

SEQUENCE LISTING

<110> Ludwig Institute for Cancer Research Ltd.

<120> Viral vectors and methods for the prevention or treatment of cancer

<130> P257619W0

<150> 1812647.4

<151> 2018-08-03

<160> 31

<170> PatentIn version 3.5

<210> 1

<211> 314

<212> PRT

<213> Homo sapiens

<400> 1

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Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Ser Thr Leu Val Glu Val
35 40 45

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

Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp
65 70 75 80

Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser
85 90 95

Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys
100 105 110

Val Ala Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu
115 120 125

Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln
130 135 140

Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Ser Ser Leu Gln Leu
145 150 155 160

Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Leu Tyr
165 170 175

Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp
180 185 190

Asn Gln Ile Met Pro Lys Ala Gly Leu Leu Ile Ile Val Leu Ala Ile
195 200 205

Ile Ala Arg Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu
210 215 220

Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Ile Leu Gly
225 230 235 240

Asp Pro Lys Lys Leu Leu Thr Gln His Phe Val Gln Glu Asn Tyr Leu
245 250 255

Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu
260 265 270

Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr Val Lys Val Leu His
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His Met Val Lys Ile Ser Gly Gly Pro His Ile Ser Tyr Pro Pro Leu
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His Glu Trp Val Leu Arg Glu Gly Glu Glu

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<211> 1753

<212> PRT

<213> Homo sapiens

<400> 2

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Ala Ala Gly Cys Cys Gly Gly Cys Cys Cys Ala Gly Gly Cys Thr Cys
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165 170 175

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Cys Cys Cys Thr Gly Ala Cys Cys Ala Gly Ala Gly Thr Cys Ala Thr
195 200 205

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325 330 335

Cys Thr Ala Cys Thr Cys Thr Ala Gly Thr Thr Gly Ala Ala Gly Thr
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Cys Ala Cys Cys Cys Thr Gly Gly Gly Gly Gly Ala Gly Gly Thr Gly
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Cys Cys Thr Gly Cys Thr Gly Cys Cys Gly Ala Gly Thr Cys Ala Cys
370 375 380

Cys Ala Gly Ala Thr Cys Cys Thr Cys Cys Cys Cys Ala Gly Ala Gly
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Cys Ala Cys Cys Thr Thr Cys Cys Cys Thr Gly Ala Cys Cys Thr Gly
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Gly Ala Gly Thr Cys Cys Gly Ala Gly Thr Thr Cys Cys Ala Ala Gly
515 520 525

Cys Ala Gly Cys Ala Cys Thr Cys Ala Gly Thr Ala Gly Gly Ala Ala
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Gly Gly Thr Gly Gly Cys Cys Gly Ala Gly Thr Thr Gly Gly Thr Thr
545 550 555 560

Cys Ala Thr Thr Thr Thr Cys Thr Gly Cys Thr Cys Cys Thr Cys Ala
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Ala Gly Thr Ala Thr Cys Gly Ala Gly Cys Cys Ala Gly Gly Gly Ala
580 585 590

Gly Cys Cys Gly Gly Thr Cys Ala Cys Ala Ala Ala Gly Gly Cys Ala
595 600 605

Gly Ala Ala Ala Thr Gly Cys Thr Gly Gly Gly Gly Ala Gly Thr Gly
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Thr Cys Gly Thr Cys Gly Gly Ala Ala Ala Thr Thr Gly Gly Cys Ala
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Ala Thr Cys Thr Thr Cys Ala Gly Cys Ala Ala Ala Gly Cys Thr Thr
660 665 670

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675 680 685

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690 695 700

Cys Thr Gly Ala Thr Gly Gly Ala Ala Gly Thr Gly Gly Ala Cys Cys
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Cys Cys Ala Thr Cys Gly Gly Cys Cys Ala Cys Thr Thr Gly Thr Ala
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Cys Ala Thr Cys Thr Thr Thr Gly Cys Cys Ala Cys Cys Thr Gly Cys
740 745 750

Cys Thr Gly Gly Gly Cys Cys Thr Cys Thr Cys Cys Thr Ala Cys Gly
755 760 765

Ala Thr Gly Gly Cys Cys Thr Gly Cys Thr Gly Gly Gly Thr Gly Ala
770 775 780

Cys Ala Ala Thr Cys Ala Gly Ala Thr Cys Ala Thr Gly Cys Cys Cys
785 790 795 800

Ala Ala Gly Gly Cys Ala Gly Gly Cys Cys Thr Cys Cys Thr Gly Ala
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Thr Ala Ala Thr Cys Gly Thr Cys Cys Thr Gly Gly Cys Cys Ala Thr
820 825 830

Ala Ala Thr Cys Gly Cys Ala Ala Gly Ala Gly Ala Gly Gly Gly Cys
835 840 845

Gly Ala Cys Thr Gly Thr Gly Cys Cys Cys Cys Thr Gly Ala Gly Gly
850 855 860

Ala Gly Ala Ala Ala Ala Thr Cys Thr Gly Gly Gly Ala Gly Gly Ala
865 870 875 880

Gly Cys Thr Gly Ala Gly Thr Gly Thr Gly Thr Thr Ala Gly Ala Gly
885 890 895

Gly Thr Gly Thr Thr Thr Gly Ala Gly Gly Gly Gly Ala Gly Gly Gly
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Ala Ala Gly Ala Cys Ala Gly Thr Ala Thr Cys Thr Thr Gly Gly Gly
915 920 925

Gly Gly Ala Thr Cys Cys Cys Ala Ala Gly Ala Ala Gly Cys Thr Gly
930 935 940

Cys Thr Cys Ala Cys Cys Cys Ala Ala Cys Ala Thr Thr Thr Cys Gly
945 950 955 960

Thr Gly Cys Ala Gly Gly Ala Ala Ala Ala Cys Thr Ala Cys Cys Thr
965 970 975

Gly Gly Ala Gly Thr Ala Cys Cys Gly Gly Cys Ala Gly Gly Thr Cys
980 985 990

Cys Cys Cys Gly Gly Cys Ala Gly Thr Gly Ala Thr Cys Cys Thr Gly
995 1000 1005

Cys Ala Thr Gly Thr Thr Ala Thr Gly Ala Ala Thr Thr Cys Cys
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Cys Cys Cys Thr Cys Gly Thr Thr Gly Ala Ala Ala Cys Cys Ala
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Thr Gly Cys Ala Cys Cys Ala Thr Ala Thr Gly Gly Thr Ala Ala
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1115 1120 1125

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1160 1165 1170

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Cys Thr Thr Thr Thr Ala Ala Cys Gly Gly Ala Thr Gly Gly Thr
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Ala Gly Thr Cys Thr Thr Gly Thr Thr Thr Thr Thr Thr Ala Cys
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Thr Cys Ala Ala Ala Thr Thr Gly Gly Gly Ala Ala Ala Thr Cys
1475 1480 1485

Cys Ala Thr Thr Cys Cys Ala Thr Thr Thr Thr Gly Thr Gly Ala
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Ala Thr Thr Gly Thr Gly Ala Cys Ala Thr Ala Ala Thr Ala Ala
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Thr Ala Gly Cys Ala Gly Thr Gly Gly Thr Ala Ala Ala Ala Gly
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Thr Ala Thr Thr Thr Gly Cys Thr Thr Ala Ala Ala Ala Thr Thr
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Ala Thr Ala Ala Cys Ala Thr Ala Cys Ala Thr Gly Ala Gly Ala
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Thr Ala Ala Cys Thr Cys Ala Ala Gly Ala Ala Ala Thr Cys Ala
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1595 1600 1605

Thr Thr Gly Cys Cys Thr Thr Gly Thr Ala Cys Cys Thr Cys Ala
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Ala Thr Cys Thr Ala Thr Thr Cys Thr Gly Thr Ala Ala Ala Ala
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Thr Thr Ala Ala Ala Cys Ala Ala Ala Thr Ala Thr Gly Cys Ala
1640 1645 1650

Ala Ala Cys Cys Ala Gly Gly Ala Thr Thr Thr Cys Cys Thr Thr
1655 1660 1665

Gly Ala Cys Thr Thr Cys Thr Thr Thr Gly Ala Gly Ala Ala Thr
1670 1675 1680

Gly Cys Ala Ala Gly Cys Gly Ala Ala Ala Thr Thr Ala Ala Ala
1685 1690 1695

Thr Cys Thr Gly Ala Ala Thr Ala Ala Ala Thr Ala Ala Thr Thr
1700 1705 1710

Cys Thr Thr Cys Cys Thr Cys Thr Thr Cys Ala Ala Ala Ala Ala
1715 1720 1725

Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
1730 1735 1740

Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
1745 1750

<210> 3
<211> 180
<212> PRT
<213> Homo sapiens

<400> 3

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Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
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Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
50 55 60

His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
65 70 75 80

Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
85 90 95

Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
100 105 110

Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
115 120 125

Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
130 135 140

Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
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Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser
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Gly Gln Arg Arg
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<211> 752
<212> DNA
<213> Homo sapiens

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ttcctgatgg cccagggggc aatgctggcg gcccaggaga ggcgggtgcc acgggcggca 180
gagggtcccc gggcgagggg gcagcaaggg cctcggggcc gggaggaggc gccccgcggg 240
gtccgcatgg cggcgaggct tcagggtgta atggatgctg cagatgcggg gccagggggc 300
cggagagccg cctgcttgag ttctacctcg ccatgccttt cgcgacaccc atggaagcag 360
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cgcagtgctt tctgcccgtg tttttggctc agcctccctc agggcagagg cgctaagccc 600
agcctggcgc cccttcctag gtcatgcctc ctcccctagg gaatgggtccc agcacgagtg 660
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ttctgtagaa aataaaaactg agctacgaaa aa 752

<210> 5
<211> 180
<212> PRT
<213> Homo sapiens

<400> 5

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Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
50 55 60

His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
65 70 75 80

Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe
85 90 95

Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp
100 105 110

Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val
115 120 125

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

Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
145 150 155 160

Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser
165 170 175

Gly Gln Arg Arg
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<210> 6
<211> 296
<212> PRT
<213> Homo sapiens

<400> 6

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val
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Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met
20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala
35 40 45

Leu Tyr Thr Gly Phe Ser Ile Leu Val Thr Leu Leu Leu Ala Gly Gln
50 55 60

Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys
65 70 75 80

Leu Thr Val Thr Ser Gln Asn Leu Gln Leu Glu Asn Leu Arg Met Lys
85 90 95

Leu Pro Lys Pro Pro Lys Pro Val Ser Lys Met Arg Met Ala Thr Pro
100 105 110

Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met
115 120 125

Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His
130 135 140

Leu Leu Gln Asn Ala Asp Pro Leu Lys Val Tyr Pro Pro Leu Lys Gly
145 150 155 160

Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile
165 170 175

Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu Phe Glu
180 185 190

Met Ser Arg His Ser Leu Glu Gln Lys Pro Thr Asp Ala Pro Pro Lys
195 200 205

Val Leu Thr Lys Cys Gln Glu Glu Val Ser His Ile Pro Ala Val His
210 215 220

Pro Gly Ser Phe Arg Pro Lys Cys Asp Glu Asn Gly Asn Tyr Leu Pro
225 230 235 240

Leu Gln Cys Tyr Gly Ser Ile Gly Tyr Cys Trp Cys Val Phe Pro Asn
245 250 255

Gly Thr Glu Val Pro Asn Thr Arg Ser Arg Gly His His Asn Cys Ser
260 265 270

Glu Ser Leu Glu Leu Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys
275 280 285

Gln Asp Leu Gly Pro Val Pro Met
290 295

<210> 7
<211> 26
<212> PRT
<213> Homo sapiens

<400> 7

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Gly Gln Ala Thr Thr Ala Tyr Phe Leu Tyr

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25

<210> 8
 <211> 562
 <212> PRT
 <213> Homo sapiens

<400> 8

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 20 25 30

Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
 35 40 45

Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
 50 55 60

Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
 65 70 75 80

Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
 85 90 95

Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
 100 105 110

Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
 115 120 125

Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
 130 135 140

Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
 145 150 155 160

Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
165 170 175

Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
180 185 190

Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
195 200 205

Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
210 215 220

Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
225 230 235 240

Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
245 250 255

Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
260 265 270

Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
275 280 285

Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr
290 295 300

Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala
305 310 315 320

Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro
325 330 335

Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile
340 345 350

Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu
355 360 365

Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu
370 375 380

Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp
385 390 395 400

Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser
405 410 415

Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro
420 425 430

Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly
435 440 445

Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
450 455 460

Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His
465 470 475 480

Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr
485 490 495

Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp
500 505 510

Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val
515 520 525

Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly
530 535 540

Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
545 550 555 560

Arg Pro

<210> 9
<211> 21
<212> PRT
<213> Homo sapiens

<400> 9

Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala
1 5 10 15

Val Phe Val Ser Pro
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<210> 10
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide construct for vector ChAdOx1_MAGE_NYES0

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gaagctctgg gactcgtggg agcacaggct ccagccaccg aagaacagga agccgccagc 120
agcagctcca ccctggtgga agtgacactg ggcgaagtgc ctgccgccga gtctcctgat 180
cctcctcagt ctcctcaggg cgccagctct ctgcccacca ccatgaacta ccccctgtgg 240
tcccagtcct acgaggacag cagcaaccag gaagaagagg gccccagcac cttccccgac 300
ctggaatctg aattccaggc cgccctgagc cggaagggtg ccgaactggt gcacttcctg 360
ctgctgaagt accgggccag agaaccctg accaaggccg agatgctggg cagcgtcgtg 420
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gaccccaaga agctgctgac ccagcacttc gtgcaggaaa actacctgga gtatagacag	780
gtgcccggca gcgaccctgc ctgctacgaa tttctgtggg gccctagagc actggtggaa	840
accagctacg tgaaagtgct gcaccacatg gtcaagatca gcggcggacc ccacatcagc	900
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ggacccggaa ttccagatgg ccctggcgga aatgctggcg ggcctggcga agctggcgct	1080
acaggcggaa gaggacctag aggcgctggc gccgctagag cttctggacc agggggaggc	1140
gctcctagag gacctcatgg cggagctgcc tctggcctga acggctgctg tagatgtggc	1200
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gccgaccaca gacagctgca gctgagcatc agcagctgcc tgcagcagct gtccctgctg	1440
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<210> 11
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Translated protein of ChAdOx1_MAGE_NYESO

<400> 11

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			20					25					30		

Thr	Glu	Glu	Gln	Glu	Ala	Ala	Ser	Ser	Ser	Ser	Thr	Leu	Val	Glu	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

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

Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp
 65 70 75 80

Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser
 85 90 95

Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys
 100 105 110

Val Ala Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu
 115 120 125

Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln
 130 135 140

Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Ser Ser Leu Gln Leu
 145 150 155 160

Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Leu Tyr
 165 170 175

Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp
 180 185 190

Asn Gln Ile Met Pro Lys Ala Gly Leu Leu Ile Ile Val Leu Ala Ile
 195 200 205

Ile Ala Arg Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu
 210 215 220

Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Ile Leu Gly
 225 230 235 240

Asp Pro Lys Lys Leu Leu Thr Gln His Phe Val Gln Glu Asn Tyr Leu
245 250 255

Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu
260 265 270

Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr Val Lys Val Leu His
275 280 285

His Met Val Lys Ile Ser Gly Gly Pro His Ile Ser Tyr Pro Pro Leu
290 295 300

His Glu Trp Val Leu Arg Glu Gly Glu Glu Gly Gly Gly Pro Gly Gly
305 310 315 320

Gly Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala
325 330 335

Asp Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala
340 345 350

Gly Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly
355 360 365

Ala Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly
370 375 380

Pro His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly
385 390 395 400

Ala Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro
405 410 415

Phe Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln
420 425 430

Asp Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr

435

440

445

Val Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg
 450 455 460

Gln Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu
 465 470 475 480

Met Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro
 485 490 495

Ser Gly Gln Arg Arg
 500

<210> 12

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide construct for vector ChAdOx1_hIi_MAGE_NY-ESO-1

<400> 12

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accaccgcct actttctgta ccccttgga cagcggagcc agcactgcaa gcctgaggaa      120
ggcctggaag ccagaggcga agctctggga ctcgtgggag cacaggctcc agccaccgaa      180
gaacaggaag ccgccagcag ctctagcacc ctggtggaag tgacactggg cgaagtgcct      240
gccgccgagt ctctgatcc tcctcagtct cctcagggcg ccagctctct gccaccacc      300
atgaactacc ccctgtggtc ccagtcctac gaggacagca gcaaccagga agaagagggc      360
cccagcacct tccccgacct ggaatctgaa ttccaggccg ccctgagccg gaagggtggc      420
gaactggtgc actttctgct gctgaagtac cgggccagag aaccctgac caaggccgag      480
atgctgggca gcgtcgtggg caactggcag tacttcttcc ccgtgatctt ctccaaggcc      540
agctccagcc tgcagctggg gttcggcatc gagctgatgg aagtggaccc catcggacac      600
ctgtacatct tcgccacctg tctgggcctg agctacgatg gcctgctggg cgacaaccag      660

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atcatgcca aagccggcct gctgatcatc gtgctggcca tcattgcccg cgagggcgat	720
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gaggactcca tcctgggcga cccaagaag ctgctgaccc agcacttcgt gcaggaaaac	840
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cctagagcac tgggtgaaac cagctacgtg aaagtgctgc accacatggt caagatcagc	960
ggcggacccc acatcagcta cccccctctg catgaatggg tgctgagaga gggcgaggaa	1020
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gacgctgatg gaccaggcgg acccggaatt ccagatggcc ctggcggaaa tgctggcggg	1140
cctggcgaag ctggcgctac aggcggaaga ggacctagag gcgctggcgc cgctagagca	1200
tctggaccag ggggaggcgc tcctagagga cctcatggcg gagctgcctc tggcctgaac	1260
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cctccactgc ctgtgccagg cgtgctgctg aaagaattca ccgtgtccgg caacatcctg	1440
accatccggc tgacagccgc cgaccacaga cagctgcagc tgagcatcag cagctgcctg	1500
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cctcctagcg gacagcggag atga	1584

<210> 13
 <211> 527
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Translated protein sequence of ChAdOx1_hIi_MAGE_NY-ESO-1

<400> 13

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1				5					10					15	

Ala	Gly	Gln	Ala	Thr	Thr	Ala	Tyr	Phe	Leu	Tyr	Pro	Leu	Glu	Gln	Arg
			20					25					30		

Ser Gln His Cys Lys Pro Glu Glu Gly Leu Glu Ala Arg Gly Glu Ala
35 40 45

Leu Gly Leu Val Gly Ala Gln Ala Pro Ala Thr Glu Glu Gln Glu Ala
50 55 60

Ala Ser Ser Ser Ser Thr Leu Val Glu Val Thr Leu Gly Glu Val Pro
65 70 75 80

Ala Ala Glu Ser Pro Asp Pro Pro Gln Ser Pro Gln Gly Ala Ser Ser
85 90 95

Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp Ser Gln Ser Tyr Glu Asp
100 105 110

Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser Thr Phe Pro Asp Leu Glu
115 120 125

Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys Val Ala Glu Leu Val His
130 135 140

Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu Pro Val Thr Lys Ala Glu
145 150 155 160

Met Leu Gly Ser Val Val Gly Asn Trp Gln Tyr Phe Phe Pro Val Ile
165 170 175

Phe Ser Lys Ala Ser Ser Ser Leu Gln Leu Val Phe Gly Ile Glu Leu
180 185 190

Met Glu Val Asp Pro Ile Gly His Leu Tyr Ile Phe Ala Thr Cys Leu
195 200 205

Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp Asn Gln Ile Met Pro Lys
210 215 220

Ala Gly Leu Leu Ile Ile Val Leu Ala Ile Ile Ala Arg Glu Gly Asp

225		230		235		240									
Cys	Ala	Pro	Glu	Glu	Lys	Ile	Trp	Glu	Glu	Leu	Ser	Val	Leu	Glu	Val
			245					250						255	
Phe	Glu	Gly	Arg	Glu	Asp	Ser	Ile	Leu	Gly	Asp	Pro	Lys	Lys	Leu	Leu
			260					265					270		
Thr	Gln	His	Phe	Val	Gln	Glu	Asn	Tyr	Leu	Glu	Tyr	Arg	Gln	Val	Pro
		275					280					285			
Gly	Ser	Asp	Pro	Ala	Cys	Tyr	Glu	Phe	Leu	Trp	Gly	Pro	Arg	Ala	Leu
	290					295					300				
Val	Glu	Thr	Ser	Tyr	Val	Lys	Val	Leu	His	His	Met	Val	Lys	Ile	Ser
305					310					315					320
Gly	Gly	Pro	His	Ile	Ser	Tyr	Pro	Pro	Leu	His	Glu	Trp	Val	Leu	Arg
				325					330					335	
Glu	Gly	Glu	Glu	Gly	Gly	Gly	Pro	Gly	Gly	Gly	Met	Gln	Ala	Glu	Gly
			340					345					350		
Arg	Gly	Thr	Gly	Gly	Ser	Thr	Gly	Asp	Ala	Asp	Gly	Pro	Gly	Gly	Pro
		355					360					365			
Gly	Ile	Pro	Asp	Gly	Pro	Gly	Gly	Asn	Ala	Gly	Gly	Pro	Gly	Glu	Ala
	370					375					380				
Gly	Ala	Thr	Gly	Gly	Arg	Gly	Pro	Arg	Gly	Ala	Gly	Ala	Ala	Arg	Ala
385					390					395					400
Ser	Gly	Pro	Gly	Gly	Gly	Ala	Pro	Arg	Gly	Pro	His	Gly	Gly	Ala	Ala
			405					410						415	
Ser	Gly	Leu	Asn	Gly	Cys	Cys	Arg	Cys	Gly	Ala	Arg	Gly	Pro	Glu	Ser
			420					425					430		

Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe Ala Thr Pro Met Glu
435 440 445

Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp Ala Pro Pro Leu Pro
450 455 460

Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val Ser Gly Asn Ile Leu
465 470 475 480

Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu Gln Leu Ser Ile
485 490 495

Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp Ile Thr Gln Cys
500 505 510

Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly Gln Arg Arg
515 520 525

<210> 14

<211> 1569

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide construct for vector ChAdOx1_tPA_MAGE_NY-ESO-1

<400> 14

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tccccccac tggaacagag aagccagcac tgcaagcccg aggaaggcct ggaagccaga	120
ggcgaagctc tgggactcgt gggagcacag gctccagcca ccgaagaaca ggaagccgcc	180
agcagctcta gcaccctggg ggaagtgaca ctgggcgaag tgcctgccgc cgagtctcct	240
gatcctcctc agtctcctca gggcgccagc tctctgcca ccaccatgaa ctaccccctg	300
tggtcccagt cctacgagga cagcagcaac caggaagaag aggccccag caccttcccc	360
gacctggaat ctgaattcca ggccgccctg agccggaagg tggccgaact ggtgcacttc	420
ctgctgctga agtaccgggc cagagaaccc gtgaccaagg ccgagatgct gggcagcgtc	480

gtgggcaact ggcagtactt cttccccgtg atcttctcca aggccagctc cagcctgcag	540
ctggtgttcg gcatcgagct gatggaagtg gaccccatcg gacacctgta catcttcgcc	600
acctgtctgg gcctgagcta cgatggcctg ctgggcgaca accagatcat gcccaaagcc	660
ggcctgctga tcatcgtgct ggccatcatt gcccgcgagg gcgattgtgc ccccgaggaa	720
aagatctggg aggaactgag cgtgctggaa gtgttcgagg gaagagagga ctccatcctg	780
ggcgacccca agaagctgct gacccagcac ttcgtgcagg aaaactacct ggagtataga	840
cagggtgccc ggcagcgaccc tgcctgctac gaatttctgt ggggccctag agcactgggtg	900
gaaaccagct acgtgaaagt gctgcaccac atggtcaaga tcagcggcgg accccacatc	960
agctacccac ctctgcacga atgggtgctg agagagggcg aagaaggcgg aggacctggc	1020
ggaggaatgc aggctgaagg cagaggcaca ggcggctcta caggcgacgc tgatggacca	1080
ggcggacccg gaattccaga tggccctggc ggaaatgctg gcgggcctgg cgaagctggc	1140
gctacaggcg gaagaggacc tagaggcgct ggcgccgcta gagcatctgg accaggggga	1200
ggcgctccta gaggacctca tggcggagct gcctctggcc tgaatggctg ctgtagatgt	1260
ggcgccagag gccccgaaag cagactgctg gaattctacc tggccatgcc tttcgccacc	1320
cccatggaag ctgagctggc cagaagaagc ctggcccagg acgctcctcc actgcctgtg	1380
ccaggggtgc tgctgaaaga attcaccgtg tccggcaaca tcctgaccat ccggctgaca	1440
gccgccgacc acagacagct gcagctgagc atcagcagct gcctgcagca gctgtccctg	1500
ctgatgtgga tcaccagtg ctttctgccc gtgtttctgg cccagcctcc tagcggacag	1560
cggagatga	1569

<210> 15

<211> 522

<212> PRT

<213> Artificial Sequence

<220>

<223> Translated protein of ChAdOx1_tPA_MAGE_NY-ESO-1

<400> 15

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly

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

Gly Leu Leu Gly Asp Asn Gln Ile Met Pro Lys Ala Gly Leu Leu Ile
210 215 220

Ile Val Leu Ala Ile Ile Ala Arg Glu Gly Asp Cys Ala Pro Glu Glu
225 230 235 240

Lys Ile Trp Glu Glu Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu
245 250 255

Asp Ser Ile Leu Gly Asp Pro Lys Lys Leu Leu Thr Gln His Phe Val
260 265 270

Gln Glu Asn Tyr Leu Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala
275 280 285

Cys Tyr Glu Phe Leu Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr
290 295 300

Val Lys Val Leu His His Met Val Lys Ile Ser Gly Gly Pro His Ile
305 310 315 320

Ser Tyr Pro Pro Leu His Glu Trp Val Leu Arg Glu Gly Glu Glu Gly
325 330 335

Gly Gly Pro Gly Gly Gly Met Gln Ala Glu Gly Arg Gly Thr Gly Gly
340 345 350

Ser Thr Gly Asp Ala Asp Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly
355 360 365

Pro Gly Gly Asn Ala Gly Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly
370 375 380

Arg Gly Pro Arg Gly Ala Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly
385 390 395 400

Gly Ala Pro Arg Gly Pro His Gly Gly Ala Ala Ser Gly Leu Asn Gly

405

410

415

Cys Cys Arg Cys Gly Ala Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe
 420 425 430

Tyr Leu Ala Met Pro Phe Ala Thr Pro Met Glu Ala Glu Leu Ala Arg
 435 440 445

Arg Ser Leu Ala Gln Asp Ala Pro Pro Leu Pro Val Pro Gly Val Leu
 450 455 460

Leu Lys Glu Phe Thr Val Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr
 465 470 475 480

Ala Ala Asp His Arg Gln Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln
 485 490 495

Gln Leu Ser Leu Leu Met Trp Ile Thr Gln Cys Phe Leu Pro Val Phe
 500 505 510

Leu Ala Gln Pro Pro Ser Gly Gln Arg Arg
 515 520

<210> 16
 <211> 945
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polynucleotide construct for vector MVA_MAGEA3

<400> 16
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 agcagctcca ccctggtgga agtgacactg ggcgaagtgc ctgccgccga gtctcctgat 180
 cctcctcagt ctctcaggg cgccagctct ctgcccacca ccatgaacta ccccctgtgg 240
 tcccagtcct acgaggacag cagcaaccag gaagaagagg gccccagcac cttccccgac 300

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ctggaatctg aattccaggc cgccctgagc cggaagggtgg ccgaactggt gcacttcctg      360
ctgctgaagt accgggccag agaaccctgt accaaggccg agatgctggg cagcgtcgtg      420
ggcaactggc agtacttctt ccccgatgat ttctccaagg ccagctccag cctgcagctg      480
gtgttcggca tcgagctgat ggaagtggac cccatcggac acctgtacat cttcgccacc      540
tgtctgggcc tgagctacga tggcctgctg ggcgacaacc agatcatgcc caaagccggc      600
ctgctgatca tcgtgctggc catcattgcc cgcgagggcg attgtgcccc cgaggaaaag      660
atctgggagg aactgagcgt gctggaagtg ttcgagggaa gagaggactc catcctgggc      720
gacccaaga agctgctgac ccagcacttc gtgcaggaaa actacctgga gtatagacag      780
gtgcccggca gcgaccctgc ctgctacgaa tttctgtggg gccctagagc actggtggaa      840
accagctacg tgaaagtgct gcaccacatg gtcaagatca gcggcggacc ccacatcagc      900
tacccccctc tgcataaatg ggtgctgcgg gaaggcgaag agtga                        945

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<210> 17
<211> 314
<212> PRT
<213> Artificial Sequence

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<220>
<223> Translated protein of MVA_MAGEA3

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<400> 17

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Met Pro Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu
1           5           10          15

```

```

Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala
20           25           30

```

```

Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Ser Thr Leu Val Glu Val
35           40           45

```

```

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

```

```

Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp

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80

95

110

125

140

160

175

190

205

220

240

255

270

Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr Val Lys Val Leu His
275 280 285

His Met Val Lys Ile Ser Gly Gly Pro His Ile Ser Tyr Pro Pro Leu
290 295 300

His Glu Trp Val Leu Arg Glu Gly Glu Glu
305 310

<210> 18
<211> 543
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide construct for vector MVA_NYESO

<400> 18
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cctggcattc cagatggccc aggcggaaat gctggcggac caggcgaagc tggcgctaca 120
ggcgggaagag gacctagagg cgctggcgcc gctagagctt ctggacctgg gggaggcgct 180
cctagaggac ctcatggcgg agctgcctct ggcctgaatg gctgctgtag atgtggcgcc 240
agaggccccg aaagccggct gctggaattc tacctggcca tgcccttcgc ccccccatg 300
gaagctgagc tggccagaag aagcctggcc caggacgctc ctccctctgcc tgtgcctggc 360
gtgctgctga aagaattcac cgtgtccggc aacatcctga ccatccggct gacagccgcc 420
gaccacagac agctgcagct gagcatcagc agctgcctgc agcagctgtc cctgctgatg 480
tggatcaccc agtgctttct gcccgtgttt ctggcccagc ctccctagcg ccagcggcgc 540
taa 543

<210> 19
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<223> Translated protein of MVA_NYESO

<400> 19

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
1 5 10 15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
20 25 30

Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
50 55 60

His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
65 70 75 80

Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
85 90 95

Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
100 105 110

Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
115 120 125

Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
130 135 140

Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
145 150 155 160

Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser
165 170 175

Gly Gln Arg Arg
180

<210> 20
<211> 1008
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide construct for vector MVA_tPA_MAGEA3

<400> 20
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ggcgaagctc tgggactcgt gggagcacag gctccagcca ccgaagaaca ggaagccgcc 180
agcagctcta gcaccctggg ggaagtgaca ctgggcgaag tgcctgccgc cgagtctcct 240
gatcctcctc agtctcctca gggcgccagc tctctgcccc ccaccatgaa ctacccctg 300
tgggtcccagt cctacgagga cagcagcaac caggaagaag agggccccag caccttcccc 360
gacctggaat ctgaattcca ggccgccctg agccggaagg tggccgaact ggtgcacttc 420
ctgctgctga agtaccgggc cagagaaccc gtgaccaagg ccgagatgct gggcagcgtc 480
gtgggcaact ggcagtactt cttccccgtg atctttctcca aggccagctc cagcctgcag 540
ctggtgttcg gcatcgagct gatggaagtg gaccccatcg gacacctgta catcttcgcc 600
acctgtctgg gcctgagcta cgatggcctg ctgggcgaca accagatcat gccc aaagcc 660
ggcctgctga tcatcgtgct ggccatcatt gcccgcgagg gcgattgtgc ccccgaggaa 720
aagatctggg aggaactgag cgtgctggaa gtgttcgagg gaagagagga ctccatcctg 780
ggcgacccca agaagctgct gaccagcac ttcgtgcagg aaaactacct ggagtataga 840
caggtgcccc gcagcgaccc tgcctgctac gaatttctgt ggggccctag agcactgggtg 900
gaaaccagct acgtgaaagt gctgcaccac atggtcaaga tcagcggcgg accccacatc 960
agctaccac ctctgcacga atgggtgctg cgggaaggcg aagagtga 1008

<210> 21
<211> 335
<212> PRT
<213> Artificial Sequence

<220>

<223> Translated protein of MVA_tPA_MAGEA3

<400> 21

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
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Ala Val Phe Val Ser Pro Pro Leu Glu Gln Arg Ser Gln His Cys Lys
20 25 30

Pro Glu Glu Gly Leu Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly
35 40 45

Ala Gln Ala Pro Ala Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Ser
50 55 60

Thr Leu Val Glu Val Thr Leu Gly Glu Val Pro Ala Ala Glu Ser Pro
65 70 75 80

Asp Pro Pro Gln Ser Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met
85 90 95

Asn Tyr Pro Leu Trp Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu
100 105 110

Glu Glu Gly Pro Ser Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala
115 120 125

Ala Leu Ser Arg Lys Val Ala Glu Leu Val His Phe Leu Leu Leu Lys
130 135 140

Tyr Arg Ala Arg Glu Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val
145 150 155 160

Val Gly Asn Trp Gln Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser
165 170 175

Ser Ser Leu Gln Leu Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro

180

185

190

Ile Gly His Leu Tyr Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp
 195 200 205

Gly Leu Leu Gly Asp Asn Gln Ile Met Pro Lys Ala Gly Leu Leu Ile
 210 215 220

Ile Val Leu Ala Ile Ile Ala Arg Glu Gly Asp Cys Ala Pro Glu Glu
 225 230 235 240

Lys Ile Trp Glu Glu Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu
 245 250 255

Asp Ser Ile Leu Gly Asp Pro Lys Lys Leu Leu Thr Gln His Phe Val
 260 265 270

Gln Glu Asn Tyr Leu Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala
 275 280 285

Cys Tyr Glu Phe Leu Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr
 290 295 300

Val Lys Val Leu His His Met Val Lys Ile Ser Gly Gly Pro His Ile
 305 310 315 320

Ser Tyr Pro Pro Leu His Glu Trp Val Leu Arg Glu Gly Glu Glu
 325 330 335

<210> 22

<211> 606

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide construct for vector MVA_tPA_NYES0

<400> 22

atggacgcca tgaagcgggg cctgtgctgc gtgctgctgc tgtgtggcgc tgtgttcgtg

60

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acaggcggaa gaggacctag aggcgctggc gccgctagag cttctggacc tgggggaggc      240
gctcctagag gacctcatgg cggagctgcc tctggcctga atggctgctg tagatgtggc      300
gccagaggcc ccgaaagccg gctgctggaa ttctacctgg ccatgccctt cgccaccccc      360
atggaagctg agctggccag aagaagcctg gcccaggacg ctctccact gcctgtgcca      420
ggggtgctgc tgaaagaatt caccgtgtcc ggcaacatcc tgaccatccg gctgacagcc      480
gccgaccaca gacagctgca gctgagcatc agcagctgcc tgcagcagct gtccctgctg      540
atgtggatca cccagtgcct tctgcccgtg tttctggccc agcctcctag cggccagcgg      600
cgctaa                                          606

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<210> 23
<211> 201
<212> PRT
<213> Artificial Sequence

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<220>
<223> Translated protein of MVA_tPA_NYES0

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<400> 23

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1           5           10          15

```

```

Ala Val Phe Val Ser Pro Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser
          20          25          30

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ctcccgttac catataaacc tctgattaaa catggcgcca tccaccacca tcctaaacca	37320
gctggccaaa acctgcccgc cggctataca ctgcaggga cgggactgg aacaatgaca	37380
gtggagagcc caggactcgt aaccatggat catcatgctc gtcatgatat caatgttggc	37440
acaacacagg cacacgtgca tacacttcct caggattaca agctcctccc gcgttagaac	37500
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tcgcacgtaa ctcacgttgt gcattgtcaa agtgttacat tcgggcagca gcggatgatc	37620
ctccagtatg gtagcgcggg tttctgtctc aaaaggaggt agacgatccc tactgtacgg	37680
agtgcgccga gacaaccgag atcgtgttgg tcgtagtgct atgccaaatg gaacgccgga	37740
cgtagtcata tttcctgaag caaaaccagg tgcgggcgtg acaaacagat ctgcgtctcc	37800
ggtctcgccg cttagatcgc tctgtgtagt agttgtagta tatccactct ctcaaagcat	37860
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acacgggagg agcgggaaga gctggaagaa ccatgattaa ctttattcca aacggctctcg	38040
gagcacttca aaatgcagggt cccggagggtg gcacctctcg cccccactgt gttggtggaa	38100
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agcgccctcc accggcattc ttaagcacac cctcataatt ccaagagatt ctgctcctgg	38400
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ccgccaggaa taagagcagg gcaagccaca ttacagataa agcgaagtcc tccccagtgw	38580
gcattgccaa atgtaagatt gaaataagca tgctggctag accctgtgat atcttccaga	38640
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tccggcgcga ccctcgtaga agctgtcgcc atgattgaaa agcatcaccg agagaccttc	38940
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ctcaaaaaaa tacgtgcgct tcctcaaacg cccaaaccgg cgtcatttcc gggttcccac	39420
gctacgtcac cgctcagcga ctttcaaatt ccgtcgaccg ttaaaaaagt cactcgcccc	39480
gcccctaacg gtcgcccctt tctcgcccaa tcaccttcct cccttcccaa attcaaacgc	39540
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<210> 26

<211> 675

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide construct for vector ChAdOx1_P1A

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<400> 26
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aacagatgta acctgctgca cagatacagc ctggaagaga tcctgcccta cctgggctgg      120
ctggtgttcg ccgtcgtgac aacaagcttc ctggccctgc agatgttcat cgacgccctg      180
tacgaggaac agtacgagag ggacgtggcc tggatcgcca gacagagcaa gagaatgagc      240
agcgtggacg aggacgagga tgatgaggac gacgaagatg actactacga cgatgaggat      300
gacgacgacg acgccttcta cgatgacgag gacgatgaag aggaagaact ggaaaacctg      360
atggacgacg agtccgagga tgaggccgag gaagagatga gcgtggaaat gggcgctggc      420
gccgaagaga tgggagccgg cgctaactgt gcttgcgtgc caggacacca cctgagaaag      480
aacgaagtga agtgccggat gatctacttc ttccacgacc ccaactttct ggtgtccatc      540
cccgtgaacc ccaaagaaca gatggaatgc agatgcgaga acgccgacga agagggtggcc      600
atggaagaag aagaggaaga ggaagaagaa gaagaagagg aagaaatggg caacccccgac      660
ggcttcagcc cctga                                                         675

```

```

<210> 27
<211> 224
<212> PRT
<213> Artificial Sequence

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<220>
<223> Translated protein of ChAdOx1_P1A

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<400> 27

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Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
1           5           10           15

```

```

Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
20           25           30

```

```

Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
35           40           45

```

```

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

```

50

55

60

Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
65 70 75 80

Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
85 90 95

Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
100 105 110

Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
115 120 125

Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
130 135 140

Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
145 150 155 160

Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
165 170 175

Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
180 185 190

Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu
195 200 205

Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
210 215 220

<210> 28

<211> 753

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide construct for vector ChAdOx1_mIi_P1A

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<400> 28
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ggcggagatg gcgacggcaa cagatgtaac ctgctgcaca gatacagcct ggaagagatc      180
ctgccctacc tgggctggct ggtgttcgcc gtcgtgacaa caagcttcct ggccctgcag      240
atgttcatcg acgccctgta cgaggaacag tacgagaggg acgtggcctg gatcgccaga      300
cagagcaaga gaatgagcag cgtggacgag gacgaggatg atgaggacga cgaagatgac      360
tactacgacg atgaggatga cgacgacgac gccttctacg atgacgagga cgatgaagag      420
gaagaactgg aaaacctgat ggacgacgag tccgaggatg aggccgagga agagatgagc      480
gtggaaaatgg gcgctggcgc cgaagagatg ggagccggcg ctaactgtgc ttgcgtgcca      540
ggacaccacc tgagaaagaa cgaagtgaag tgccggatga tctacttctt ccacgacccc      600
aactttctgg tgtccatccc cgtgaacccc aaagaacaga tggaatgcag atgcgagaac      660
gccgacgaag aggtggccat ggaagaagaa gaggaagagg aagaagaaga agaagaggaa      720
gaaatgggca accccgacgg cttcagcccc tga                                     753

```

```

<210> 29
<211> 250
<212> PRT
<213> Artificial Sequence

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<220>
<223> Translated protein ChAdOx1_mIi_P1A

```

```

<400> 29
Met Gly Ala Leu Tyr Thr Gly Val Ser Val Leu Val Ala Leu Leu Leu
1           5           10           15

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

Pro Asp Lys Ala His Ser Gly Ser Gly Gly Asp Gly Asp Gly Asn Arg
35           40           45

```

Cys Asn Leu Leu His Arg Tyr Ser Leu Glu Glu Ile Leu Pro Tyr Leu
50 55 60

Gly Trp Leu Val Phe Ala Val Val Thr Thr Ser Phe Leu Ala Leu Gln
65 70 75 80

Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln Tyr Glu Arg Asp Val Ala
85 90 95

Trp Ile Ala Arg Gln Ser Lys Arg Met Ser Ser Val Asp Glu Asp Glu
100 105 110

Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr Asp Asp Glu Asp Asp Asp
115 120 125

Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp Glu Glu Glu Glu Leu Glu
130 135 140

Asn Leu Met Asp Asp Glu Ser Glu Asp Glu Ala Glu Glu Glu Met Ser
145 150 155 160

Val Glu Met Gly Ala Gly Ala Glu Glu Met Gly Ala Gly Ala Asn Cys
165 170 175

Ala Cys Val Pro Gly His His Leu Arg Lys Asn Glu Val Lys Cys Arg
180 185 190

Met Ile Tyr Phe Phe His Asp Pro Asn Phe Leu Val Ser Ile Pro Val
195 200 205

Asn Pro Lys Glu Gln Met Glu Cys Arg Cys Glu Asn Ala Asp Glu Glu
210 215 220

Val Ala Met Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
225 230 235 240

Glu Met Gly Asn Pro Asp Gly Phe Ser Pro

<210> 30
 <211> 675
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polynucleotide construct for vector MVA_P1A

<400> 30
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 aacagatgta acctgctgca cagatacagc ctggaagaga tcctgcccta cctgggctgg 120
 ctggtgttcg ccgtcgtgac aacaagcttc ctggccctgc agatgttcat cgacgccctg 180
 tacgaggaac agtacgagag ggacgtggcc tggatcgcca gacagagcaa gagaatgagc 240
 agcgtggacg aggacgagga tgatgaggac gacgaagatg actactacga cgatgaggat 300
 gacgacgacg acgccttcta cgatgacgag gacgatgaag aggaagaact ggaaaacctg 360
 atggacgacg agtccgagga tgaggccgag gaagagatga gcgtggaaat gggcgctggc 420
 gccgaagaga tgggagccgg cgctaactgt gcttgcgtgc caggacacca cctgagaaag 480
 aacgaagtga agtgccggat gatctacttc ttccacgacc ccaactttct ggtgtccatc 540
 cccgtgaacc ccaaagaaca gatggaatgc agatgcgaga acgccgacga agaggtggcc 600
 atggaagaag aagaggaaga ggaagaagaa gaagaagagg aagaaatggg caaccccgcac 660
 ggcttcagcc cctga 675

<210> 31
 <211> 224
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Translated protein of MVA_P1A

<400> 31

Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
 1 5 10 15

Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
20 25 30

Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
35 40 45

Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
50 55 60

Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
65 70 75 80

Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
85 90 95

Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
100 105 110

Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
115 120 125

Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
130 135 140

Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
145 150 155 160

Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
165 170 175

Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
180 185 190

Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
195 200 205

Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro

210

215

220