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SEQUENCE LISTING

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<120> Induction of Gene Expression in Arthropods  
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Gly Leu Ser Thr Pro Leu Thr His Ile Pro His Ala Leu Thr Leu Ile  
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Ile Asp Leu Leu Ile Val Ile Asn Tyr Gly Val Ile Ser Ser Pro Ile  
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Tyr Gly Val Pro Arg Tyr Ile Thr Tyr Gly Lys Trp Pro Ala Trp Leu  
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Ser Asn Ala Asn Arg Asp Phe Pro Leu Thr Ser Met Gly Gly Leu Phe

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Thr Val Asn Cys Pro Leu Gly Ser Thr Ser Ser Val Ser Tyr Ala Lys  
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Tyr Ala Pro Tyr Arg Gln Arg Met Ala Arg Leu Ala Leu Cys Pro Val  
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His Arg Tyr Tyr His Gly Asp Ala Val Leu Ala Val His Gln Trp Ala  
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Trp Ile Ala Val Leu Thr Gly Ile Ser Lys Ser Pro Pro His Arg Gln  
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Trp Glu Phe Val Leu Ala Pro Lys Ser Thr Gly Leu Ser Lys Met Ser  
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Gln Leu Arg Pro Ile Asp Ala Asn Gly Arg Ala Cys Thr Val Gly Gly  
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Leu Tyr Lys Gln Ser Ser Leu Ala Asn Arg Thr His Cys Leu Leu Ala  
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Tyr Arg Asn Tyr Asp Ser Leu Gly Asp Pro Ser Trp Leu Ala Phe Lys  
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Leu Lys Leu Gly Thr Glu Leu Gly Ser Ala Thr Met Val Ser Lys Gly  
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Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys  
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Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val  
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Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe  
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Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe  
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Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly  
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Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp  
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His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
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Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
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Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
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Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly Pro Val Thr Arg Ser  
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Pro Val Pro Ser Leu Thr Leu Glu Gly Ala Thr Pro Thr Val Leu Ser  
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Val Arg Leu Gly Ser Pro Ala Lys Thr Gly Trp Leu Ser Arg Arg Gln  
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Asp Arg Phe Ala Leu Asn Lys Met Asp Cys Thr Gln Val Leu Arg Pro  
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675

680

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Arg Gln Arg Tyr Arg Gly Trp Pro Arg Arg Ala Phe Leu Ala Gln Leu  
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Cys Ser Thr Leu Ser Leu Lys Arg Glu Gly Thr Gly Cys Tyr Trp Ala  
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Lys Cys Arg Gly Arg Ile Ser Cys His Leu Thr Leu Leu Leu Pro Arg  
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Arg Leu Pro Ala His Ser Thr Thr Lys Arg Asn Ile Ala Ser Ser Glu  
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His Val Leu Gly Trp Lys Pro Val Leu Ser Ile Arg Met Ile Trp Thr  
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Lys Ser Ile Arg Gly Ser Arg Gln Pro Asn Cys Ser Pro Gly Ser Arg  
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Arg Ala Cys Pro Thr Ala Arg Ile Ser Ser Pro Met Ala Met Pro Ala  
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Cys Arg Ile Ser Trp Trp Lys Met Ala Ala Phe Leu Asp Ser Ser Thr  
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Cys Phe Thr Val Ser Pro Leu Pro Ile Arg Ser Ala Ser Pro Ser Ile  
 915 920 925

Ala Phe Leu Thr Ser Ser Ser Glu Leu Leu Thr Leu Thr Ile Ser Cys  
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Gly Ile Phe Ser Leu Arg Ile Cys Ala Val Phe His Thr Ala Tyr Arg





1205

1210

1215

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Pro Gly Asp Phe Pro His Pro Asn His Thr Phe His Thr Arg His Leu  
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Leu Thr Ser Tyr Ser Ile Thr Gly Ser Leu Val His Ser Pro Tyr Met  
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Glu Phe Arg Val Thr Leu Thr Val Asn Gly Pro Pro Gly Pro Pro Asn  
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Asp Pro Arg Pro Leu Thr Ser Ile Met Thr Tyr Val Pro Ile Val Thr  
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Pro Ile Gly Thr Phe His Arg Gln Trp Val Asp Tyr Leu Arg Thr Ala  
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His Leu Ala Val His Gln Val Tyr His Met Pro Ser Thr Pro Pro Ile  
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Asp Val Asn Asp Gly Lys Trp Pro Ala Trp His Tyr Ala Gln Tyr Met  
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 cggtaccaag ctttaagctcg agcttgagtg gagagagaga gctagttata agcgtgtgtg 3000  
 tgcgctcttg tgactgaatc gaggagctaa cacgggctct tatatacaca aatatgctcc 3060  
 gccacaaca gcgattacac catttctagg aataaatgag taacaagggg taccactagc 3120  
 taataatcaa tgtcaacgcg tgtggaatgt gtgtcagtta ggggtgtggaa agtccccagg 3180  
 ctccccagca ggcagaagta tgcaaagcat gcatctcaat tagtcagcaa ccaggtgtgg 3240  
 aaagtcccca ggctccccag caggcagaag tatgcaaagc atgcatctca attagtcagc 3300  
 aaccatagtc ccgcccctaa ctccgcccac cccgccccta actccacgcg tatatctggc 3360  
 ccgtacatcg cgaagagtc 3379

<210> 8  
 <211> 1096  
 <212> PRT  
 <213> artificial sequences  
 <220>  
 <223> pVAX-EGFP-SV40-wssvie1 first reading frame  
 <400> 8

Asp Ser Ser Arg Cys Thr Gly Gln Ile Tyr Ala Trp Ser Gly Arg Asp  
 1 5 10 15

Gly Arg Ser Gly Arg Asp Tyr Gly Cys Leu Ile Glu Met His Ala Leu  
 20 25 30

His Thr Ser Ala Cys Trp Gly Ala Trp Gly Leu Ser Thr Pro Gly Cys  
 35 40 45

Leu Ile Glu Met His Ala Leu His Thr Ser Ala Cys Trp Gly Ala Trp  
 50 55 60

Gly Leu Ser Thr Pro Leu Thr His Ile Pro His Ala Leu Thr Leu Ile  
 65 70 75 80

Ile Asp Trp Tyr Pro Leu Leu Leu Ile Tyr Ser Lys Trp Cys Asn Arg  
 85 90 95

Cys Cys Gly Arg Ser Ile Phe Val Tyr Ile Arg Ala Arg Val Ser Ser  
 100 105 110

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



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

Ala Ser Ser Glu His Val Leu Gly Trp Lys Pro Val Leu Ser Ile Arg  
 660 665 670  
 Met Ile Trp Thr Lys Ser Ile Arg Gly Ser Arg Gln Pro Asn Cys Ser  
 675 680 685  
 Pro Gly Ser Arg Arg Ala Cys Pro Thr Ala Arg Ile Ser Ser Pro Met  
 690 695 700  
 Ala Met Pro Ala Cys Arg Ile Ser Trp Trp Lys Met Ala Ala Phe Leu  
 705 710 715 720  
 Asp Ser Ser Thr Val Ala Gly Trp Val Trp Arg Thr Ala Ile Arg Thr  
 725 730 735  
 Arg Trp Leu Pro Val Ile Leu Leu Lys Ser Leu Ala Ala Asn Gly Leu  
 740 745 750  
 Thr Ala Ser Ser Cys Phe Thr Val Ser Pro Leu Pro Ile Arg Ser Ala  
 755 760 765  
 Ser Pro Ser Ile Ala Phe Leu Thr Ser Ser Ser Glu Leu Leu Thr Leu  
 770 775 780  
 Thr Ile Ser Cys Gly Ile Phe Ser Leu Arg Ile Cys Ala Val Phe His  
 785 790 795 800  
 Thr Ala Tyr Arg Trp His Phe Ser Gly Lys Cys Ala Arg Asn Pro Tyr  
 805 810 815  
 Leu Phe Ile Phe Leu Asn Thr Phe Lys Tyr Val Ser Ala His Glu Thr  
 820 825 830  
 Ile Thr Leu Ile Asn Ala Ser Ile Ile Ala Arg Ala Lys Thr Ser Phe  
 835 840 845  
 Leu Ile Lys Asp Leu Gly Glu Asp Pro Phe Ser His Asp Gln Asn Pro  
 850 855 860  
 Leu Thr Val Phe Val Pro Leu Ser Val Arg Pro Arg Arg Lys Asp Gln  
 865 870 875 880  
 Arg Ile Phe Leu Arg Ser Phe Phe Ser Ala Arg Asn Leu Leu Leu Ala  
 885 890 895  
 Asn Lys Lys Thr Thr Ala Thr Ser Gly Gly Leu Phe Ala Gly Ser Arg  
 900 905 910  
 Ala Thr Asn Ser Phe Ser Glu Gly Asn Trp Leu Gln Gln Ser Ala Asp  
 915 920 925

Thr Lys Tyr Cys Pro Ser Ser Val Ala Val Val Arg Pro Pro Leu Gln  
 930 935 940

Glu Leu Cys Ser Thr Ala Tyr Ile Pro Arg Ser Ala Asn Pro Val Thr  
 945 950 955 960

Ser Gly Cys Cys Gln Trp Arg Val Val Ser Tyr Arg Val Gly Leu Lys  
 965 970 975

Thr Ile Val Thr Gly Gly Ala Ala Val Gly Leu Asn Gly Gly Phe Val  
 980 985 990

His Thr Ala Gln Leu Gly Ala Asn Asp Leu His Arg Thr Glu Ile Pro  
 995 1000 1005

Thr Ala Ala Met Arg Lys Arg His Ala Ser Arg Arg Glu Lys Gly  
 1010 1015 1020

Gly Gln Val Ser Gly Lys Arg Gln Gly Arg Asn Arg Arg Ala His  
 1025 1030 1035

Glu Gly Ala Ser Arg Gly Lys Arg Leu Val Ser Leu Ser Cys Arg  
 1040 1045 1050

Val Ser Pro Pro Leu Thr Ala Ser Ile Phe Val Met Leu Val Arg  
 1055 1060 1065

Gly Ala Glu Pro Met Glu Lys Arg Gln Gln Arg Gly Leu Phe Thr  
 1070 1075 1080

Val Pro Gly Leu Leu Leu Ala Phe Cys Ser His Val Leu  
 1085 1090 1095

<210> 9  
 <211> 1072  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> pVAX-EGFP-SV40-WSSViel second reading frame

<400> 9

Thr Leu Arg Asp Val Arg Ala Arg Tyr Thr Arg Gly Val Arg Gly Gly  
 1 5 10 15

Met Gly Gly Val Arg Gly Gly Thr Met Val Ala Asp Leu Arg Cys Met  
 20 25 30

Leu Cys Ile Leu Leu Pro Ala Gly Glu Pro Gly Asp Phe Pro His Leu  
 35 40 45

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

Pro Pro Ser Ala Thr Ala Pro Cys Cys Cys Pro Thr Thr Thr Thr Ala  
 325 330 335  
 Pro Ser Pro Pro Ala Lys Thr Pro Thr Arg Ser Ala Ile Thr Trp Ser  
 340 345 350  
 Cys Trp Ser Ser Pro Pro Pro Gly Ser Leu Ser Ala Trp Thr Ser Cys  
 355 360 365  
 Thr Ser Lys Gly Pro Phe Lys Pro Ala Asp Gln Pro Arg Leu Cys Leu  
 370 375 380  
 Leu Val Ala Ser His Leu Leu Phe Ala Pro Pro Pro Cys Leu Pro Pro  
 385 390 395 400  
 Trp Lys Val Pro Leu Pro Leu Ser Phe Pro Asn Lys Met Arg Lys Leu  
 405 410 415  
 His Arg Ile Val Val Gly Val Ile Leu Phe Trp Gly Val Gly Trp Gly  
 420 425 430  
 Arg Thr Ala Arg Gly Arg Ile Gly Lys Thr Ile Ala Gly Met Leu Gly  
 435 440 445  
 Met Arg Trp Ala Leu Trp Leu Leu Gly Gly Phe Met Met Asp Ser  
 450 455 460  
 Lys Arg Thr Gly Ile Ala Ser Trp Gly Ala Leu Trp Gly Trp Glu Ala  
 465 470 475 480  
 Leu Gln Ser Lys Leu Asp Gly Phe Leu Ala Ala Lys Asp Leu Met Ala  
 485 490 495  
 Gln Gly Ile Lys Leu Ser Arg Asp Arg Met Arg Ile Val Ser His Asp  
 500 505 510  
 Thr Arg Trp Ile Ala Arg Arg Phe Ser Gly Arg Leu Gly Gly Glu Glu  
 515 520 525  
 Ala Ile Arg Leu Leu Gly Thr Thr Asp Asn Arg Leu Leu Cys Arg Arg  
 530 535 540  
 Val Pro Ala Val Ser Ala Gly Ala Pro Gly Ser Phe Cys Gln Asp Arg  
 545 550 555 560  
 Pro Val Arg Cys Pro Glu Thr Ala Arg Arg Gly Ser Ala Ala Ile Val  
 565 570 575  
 Ala Gly His Asp Gly Arg Ser Leu Arg Ser Cys Ala Arg Arg Cys His  
 580 585 590

Ser Gly Lys Gly Leu Ala Ala Ile Gly Arg Ser Ala Gly Ala Gly Ser  
 595 600 605  
 Pro Val Ile Ser Pro Cys Ser Cys Arg Glu Ser Ile His His Gly Cys  
 610 615 620  
 Asn Ala Ala Ala Ala Tyr Ala Ser Gly Tyr Leu Pro Ile Arg Pro Pro  
 625 630 635 640  
 Ser Glu Thr Ser His Arg Ala Ser Thr Tyr Ser Asp Gly Ser Arg Ser  
 645 650 655  
 Cys Arg Ser Gly Ser Gly Arg Arg Ala Ser Gly Ala Arg Ala Ser Arg  
 660 665 670  
 Thr Val Arg Gln Ala Gln Gly Glu His Ala Arg Arg Arg Gly Ser Arg  
 675 680 685  
 Arg Asp Pro Trp Arg Cys Leu Leu Ala Glu Tyr His Gly Gly Lys Trp  
 690 695 700  
 Pro Leu Phe Trp Ile His Arg Leu Trp Pro Ala Gly Cys Gly Gly Pro  
 705 710 715 720  
 Leu Ser Gly His Ser Val Gly Tyr Pro Tyr Cys Arg Ala Trp Arg Arg  
 725 730 735  
 Met Gly Pro Leu Pro Arg Ala Leu Arg Tyr Arg Arg Ser Arg Phe Ala  
 740 745 750  
 Ala His Arg Leu Leu Ser Pro Ser Arg Val Leu Leu Asn Tyr Arg Leu  
 755 760 765  
 Gln Phe Pro Asp Ala Val Phe Ser Pro Tyr Ala Ser Val Arg Tyr Phe  
 770 775 780  
 Thr Pro His Thr Gly Gly Thr Phe Arg Gly Asn Val Arg Gly Thr Pro  
 785 790 795 800  
 Ile Cys Leu Phe Phe Ile His Ser Asn Met Tyr Pro Leu Met Arg Gln  
 805 810 815  
 Pro Met Leu Gln His Val Leu Lys Leu His Phe Phe Lys Arg Ile Val  
 820 825 830  
 Lys Ile Leu Phe Asp Asn Leu Met Thr Lys Ile Pro Arg Glu Phe Ser  
 835 840 845  
 Phe His Ala Ser Asp Pro Val Glu Lys Ile Lys Gly Ser Ser Asp Pro  
 850 855 860

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Phe Phe Leu Arg Val Ile Cys Cys Leu Gln Thr Lys Lys Pro Pro Leu  
 865 870 875 880  
 Pro Ala Val Val Cys Leu Pro Asp Gln Glu Leu Pro Thr Leu Phe Pro  
 885 890 895  
 Lys Val Thr Gly Phe Ser Arg Ala Gln Ile Pro Asn Thr Val Leu Leu  
 900 905 910  
 Val Pro Leu Gly His His Phe Lys Asn Ser Val Ala Pro Pro Thr Tyr  
 915 920 925  
 Leu Ala Leu Leu Ile Leu Leu Pro Val Ala Ala Ala Ser Gly Asp Lys  
 930 935 940  
 Ser Cys Leu Thr Gly Leu Asp Ser Arg Arg Leu Pro Asp Lys Ala Gln  
 945 950 955 960  
 Arg Ser Gly Thr Gly Gly Ser Cys Thr Gln Pro Ser Leu Glu Arg Thr  
 965 970 975  
 Thr Tyr Thr Glu Leu Arg Tyr Leu Gln Arg Glu Leu Glu Ser Ala Thr  
 980 985 990  
 Leu Pro Glu Gly Arg Lys Ala Asp Arg Tyr Pro Val Ser Gly Arg Val  
 995 1000 1005  
 Gly Thr Gly Glu Arg Thr Arg Glu Leu Pro Gly Gly Asn Ala Trp  
 1010 1015 1020  
 Tyr Leu Tyr Ser Pro Val Gly Phe Arg His Leu Leu Glu Arg Arg  
 1025 1030 1035  
 Phe Leu Cys Ser Ser Gly Gly Arg Ser Leu Trp Lys Asn Ala Ser  
 1040 1045 1050  
 Asn Ala Ala Phe Leu Arg Phe Leu Gly Phe Cys Trp Pro Phe Ala  
 1055 1060 1065  
 His Met Phe Leu  
 1070

<210> 10  
 <211> 1100  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> plasmid pVAX-EGFP-SV40-WSSvie1 third reading frame  
 <400> 10

Leu Phe Ala Met Tyr Gly Pro Asp Ile Arg Val Glu Leu Gly Ala Gly  
 1 5 10 15

Trp Ala Glu Leu Gly Ala Gly Leu Trp Leu Leu Thr Asn Asp Ala Cys  
 20 25 30  
 Phe Ala Tyr Phe Cys Leu Leu Gly Ser Leu Gly Thr Phe His Thr Trp  
 35 40 45  
 Leu Leu Thr Asn Asp Ala Cys Phe Ala Tyr Phe Cys Leu Leu Gly Ser  
 50 55 60  
 Leu Gly Thr Phe His Thr Leu Thr Asp Thr His Ser Thr Arg Val Asp  
 65 70 75 80  
 Ile Asp Tyr Leu Val Val Pro Leu Val Thr His Leu Phe Leu Glu Met  
 85 90 95  
 Val Ser Leu Leu Trp Ala Glu His Ile Cys Val Tyr Lys Ser Pro Cys  
 100 105 110  
 Leu Leu Asp Ser Val Thr Arg Ala His Thr His Ala Tyr Asn Leu Ser  
 115 120 125  
 Leu Ser Thr Gln Ala Arg Ala Ala Trp Tyr Arg Ala Arg Ile Arg His  
 130 135 140  
 His Gly Glu Gln Gly Arg Gly Ala Val His Arg Gly Gly Ala His Pro  
 145 150 155 160  
 Gly Arg Ala Gly Arg Arg Arg Lys Arg Pro Gln Val Gln Arg Val Arg  
 165 170 175  
 Arg Gly Arg Gly Arg Cys His Leu Arg Gln Ala Asp Pro Glu Val His  
 180 185 190  
 Leu His His Arg Gln Ala Ala Arg Ala Leu Ala His Pro Arg Asp His  
 195 200 205  
 Pro Asp Leu Arg Arg Ala Val Leu Gln Pro Leu Pro Arg Pro His Glu  
 210 215 220  
 Ala Ala Arg Leu Leu Gln Val Arg His Ala Arg Arg Leu Arg Pro Gly  
 225 230 235 240  
 Ala His His Leu Leu Gln Gly Arg Arg Gln Leu Gln Asp Pro Arg Arg  
 245 250 255  
 Gly Glu Val Arg Gly Arg His Pro Gly Glu Pro His His Arg Ala Glu  
 260 265 270  
 Gly His Arg Leu Gln Gly Gly Arg Gln His Pro Gly Ala Gln Ala Gly  
 275 280 285



Val Gln Leu Gln Gln Pro Gln Arg Leu Tyr His Gly Arg Gln Ala Glu  
 290 295 300  
 Glu Arg His Gln Gly Glu Leu Gln Asp Pro Pro Gln His Arg Gly Arg  
 305 310 315 320  
 Gln Arg Ala Ala Arg Arg Pro Leu Pro Ala Glu His Pro His Arg Arg  
 325 330 335  
 Pro Arg Ala Ala Ala Arg Gln Pro Leu Pro Glu His Pro Val Arg Pro  
 340 345 350  
 Glu Gln Arg Pro Gln Arg Glu Ala Arg Ser His Gly Pro Ala Gly Val  
 355 360 365  
 Arg Asp Arg Arg Arg Asp His Ser Arg His Gly Arg Ala Val Gln Val  
 370 375 380  
 Arg Ala Arg Leu Asn Pro Leu Ile Ser Leu Asp Cys Ala Phe Leu Pro  
 385 390 395 400  
 Ala Ile Cys Cys Leu Pro Leu Pro Arg Ala Phe Leu Asp Pro Gly Arg  
 405 410 415  
 Cys His Ser His Cys Pro Phe Leu Ile Lys Gly Asn Cys Ile Ala Leu  
 420 425 430  
 Ser Glu Val Ser Phe Tyr Ser Gly Gly Trp Gly Gly Ala Gly Gln Gln  
 435 440 445  
 Gly Gly Gly Leu Gly Arg Gln Gln Ala Cys Trp Gly Cys Gly Gly Leu  
 450 455 460  
 Tyr Gly Phe Tyr Trp Ala Val Leu Trp Thr Ala Ser Glu Pro Glu Leu  
 465 470 475 480  
 Pro Ala Gly Ala Pro Ser Gly Lys Val Gly Lys Pro Cys Lys Val Asn  
 485 490 495  
 Trp Met Ala Phe Ser Pro Pro Arg Ile Trp Arg Arg Gly Ser Ser Ser  
 500 505 510  
 Asp Gln Glu Thr Gly Gly Ser Phe Arg Met Ile Glu Gln Asp Gly Leu  
 515 520 525  
 His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly Tyr Asp  
 530 535 540  
 Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala Ala Val Phe Arg Leu  
 545 550 555 560

Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu Ser Gly  
 565 570 575  
 Ala Leu Asn Glu Leu Gln Asp Glu Ala Ala Arg Leu Ser Trp Leu Ala  
 580 585 590  
 Thr Thr Gly Val Pro Cys Ala Ala Val Leu Asp Val Val Thr Glu Ala  
 595 600 605  
 Gly Arg Asp Trp Leu Leu Leu Gly Glu Val Pro Gly Gln Asp Leu Leu  
 610 615 620  
 Ser Ser His Leu Ala Pro Ala Glu Lys Val Ser Ile Met Ala Asp Ala  
 625 630 635 640  
 Met Arg Arg Leu His Thr Leu Asp Pro Ala Thr Cys Pro Phe Asp His  
 645 650 655  
 Gln Ala Lys His Arg Ile Glu Arg Ala Arg Thr Arg Met Glu Ala Gly  
 660 665 670  
 Leu Val Asp Gln Asp Asp Leu Asp Glu Glu His Gln Gly Leu Ala Pro  
 675 680 685  
 Ala Glu Leu Phe Ala Arg Leu Lys Ala Ser Met Pro Asp Gly Glu Asp  
 690 695 700  
 Leu Val Val Thr His Gly Asp Ala Cys Leu Pro Asn Ile Met Val Glu  
 705 710 715 720  
 Asn Gly Arg Phe Ser Gly Phe Ile Asp Cys Gly Arg Leu Gly Val Ala  
 725 730 735  
 Asp Arg Tyr Gln Asp Ile Ala Leu Ala Thr Arg Asp Ile Ala Glu Glu  
 740 745 750  
 Leu Gly Gly Glu Trp Ala Asp Arg Phe Leu Val Leu Tyr Gly Ile Ala  
 755 760 765  
 Ala Pro Asp Ser Gln Arg Ile Ala Phe Tyr Arg Leu Leu Asp Glu Phe  
 770 775 780  
 Phe Ile Ile Asn Ala Tyr Asn Phe Leu Met Arg Tyr Phe Leu Leu Thr  
 785 790 795 800  
 His Leu Cys Gly Ile Ser His Arg Ile Gln Val Ala Leu Phe Gly Glu  
 805 810 815  
 Met Cys Cys Ala Glu Pro Leu Phe Val Tyr Phe Ser Lys Tyr Ile Gln  
 820 825 830

• Ile Cys Ile Arg Ser Asp Asn Asn Pro Asp Lys Cys Cys Phe Asn Asn  
 835 840 845  
 :  
 • Ser Thr Cys Asn Phe Ile Phe Asn Leu Lys Gly Ser Arg Arg Ser Phe  
 850 855 860  
 Leu Ile Ile Ser Pro Lys Ser Leu Asn Val Ser Phe Arg Ser Thr Glu  
 865 870 875 880  
 Arg Gln Thr Pro Lys Arg Ser Lys Asp Leu Leu Glu Ile Leu Phe Phe  
 885 890 895  
 Cys Ala Ser Ala Ala Cys Lys Gln Lys Asn His Arg Tyr Gln Arg Trp  
 900 905 910  
 Phe Val Cys Arg Ile Lys Ser Tyr Gln Leu Phe Phe Arg Arg Leu Ala  
 915 920 925  
 Ser Ala Glu Arg Arg Tyr Gln Ile Leu Ser Phe Cys Ser Arg Ser Ala  
 930 935 940  
 Thr Thr Ser Arg Thr Leu His Arg Leu His Thr Ser Leu Cys Ser Cys  
 945 950 955 960  
 Tyr Gln Trp Leu Leu Pro Val Ala Ile Ser Arg Val Leu Pro Gly Trp  
 965 970 975  
 Thr Gln Asp Asp Ser Tyr Arg Ile Arg Arg Ser Gly Arg Ala Glu Arg  
 980 985 990  
 Gly Val Arg Ala His Ser Pro Ala Trp Ser Glu Arg Pro Thr Pro Asn  
 995 1000 1005  
 Asp Thr Tyr Ser Val Ser Tyr Glu Lys Ala Pro Arg Phe Pro Lys  
 1010 1015 1020  
 Gly Glu Arg Arg Thr Gly Ile Arg Ala Ala Gly Ser Glu Gln Glu  
 1025 1030 1035  
 Ser Ala Arg Gly Ser Phe Gln Gly Glu Thr Pro Gly Ile Phe Ile  
 1040 1045 1050  
 Val Leu Ser Gly Phe Ala Thr Ser Asp Leu Ser Val Asp Phe Cys  
 1055 1060 1065  
 Asp Ala Arg Gln Gly Gly Gly Ala Tyr Gly Lys Thr Pro Ala Thr  
 1070 1075 1080  
 Arg Pro Phe Tyr Gly Ser Trp Ala Phe Ala Gly Leu Leu Leu Thr  
 1085 1090 1095

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■ Cys Ser  
: 1100  
■