ST25.txt

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 260 265 270
 Gly Asn Gly Lys Thr Tyr Lys Val Thr Ser Leu Pro Asp Ile Ser Arg
 275 280 285
 Phe Ile Asn Thr Arg Phe Val Tyr Glu Arg Ile Pro Gly Gln Pro Leu
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 Tyr Tyr Ala Ser Glu Glu Phe Val Gln Gly Glu Leu Phe Lys Ile Thr
 305 310 315 320
 Asp Thr Pro Tyr Tyr Asn Ala Trp Pro Gln Asp Lys Ala Phe Val Tyr
 325 330 335
 Glu Asn Val Ile Tyr Ala Pro Tyr Met Gly Ser Asp Arg His Gly Val
 340 345 350
 Ser Arg Leu His Val Ser Trp Val Lys Ser Gly Asp Asp Gly Gln Thr
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 Trp Ser Thr Pro Glu Trp Leu Thr Asp Leu His Pro Asp Tyr Pro Thr
 370 375 380
 Val Asn Tyr His Cys Met Ser Met Gly Val Cys Arg Asn Arg Leu Phe
 385 390 395 400
 Ala Met Ile Glu Thr Arg Thr Leu Ala Lys Asn Ala Leu Thr Asn Cys
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 Ala Leu Trp Asp Arg Pro Met Ser Arg Ser Leu His Leu Thr Gly Gly
 420 425 430
 Ile Thr Lys Ala Ala Asn Gln Arg Tyr Ala Thr Ile His Val Pro Asp
 435 440 445
 His Gly Leu Phe Val Gly Asp Phe Val Asn Phe Ser Asn Ser Ala Val
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 Thr Gly Val Ser Gly Asp Met Thr Val Ala Thr Val Ile Asp Lys Asp
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SEQ Prot 20236_ST25.txt

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 500 505 510
 Arg Lys Thr Asp Leu Gly Leu Ile Pro Ser Val Thr Glu Val His Ser
 515 520 525
 Phe Ala Thr Ile Asp Asn Asn Gly Phe Ala Met Gly Tyr His Gln Gly
 530 535 540
 Asp Val Ala Pro Arg Glu Val Gly Leu Phe Tyr Phe Pro Asp Ala Phe
 545 550 555 560
 Asn Ser Pro Ser Asn Tyr Val Arg Arg Gln Ile Pro Ser Glu Tyr Glu
 565 570 575
 Pro Asp Ala Ser Glu Pro Cys Ile Lys Tyr Tyr Asp Gly Val Leu Tyr
 580 585 590
 Leu Ile Thr Arg Gly Thr Arg Gly Asp Arg Leu Gly Ser Ser Leu His
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 Arg Ser Arg Asp Ile Gly Gln Thr Trp Glu Ser Leu Arg Phe Pro His
 610 615 620
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 625 630 635 640
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 645 650 655
 Pro Asp Asp Arg Tyr Lys Ala Ser Tyr Pro Arg Thr Phe Tyr Ala Arg
 660 665 670
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 Thr Asp Gln Ile Tyr Gln Gly Gly Ile Val Asn Ser Gly Val Gly Val
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 Glu Asp His Phe Asn Pro Trp Thr Tyr Gly Asp Asn Ser Ala Lys Asp
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 Pro Phe Lys Ser Asp Gly His Pro Ser Asp Leu Tyr Cys Tyr Lys Met
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SEQ Prot 20236_ST25.txt

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 785 790 795 800
 Val Thr Ile Arg Ala Ser Thr Ser Ser Asn Ile Arg Ser Glu Val Leu
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 Pro Ala Gly Gln Arg Ile Ile Phe Cys Gly Gly Glu Gly Thr Ser Ser
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 Val Lys Pro Tyr Asn Asp Asn Val Thr Ala Leu Gly Gly Pro Ser Asn
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 Arg Phe Thr Thr Ala Tyr Leu Gly Ser Asn Pro Ile Val Thr Ser Asn
 900 905 910
 Gly Glu Arg Lys Thr Glu Pro Val Val Phe Asp Asp Ala Phe Leu Asp
 915 920 925
 Ala Trp Gly Asp Val His Tyr Ile Met Tyr Gln Trp Leu Asp Ala Val
 930 935 940
 Gln Leu Lys Gly Asn Asp Ala Arg Ile His Phe Gly Val Ile Ala Gln
 945 950 955 960
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 965 970 975
 Thr Asn Cys Arg Tyr Ala Val Leu Cys Tyr Asp Lys Tyr Pro Arg Met
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SEQ Prot 20236_ST25.txt

Val Ile His Glu Glu Gly Glu Glu Trp Gly Val Arg Pro Asp Gly
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<210> 5
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SEQ Prot 20236_ST25.txt

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SEQ Prot 20236_ST25.txt

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 50 55 60
 Gly Phe Phe Asp Gly Asn Leu Thr Lys Ile Thr Asp Thr Pro Phe Tyr
 65 70 75 80
 Asn Ala Trp Thr Gln Asp Lys Thr Phe Val Tyr Asp Asn Val Ile Tyr
 85 90 95
 Ala Pro Phe Met Ala Gly Glu Arg His Gly Val Gln Asn Leu His Val
 100 105 110
 Ala Trp Val Lys Ser Gly Asp Asp Gly Gln Thr Trp Ser Met Pro Glu
 115 120 125
 Trp Leu Thr Pro Ile His Pro Asp Tyr Thr Ala Asp Lys Val Asn Tyr
 130 135 140
 His Cys Met Ser Met Gly Val Cys Gly Asn Arg Leu Tyr Ala Val Ile
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 165 170 175
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 195 200 205
 Lys Val Gly Asp Ala Val Asn Phe Ser Asn Ser Gly Ala Thr Gly Val
 210 215 220
 Ser Gly Asn Met Thr Val Ala Ser Val Ile Asn Lys Asp Thr Phe Thr
 225 230 235 240
 Val Thr Leu Ala Arg Ala Ala Thr Ser Asn Ile Asp Asn Thr Gly Thr
 245 250 255
 Thr Trp His Phe Gly Thr Arg Phe Trp Asp Ser Pro Trp Glu Ile Thr
 260 265 270
 Glu Leu Pro Asp Val Ala Tyr Ser Thr Asn Ala Asp Leu Cys Val Thr
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SEQ Prot 20236_ST25.txt

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 325 330 335
 Ile Ser Gln Glu Tyr Ala Asp Asn Ala Ala Glu Pro Cys Ile Lys Tyr
 340 345 350
 Tyr Asp Gly Ile Leu Tyr Leu Thr Thr Arg Gly Thr Ser Thr Ser Ala
 355 360 365
 Ala Gly Ser Thr Leu Ala Met Ser Ala Asp Leu Gly Glu Asn Trp Asn
 370 375 380
 Tyr Leu Arg Phe Pro Asn Asn Val His His Thr Asn Leu Pro Phe Ala
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 Lys Val Gly Asp Tyr Leu Tyr Ile Phe Gly Thr Glu Arg Ser Phe Gly
 405 410 415
 Glu Trp Glu Gly Gln Glu Leu Asp Asn Arg Tyr Lys Gly Thr Tyr Pro
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 Arg Thr Phe Met Cys Lys Ile Asn Val Ser Ser Trp Pro Val Ser Leu
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 Ser Asn Val Gln Trp Phe Asn Ile Thr Asp Gln Ile Tyr Gln Gly His
 450 455 460
 Ile Val Asn Ser Ala Cys Gly Val Gly Ser Val Cys Val Lys Asp Gly
 465 470 475 480
 Trp Leu Tyr Tyr Ile Phe Gly Gly Glu Asp Phe Leu Ser Pro Trp Ser
 485 490 495
 Ile Gly Asp Asn Ser Lys Lys Leu Trp Tyr Lys His Asp Gly His Pro
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 Ala Asp Leu Tyr Ser Tyr Arg Leu Lys Ile Thr Glu His Asp Phe Val
 515 520 525
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SEQ Prot 20236_ST25.txt

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 595 600 605
 Leu Ile Leu Cys Gly Gly Glu Thr Pro Tyr Thr Thr Asp Gly Ser Leu
 610 615 620
 Leu Gln Leu Tyr Gly Ser Asn His Thr Tyr Pro Asn Arg Ala Ile Leu
 625 630 635 640
 Tyr Ala Pro Gly Gly Ala Tyr Thr Gln Asn Asn Phe Met Pro Tyr Leu
 645 650 655
 Asp Gly Gln Val Ser Leu Gly Gly Ala Ser Asn Arg Trp Ser Glu Val
 660 665 670
 Tyr Ala Ser Thr Gly Thr Ile Asn Thr Ser Asp Gly Thr Leu Lys Thr
 675 680 685
 Lys Pro Thr Glu Ile Glu Asp Ile Leu Leu Lys Ala Trp Glu Asp Ile
 690 695 700
 His Val Ile Ser Tyr Gln Trp Leu Ser Ala Val Ala Glu Lys Gly Asp
 705 710 715 720
 Ser Ala Arg Ile His Phe Gly Val Ile Ala Gln Asp Val Arg Asp Ile
 725 730 735
 Leu Ile Asn Tyr Gly Leu Met Asp Glu Asn Ser Thr Asp Cys Lys Tyr
 740 745 750
 Ala Phe Leu Cys Tyr Asp Glu Tyr Pro Ala Met Tyr Asp Ser Val Val
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 Thr Gly Gln Lys Glu Ile Thr Leu Leu Asp Asp Glu Gly Asn Asn Val
 770 775 780
 Ile Asp Glu Glu Gly Asn Pro Val Thr Ile Val Glu Asp Val Val Glu
 785 790 795 800
 Thr Ile Glu Val Ile Pro Ala Gly Ser Arg Trp Gly Ile Arg Ala Asp
 805 810 815
 Gln Met Phe Phe Ile Glu Met Ala Tyr Gln Arg Lys Lys Leu Lys Ala
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SEQ Prot 20236_ST25.txt

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SEQ Prot 20236_ST25.txt

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Tyr	Lys	Val	Thr	Ser	Leu	Pro	Asp	Ile	Ser	Arg	Phe	Ile	Asn	Thr	Arg
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Phe	Val	Tyr	Glu	Arg	Ile	Pro	Gly	Gln	Pro	Leu	Tyr	Tyr	Ala	Ser	Glu
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Glu	Phe	Val	Gln	Gly	Glu	Leu	Phe	Lys	Ile	Thr	Asp	Thr	Pro	Tyr	Tyr
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Asn	Ala	Trp	Pro	Gln	Asp	Lys	Ala	Phe	Val	Tyr	Glu	Asn	Val	Ile	Tyr
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SEQ Prot 20236_ST25.txt

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Ser Trp Val Lys Ser Gly Asp Asp Gly Gln Thr Trp Ser Thr Pro Glu
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Trp Leu Thr Asp Leu His Pro Asp Tyr Pro Thr Val Asn Tyr His Cys
130 135 140

Met Ser Met Gly Val Cys Arg Asn Arg Leu Phe Ala Met Ile Glu Thr
145 150 155 160

Arg Thr Leu Ala Lys Asn Ala Leu Thr Asn Cys Ala Leu Trp Asp Arg
165 170 175

Pro Met Ser Arg Ser Leu His Leu Thr Gly Gly Ile Thr Lys Ala Ala
180 185 190

Asn Gln Arg Tyr Ala Thr Ile His Val Pro Asp His Gly Leu Phe Val
195 200 205

Gly Asp Phe Val Asn Phe Ser Asn Ser Ala Val Thr Gly Val Ser Gly
210 215 220

Asp Met Thr Val Ala Thr Val Ile Asp Lys Asp Asn Phe Thr Val Leu
225 230 235 240

Thr Pro Asn Gln Gln Thr Ser Asp Leu Asn Asn Ala Gly Lys Asn Trp
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His Met Gly Thr Ser Phe His Lys Ser Pro Trp Arg Lys Thr Asp Leu
260 265 270

Gly Leu Ile Pro Ser Val Thr Glu Val His Ser Phe Ala Thr Ile Asp
275 280 285

Asn Asn Gly Phe Ala Met Gly Tyr His Gln Gly Asp Val Ala Pro Arg
290 295 300

Glu Val Gly Leu Phe Tyr Phe Pro Asp Ala Phe Asn Ser Pro Ser Asn
305 310 315 320

Tyr Val Arg Arg Gln Ile Pro Ser Glu Tyr Glu Pro Asp Ala Ser Glu
325 330 335

Pro Cys Ile Lys Tyr Tyr Asp Gly Val Leu Tyr Leu Ile Thr Arg Gly
340 345 350

Thr Arg Gly Asp Arg Leu Gly Ser Ser Leu His Arg Ser Arg Asp Ile
355 360 365

SEQ Prot 20236_ST25.txt

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 Thr Leu Pro Phe Ala Lys Val Gly Asp Asp Leu Ile Met Phe Gly Ser
 385 390 395 400
 Glu Arg Ala Glu Asn Glu Trp Glu Ala Gly Ala Pro Asp Asp Arg Tyr
 405 410 415
 Lys Ala Ser Tyr Pro Arg Thr Phe Tyr Ala Arg Leu Asn Val Asn Asn
 420 425 430
 Trp Asn Ala Asp Asp Ile Glu Trp Val Asn Ile Thr Asp Gln Ile Tyr
 435 440 445
 Gln Gly Gly Ile Val Asn Ser Gly Val Gly Val Gly Ser Val Val Val
 450 455 460
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 Met Glu Phe Thr Gly Asp Leu Gly Leu Gly His Val Thr Ile Arg Ala
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 565 570 575
 Gly Phe Ile Gly Lys Ser Ile Pro Thr Asp Asn Pro Ala Gly Gln Arg
 580 585 590
 Ile Ile Phe Cys Gly Gly Glu Gly Thr Ser Ser Thr Thr Gly Ala Gln
 595 600 605
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 Asn Gly Asp Glu His Leu Phe Gln Ser Ala Asp Val Lys Pro Tyr Asn
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SEQ Prot 20236_ST25.txt

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Glu Pro Val Val Phe Asp Asp Ala Phe Leu Asp Ala Trp Gly Asp Val
675 680 685

His Tyr Ile Met Tyr Gln Trp Leu Asp Ala Val Gln Leu Lys Gly Asn
690 695 700

Asp Ala Arg Ile His Phe Gly Val Ile Ala Gln Gln Ile Arg Asp Val
705 710 715 720

Phe Ile Ala His Gly Leu Met Asp Glu Asn Ser Thr Asn Cys Arg Tyr
725 730 735

Ala Val Leu Cys Tyr Asp Lys Tyr Pro Arg Met Thr Asp Thr Val Phe
740 745 750

Ser His Asn Glu Ile Val Glu His Thr Asp Glu Glu Gly Asn Val Thr
755 760 765

Thr Thr Glu Glu Pro Val Tyr Thr Glu Val Val Ile His Glu Glu Gly
770 775 780

Glu Glu Trp Gly Val Arg Pro Asp Gly Ile Phe Phe Ala Glu Ala Ala
785 790 795 800

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Glu Gln Lys

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SEQ Prot 20236_ST25.txt

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SEQ Prot 20236_ST25.txt

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caaatgtcgc gctggagaga tgaaggatgat cctagaggat ggggagcagt aggtgacgga	240
gcaacagacg atactaatgc tataacacag cttcttgctg ctatgcctga tggatggatt	300
attgatgggc gtaatctcac tttcaagggtt acaacactac cagatataag caagtttaaa	360
aacgctgctt ttgtttacga gcgtattgtt ggacaacccc ttacttatgt atctgaagg	420
ttcttcgatg gaaatctgac aaagattacg gatacaccat tttacaatgc ttggacgcaa	480
gataagacgt ttgtttatga taatgttata tatgcaccat ttatggctgg cgaacgtcat	540
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tgtatgagta tgggtgtatg tggtaatcgc ctatatgcag tcatcgaaac ccgttactta	720
tctaacatgc gattgaagaa agcagaactt tgggtcacgtc caatgcctta ttatagaagg	780
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SEQ Prot 20236_ST25.txt

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aatagtactg attgtaagta tgcttttcta tgttatgatg aataccctgc tatgtatgat	2520
agtgttgtta cgggacaaaa agaaatcact ttacttgacg atgaaggaaa taatgtaatt	2580
gatgaagaag gtaatccagt aacaattgta gaagatgttg tagaaactat cgaagtaatt	2640
ccagcaggat cgcgatggg tatccgcgct gaccaaattg tttttattga gatggcttat	2700
caacgtaaaa agttaaagc tcttgaagaa agacttgcaa ccctagaaag taaataa	2757

<210> 11
 <211> 918
 <212> PRT
 <213> Enterobacteria phage phi92

<220>
 <221> MISC_FEATURE
 <222> (303)..(303)
 <223> M303R mutant of SEQ ID No. 2

<400> 11

SEQ Prot 20236_ST25.txt

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Ser Asp Tyr Leu Val Leu Asp Gln Pro Asp Lys Thr Val Lys Ser Thr
20 25 30

Val Ser Asn Phe Leu Ala Asp Thr Gly Val Val Leu Ala Thr Gln Leu
35 40 45

Lys Asp Thr Ser Gly Ala Thr Lys Tyr Pro Glu Leu Gln Met Ser Arg
50 55 60

Trp Arg Asp Glu Gly Asp Pro Arg Gly Trp Gly Ala Val Gly Asp Gly
65 70 75 80

Ala Thr Asp Asp Thr Asn Ala Ile Thr Gln Leu Leu Ala Ala Met Pro
85 90 95

Asp Gly Trp Ile Ile Asp Gly Arg Asn Leu Thr Phe Lys Val Thr Thr
100 105 110

Leu Pro Asp Ile Ser Lys Phe Lys Asn Ala Ala Phe Val Tyr Glu Arg
115 120 125

Ile Val Gly Gln Pro Leu Thr Tyr Val Ser Glu Gly Phe Phe Asp Gly
130 135 140

Asn Leu Thr Lys Ile Thr Asp Thr Pro Phe Tyr Asn Ala Trp Thr Gln
145 150 155 160

Asp Lys Thr Phe Val Tyr Asp Asn Val Ile Tyr Ala Pro Phe Met Ala
165 170 175

Gly Glu Arg His Gly Val Gln Asn Leu His Val Ala Trp Val Lys Ser
180 185 190

Gly Asp Asp Gly Gln Thr Trp Ser Met Pro Glu Trp Leu Thr Pro Ile
195 200 205

His Pro Asp Tyr Thr Ala Asp Lys Val Asn Tyr His Cys Met Ser Met
210 215 220

Gly Val Cys Gly Asn Arg Leu Tyr Ala Val Ile Glu Thr Arg Tyr Leu
225 230 235 240

Ser Asn Met Arg Leu Lys Lys Ala Glu Leu Trp Ser Arg Pro Met Pro
245 250 255

Tyr Tyr Arg Arg Pro Thr Gly Gly Ile Thr Ile Ser Ser Gly Ser Thr
260 265 270

SEQ Prot 20236_ST25.txt

Thr Ala Thr Ile Val Leu Lys Lys His Gly Leu Lys Val Gly Asp Ala
275 280 285

Val Asn Phe Ser Asn Ser Gly Ala Thr Gly Val Ser Gly Asn Arg Thr
290 295 300

Val Ala Ser Val Ile Asn Lys Asp Thr Phe Thr Val Thr Leu Ala Arg
305 310 315 320

Ala Ala Thr Ser Asn Ile Asp Asn Thr Gly Thr Thr Trp His Phe Gly
325 330 335

Thr Arg Phe Trp Asp Ser Pro Trp Glu Ile Thr Glu Leu Pro Asp Val
340 345 350

Ala Tyr Ser Thr Asn Ala Asp Leu Cys Val Thr Glu Thr His Ser Phe
355 360 365

Thr Val Ile Asp Asp Asp Asn Tyr Thr Phe Ala Val Gly Tyr His Asn
370 375 380

Gly Asp Ile Ser Pro Arg Arg Leu Gly Ile Leu Tyr Phe Asn Asn Ala
385 390 395 400

Tyr Ser Asp Pro Ser Ser Phe Thr Arg Arg Thr Ile Ser Gln Glu Tyr
405 410 415

Ala Asp Asn Ala Ala Glu Pro Cys Ile Lys Tyr Tyr Asp Gly Ile Leu
420 425 430

Tyr Leu Thr Thr Arg Gly Thr Ser Thr Ser Ala Ala Gly Ser Thr Leu
435 440 445

Ala Met Ser Ala Asp Leu Gly Glu Asn Trp Asn Tyr Leu Arg Phe Pro
450 455 460

Asn Asn Val His His Thr Asn Leu Pro Phe Ala Lys Val Gly Asp Tyr
465 470 475 480

Leu Tyr Ile Phe Gly Thr Glu Arg Ser Phe Gly Glu Trp Glu Gly Gln
485 490 495

Glu Leu Asp Asn Arg Tyr Lys Gly Thr Tyr Pro Arg Thr Phe Met Cys
500 505 510

Lys Ile Asn Val Ser Ser Trp Pro Val Ser Leu Ser Asn Val Gln Trp
515 520 525

Phe Asn Ile Thr Asp Gln Ile Tyr Gln Gly His Ile Val Asn Ser Ala
530 535 540

SEQ Prot 20236_ST25.txt

cys Gly Val Gly Ser Val Cys Val Lys Asp Gly Trp Leu Tyr Tyr Ile
 545 550 555 560
 Phe Gly Gly Glu Asp Phe Leu Ser Pro Trp Ser Ile Gly Asp Asn Ser
 565 570 575
 Lys Lys Leu Trp Tyr Lys His Asp Gly His Pro Ala Asp Leu Tyr Ser
 580 585 590
 Tyr Arg Leu Lys Ile Thr Glu His Asp Phe Val Ser Arg Asp Phe Lys
 595 600 605
 Tyr Gly Ala Thr Pro Asn Arg Thr Leu Pro Val Ser Met Gly Thr Asp
 610 615 620
 Gly Val Arg His Val Ser Ala Pro Val Thr Phe Asp Asn Asp Val Gln
 625 630 635 640
 Met Tyr Ser Leu Thr Val Thr Gly Leu Glu His Asp Gly Thr Gln Gln
 645 650 655
 Ser Ala Val Arg Val Lys Leu Asp Gly Asp Tyr Gly Val Ile Ala Lys
 660 665 670
 Asn Ile Pro Ile Lys Asn Pro Ser Glu Gln Arg Leu Ile Leu Cys Gly
 675 680 685
 Gly Glu Thr Pro Tyr Thr Thr Asp Gly Ser Leu Leu Gln Leu Tyr Gly
 690 695 700
 Ser Asn His Thr Tyr Pro Asn Arg Ala Ile Leu Tyr Ala Pro Gly Gly
 705 710 715 720
 Ala Tyr Thr Gln Asn Asn Phe Met Pro Tyr Leu Asp Gly Gln Val Ser
 725 730 735
 Leu Gly Gly Ala Ser Asn Arg Trp Ser Glu Val Tyr Ala Ser Thr Gly
 740 745 750
 Thr Ile Asn Thr Ser Asp Gly Thr Leu Lys Thr Lys Pro Thr Glu Ile
 755 760 765
 Glu Asp Ile Leu Leu Lys Ala Trp Glu Asp Ile His Val Ile Ser Tyr
 770 775 780
 Gln Trp Leu Ser Ala Val Ala Glu Lys Gly Asp Ser Ala Arg Ile His
 785 790 795 800
 Phe Gly Val Ile Ala Gln Asp Val Arg Asp Ile Leu Ile Asn Tyr Gly
 805 810 815

SEQ Prot 20236_ST25.txt

Leu Met Asp Glu Asn Ser Thr Asp Cys Lys Tyr Ala Phe Leu Cys Tyr
820 825 830

Asp Glu Tyr Pro Ala Met Tyr Asp Ser Val Val Thr Gly Gln Lys Glu
835 840 845

Ile Thr Leu Leu Asp Asp Glu Gly Asn Asn Val Ile Asp Glu Glu Gly
850 855 860

Asn Pro Val Thr Ile Val Glu Asp Val Val Glu Thr Ile Glu Val Ile
865 870 875 880

Pro Ala Gly Ser Arg Trp Gly Ile Arg Ala Asp Gln Met Phe Phe Ile
885 890 895

Glu Met Ala Tyr Gln Arg Lys Lys Leu Lys Ala Leu Glu Glu Arg Leu
900 905 910

Ala Thr Leu Glu Ser Lys
915

<210> 12
<211> 918
<212> PRT
<213> Enterobacteria phage phi92

<220>
<221> MISC_FEATURE
<222> (303)..(303)
<223> M303K mutant of SEQ ID No. 2

<400> 12

Met Ser Thr Thr Ile Thr Asn Leu Pro Glu Thr Ser Lys Val Asn Ser
1 5 10 15

Ser Asp Tyr Leu Val Leu Asp Gln Pro Asp Lys Thr Val Lys Ser Thr
20 25 30

Val Ser Asn Phe Leu Ala Asp Thr Gly Val Val Leu Ala Thr Gln Leu
35 40 45

Lys Asp Thr Ser Gly Ala Thr Lys Tyr Pro Glu Leu Gln Met Ser Arg
50 55 60

Trp Arg Asp Glu Gly Asp Pro Arg Gly Trp Gly Ala Val Gly Asp Gly
65 70 75 80

Ala Thr Asp Asp Thr Asn Ala Ile Thr Gln Leu Leu Ala Ala Met Pro
85 90 95

Asp Gly Trp Ile Ile Asp Gly Arg Asn Leu Thr Phe Lys Val Thr Thr
100 105 110

SEQ Prot 20236_ST25.txt

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

SEQ Prot 20236_ST25.txt

Gly Asp Ile Ser Pro Arg Arg Leu Gly Ile Leu Tyr Phe Asn Asn Ala
 385 390 395 400
 Tyr Ser Asp Pro Ser Ser Phe Thr Arg Arg Thr Ile Ser Gln Glu Tyr
 405 410 415
 Ala Asp Asn Ala Ala Glu Pro Cys Ile Lys Tyr Tyr Asp Gly Ile Leu
 420 425 430
 Tyr Leu Thr Thr Arg Gly Thr Ser Thr Ser Ala Ala Gly Ser Thr Leu
 435 440 445
 Ala Met Ser Ala Asp Leu Gly Glu Asn Trp Asn Tyr Leu Arg Phe Pro
 450 455 460
 Asn Asn Val His His Thr Asn Leu Pro Phe Ala Lys Val Gly Asp Tyr
 465 470 475 480
 Leu Tyr Ile Phe Gly Thr Glu Arg Ser Phe Gly Glu Trp Glu Gly Gln
 485 490 495
 Glu Leu Asp Asn Arg Tyr Lys Gly Thr Tyr Pro Arg Thr Phe Met Cys
 500 505 510
 Lys Ile Asn Val Ser Ser Trp Pro Val Ser Leu Ser Asn Val Gln Trp
 515 520 525
 Phe Asn Ile Thr Asp Gln Ile Tyr Gln Gly His Ile Val Asn Ser Ala
 530 535 540
 Cys Gly Val Gly Ser Val Cys Val Lys Asp Gly Trp Leu Tyr Tyr Ile
 545 550 555 560
 Phe Gly Gly Glu Asp Phe Leu Ser Pro Trp Ser Ile Gly Asp Asn Ser
 565 570 575
 Lys Lys Leu Trp Tyr Lys His Asp Gly His Pro Ala Asp Leu Tyr Ser
 580 585 590
 Tyr Arg Leu Lys Ile Thr Glu His Asp Phe Val Ser Arg Asp Phe Lys
 595 600 605
 Tyr Gly Ala Thr Pro Asn Arg Thr Leu Pro Val Ser Met Gly Thr Asp
 610 615 620
 Gly Val Arg His Val Ser Ala Pro Val Thr Phe Asp Asn Asp Val Gln
 625 630 635 640
 Met Tyr Ser Leu Thr Val Thr Gly Leu Glu His Asp Gly Thr Gln Gln
 645 650 655

SEQ Prot 20236_ST25.txt

Ser Ala Val Arg Val Lys Leu Asp Gly Asp Tyr Gly Val Ile Ala Lys
660 665 670

Asn Ile Pro Ile Lys Asn Pro Ser Glu Gln Arg Leu Ile Leu Cys Gly
675 680 685

Gly Glu Thr Pro Tyr Thr Thr Asp Gly Ser Leu Leu Gln Leu Tyr Gly
690 695 700

Ser Asn His Thr Tyr Pro Asn Arg Ala Ile Leu Tyr Ala Pro Gly Gly
705 710 715 720

Ala Tyr Thr Gln Asn Asn Phe Met Pro Tyr Leu Asp Gly Gln Val Ser
725 730 735

Leu Gly Gly Ala Ser Asn Arg Trp Ser Glu Val Tyr Ala Ser Thr Gly
740 745 750

Thr Ile Asn Thr Ser Asp Gly Thr Leu Lys Thr Lys Pro Thr Glu Ile
755 760 765

Glu Asp Ile Leu Leu Lys Ala Trp Glu Asp Ile His Val Ile Ser Tyr
770 775 780

Gln Trp Leu Ser Ala Val Ala Glu Lys Gly Asp Ser Ala Arg Ile His
785 790 795 800

Phe Gly Val Ile Ala Gln Asp Val Arg Asp Ile Leu Ile Asn Tyr Gly
805 810 815

Leu Met Asp Glu Asn Ser Thr Asp Cys Lys Tyr Ala Phe Leu Cys Tyr
820 825 830

Asp Glu Tyr Pro Ala Met Tyr Asp Ser Val Val Thr Gly Gln Lys Glu
835 840 845

Ile Thr Leu Leu Asp Asp Glu Gly Asn Asn Val Ile Asp Glu Glu Gly
850 855 860

Asn Pro Val Thr Ile Val Glu Asp Val Val Glu Thr Ile Glu Val Ile
865 870 875 880

Pro Ala Gly Ser Arg Trp Gly Ile Arg Ala Asp Gln Met Phe Phe Ile
885 890 895

Glu Met Ala Tyr Gln Arg Lys Lys Leu Lys Ala Leu Glu Glu Arg Leu
900 905 910

Ala Thr Leu Glu Ser Lys
915

SEQ Prot 20236_ST25.txt

<210> 13
 <211> 3195
 <212> DNA
 <213> Enterobacteria phage K1F

<220>
 <221> mutation
 <222> (624)..(1801)
 <223> T624A, G1230T, T1412G, and G1801A mutant of SEQ ID No.3

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gccatgattg aaacacgtac cttagccaat aacgcattaa ccaattgtgc attgtgggat     1260
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aattctgcgg taacaggtgt atccggtgat aggactgttg caaccgtaat agataaggac     1440
aacttcacgg ttcttacacc caaccagcag acttcagatt tgaataacgc tggaaagaat     1500
tggcacatgg gtacttcttt ccataagtct ccatggcgta agacagatct tgggtctaate     1560
cctagtgtca cagaggtgca tagctttgct actattgata acaatggctt tgctatgggc     1620
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SEQ Prot 20236_ST25.txt

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gatagactag	gtagctcttt	gcatcgtagt	agagacatag	gtcagacttg	ggagtcactg	1860
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tacaaggcat	cttatcctcg	caccttctat	gcacgcttga	atgtaaacia	ttggaatgca	2040
gatgatattg	aatgggttaa	catcactgac	cagatttatc	agggcggaat	agttaactca	2100
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caaattcgtg	atgtattcat	tgacatgggt	ctgatggatg	aaaacagtac	gaattgtcgt	2940
tatgctgttc	tgtgctatga	caagtatcca	cggatgaccg	atacgggtatt	ttcgacacaa	3000
gaaatcggtg	aacacactga	cgaggagggt	aatgtcacta	ctacggaaga	acctgtgtac	3060
accgaggtgg	ttattcacga	agagggtgag	gagtgggggtg	ttcggcctga	cggaattttc	3120
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<210> 14
 <211> 1064
 <212> PRT
 <213> Enterobacteria phage K1F

<220>
 <221> PEPTIDE
 <222> (208)..(601)
 <223> S208R, K410N, M471R, and D601N

<220>
 <221> PEPTIDE
 <222> (208)..(601)

<223> S208R, K410N, M471R, and D601N mutant of SEQ ID No. 4

<400> 14

Met Ser Thr Ile Thr Gln Phe Pro Ser Gly Asn Thr Gln Tyr Arg Ile
 1 5 10 15
 Glu Phe Asp Tyr Leu Ala Arg Thr Phe Val Val Val Thr Leu Val Asn
 20 25 30
 Ser Ser Asn Pro Thr Leu Asn Arg Val Leu Glu Val Gly Arg Asp Tyr
 35 40 45
 Arg Phe Leu Asn Pro Thr Met Ile Glu Met Leu Val Asp Gln Ser Gly
 50 55 60
 Phe Asp Ile Val Arg Ile His Arg Gln Thr Gly Thr Asp Leu Val Val
 65 70 75 80
 Asp Phe Arg Asn Gly Ser Val Leu Thr Ala Ser Asp Leu Thr Thr Ala
 85 90 95
 Glu Leu Gln Ala Ile His Ile Ala Glu Glu Gly Arg Asp Gln Thr Val
 100 105 110
 Asp Leu Ala Lys Glu Tyr Ala Asp Ala Ala Gly Ser Ser Ala Gly Asn
 115 120 125
 Ala Lys Asp Ser Glu Asp Glu Ala Arg Arg Ile Ala Glu Ser Ile Arg
 130 135 140
 Ala Ala Gly Leu Ile Gly Tyr Met Thr Arg Arg Ser Phe Glu Lys Gly
 145 150 155 160
 Tyr Asn Val Thr Thr Trp Ser Glu Val Leu Leu Trp Glu Glu Asp Gly
 165 170 175
 Asp Tyr Tyr Arg Trp Asp Gly Thr Leu Pro Lys Asn Val Pro Ala Gly
 180 185 190
 Ser Thr Pro Glu Thr Ser Gly Gly Ile Gly Leu Gly Ala Trp Val Arg
 195 200 205
 Val Gly Asp Ala Ala Leu Arg Ser Gln Ile Ser Asn Pro Glu Gly Ala
 210 215 220
 Ile Leu Tyr Pro Glu Leu His Arg Ala Arg Trp Leu Asp Glu Lys Asp
 225 230 235 240
 Ala Arg Gly Trp Gly Ala Lys Gly Asp Gly Val Thr Asp Asp Thr Ala
 245 250 255

SEQ Prot 20236_ST25.txt

Ala Leu Thr Ser Ala Leu Asn Asp Thr Pro Val Gly Gln Lys Ile Asn
260 265 270

Gly Asn Gly Lys Thr Tyr Lys Val Thr Ser Leu Pro Asp Ile Ser Arg
275 280 285

Phe Ile Asn Thr Arg Phe Val Tyr Glu Arg Ile Pro Gly Gln Pro Leu
290 295 300

Tyr Tyr Ala Ser Glu Glu Phe Val Gln Gly Glu Leu Phe Lys Ile Thr
305 310 315 320

Asp Thr Pro Tyr Tyr Asn Ala Trp Pro Gln Asp Lys Ala Phe Val Tyr
325 330 335

Glu Asn Val Ile Tyr Ala Pro Tyr Met Gly Ser Asp Arg His Gly Val
340 345 350

Ser Arg Leu His Val Ser Trp Val Lys Ser Gly Asp Asp Gly Gln Thr
355 360 365

Trp Ser Thr Pro Glu Trp Leu Thr Asp Leu His Pro Asp Tyr Pro Thr
370 375 380

Val Asn Tyr His Cys Met Ser Met Gly Val Cys Arg Asn Arg Leu Phe
385 390 395 400

Ala Met Ile Glu Thr Arg Thr Leu Ala Asn Asn Ala Leu Thr Asn Cys
405 410 415

Ala Leu Trp Asp Arg Pro Met Ser Arg Ser Leu His Leu Thr Gly Gly
420 425 430

Ile Thr Lys Ala Ala Asn Gln Arg Tyr Ala Thr Ile His Val Pro Asp
435 440 445

His Gly Leu Phe Val Gly Asp Phe Val Asn Phe Ser Asn Ser Ala Val
450 455 460

Thr Gly Val Ser Gly Asp Arg Thr Val Ala Thr Val Ile Asp Lys Asp
465 470 475 480

Asn Phe Thr Val Leu Thr Pro Asn Gln Gln Thr Ser Asp Leu Asn Asn
485 490 495

Ala Gly Lys Asn Trp His Met Gly Thr Ser Phe His Lys Ser Pro Trp
500 505 510

Arg Lys Thr Asp Leu Gly Leu Ile Pro Ser Val Thr Glu Val His Ser
515 520 525

SEQ Prot 20236_ST25.txt

Phe Ala Thr Ile Asp Asn Asn Gly Phe Ala Met Gly Tyr His Gln Gly
530 535 540

Asp Val Ala Pro Arg Glu Val Gly Leu Phe Tyr Phe Pro Asp Ala Phe
545 550 555 560

Asn Ser Pro Ser Asn Tyr Val Arg Arg Gln Ile Pro Ser Glu Tyr Glu
565 570 575

Pro Asp Ala Ser Glu Pro Cys Ile Lys Tyr Tyr Asp Gly Val Leu Tyr
580 585 590

Leu Ile Thr Arg Gly Thr Arg Gly Asn Arg Leu Gly Ser Ser Leu His
595 600 605

Arg Ser Arg Asp Ile Gly Gln Thr Trp Glu Ser Leu Arg Phe Pro His
610 615 620

Asn Val His His Thr Thr Leu Pro Phe Ala Lys Val Gly Asp Asp Leu
625 630 635 640

Ile Met Phe Gly Ser Glu Arg Ala Glu Asn Glu Trp Glu Ala Gly Ala
645 650 655

Pro Asp Asp Arg Tyr Lys Ala Ser Tyr Pro Arg Thr Phe Tyr Ala Arg
660 665 670

Leu Asn Val Asn Asn Trp Asn Ala Asp Asp Ile Glu Trp Val Asn Ile
675 680 685

Thr Asp Gln Ile Tyr Gln Gly Gly Ile Val Asn Ser Gly Val Gly Val
690 695 700

Gly Ser Val Val Val Lys Asp Asn Tyr Ile Tyr Tyr Met Phe Gly Gly
705 710 715 720

Glu Asp His Phe Asn Pro Trp Thr Tyr Gly Asp Asn Ser Ala Lys Asp
725 730 735

Pro Phe Lys Ser Asp Gly His Pro Ser Asp Leu Tyr Cys Tyr Lys Met
740 745 750

Lys Ile Gly Pro Asp Asn Arg Val Ser Arg Asp Phe Arg Tyr Gly Ala
755 760 765

Val Pro Asn Arg Ala Val Pro Val Phe Phe Asp Thr Asn Gly Val Arg
770 775 780

Thr Val Pro Ala Pro Met Glu Phe Thr Gly Asp Leu Gly Leu Gly His
785 790 795 800

SEQ Prot 20236_ST25.txt

Val Thr Ile Arg Ala Ser Thr Ser Ser Asn Ile Arg Ser Glu Val Leu
805 810 815

Met Glu Gly Glu Tyr Gly Phe Ile Gly Lys Ser Ile Pro Thr Asp Asn
820 825 830

Pro Ala Gly Gln Arg Ile Ile Phe Cys Gly Gly Glu Gly Thr Ser Ser
835 840 845

Thr Thr Gly Ala Gln Ile Thr Leu Tyr Gly Ala Asn Asn Thr Asp Ser
850 855 860

Arg Arg Ile Val Tyr Asn Gly Asp Glu His Leu Phe Gln Ser Ala Asp
865 870 875 880

Val Lys Pro Tyr Asn Asp Asn Val Thr Ala Leu Gly Gly Pro Ser Asn
885 890 895

Arg Phe Thr Thr Ala Tyr Leu Gly Ser Asn Pro Ile Val Thr Ser Asn
900 905 910

Gly Glu Arg Lys Thr Glu Pro Val Val Phe Asp Asp Ala Phe Leu Asp
915 920 925

Ala Trp Gly Asp Val His Tyr Ile Met Tyr Gln Trp Leu Asp Ala Val
930 935 940

Gln Leu Lys Gly Asn Asp Ala Arg Ile His Phe Gly Val Ile Ala Gln
945 950 955 960

Gln Ile Arg Asp Val Phe Ile Ala His Gly Leu Met Asp Glu Asn Ser
965 970 975

Thr Asn Cys Arg Tyr Ala Val Leu Cys Tyr Asp Lys Tyr Pro Arg Met
980 985 990

Thr Asp Thr Val Phe Ser His Asn Glu Ile Val Glu His Thr Asp Glu
995 1000 1005

Glu Gly Asn Val Thr Thr Thr Glu Glu Pro Val Tyr Thr Glu Val
1010 1015 1020

Val Ile His Glu Glu Gly Glu Glu Trp Gly Val Arg Pro Asp Gly
1025 1030 1035

Ile Phe Phe Ala Glu Ala Ala Tyr Gln Arg Arg Lys Leu Glu Arg
1040 1045 1050

Ile Glu Ala Arg Leu Ser Ala Leu Glu Gln Lys
1055 1060

SEQ Prot 20236_ST25.txt

<210> 15
 <211> 2532
 <212> DNA
 <213> Enterobacteria phage phi92

<220>
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 <222> (682)..(682)
 <223> SEQ ID No. 9 N-terminally truncated

T682G

<220>
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 <222> (682)..(682)
 <223> T682G; N-terminally truncated SEQ ID No. 9

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ataagcaagt ttaaaaacgc tgcttttgtt tacgagcgta ttgttggaca accccttact      180
tatgtatctg aaggtttctt cgatggaaat ctgacaaaga ttacggatac accattttac      240
aatgcttgga cgcaagataa gacgtttgtt tatgataatg ttatatatgc accatttatg      300
gctggcgaac gtcattggtg acaaaacctc catgtagcgt gggttaaatc aggagatgat      360
ggacaaactt ggtctatgcc agaattggtta actccaattc atcctgatta tacagcagac      420
aaagttaact atcattgtat gaggatgggt gtatgtggta atcgctataa tgcagtcatc      480
gaaacccgtt acttatctaa catgcgattg aagaaagcag aactttgggtc acgtccaatg      540
ccttattata gaaggccaac tggaggataa acaattagtt ctgggtctac tacggcgacg      600
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gcaactggtg tatctggaaa taggactggt gcatctgtaa ttaacaagga tacattttacg      720
gttacattag caagggtgac cacatctaata atagataata caggaaactac ttggcatttt      780
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actaatgcag acttatgtgt tacagaaacc catagtttta cagttataga tgatgataat      900
tacacttttg ctgtgggtta tcacaatggt gatatttccc caagaagatt aggtattttg      960
tacttcaata atgcttactc tgaccaagt tcttttactc gtagaacaat tagtcaagaa     1020
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accaggggta cttcaacttc tgctgctggt tctacattag caatgagtgc tgaccttgga     1140
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aaagttggtg attatcttta tatctttggt acagaacgtt catttgagga gtgggaaggg     1260
caagaactag ataataagata taaaggtagc tatcctcgaa cgtttatgtg caagattaat     1320
gtatcttcat ggcctgtatc tttatccaat gttcaatggt ttaatatcac tgatcagata     1380
tatcaagggc atattgttaa ttctgcatgt ggcgttggtt cggtatgtgt taaagatggc     1440
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SEQ Prot 20236_ST25.txt

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gataatgatg tacagatgta ctctttaaca gttactgggtc ttgagcatga tgggacacaa	1740
caatctgccg ttagagtaaa attagatggt gattatgggg ttattgcaaa aaatatccca	1800
ataaaaaatc cttctgaaca gcgactaatc ttatgtggag gagaaactcc ttacactact	1860
gatggatcgt tattacaatt gtatggttca aaccatacgt atccaaacag agcaatttta	1920
tatgccccag gaggagcata tacacaaaat aatttcatgc cgtacttaga tggacaagtt	1980
tcattaggtg gtgcatctaa tagatgggtca gaagtgtatg catctacagg aaccattaat	2040
acttcagacg gaacattaaa aactaaacct acagagattg aagatatttt actgaaagca	2100
tgggaagata ttcattgtaat ctcttaccaa tggcttagtg ctgtcgcgga gaaaggagat	2160
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ggtttaatgg atgaaaatag tactgattgt aagtatgctt ttctatgtta tgatgaatac	2280
cctgctatgt atgatagtgt tgttacggga caaaaagaaa tcactttact tgacgatgaa	2340
ggaaataatg taattgatga agaaggtaat ccagtaacaa ttgtagaaga tgtttagtaa	2400
actatcgaag taattccagc aggatcgca tggggatatcc gcgctgacca aatgtttttt	2460
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gaaagtaaat aa	2532

<210> 16
 <211> 2532
 <212> DNA
 <213> Enterobacteria phage phi 92

<220>
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 <222> (682)..(682)
 <223> SEQ ID No. 10 N-terminally truncated;

T682A

<220>
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 <222> (682)..(682)
 <223> T682A; N-terminally truncated SEQ ID No. 10

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ataagcaagt ttaaaaacgc tgcttttgtt tacgagcgta ttgttgaca accccttact	180
tatgtatctg aaggtttctt cgatggaaat ctgacaaaga ttacggatac accattttac	240
aatgcttgga cgcaagataa gacgtttgtt tatgataatg ttatatatgc accatttatg	300
gctggcgaac gtcatggtgt acaaaacctc catgtagcgt gggttaaatc aggagatgat	360

SEQ Prot 20236_ST25.txt

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gaaaccggtt acttatctaa catgcgattg aagaaagcag aactttgggtc acgtccaatg	540
ccttattata gaaggccaac tggaggtata acaattagtt ctgggtctac tacggcgacg	600
attgttttaa aaaagcatgg tcttaaagtt ggagatgctg ttaacttttc caattcgggt	660
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gttacattag caagggctgc cacatctaata atagataata caggaactac ttggcatttt	780
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cctgctatgt atgatagtgt tgttacggga caaaaagaaa tcactttact tgacgatgaa	2340
ggaaataatg taattgatga agaaggtaat ccagtaacaa ttgtagaaga tgttgtagaa	2400

SEQ Prot 20236_ST25.txt

actatcgaag taattccagc aggatcgcga tggggatatcc gcgctgacca aatgtttttt 2460
attgagatgg cttatcaacg taaaaagtta aaagctcttg aagaaagact tgcaacccta 2520
gaaagtaa at aa 2532

<210> 17
<211> 843
<212> PRT
<213> Enterobacteria phage phi92

<220>
<221> MISC_FEATURE
<222> (228)..(228)
<223> SEQ ID No. 11 N-terminally truncated by 75 amino acids;

M228R

<220>
<221> MISC_FEATURE
<222> (228)..(228)
<223> M228R; SEQ ID No. 11 N-terminally truncated by 75 amino acids

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Phe Lys Val Thr Thr Leu Pro Asp Ile Ser Lys Phe Lys Asn Ala Ala
35 40 45

Phe Val Tyr Glu Arg Ile Val Gly Gln Pro Leu Thr Tyr Val Ser Glu
50 55 60

Gly Phe Phe Asp Gly Asn Leu Thr Lys Ile Thr Asp Thr Pro Phe Tyr
65 70 75 80

Asn Ala Trp Thr Gln Asp Lys Thr Phe Val Tyr Asp Asn Val Ile Tyr
85 90 95

Ala Pro Phe Met Ala Gly Glu Arg His Gly Val Gln Asn Leu His Val
100 105 110

Ala Trp Val Lys Ser Gly Asp Asp Gly Gln Thr Trp Ser Met Pro Glu
115 120 125

Trp Leu Thr Pro Ile His Pro Asp Tyr Thr Ala Asp Lys Val Asn Tyr
130 135 140

His Cys Met Ser Met Gly Val Cys Gly Asn Arg Leu Tyr Ala Val Ile
145 150 155 160

SEQ Prot 20236_ST25.txt

Glu Thr Arg Tyr Leu Ser Asn Met Arg Leu Lys Lys Ala Glu Leu Trp
165 170 175

Ser Arg Pro Met Pro Tyr Tyr Arg Arg Pro Thr Gly Gly Ile Thr Ile
180 185 190

Ser Ser Gly Ser Thr Thr Ala Thr Ile Val Leu Lys Lys His Gly Leu
195 200 205

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

Ser Gly Asn Arg Thr Val Ala Ser Val Ile Asn Lys Asp Thr Phe Thr
225 230 235 240

Val Thr Leu Ala Arg Ala Ala Thr Ser Asn Ile Asp Asn Thr Gly Thr
245 250 255

Thr Trp His Phe Gly Thr Arg Phe Trp Asp Ser Pro Trp Glu Ile Thr
260 265 270

Glu Leu Pro Asp Val Ala Tyr Ser Thr Asn Ala Asp Leu Cys Val Thr
275 280 285

Glu Thr His Ser Phe Thr Val Ile Asp Asp Asp Asn Tyr Thr Phe Ala
290 295 300

Val Gly Tyr His Asn Gly Asp Ile Ser Pro Arg Arg Leu Gly Ile Leu
305 310 315 320

Tyr Phe Asn Asn Ala Tyr Ser Asp Pro Ser Ser Phe Thr Arg Arg Thr
325 330 335

Ile Ser Gln Glu Tyr Ala Asp Asn Ala Ala Glu Pro Cys Ile Lys Tyr
340 345 350

Tyr Asp Gly Ile Leu Tyr Leu Thr Thr Arg Gly Thr Ser Thr Ser Ala
355 360 365

Ala Gly Ser Thr Leu Ala Met Ser Ala Asp Leu Gly Glu Asn Trp Asn
370 375 380

Tyr Leu Arg Phe Pro Asn Asn Val His His Thr Asn Leu Pro Phe Ala
385 390 395 400

Lys Val Gly Asp Tyr Leu Tyr Ile Phe Gly Thr Glu Arg Ser Phe Gly
405 410 415

Glu Trp Glu Gly Gln Glu Leu Asp Asn Arg Tyr Lys Gly Thr Tyr Pro
420 425 430

SEQ Prot 20236_ST25.txt

Arg Thr Phe Met Cys Lys Ile Asn Val Ser Ser Trp Pro Val Ser Leu
435 440 445

Ser Asn Val Gln Trp Phe Asn Ile Thr Asp Gln Ile Tyr Gln Gly His
450 455 460

Ile Val Asn Ser Ala Cys Gly Val Gly Ser Val Cys Val Lys Asp Gly
465 470 475 480

Trp Leu Tyr Tyr Ile Phe Gly Gly Glu Asp Phe Leu Ser Pro Trp Ser
485 490 495

Ile Gly Asp Asn Ser Lys Lys Leu Trp Tyr Lys His Asp Gly His Pro
500 505 510

Ala Asp Leu Tyr Ser Tyr Arg Leu Lys Ile Thr Glu His Asp Phe Val
515 520 525

Ser Arg Asp Phe Lys Tyr Gly Ala Thr Pro Asn Arg Thr Leu Pro Val
530 535 540

Ser Met Gly Thr Asp Gly Val Arg His Val Ser Ala Pro Val Thr Phe
545 550 555 560

Asp Asn Asp Val Gln Met Tyr Ser Leu Thr Val Thr Gly Leu Glu His
565 570 575

Asp Gly Thr Gln Gln Ser Ala Val Arg Val Lys Leu Asp Gly Asp Tyr
580 585 590

Gly Val Ile Ala Lys Asn Ile Pro Ile Lys Asn Pro Ser Glu Gln Arg
595 600 605

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

Leu Gln Leu Tyr Gly Ser Asn His Thr Tyr Pro Asn Arg Ala Ile Leu
625 630 635 640

Tyr Ala Pro Gly Gly Ala Tyr Thr Gln Asn Asn Phe Met Pro Tyr Leu
645 650 655

Asp Gly Gln Val Ser Leu Gly Gly Ala Ser Asn Arg Trp Ser Glu Val
660 665 670

Tyr Ala Ser Thr Gly Thr Ile Asn Thr Ser Asp Gly Thr Leu Lys Thr
675 680 685

Lys Pro Thr Glu Ile Glu Asp Ile Leu Leu Lys Ala Trp Glu Asp Ile
690 695 700

SEQ Prot 20236_ST25.txt

His Val Ile Ser Tyr Gln Trp Leu Ser Ala Val Ala Glu Lys Gly Asp
705 710 715 720

Ser Ala Arg Ile His Phe Gly Val Ile Ala Gln Asp Val Arg Asp Ile
725 730 735

Leu Ile Asn Tyr Gly Leu Met Asp Glu Asn Ser Thr Asp Cys Lys Tyr
740 745 750

Ala Phe Leu Cys Tyr Asp Glu Tyr Pro Ala Met Tyr Asp Ser Val Val
755 760 765

Thr Gly Gln Lys Glu Ile Thr Leu Leu Asp Asp Glu Gly Asn Asn Val
770 775 780

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

Thr Ile Glu Val Ile Pro Ala Gly Ser Arg Trp Gly Ile Arg Ala Asp
805 810 815

Gln Met Phe Phe Ile Glu Met Ala Tyr Gln Arg Lys Lys Leu Lys Ala
820 825 830

Leu Glu Glu Arg Leu Ala Thr Leu Glu Ser Lys
835 840

<210> 18
<211> 843
<212> PRT
<213> Enterobacteria phage phi92

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<223> SEQ ID No. 12 N-terminally truncated by 75 amino acids;

M228K

<220>
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<223> M228K; SEQ ID No. 12 N-terminally truncated by 75 amino acids;

<400> 18

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20 25 30

Phe Lys Val Thr Thr Leu Pro Asp Ile Ser Lys Phe Lys Asn Ala Ala
35 40 45

SEQ Prot 20236_ST25.txt

Phe Val Tyr Glu Arg Ile Val Gly Gln Pro Leu Thr Tyr Val Ser Glu
50 55 60

Gly Phe Phe Asp Gly Asn Leu Thr Lys Ile Thr Asp Thr Pro Phe Tyr
65 70 75 80

Asn Ala Trp Thr Gln Asp Lys Thr Phe Val Tyr Asp Asn Val Ile Tyr
85 90 95

Ala Pro Phe Met Ala Gly Glu Arg His Gly Val Gln Asn Leu His Val
100 105 110

Ala Trp Val Lys Ser Gly Asp Asp Gly Gln Thr Trp Ser Met Pro Glu
115 120 125

Trp Leu Thr Pro Ile His Pro Asp Tyr Thr Ala Asp Lys Val Asn Tyr
130 135 140

His Cys Met Ser Met Gly Val Cys Gly Asn Arg Leu Tyr Ala Val Ile
145 150 155 160

Glu Thr Arg Tyr Leu Ser Asn Met Arg Leu Lys Lys Ala Glu Leu Trp
165 170 175

Ser Arg Pro Met Pro Tyr Tyr Arg Arg Pro Thr Gly Gly Ile Thr Ile
180 185 190

Ser Ser Gly Ser Thr Thr Ala Thr Ile Val Leu Lys Lys His Gly Leu
195 200 205

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

Ser Gly Asn Lys Thr Val Ala Ser Val Ile Asn Lys Asp Thr Phe Thr
225 230 235 240

Val Thr Leu Ala Arg Ala Ala Thr Ser Asn Ile Asp Asn Thr Gly Thr
245 250 255

Thr Trp His Phe Gly Thr Arg Phe Trp Asp Ser Pro Trp Glu Ile Thr
260 265 270

Glu Leu Pro Asp Val Ala Tyr Ser Thr Asn Ala Asp Leu Cys Val Thr
275 280 285

Glu Thr His Ser Phe Thr Val Ile Asp Asp Asp Asn Tyr Thr Phe Ala
290 295 300

Val Gly Tyr His Asn Gly Asp Ile Ser Pro Arg Arg Leu Gly Ile Leu
305 310 315 320

SEQ Prot 20236_ST25.txt

Tyr Phe Asn Asn Ala Tyr Ser Asp Pro Ser Ser Phe Thr Arg Arg Thr
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 Ile Ser Gln Glu Tyr Ala Asp Asn Ala Ala Glu Pro Cys Ile Lys Tyr
 340 345 350
 Tyr Asp Gly Ile Leu Tyr Leu Thr Thr Arg Gly Thr Ser Thr Ser Ala
 355 360 365
 Ala Gly Ser Thr Leu Ala Met Ser Ala Asp Leu Gly Glu Asn Trp Asn
 370 375 380
 Tyr Leu Arg Phe Pro Asn Asn Val His His Thr Asn Leu Pro Phe Ala
 385 390 395 400
 Lys Val Gly Asp Tyr Leu Tyr Ile Phe Gly Thr Glu Arg Ser Phe Gly
 405 410 415
 Glu Trp Glu Gly Gln Glu Leu Asp Asn Arg Tyr Lys Gly Thr Tyr Pro
 420 425 430
 Arg Thr Phe Met Cys Lys Ile Asn Val Ser Ser Trp Pro Val Ser Leu
 435 440 445
 Ser Asn Val Gln Trp Phe Asn Ile Thr Asp Gln Ile Tyr Gln Gly His
 450 455 460
 Ile Val Asn Ser Ala Cys Gly Val Gly Ser Val Cys Val Lys Asp Gly
 465 470 475 480
 Trp Leu Tyr Tyr Ile Phe Gly Gly Glu Asp Phe Leu Ser Pro Trp Ser
 485 490 495
 Ile Gly Asp Asn Ser Lys Lys Leu Trp Tyr Lys His Asp Gly His Pro
 500 505 510
 Ala Asp Leu Tyr Ser Tyr Arg Leu Lys Ile Thr Glu His Asp Phe Val
 515 520 525
 Ser Arg Asp Phe Lys Tyr Gly Ala Thr Pro Asn Arg Thr Leu Pro Val
 530 535 540
 Ser Met Gly Thr Asp Gly Val Arg His Val Ser Ala Pro Val Thr Phe
 545 550 555 560
 Asp Asn Asp Val Gln Met Tyr Ser Leu Thr Val Thr Gly Leu Glu His
 565 570 575
 Asp Gly Thr Gln Gln Ser Ala Val Arg Val Lys Leu Asp Gly Asp Tyr
 580 585 590

SEQ Prot 20236_ST25.txt

Gly Val Ile Ala Lys Asn Ile Pro Ile Lys Asn Pro Ser Glu Gln Arg
595 600 605

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

Leu Gln Leu Tyr Gly Ser Asn His Thr Tyr Pro Asn Arg Ala Ile Leu
625 630 635 640

Tyr Ala Pro Gly Gly Ala Tyr Thr Gln Asn Asn Phe Met Pro Tyr Leu
645 650 655

Asp Gly Gln Val Ser Leu Gly Gly Ala Ser Asn Arg Trp Ser Glu Val
660 665 670

Tyr Ala Ser Thr Gly Thr Ile Asn Thr Ser Asp Gly Thr Leu Lys Thr
675 680 685

Lys Pro Thr Glu Ile Glu Asp Ile Leu Leu Lys Ala Trp Glu Asp Ile
690 695 700

His Val Ile Ser Tyr Gln Trp Leu Ser Ala Val Ala Glu Lys Gly Asp
705 710 715 720

Ser Ala Arg Ile His Phe Gly Val Ile Ala Gln Asp Val Arg Asp Ile
725 730 735

Leu Ile Asn Tyr Gly Leu Met Asp Glu Asn Ser Thr Asp Cys Lys Tyr
740 745 750

Ala Phe Leu Cys Tyr Asp Glu Tyr Pro Ala Met Tyr Asp Ser Val Val
755 760 765

Thr Gly Gln Lys Glu Ile Thr Leu Leu Asp Asp Glu Gly Asn Asn Val
770 775 780

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

Thr Ile Glu Val Ile Pro Ala Gly Ser Arg Trp Gly Ile Arg Ala Asp
805 810 815

Gln Met Phe Phe Ile Glu Met Ala Tyr Gln Arg Lys Lys Leu Lys Ala
820 825 830

Leu Glu Glu Arg Leu Ala Thr Leu Glu Ser Lys
835 840

<210> 19

<211> 2460

<212> DNA

<213> Enterobacteria phage K1F

SEQ Prot 20236_ST25.txt

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 <222> (495)..(1066)
 <223> SEQ ID No. 13 N-terminally truncated;

G495T, T677G, and G1066A

<220>
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 <222> (495)..(1066)
 <223> G495T, T677G, and G1066A; SEQ ID No. 13 N-terminally truncated

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attagtcgct tcatcaacac tcgtttcggt tatgagcgca ttcccggaca acctctttat      180
tatgcctctg aagaatttgt tcaggggtgag ctattcaaaa taacggacac cccttattac      240
aatgcgtggc ctcaggataa agcgttcgta tatgagaatg tgatatatgc accttacatg      300
ggtagcgatc gtcattggtg tagtcgtctg catgtatcat gggttaagtc tggatgatgat      360
ggtcaaacat ggtctactcc agagtgggta actgatctgc atccagatta ccctacagtg      420
aactatcatt gtatgagtat ggggtgatgt cgcaaccgtc tgtttgccat gattgaaaca      480
cgtaccttag ccaataacgc attaaccaat tgtgcattgt gggatcgccc catgtctcgt      540
agcctgcatc ttactggtgg tatcactaaa gctgcaaadc agcgatatgc aacaatacat      600
gtaccagacc acggactatt cgtgggtgat tttgttaact tctctaattc tgcggtaaca      660
ggtgtatccg gtgataggac tggtgcaacc gtaatagata aggacaactt cacggttctt      720
acaccaacc  agcagacttc agatttgaat aacgctggaa agaattggca catgggtact      780
tctttccata agtctccatg gcgtaagaca gatcttggtc taatccctag tgtcacagag      840
gtgcatagct ttgctactat tgataacaat ggctttgcta tgggctatca tcaagggtgat      900
gtagctccac gagaagttgg gcttttctac ttccctgatg ctttcaatag cccatctaata      960
tatgttcgct gtcagatacc atctgagtat gaaccagatg cgtcagagcc gtgcatcaag     1020
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tctttgcatc gtagtagaga cataggtcag acttgggagt cactgagatt tccacataat     1140
gttcatcata ctacattacc ttttgctaaa gtaggggatg accttattat gtttggttca     1200
gaacgtgcag aaaatgaatg ggaagcaggt gcaccagatg atcgttacaa ggcattcttat     1260
cctgcacact tctatgcacg cttgaatgta aacaattgga atgcagatga tattgaatgg     1320
gttaacatca ctgaccagat ttatcagggc ggaatagtta actcaggtgt aggtgttggt     1380
tcggtagtgt tgaaggataa ttacatctac tacatgtttg gtggagagga ccattttaac     1440
ccatggacat atggagataa ctcagcgaac gaccatttca aatcggatgg tcacccctcg     1500
gatttgtatt gctacaaaat gaagattggc ccagacaatc gtgtttccag agatttcaga     1560
tatggtgctg tacccaacag agctgttccc gtgttttttg atacgaatgg gggttcgcact     1620
    
```


SEQ Prot 20236_ST25.txt

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gttcctgcgc caatggaatt tacaggggat ttgggttttag gtcattgtgac cattagagcc 1680
agcaccagta gtaacattcg ctctgaagtt ttaatggaag gtgaatatgg gtttatcggg 1740
aaatctatac cgactgataa cccggcaggg cagcgcacatca ttttttgcgg ggggtgaaggc 1800
accagttcaa cgactggcgc acagattacg ctatatggtg caaataacac cgactcaagg 1860
cgaatagttt acaacggaga tgagcatcta tttcagagtg ctgatgttaa gccttataac 1920
gataacgtca ctgcgcttgg tgggcctagc aaccgtttca ccactgcata cctcggaagc 1980
aaccctattg ttactttctaa cggggagagg aaaacagagc cggtagtttt tgatgatgct 2040
ttcctggatg cctgggggtga cgttcactac atcatgtacc agtgggttaga tgctgttcaa 2100
ctgaaaggca atgatgctcg tttcacttc ggggttattg ctcagcaaat tcgtgatgta 2160
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actgacgagg agggtaatgt cactactacg gaagaacctg tgtacaccga ggtgggttatt 2340
cacgaagagg gtgaggagtg ggggtgttcgg cctgacggaa ttttctttgc tgaagccgct 2400
tatcagagaa gaaaactgga aagaatcgaa gccagacttt ctgctcttga acagaagtaa 2460
```

```
<210> 20
<211> 819
<212> PRT
<213> Enterobacteria phage K1F
```

```
<220>
<221> MISC_FEATURE
<222> (165)..(356)
<223> SEQ ID No. 14 N-terminally truncated by 245 amino acids;
      K165N, M226R, and D356N
```

```
<220>
<221> MISC_FEATURE
<222> (165)..(356)
<223> K165N, M226R, and D356N; SEQ ID No. 14 N-terminally truncated by
      245 amino acids
```

```
<400> 20
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```
Ala Lys Gly Asp Gly Val Thr Asp Asp Thr Ala Ala Leu Thr Ser Ala
 1           5           10           15
```

```
Leu Asn Asp Thr Pro Val Gly Gln Lys Ile Asn Gly Asn Gly Lys Thr
 20           25           30
```

```
Tyr Lys Val Thr Ser Leu Pro Asp Ile Ser Arg Phe Ile Asn Thr Arg
 35           40           45
```

```
Phe Val Tyr Glu Arg Ile Pro Gly Gln Pro Leu Tyr Tyr Ala Ser Glu
 50           55           60
```

```
Glu Phe Val Gln Gly Glu Leu Phe Lys Ile Thr Asp Thr Pro Tyr Tyr
                               Seite 49
```

SEQ Prot 20236_ST25.txt
75

65 70 80

Asn Ala Trp Pro Gln Asp Lys Ala Phe Val Tyr Glu Asn Val Ile Tyr
85 90 95

Ala Pro Tyr Met Gly Ser Asp Arg His Gly Val Ser Arg Leu His Val
100 105 110

Ser Trp Val Lys Ser Gly Asp Asp Gly Gln Thr Trp Ser Thr Pro Glu
115 120 125

Trp Leu Thr Asp Leu His Pro Asp Tyr Pro Thr Val Asn Tyr His Cys
130 135 140

Met Ser Met Gly Val Cys Arg Asn Arg Leu Phe Ala Met Ile Glu Thr
145 150 155 160

Arg Thr Leu Ala Asn Asn Ala Leu Thr Asn Cys Ala Leu Trp Asp Arg
165 170 175

Pro Met Ser Arg Ser Leu His Leu Thr Gly Gly Ile Thr Lys Ala Ala
180 185 190

Asn Gln Arg Tyr Ala Thr Ile His Val Pro Asp His Gly Leu Phe Val
195 200 205

Gly Asp Phe Val Asn Phe Ser Asn Ser Ala Val Thr Gly Val Ser Gly
210 215 220

Asp Arg Thr Val Ala Thr Val Ile Asp Lys Asp Asn Phe Thr Val Leu
225 230 235 240

Thr Pro Asn Gln Gln Thr Ser Asp Leu Asn Asn Ala Gly Lys Asn Trp
245 250 255

His Met Gly Thr Ser Phe His Lys Ser Pro Trp Arg Lys Thr Asp Leu
260 265 270

Gly Leu Ile Pro Ser Val Thr Glu Val His Ser Phe Ala Thr Ile Asp
275 280 285

Asn Asn Gly Phe Ala Met Gly Tyr His Gln Gly Asp Val Ala Pro Arg
290 295 300

Glu Val Gly Leu Phe Tyr Phe Pro Asp Ala Phe Asn Ser Pro Ser Asn
305 310 315 320

Tyr Val Arg Arg Gln Ile Pro Ser Glu Tyr Glu Pro Asp Ala Ser Glu
325 330 335

Pro Cys Ile Lys Tyr Tyr Asp Gly Val Leu Tyr Leu Ile Thr Arg Gly

SEQ Prot 20236_ST25.txt

340

345

350

Thr Arg Gly Asn Arg Leu Gly Ser Ser Leu His Arg Ser Arg Asp Ile
355 360 365

Gly Gln Thr Trp Glu Ser Leu Arg Phe Pro His Asn Val His His Thr
370 375 380

Thr Leu Pro Phe Ala Lys Val Gly Asp Asp Leu Ile Met Phe Gly Ser
385 390 395 400

Glu Arg Ala Glu Asn Glu Trp Glu Ala Gly Ala Pro Asp Asp Arg Tyr
405 410 415

Lys Ala Ser Tyr Pro Arg Thr Phe Tyr Ala Arg Leu Asn Val Asn Asn
420 425 430

Trp Asn Ala Asp Asp Ile Glu Trp Val Asn Ile Thr Asp Gln Ile Tyr
435 440 445

Gln Gly Gly Ile Val Asn Ser Gly Val Gly Val Gly Ser Val Val Val
450 455 460

Lys Asp Asn Tyr Ile Tyr Tyr Met Phe Gly Gly Glu Asp His Phe Asn
465 470 475 480

Pro Trp Thr Tyr Gly Asp Asn Ser Ala Lys Asp Pro Phe Lys Ser Asp
485 490 495

Gly His Pro Ser Asp Leu Tyr Cys Tyr Lys Met Lys Ile Gly Pro Asp
500 505 510

Asn Arg Val Ser Arg Asp Phe Arg Tyr Gly Ala Val Pro Asn Arg Ala
515 520 525

Val Pro Val Phe Phe Asp Thr Asn Gly Val Arg Thr Val Pro Ala Pro
530 535 540

Met Glu Phe Thr Gly Asp Leu Gly Leu Gly His Val Thr Ile Arg Ala
545 550 555 560

Ser Thr Ser Ser Asn Ile Arg Ser Glu Val Leu Met Glu Gly Glu Tyr
565 570 575

Gly Phe Ile Gly Lys Ser Ile Pro Thr Asp Asn Pro Ala Gly Gln Arg
580 585 590

Ile Ile Phe Cys Gly Gly Glu Gly Thr Ser Ser Thr Thr Gly Ala Gln
595 600 605

Ile Thr Leu Tyr Gly Ala Asn Asn Thr Asp Ser Arg Arg Ile Val Tyr
Seite 51

SEQ Prot 20236_ST25.txt

610

615

620

Asn Gly Asp Glu His Leu Phe Gln Ser Ala Asp Val Lys Pro Tyr Asn
625 630 635 640

Asp Asn Val Thr Ala Leu Gly Gly Pro Ser Asn Arg Phe Thr Thr Ala
645 650 655

Tyr Leu Gly Ser Asn Pro Ile Val Thr Ser Asn Gly Glu Arg Lys Thr
660 665 670

Glu Pro Val Val Phe Asp Asp Ala Phe Leu Asp Ala Trp Gly Asp Val
675 680 685

His Tyr Ile Met Tyr Gln Trp Leu Asp Ala Val Gln Leu Lys Gly Asn
690 695 700

Asp Ala Arg Ile His Phe Gly Val Ile Ala Gln Gln Ile Arg Asp Val
705 710 715 720

Phe Ile Ala His Gly Leu Met Asp Glu Asn Ser Thr Asn Cys Arg Tyr
725 730 735

Ala Val Leu Cys Tyr Asp Lys Tyr Pro Arg Met Thr Asp Thr Val Phe
740 745 750

Ser His Asn Glu Ile Val Glu His Thr Asp Glu Glu Gly Asn Val Thr
755 760 765

Thr Thr Glu Glu Pro Val Tyr Thr Glu Val Val Ile His Glu Glu Gly
770 775 780

Glu Glu Trp Gly Val Arg Pro Asp Gly Ile Phe Phe Ala Glu Ala Ala
785 790 795 800

Tyr Gln Arg Arg Lys Leu Glu Arg Ile Glu Ala Arg Leu Ser Ala Leu
805 810 815

Glu Gln Lys