

SEQUENCE LISTING

<110> Themis Bioscience GmbH

<120> Recombinant Zika vaccines

<130> TM 5400-02WO

<150> EP15202480.8

<151> 2015-12-23

<150> DE102015122740.1

<151> 2015-12-23

<150> EP16162688.2

<151> 2016-03-29

<160> 192

<170> PatentIn version 3.5

<210> 1

<211> 10662

<212> DNA

<213> Zika virus strain BeH818995 polyprotein gene

<400> 1

gtgaatcaga ctgcgacagt tcgagtttga agcgaaagct agcaacagta tcaacaggtt	60
ttatttttgga tttggaaacg agagtttctg gtcattgaaaa acccaaaaaa gaaatccgga	120
ggattccgga ttgtcaatat gctaaaacgc ggagtagccc gtgtgagccc ctttgggggc	180
ttgaagaggc tgccagcccg acttctgctg ggtcatgggc ccatcaggat ggtcttggcg	240
attctagcct ttttgagatt cacggcaatc aagccatcac tgggtctcat caatagatgg	300
ggttcagtgg ggaaaaaaga ggctatggaa ataataaaga agttcaagaa agatctggct	360
gccatgctga gaataatcaa tgctaggaag gagaagaaga gacgaggcgc agatactagt	420
gtcgggaattg ttggcctcct gctgaccaca gctatggcag cggagggtcac tagacgtggg	480
agtgcatact atatgtactt ggacagaaac gatgctgggg aggccatatac ttttccaacc	540
acattgggga tgaataagtg ttatatacag atcatggatc ttggacacat gtgtgatgcc	600
accatgagct atgaatgccc tatgctggat gaggggggtgg aaccagatga cgtcgattgt	660
tggtgcaaca cgacgtcaac ttgggttgtg tacggaacct gccatcaciaa aaaaggtgaa	720
gcacggagat ctagaagagc tgtgacgctc ccctccatt ccactaggaa gctgcaaacg	780
cggtcgcaaa cctgggttga atcaagagaa tacacaaagc acttgattag agtcgaaaat	840
tggatattta ggaaccctgg cttcgcgtta gcagcagctg ccatcgcttg gcttttggga	900
agctcaacga gccaaaaagt catatacttg gtcattgatac tgctgattgc cccggcatac	960

agcatcaggt gcataggagt cagcaatagg gactttgtgg aaggtatgtc aggtgggacc	1020
tgggttgatg ttgtcttgga acatggaggt tgtgtcaccg taatggcaca ggacaaaccg	1080
actgtcgaca tagagctggt tacaacaaca gtcagcaaca tggcggaggt aagatcctac	1140
tgctatgagg catcaatatc agacatggct tcggacagcc gctgccaac acaaggtgaa	1200
gcctaccttg acaagcaatc agacactcaa tatgtctgca aaagaacggt agtggacaga	1260
ggctggggaa atggatgtgg actttttggc aaagggagcc tggtgacatg cgctaagttt	1320
gcatgctcca agaaaatgac cgggaagagc atccagccag agaatctgga gtaccggata	1380
atgctgtcag ttcattggctc ccagcacagt gggatgattg ttaatgacac aggacatgaa	1440
actgatgaga atagagcgaa agttgagata acgccaatt caccaagagc cgaagccacc	1500
ctgggggggtt ttggaagcct aggacttgat tgtgaaccga ggacaggcct tgacttttca	1560
gatttgtatt acttgactat gaataacaag cactggttgg ttcacaagga gtggttccac	1620
gacattccat taccttggca cgctggggca gacaccggaa ctccacactg gaacaacaaa	1680
gaagcactgg tagagttcaa ggacgcacat gccaaaaggc aaactgtcgt ggttctaggg	1740
agtcaagaag gagcagttca cacggccctt gctggagctc tggaggctga gatggatggt	1800
gcaaaggga ggctgtcctc tggccacttg aaatgtcgcc tgaaaatgga taaacttaga	1860
ttgaaggcg tgtcatactc cttgtgtact gcagcgttca cattcaccaa gatcccggct	1920
gaaacactgc acgggacagt cacagtggag gtacagtacg cagggacaga tggaccttgc	1980
aaggttccag ctcatgatggc ggtggacatg caaactctga cccagttgg gaggttgata	2040
accgctaacc ccgtaatcac tgaaagcact gagaactcta agatgatgct ggaacttgat	2100
ccaccatttg gggactctta cattgtcata ggagtcgggg agaagaagat caccaccac	2160
tggcacagga gtggcagcac cattggaaaa gcatttgaag ccactgtgag aggtgccaag	2220
agaatggcag tcttgggaga cacagcctgg gactttggat cagttggagg cgctctcaac	2280
tcattgggca agggcatcca tcaaattttt ggagcagctt tcaaatacatt gtttggagga	2340
atgtcctggt tctcaciaat tctcattgga acgttgctga tgtggttggg tctgaacaca	2400
aagaatggat ctatttccct tatgtgcttg gccttagggg gagtggtgat cttcttatcc	2460
acagccgtct ctgctgatgt ggggtgctcg gtggacttct caaagaagga gacgagatgc	2520
ggtacagggg tgttcgtcta taacgacgtt gaagcctgga gggacaggta caagtaccat	2580
cctgactccc cccgtagatt ggagcagca gtcaagcaag cctgggaaga tggatatctgc	2640
gggatctcct ctgtttcaag aatggaaaac atcatgtgga gatcagtaga aggggagctc	2700

aacgcaatcc	tggaagagaa	tggagttcaa	ctgacggtcg	ttgtgggatac	tgtaaaaaaac	2760
cccatgtgga	gaggtccaca	gagattgccc	gtgcctgtga	acgagctgcc	ccacggctgg	2820
aaggcttggg	ggaaatcgta	cttcgtcaga	gcagcaaaga	caaataacag	ctttgtcgtg	2880
gatggtgaca	cactgaagga	atgcccactc	aaacatagag	catggaacag	ctttcttgtg	2940
gaggatcatg	ggttcggggg	atttcacact	agtgtctggc	tcaaggtttag	agaagattat	3000
tcattagagt	gtgatccagc	cgttattgga	acagctgtta	agggaaagga	ggctgtacac	3060
agtgatctag	gctactggat	tgagagtga	aagaatgaca	catggaggct	gaagagggcc	3120
catctgatcg	agatgaaaac	atgtgaatgg	ccaaagtccc	acacattgtg	gacagatgga	3180
atagaagaga	gtgatctgat	catacccaag	tcttttagctg	ggccactcag	ccatcacaat	3240
accagagagg	gctacaggac	ccaaatgaaa	gggccatggc	acagtgaaga	gcttgaaatt	3300
cggtttgagg	aatgcccagg	cactaaggtc	cacgtggagg	aaacatgtgg	aacaagagga	3360
ccatctctga	gatcaaccac	tgcaagcgga	agggatgatcg	aggaatgggtg	ctgcagggag	3420
tgcacaatgc	ccccactgtc	gttccgggct	aaagatggct	gttggatatgg	aatggagata	3480
aggcccagga	aagaaccaga	aagcaactta	gtaaggtcaa	tgggtgactgc	aggatcaact	3540
gatcacatgg	accacttctc	ccttggagtg	cttgtgattc	tgctcatggg	gcaggaaggg	3600
ctgaagaaga	gaatgaccac	aaagatcatc	ataagcacat	caatggcagt	gctggtagct	3660
atgatcctgg	gaggattttc	aatgagtga	ctggctaagc	ttgcaatttt	gatgggtgcc	3720
accttcgctg	aaatgaacac	tggaggagat	gtagctcatc	tggcgctgat	agcggcattc	3780
aaagtccagc	cagcgttgct	ggtatctttc	atcttcagag	ctaattggac	accccgtaga	3840
agcatgctgc	tggccttggc	ctcgtgtctt	ttgcaaactg	cgatctccgc	cttggaaggc	3900
gacctgatgg	ttctcatcaa	tggttttgct	ttggcctggg	tggcaatacg	agcgtgggtt	3960
gttccacgca	ctgataacat	caccttggca	atcctggctg	ctctgacacc	actggcccgg	4020
ggcacactgc	ttgtggcggtg	gagagcaggc	cttgctactt	gcgggggggtt	tatgctcctc	4080
tctctgaagg	gaaaaggcag	tgtgaagaag	aacttaccat	ttgtcatggc	cctgggacta	4140
accgctgtga	ggctgggtcga	ccccatcaac	gtgggtgggac	tgctgttgct	cacaaggagt	4200
gggaagcgga	gctggccccc	tagcgaagta	ctcacagctg	ttggcctgat	atgcgcattg	4260
gctggagggt	tcgccaaggc	agatatagag	atggctgggc	ccatggccgc	ggtcggtctg	4320
ctaattgtca	gttacgtggg	ctcaggaaag	agtgtggaca	tgtacattga	aagagcaggt	4380
gacatcacat	gggaaaaaga	tgcggaagtc	actggaaaca	gtccccggct	cgatgtggcg	4440

ctagatgaga	gtggtgattt	ctccctggtg	gaggatgacg	gtccccccat	gagagagatc	4500
atactcaagg	tggtcctgat	gaccatctgt	ggcatgaacc	caatagccat	accctttgca	4560
gctggagcgt	ggtacgtata	cgtgaagact	ggaaaaagga	gtggtgctct	atgggatgtg	4620
cctgctccca	aggaagtaaa	aaagggggag	accacagatg	gagtgtacag	agtaatgact	4680
cgtagactgc	taggttcaac	acaagttgga	gtgggagtta	tgcaagaggg	ggtctttcac	4740
actatgtggc	acgtcacaaa	aggatccgcg	ctgagaagcg	gtgaagggag	acttgatcca	4800
tactggggag	atgtcaagca	ggatctggtg	tcatactgtg	gtccatggaa	gctagatgcc	4860
gcctgggacg	ggcacagcga	ggtgcagctc	ttggccgtgc	cccccgaga	gagagcgagg	4920
aacatccaga	ctctgcccgg	aatatttaag	acaaaggatg	gggacattgg	agcggttgcg	4980
ctggattacc	cagcaggaac	ttcaggatct	ccaatcctag	acaagtgtgg	gagagtgata	5040
ggactttatg	gcaatggggg	cgtgatcaaa	aatgggagtt	atgttagtgc	catcacccaa	5100
gggaggaggg	aggaagagac	tctgttgag	tgcttcgagc	cttcgatgct	gaagaagaag	5160
cagctaactg	tcttagactt	gcatactgga	gctgggaaaa	ccaggagagt	tcttcctgaa	5220
atagtccgtg	aagccataaa	aacaagactc	cgcaccgtga	tcttagctcc	aaccagggtt	5280
gtcgctgctg	aaatggagga	ggcccttaga	gggcttccag	tgcgttatat	gacaacagca	5340
gtcaatgtca	cccactctgg	aacagaaatc	gtcgacttaa	tgtgccatgc	caccttcact	5400
tcacgtctac	tacagccaat	cagagtcccc	aactataatc	tgtatattat	ggatgaggcc	5460
cacttcacag	atccctcaag	tatagcagca	agaggataca	tttcaacaag	ggttgagatg	5520
ggcgaggcgg	ctgccatctt	catgaccgcc	acgccaccag	gaaccggtga	cgcatttccg	5580
gactccaact	caccaattat	ggacaccgaa	gtggaagtcc	cagagagagc	ctggagctca	5640
ggctttgatt	gggtgacgga	tcattctgga	aaaacagttt	ggtttgttcc	aagcgtgagg	5700
aacggcaatg	agatcgcagc	ttgtctgaca	aaggctggaa	aacgggtcat	acagctcagc	5760
agaaagactt	ttgagacaga	gttccagaaa	acaaaacatc	aagagtggga	ctttgtcgtg	5820
acaactgaca	tttcagagat	gggcgccaac	tttaaagctg	accgtgtcat	agattccagg	5880
agatgcctaa	agccgggtcat	acttgatggc	gagagagtca	ttctggctgg	acccatgcct	5940
gtcacacatg	ccagcgctgc	ccagaggagg	gggcgcatag	gcaggaatcc	caacaaacct	6000
ggagatgagt	atctgtatgg	aggtgggtgc	gcagagactg	acgaagacca	tgcacactgg	6060
cttgaagcaa	gaatgctcct	tgacaatatt	tacctccaag	atggcctcat	agcctcgctc	6120
tatcgacctg	aggccgacaa	agtagcagcc	attgaggggag	agttcaagct	taggacggag	6180

caaaggaaga cttttgtgga actcatgaaa agaggagatc ttcttgtttg gctggcctat	6240
caggttgcat ctgccggaat aacctacaca gatagaagat ggtgctttga tggcacgacc	6300
aacaacacca taatggaaga cagtgtgccg gcagaggtgt ggaccagaca cggagagaaa	6360
agagtgtca aaccgaggtg gatggacgcc agagtttgtt cagatcatgc ggccctgaag	6420
tcattcaagg agtttgccgc tgggaaaaga ggagcggctt ttggagtgat ggaagccctg	6480
ggaacactgc caggacacat gacagagaga ttccaggaag ccattgacaa cctcgctgtg	6540
ctcatgcggg cagagactgg aagcaggcct taaaagccg cggcggccca attgccggag	6600
accctagaga ccattatgct tttggggttg ctgggaacag tctcgctggg aatcttcttc	6660
gtcttgatga ggaacaaggg catagggaaag atgggctttg gaatggtgac tcttggggcc	6720
agcgcattggc tcatgtggct ctcgaaatt gagccagcca gaattgcatg tgtcctcatt	6780
gttgtgtttc tattgctggt ggtgctcata cctgagccag aaaagcaaag atctcccag	6840
gacaacaaa tggcaatcat catcatggta gcagtaggtc ttctgggctt gattaccgcc	6900
aatgaactcg gatggttgga gagaacaaag agtgacctaa gccatctaata gggaaggaga	6960
gaggaggggg caaccatagg attctcaatg gacattgacc tgcggccagc ctcagcttgg	7020
gccatctatg ctgccttgac aactttcatt accccagccg tccaacatgc agtgaccact	7080
tcatacaaca actactcctt aatggcgatg gccacgcaag ctggagtgtt gtttggatatg	7140
ggcaaaggga tgccattcta cgcattggac tttggagtcc cgctgctaata gataggttgc	7200
tactcacaat taacaccctt gaccctaata gtggccatca ttttgctcgt ggcgcactac	7260
atgtacttga tcccagggtt gcaggcagca gctgcgcgtg ctgccagaa gagaacggca	7320
gctggcatca tgaagaacct tgttgtggat ggaatagtgg tgactgacat tgacacaatg	7380
acaattgacc cccaagtgga gaaaaagatg ggacaggtgc tactcatagc agtagccgtc	7440
tccagcgcca tactgtcgcg gaccgcctgg ggggtggggg aggctggggc cctgatcaca	7500
gccgcaactt ccactttgtg ggaaggctct ccgaacaagt actggaactc ctctacagcc	7560
acttcaactgt gtaacatttt taggggaagt tacttggtg gagcttctct aatctacaca	7620
gtaacaagaa acgctggctt ggtcaagaga cgtgggggtg gaacaggaga gaccctggga	7680
gagaaatgga aggcccgtt gaaccagatg tcggccctgg agttctactc ctacaaaaag	7740
tcaggcatca ccgaggtgtg cagagaagag gcccgccgcg ccctcaagga cgggtgtggca	7800
acgggaggcc atgctgtgtc ccgaggaagt gcaaagctga gatggttggt ggagcgggga	7860
tacctgcagc cctatggaaa ggtcattgat cttggatgtg gcagaggggg ctggagttac	7920

tacgccgcca	ccatccgcaa	agttcaagaa	gtgaaaggat	acacaaaagg	aggccctggt	7980
catgaagaac	ccgtgttggt	gcaaagctat	gggtggaaca	tagtccgtct	taagagtggg	8040
gtggacgtct	ttcatatggc	ggctgagccg	tgtgacacgt	tgctgtgtga	cataggtgag	8100
tcatcatcta	gtcctgaagt	ggaagaagca	cggacgctca	gagtcctctc	catggtgggg	8160
gattggcttg	aaaaaagacc	aggagccttt	tgtataaagg	tggtgtgccc	atacaccagc	8220
actatgatgg	aaaccctgga	gcgactgcag	cgtaggatatg	ggggaggact	ggtcagagtg	8280
ccactctccc	gcaactctac	acatgagatg	tattgggtct	ctggagcgaa	aagcaacacc	8340
ataaaaagtg	tgtccaccac	gagccagctc	ctcttggggc	gcatggacgg	gcctaggagg	8400
ccagtgaaat	atgaggagga	tgtggatctc	ggctctggca	cgcgggctgt	ggtaagctgc	8460
gctgaagctc	ccaacatgaa	gatcattggt	aaccgcattg	aaaggatccg	cagtgagcac	8520
gcggaaacgt	ggttctttga	cgagaaccac	ccatatagga	catgggctta	ccatggaagc	8580
tatgaggccc	ccacacaagg	gtcagcgtcc	tctctaataa	acggggttgt	caggctcctg	8640
tcaaaaccct	gggatgtggt	gactggagtc	acaggaatag	ccatgaccga	caccacaccg	8700
tatggtcagc	aaagagtttt	caaggaaaaa	gtggacacta	gggtgccaga	cccccaagaa	8760
ggcactcgtc	aggttatgag	catggtctct	tcctggttgt	ggaaagagct	aggcaaacac	8820
aaacggccac	gagtctgtac	caaagaagag	ttcatcaaca	aggttcgtag	caatgcagca	8880
ttaggggcaa	tatttgaaga	ggaaaaagag	tggaagactg	cagtgggaagc	tgtgaacgat	8940
ccaaggttct	gggctctagt	ggataaggaa	agagagcacc	acctgagagg	agagtgccag	9000
agttgtgtgt	acaacatgat	gggaaaaaga	gaaaagaaac	aaggggaatt	tggaaaggcc	9060
aagggcagcc	gcgccatctg	gtatatgtgg	ctaggggcta	gatttctaga	gttcgaagcc	9120
cttggattct	tgaacgagga	tactggatg	gggagagaga	actcaggagg	tggtgttgaa	9180
gggctgggat	tacaaagact	cggatatgtc	ctagaagaga	tgagtcgtat	accaggagga	9240
aggatgtatg	cagatgacac	tgctggctgg	gacacccgca	tcagcagggt	tgatctggag	9300
aatgaagctc	taatcaccaa	ccaaatggaa	aaagggcaca	gggccttggc	attggccata	9360
atcaagtaca	cataccaaaa	caaagtggta	aaggtcctta	gaccagctga	aaaagggaaa	9420
acagttatgg	acattatttc	gagacaagac	caaaggggga	gcggacaagt	tgtcacttac	9480
gctcttaaca	catttaccaa	cctagtgggtg	caactcattc	ggaatatgga	ggctgaggaa	9540
gttctagaga	tgcaagactt	gtggctgctg	cggaggtcag	agaaagtgac	caactggttg	9600
cagagcaacg	gatgggatatg	gctcaaacga	atggcagtca	gtggagatga	ttgcgttgtg	9660

aagccaattg atgataggtt tgcacatgcc ctcaggttct tgaatgatat gggaaaagtt	9720
aggaaggaca cacaagagtg gaaaccctca actggatggg acaactggga agaagttccg	9780
ttttgctccc accacttcaa caagctccat ctcaaggacg ggaggtccat tgtggttccc	9840
tgccgccacc aagatgaact gattggccgg gcccgcgtct ctccaggggc gggatggagc	9900
atccgggaga ctgcttgcct agcaaaatca tatgcgcaaa tgtggcagct cctttatttc	9960
cacagaaggg acctccgact gatggccaat gccatttgtt catctgtgcc agttgactgg	10020
gttccaactg ggagaactac ctggtcaatc catggaaagg gagaatggat gaccactgaa	10080
gacatgcttg tgggtgtggaa cagagtgtgg attgaggaga acgaccacat ggaagacaag	10140
accccagtta cgaaatggac agacatcccc tatttgggaa aaagggaga cttgtggtgt	10200
ggatctctca tagggcacag accgcgacc acctgggctg agaacattaa aaacacagtc	10260
aacatggtgc gcaggatcat aggtgatgaa gaaaagtaca tggactacct atccacccaa	10320
gttcgctact tgggtgaaga agggcttaca cctggagtgc tgtaagcacc agtcttaatg	10380
ttgtcaggcc tgctagtcag ccacagcttg gggaaagctg tgcagcctgt gacccccag	10440
gagaagctgg gaaaccaagc ctatagtcag gccgagaacg ccatggcacg gaagaagcca	10500
tgctgcctgt gagccccctca gaggacactg agtcaaaaaa cccacgcgc ttggaggcgc	10560
aggatgggaa aagaaggtgg cgaccttccc cacccttcaa tctggggcct gaactggaga	10620
tcagctgtgg atctccagaa gagggactag tggtagagg ag	10662

<210> 2
 <211> 10648
 <212> DNA
 <213> Zika virus isolate SSABR1, complete genome

<400> 2	
gacagttcga gtttgaagcg aaagctagca acagtatcaa caggttttat ttggatttgg	60
aaacgagagt ttctgggtcat gaaaaaccca aaaaagaaat ccggaggatt ccggattgtc	120
aatatgctaa aacgcggagt agcccgtgtg agcccctttg ggggcttgaa gaggctgcca	180
gccggacttc tgctgggtca tgggcccatc aggatggtct tggcgattct agcctttttg	240
agattcacgg caatcaagcc atcactgggt ctcatcaata gatgggggtc agtggggaaa	300
aaagaggcta tggaaataat aaagaagttc aagaaagatc tggctgccat gctgagaata	360
atcaatgcta ggaaggagaa gaagagacga ggcgcagata ctagtgtcgg aattgttggc	420
ctcctgctga ccacagctat ggcagcggag gtcactagac gtgggagtgc atactatatg	480

tacttggaca gaaacgatgc tggggaggcc atatcttttc caaccacatt ggggatgaat	540
aagtgttata tacagatcat ggatcttggga cacatgtgtg atgccaccat gagctatgaa	600
tgccctatgc tggatgaggg ggtggaacca gatgacgtcg attgttgggtg caacacgacg	660
tcaacttggg ttgtgtacgg aacctgccat cacaaaaaag gtgaagcacg gagatctaga	720
agagctgtga cgctcccctc ccattccact aggaagctgc aaacgcggtc gcaaacctgg	780
ttggaatcaa gagaatacac aaagcacttg attagagtcg aaaattggat attcaggaac	840
cctggcttcg cgttagcagc agctgccatc gcttggcttt tgggaagctc aacgagccaa	900
aaagtcatat acttgggtcat gatactgctg attgccccgg catacagcat caggtgcata	960
ggagtcagca atagggactt tgtggaaggt atgtcagggt ggacctgggt tgatgttgtc	1020
ttggaacatg gaggttgtgt caccgtaatg gcacaggaca aaccgactgt cgacatagag	1080
ctggttacia caacagtcag caacatggcg gaggtgaagat cctactgcta tgaggcatca	1140
atatcagaca tggcttcgga cagccgctgc ccaacacaag gtgaagccta ccttgacaag	1200
caatcagaca ctcaatatgt ctgcaaaaga acgttagtgg acagaggctg gggaaatgga	1260
tgtggacttt ttggcaaagg gagcctgggtg acatgcgcta agtttgcatg ctccaagaaa	1320
atgaccggga agagcatcca gccagagaat ctggagtacc ggataatgct gtcagttcat	1380
ggctcccagc acagtgggat gattgttaat gacacaggac atgaaactga tgagaataga	1440
gcgaaagtgt agataacgcc caattcacca agagccgaag ccacctggg gggttttgga	1500
agcctaggac ttgattgtga accgaggaca ggccttgact tttcagattt gtattacttg	1560
actatgaata acaagcactg gttggttcac aaggagtgggt tccacgacat tccattacct	1620
tggcacgctg gggcagacac cggaactcca cactggaaca acaaagaagc actggtagag	1680
ttcaaggacg cacatgccaa aaggcaaact gtcgtggttc tagggagtca agaaggagca	1740
gttcacacgg cccttgctgg agctctggag gctgagatgg atggtgcaaa ggaaggctg	1800
tcctctggcc acttgaaatg tcgcctgaaa atggataaac ttagattgaa gggcgtgtca	1860
tactccttgt gtactgcagc gttcacattc accaagatcc cggctgaaac actgcacggg	1920
acagtcacag tggaggtaca gtacgcaggg acagatggac cttgcaaggt tccagctcag	1980
atggcggtgg acatgcaaac tctgaccca gttgggaggt tgataaccgc taaccccgta	2040
atcactgaaa gcactgagaa ctctaagatg atgctggaac ttgatccacc atttggggac	2100
tcttacattg tcataggagt cggggagaag aagatcaccc accactggca caggagtggc	2160
agcaccattg gaaaagcatt tgaagccact gtgagaggtg ccaagagaat ggcagtcttg	2220

ggagacacag cctgggactt tggatcagtt ggaggcgctc tcaactcatt gggcaagggc	2280
atccatcaaa tttttggagc agctttcaaa tcattgtttg gaggaatgtc ctggttctca	2340
caaattctca ttggaacggt gctgatgtgg ttgggtctga acacaaagaa tggatctatt	2400
tcccttatgt gcttggcctt agggggagtg ttgatcttct tatccacagc cgtctctgct	2460
gatgtggggg gctcgggtga cttctcaaag aaggagacga gatgcggtac aggggtgttc	2520
gtctataacg acgttgaagc ctggaggggac aggtacaagt accatcctga cccccccgt	2580
agattggcag cagcagtcaa gcaagcctgg gaagatggta tctgcgggat ctctctgtt	2640
tcaagaatgg aaaacatcat gtggagatca gtagaagggg agctcaacgc aatcctggaa	2700
gagaatggag ttcaactgac ggtcgttgtg ggatctgtaa aaaaccccat gtggagaggt	2760
ccacagagat tgcccgtgcc tgtgaacgag ctgccccacg gctggaaggc ttgggggaaa	2820
tcgtacttcg tcagagcagc aaagacaaat aacagctttg tcgtggatgg tgacacactg	2880
aaggaatgcc cactcaaaca tagagcatgg aacagctttc ttgtggagga tcatgggttc	2940
ggggtatttc acactagtgt ctggctcaag gttagagaag attattcatt agagtgtgat	3000
ccagccgtta ttggaacagc tgtaagggg aaggaggctg tacacagtga tctaggctac	3060
tggattgaga gtgagaagaa tgacacatgg aggctgaaga gggcccatct gatcgagatg	3120
aaaacatgtg aatggccaaa gtcccacaca ttgtggacag atggaataga agagagtgat	3180
ctgatcatac ccaagtcttt agctgggcca ctcagccatc acaataccag agagggtac	3240
aggacccaaa tgaaagggcc atggcacagt gaagagcttg aaattcgggt tgaggaatgc	3300
ccaggcacta aggtccacgt ggaggaaaca tgtggaacaa gaggaccatc tctgagatca	3360
accactgcaa gcggaagggg gatcgaggaa tgggtgctga gggagtgcac aatgccccca	3420
ctgtcgttcc gggctaaaga tggctgttgg tatggaatgg agataaggcc caggaaagaa	3480
ccagaaagca acttagtaag gtcaatggtg actgcaggat caactgatca catggaccac	3540
ttctcccttg gagtgcttgt gattctgctc atgggtgcagg aagggtgaa gaagagaatg	3600
accacaaaga tcatcataag cacatcaatg gcagtgctgg tagctatgat cctgggagga	3660
ttttcaatga gtgacctggc taagcttgca attttgatgg gtgccacctt cgcggaaatg	3720
aacactggag gagatgtagc tcatctggcg ctgatagcgg cattcaaagt cagaccagcg	3780
ttgctggtat ctttcatctt cagagctaata tggacacccc gtgaaagcat gctgctggcc	3840
ttggcctcgt gtcttttgca aactgcgac tccgccttgg aaggcgacct gatggttctc	3900
atcaatggtt ttgctttggc ctggttggca atacgagcga tggttgttcc acgcactgat	3960

aacatcacct	tggaatcct	ggctgctctg	acaccactgg	cccgggggcac	actgcttgtg	4020
gcgtggagag	caggccttgc	tacttgccgg	gggtttatgc	tcctctctct	gaagggaaaa	4080
ggcagtgtga	agaagaactt	accatttgtc	atggccctgg	gactaaccgc	tgtgaggctg	4140
gtcgacccca	tcaacgtggt	gggactgctg	ttgctcacia	ggagtgggaa	gcggagctgg	4200
ccccctagcg	aagtactcac	agctgttggc	ctgatatgcg	cattggctgg	agggttcgcc	4260
aaggcagata	tagagatggc	tgggcccatg	gccgcggtcg	gtctgctaata	tgtcagttac	4320
gtggtctcag	gaaagagtgt	ggacatgtac	attgaaagag	caggtgacat	cacatgggaa	4380
aaagatgcgg	aagtcactgg	aaacagtccc	cggctcgatg	tggcgctaga	tgagagtggg	4440
gatttctccc	tgggtggagga	tgacgggtccc	cccatgagag	agatcatact	caaggtgggtc	4500
ctgatgacca	tctgtggcat	gaaccaata	gccataccct	ttgcagctgg	agcgtgggtac	4560
gtatacgtga	agactggaaa	aaggagtggg	gctctatggg	atgtgcctgc	tccaaggaa	4620
gtaaaaaagg	gggagaccac	agatggagtg	tacagagtaa	tgactcgtag	actgctaggt	4680
tcaacacaag	ttggagtggg	agttatgcaa	gaggggggtct	ttcacactat	gtggcacgtc	4740
acaaaaggat	ccgcgctgag	aagcggtgaa	gggagacttg	atccatactg	gggagatgtc	4800
aagcaggatc	tgggtgtcata	ctgtgggtcca	tggaaagctag	atgccgcctg	ggacggggcac	4860
agcgagggtgc	agctcttggc	cgtgcccccc	ggagagagag	cgaggaacat	ccagactctg	4920
cccggaatat	ttaagacaaa	ggatggggac	attggagcgg	ttgcgctgga	ttaccagca	4980
ggaacttcag	gatctccaat	cctagacaag	tgtgggagag	tgataggact	ttatggcaat	5040
gggggtcgtga	tcaaaaatgg	gagttatggt	agtgccatca	ccaaggagg	gagggaggaa	5100
gagactcctg	ttgagtgtct	cgagccttcg	atgctgaaga	agaagcagct	aactgtctta	5160
gacttgcata	ctggagctgg	gaaaaccagg	agagttcttc	ctgaaatagt	ccgtgaagcc	5220
ataaaaaaca	gactccgtac	tgtgatctta	gctccaacca	gggttgctgc	tgctgaaatg	5280
gaggaggccc	ttagagggtc	tccagtgcgt	tatatgacaa	cagcagtcaa	tgtcacccac	5340
tctggaacag	aaatcgtcga	cttaatgtgc	catgccacct	tcacttcacg	tctactacag	5400
ccaatcagag	tccccaaacta	taatctgtat	attatggatg	aggccactt	cacagatccc	5460
tcaagtatag	cagcaagagg	atacatttca	acaagggttg	agatgggcga	ggcggctgcc	5520
atcttcatga	ccgccacgcc	accaggaacc	cgtgacgcat	ttccggactc	caactcacca	5580
attatggaca	ccgaagtgga	agtcccagag	agagcctgga	gctcaggctt	tgattgggtg	5640
acggatcatt	ctggaaaaac	agtttggttt	gttccaagcg	tgagggaacg	caatgagatc	5700

gcagcttgtc	tgacaaaggc	tggaaaacgg	gtcatacagc	tcagcagaaa	gactttttgag	5760
acagagttcc	agaaaacaaa	acatcaagag	tgggactttg	tcgtgacaac	tgacatttca	5820
gagatgggcg	ccaactttta	agctgaccgt	gtcatagatt	ccaggagatg	cctaaagccg	5880
gtcatacttg	atggcgagag	agtcattctg	gctggaccca	tgctgtcac	acatgccagc	5940
gctgcccaga	ggagggggcg	cataggcagg	aatcccaaca	aacctggaga	tgagtatctg	6000
tatggaggtg	ggtgcgcgag	gactgacgaa	gaccatgcac	actggcttga	agcaagaatg	6060
ctccttgaca	atattttacct	ccaagatggc	ctcatagcct	cgctctatcg	acctgaggcc	6120
gacaaagtag	cagccattga	gggagagttc	aagcttagga	cggagcaaag	gaagaccttt	6180
gtggaactca	tgaaaagagg	agatcttcct	gtttggctgg	cctatcaggt	tgcatctgcc	6240
ggaataacct	acacagatag	aagatgggtg	tttgatggca	cgaccaacaa	caccataatg	6300
gaagacagtg	tgccggcgag	ggtgtggacc	agacacggag	agaaaagagt	gctcaaaccg	6360
aggtggatgg	acgccagagt	ttgttcagat	catgcggccc	tgaagtcatt	caaggagttt	6420
gccgctggga	aaagaggagc	ggcttttggg	gtgatggaag	ccctgggaac	actgccagga	6480
cacatgacag	agagattcca	ggaagccatt	gacaacctcg	ctgtgctcat	gcgggcagag	6540
actggaagca	ggccttacia	agccgcggcg	gccaatttgc	cggagaccct	agagaccatt	6600
atgcttttgg	ggttgctggg	aacagtctcg	ctgggaatct	tcttcgtctt	gatgaggaac	6660
aagggcatag	ggaagatggg	ctttggaatg	gtgactcttg	gggccagcgc	atggctcatg	6720
tggctctcgg	aaattgagcc	agccagaatt	gcatgtgtcc	tcattgttgt	gtttctattg	6780
ctggtggtgc	tcataacctga	gccagaaaag	caaagatctc	cccaggacaa	ccaaatggca	6840
atcatcatca	tggtagcagt	aggtcttctg	ggcttgatta	ccgccaatga	actcggatgg	6900
ttggagagaa	caaagagtga	cctaagccat	ctaatgggaa	ggagagagga	gggggcaacc	6960
ataggattct	caatggacat	tgacctgcgg	ccagcctcag	cttggggccat	ctatgctgcc	7020
ttgacaactt	tcattacccc	agccgtccaa	catgcagtga	ccacttcata	caacaactac	7080
tccttaatgg	cgatggccac	gcaagctgga	gtgttgtttg	gtatgggcaa	agggatgcca	7140
ttctacgcat	gggacttttg	agtcccgtg	ctaatgatag	gttgctactc	acaattaaca	7200
cccctgaccc	taatagtggc	catcattttg	ctcgtggcgc	actacatgta	cttgatccca	7260
gggctgcagg	cagcagctgc	gcgtgctgcc	cagaagagaa	cggcagctgg	catcatgaag	7320
aaccctgttg	tggatggaat	agtggtgact	gacattgaca	caatgacaat	tgacccccaa	7380
gtggagaaaa	agatgggaca	ggtgctactc	atagcagtag	ccgtctccag	cgccatactg	7440

tcgcggaccg cctgggggtg gggggaggct ggggccctga tcacagccgc aacttcact	7500
ttgtgggaag gctctccgaa caagtactgg aactcctcta cagccacttc actgtgtaac	7560
atTTTTtaggg gaagttactt ggctggagct tctctaattct acacagtaac aagaaacgct	7620
ggcttgggtca agagacgtgg gggtggaaca ggagagaccc tgggagagaa atggaaggcc	7680
cgcttgaacc agatgtcggc cctggagttc tactcctaca aaaagtcagg catcaccgag	7740
gtgtgcagag aagaggcccc cgcgcacctc aaggacggtg tggcaacggg aggccatgct	7800
gtgtcccgag gaagtgcaaa gctgagatgg ttggtggagc ggggatacct gcagccctat	7860
ggaaagggtca ttgatcttgg atgtggcaga gggggctgga gttactacgc cgccaccatc	7920
cgcaaagttc aagaagtgaaggatacaca aaaggaggcc ctggtcatga agaaccctg	7980
ttggtgcaaa gctatgggtg gaacatagtc cgtcttaaga gtgggggtgga cgtctttcat	8040
atggcggctg agccgtgtga cacgttgctg tgtgacatag gtgagtcac atctagtcct	8100
gaagtggaa aagcacggac gctcagagtc ctctccatgg tgggggattg gcttgaaaaa	8160
agaccaggag ctttttgtat aaagggtgtg tgcccataca ccagcactat gatggaaacc	8220
ctggagcgac tgcagcgtag gtatggggga ggactggtca gagtgccact ctcccgcaac	8280
tctacacatg agatgtattg ggtctctgga gcgaaaagca acaccataaa aagtgtgtcc	8340
accacgagcc agctcctctt ggggcgcagt gacgggccta ggaggccagt gaaatatgag	8400
gaggatgtga atctcggtc tggcacgcgg gctgtggtaa gctgcgctga agtcccaac	8460
atgaagatca ttggtaaacc cattgaaagg atccgcagt agcacgcgga aacgtggttc	8520
tttgacgaga accaccata taggacatgg gcttaccatg gaagctatga ggccccaca	8580
caagggtcag cgtcctctct aataaacggg gttgtcaggc tcctgtcaaa accctgggat	8640
gtggtgactg gagtcacagg aatagccatg accgacacca caccgtatgg tcagcaaaga	8700
gttttcaagg aaaaagtgga cactaggggt ccagaccccc aagaaggcac tcgtcaggtt	8760
atgagcatgg tctcttcctg gttgtggaaa gagctaggca aacacaaacg gccacgagtc	8820
tgtaccaaag aagagttcat caacaagggt cgtagcaatg cagcattagg ggcaatattt	8880
gaagaggaaa aagagtggaa gactgcagt gaagctgtga acgatccaag gttctgggct	8940
ctagtggata aggaaagaga gcaccacctg agaggagagt gccagagttg tgtgtacaac	9000
atgatgggaa aaagagaaaa gaaacaagg gaatttggaaggccaagg cagccgcgcc	9060
atctggtata tgtggctagg ggctagatct ctagagtctg aagcccttgg attcttgaac	9120
gaggatcact ggatggggag agagaactca ggagggtggt ttgaagggtt gggattacaa	9180

agactcggat atgtcctaga agagatgagt cgtataccag gaggaaggat gtatgcagat	9240
gacactgctg gctgggacac ccgcatcagc aggtttgatc tggagaatga agctctaadc	9300
accaacaaaa tggaaaaagg gcacagggcc ttggcattgg ccataatcaa gtacacatac	9360
caaaacaaag tggtaaaggc ccttagacca gctgaaaaag ggaaaacagt tatggacatt	9420
atttcgagac aagaccaaag ggggagcgga caagttgtca cttacgctct taacacattt	9480
accaacctag tgggtgcaact cattcggaat atggaggctg aggaagttct agagatgcaa	9540
gacttgtggc tgctgcggag gtcagagaaa gtgaccaact ggttgcagag caacggatgg	9600
gataggctca aacgaatggc agtcagtga gatgattgag ttgtgaagcc aattgatgat	9660
aggtttgcac atgccctcag gttcttgaat gatatgggaa aagttaggaa ggacacacaa	9720
gagtggaaac cctcaactgg atgggacaac tgggaagaag ttccgttttg ctcccaccac	9780
ttcaacaagc tccatctcaa ggacgggagg tccattgtgg ttccctgccg ccaccaagat	9840
gaactgattg gccggggccc cgtctctcca ggggcgggat ggagcatccg ggagactgct	9900
tgcctagcaa aatcatatgc gcaaatgtgg cagctccttt atttccacag aagggacctc	9960
cgactgatgg ccaatgccat ttgttcatct gtgccagttg actgggttcc aactgggaga	10020
actacctggt caatccatgg aaaggagaaa tggatgacca ctgaagacat gcttgtggtg	10080
tggaaacagag tgtggattga ggagaacgac cacatggaag acaagacccc agttacgaaa	10140
tggacagaca tcccctatct gggaaaaagg gaagacttgt ggtgtggatc tctcataggg	10200
cacagaccgc gcaccacctg ggctgagaac attaaaaaca cagtcaacat ggtgcgcagg	10260
atcataggtg atgaagaaaa gtacatggac tacctatcca cccaagtctg ctacttgggt	10320
gaagaagggc ctacacctgg agtgctgtaa gcaccagtct taatgttgctc aggctgcta	10380
gtcagccaca gcttggggaa agctgtgcag cctgtgacct cccagggaga agctgggaaa	10440
ccaagcctat agtcaggccg agaacgcat ggcacggaag aagccatgct gcctgtgagc	10500
ccctcagagg aactgagtc aaaaaacccc acgcgcttgg aggcgcagga tgggaaaaga	10560
aggtggcgac cttccccacc cttcaatctg gggcctgaac tggagatcag ctgtggatct	10620
ccagaagagg gactagtggc tagaggag	10648

<210> 3
 <211> 10808
 <212> DNA
 <213> Zika virus strain Natal RGN, complete genome

<400> 3	
agttgttgat ctgtgtgaat cagactgcga cagttcgagt ttgaagcgaa agctagcaac	60

agtatcaaca ggtttttatatt tggatttgga aacgagagtt tctgggtcatg aaaaacccaa	120
aaaagaaatc cggaggattc cggattgtca atatgctaaa acgcgaggta gcccgtgtga	180
gccccttttg gggcttgaag aggctgccag ccggacttct gctgggtcat gggcccatca	240
ggatgggtctt ggcaattcta gcctttttga gattcacggc aatcaagcca tctactgggtc	300
tcatcaatag atgggggttca gtggggaaaa aagaggctat ggaaataata aagaagttca	360
agaaagatct ggctgccatg ctgagaataa tcaatgctag gaaggagaag aagagacgag	420
gcgcagatac tagtgctcga attgttggcc tcctgctgac cacagctatg gcagcggagg	480
tacttagacg tgggagtgca tactatatgt acttgacag aaacgatgct ggggaggcca	540
tatcttttcc aaccacattg gggatgaata agtggtatat acagatcatg gatcttggac	600
acatgtgtga tgccaccatg agctatgaat gccctatgct ggatgagggg gtggaaccag	660
atgacgtcga ttgttggtgc aacacgacgt caacttgggt tgtgtacgga acctgccatc	720
acaaaaaagg tgaagcacgg agatctagaa gagctgtgac gctcccctcc cattccacta	780
ggaagctgca aacgcggtcg caaacctggt tggaatcaag agaatacaca aagcacttga	840
ttagagtcga aaattggata ttcaggaacc ctggcttcgc gttagcagca gctgccatcg	900
cttggttttt gggaagctca acgagccaaa aagtcataata cttgggtcatg atactgctga	960
ttgccccggc atacagcatc aggtgcatag gagtcagcaa tagggacttt gtggaaggta	1020
tgtcagggtg gacttgggtt gatgttgtct tggaacatgg aggttgtgtc accgtaatgg	1080
cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc aacatggcgg	1140
aggtaagatc ctactgctat gaggcacaa tatcagacat ggcttcggac agccgctgcc	1200
caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc tgcaaaagaa	1260
cgtagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg agcctgggtga	1320
catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag ccagagaatc	1380
tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg atcgttaatg	1440
acacaggaca tgaaactgat gagaatagag cgaagggtga gataacgccc aattcaccaa	1500
gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa ccgaggacag	1560
gccttgactt ttcagatttg tattacttga ctatgaataa caagcactgg ttggtccaca	1620
aggagtgggt ccacgacatt ccattacctt ggcacgctgg ggcagacacc ggaactccac	1680
actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa aggcaaactg	1740
tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga gctctggagg	1800

ctgagatgga	tgggtgcaaag	ggaaggctgt	cctctggcca	cttgaaatgt	cgctgaaaa	1860
tggataaact	tagattgaag	ggcgtgtcat	actccttggt	taccgcagcg	ttcacattca	1920
ccaagatccc	ggctgaaaca	ctgcacggga	cagtcacagt	ggaggtacag	tacgcaggga	1980
cagatggacc	ttgcaagggt	ccagctcaga	tggcgggtga	catgcaaact	ctgaccccag	2040
ttgggaggtt	gataaccgct	aaccccgtaa	tactgaaag	cactgagaac	tctaagatga	2100
tgctggaact	tgatccacca	tttggggact	cttacattgt	cataggagtc	ggggagaaga	2160
agatcaccca	ccactggcac	aggagtggca	gcaccattgg	aaaagcattt	gaagccactg	2220
tgagaggtgc	caagagaatg	gcagtcttgg	gagacacagc	ctgggacttt	ggatcagttg	2280
gaggcgctct	caactcattg	ggcaagggca	tccatcaaat	ttttggagca	gctttcaaat	2340
cattgttttg	aggaatgtcc	tggttctcac	aaatcctcat	tggaacgttg	ctgatgtggt	2400
tgggtctgaa	cacaaagaat	ggatctattt	cccttatgtg	cttggcctta	gggggagtgt	2460
tgatcttctt	atccacagcc	gtctctgctg	atgtggggtg	ctcgggtggac	ttctcaaaga	2520
aggagacgag	atgcggtaca	ggggtgttcg	tctataacga	cgttgaagcc	tggagggaca	2580
ggtacaagta	ccatcctgac	tcccccgta	gattggcagc	agcagtcaag	caagcctggg	2640
aagatggtat	ctgcgggata	tcctctgttt	caagaatgga	gaacatcatg	tggagatcag	2700
tagaagggga	gctcaacgca	atcttggaag	agaatggagt	tcaactgacg	gtcgttgttg	2760
gatctgtaaa	aaaccccatg	tggagaggtc	cacagagatt	gcccgctgct	gtgaacgagc	2820
tgccccacgg	ctggaaggct	tgggggaaat	cgtacttcgt	cagagcagca	aagacaaata	2880
acagctttgt	cgtggatggt	gacacactga	aggaatgccc	actcgaacat	agagcatgga	2940
acagctttct	tgtggaggat	catgggttcg	gggtatttca	cactagtgtc	tggctcaagg	3000
ttagagaaga	ttattcatta	gagtgtgata	cagccgttat	tggaacagct	gttaagggga	3060
aggaggctgt	acacagtgat	ctaggctact	ggattgagag	tgagaagaat	gacacatgga	3120
ggctgaagag	ggcccatcta	atcgagatga	aaacatgtga	atggccaaag	tcccacacat	3180
tgtgggcaga	tggaatagaa	gagagtgate	tgatcattcc	caagtcttta	gctggggccac	3240
tcagccatca	caataccaga	gagggttaca	ggacccaaat	gaaagggcca	tggcacagtg	3300
aagagcttga	aattcggttt	gaggaatgcc	cgggcactaa	ggtccacgtg	gaggaaacat	3360
gtggaacaag	aggaccatct	ctgagatcaa	ccactgcaag	cggaaggggtg	atcgaggaat	3420
ggtgctgcag	ggagtgcaca	atgcccccac	tgtcgttccg	ggctaaagat	ggctgttggt	3480
atggaatgga	gataaggccc	aggaaagaac	cagaaagcaa	cttagtaagg	tcagtgggtga	3540

ctgcaggatc aactgatcac atggatcact tctcccttgg agtgcttgtg attctgctca	3600
tggtgcagga agggctgaag aagagaatga ccacaaagat catcataagc acatcaatgg	3660
cagtgcctgg agctatgatc ctgggaggat tttcaatgag tgacctggct aagcttgcaa	3720
ttttgatggg cgccaccttc gcggaaatga aacttgagg agatgtagct catctggcgc	3780
tgatagcggc attcaaagtc agaccagcgt tgctggatc tttcatcttc agagctaatt	3840
ggacaccccg tgaaagcatg ctgctggcct tggcctcgtg tcttttgcaa actgcgatct	3900
ccgccttgga aggcgacctg atggttctca tcaatggttt tgctttggcc tggttggcaa	3960
tacgagcgat ggttggtcca cgcactgata acatcacctt ggcaatcctg gctgctctga	4020
caccactggc ccggggcaca ctgcttgtgg cgtggagagc aggccttgct acttgccggg	4080
ggtttatgct cctctctctg aagggaagag gcagtgtgaa gaagaactta ccatttgtca	4140
tggccctggg actaaccgct gtgaggctgg tcgaccccat caacgtgggtg ggactgctgt	4200
tgctcacaag gagtgggaag cggagctggc cccctagcga agtactcaca gctgttggcc	4260
tgatatgccc attggctgga gggttcgcca aggcagatat agagatggct gggcccatgg	4320
ccgcggtcgg tctgctaatt gtcagttacg tgggtctcagg aaagagtgtg gacatgtaca	4380
ttgaaagagc aggtgacatc acatgggaaa aagatgcgga agtcactgga aacagtcccc	4440
ggctcgatgt ggcgctagat gagagtgggtg atttctccct ggtggaggat gacgggtccc	4500
ccatgagaga gatcatactc aagggtgtcc tgatgacctt ctgtggcatg aaccaatag	4560
ccataccctt tgcagctgga gcgtggtacg tatacgtgaa gactggaaaa aggagtgggtg	4620
ctctatggga tgtgcctgct cccaaggaag taaaaaaggg ggagaccaca gatggagtgt	4680
acagagtaat gactcgtaga ctgctagggt caacacaagt tggagtggga gttatgcaag	4740
aggggggtctt tcacactatg tggcacgtca caaaaggatc cgcgctgaga agcgggtgaag	4800
ggagacttga tccatactgg ggagatgtca agcaggatct ggtgtcatac tgtggtccat	4860
ggaagctaga tgccgcctgg gacgggcaca gcgaggtgca gctcttggcc gtgccccccg	4920
gagagagagc gaggaacatc cagactctgc ccggaatatt taagacaaag gatggggaca	4980
ttggagcggg tgcgctggat taccagcag gaacttcagg atctccaatc ctagacaagt	5040
gtgggagagt gataggactt tatggcaatg gggctcgtgat caaaaatggg agttatgtta	5100
gtgccatcac ccaaggagag agggaggaag agactcctgt tgagtgcctc gacgttcga	5160
tgctgaagaa gaagcagcta actgtcttag acttgcattc tggagctggg aaaaccagga	5220
gagttcttcc tgaaatagtc cgtgaagcca taaaaacaag actccgtact gtgatcttag	5280

ctccaaccag ggttgtcgct gctgaaatgg aggaagccct tagaggggctt ccagtgcggt	5340
atatgacaac agcagtcaat gtcacccact ctggaacaga aatcgtcgac ttaatgtgcc	5400
atgccacctt cacttcacgt ctactacagc caatcagagt ccccaactat aatctgtata	5460
ttatggatga ggcccacttc acagatccct caagtatagc agcaagagga tacatttcaa	5520
caagggttga gatgggagc gcggtgcca tcttcatgac cgccacgcca ccaggaaccc	5580
gtgacgcatt tccggactcc aactcaccaa ttatggacac cgaagtggaa gtcccagaga	5640
gagcctggag ctgaggcttt gattgggtga cggatcattc tggaaaaaca gtttggtttg	5700
ttccaagcgt gaggaacggc aatgagatcg cagcttgtct gacaaaggct ggaaaacggg	5760
tcatacagct cagcagaaag acttttgaga cagagttcca gaaaacaaaa catcaagagt	5820
gggactttgt cgtgacaact gacatttcag agatgggagc caactttaaa gctgaccgtg	5880
tcatagattc caggagatgc ctaaagccgg tcatacttga tggcgagaga gtcattttgg	5940
ctggaccat gcctgtcaca catgccagcg ctgcccagag gagggggagc ataggcagga	6000
atcccaacaa acctggagat gagtatctgt atggaggtgg gtgagcagag actgacgaag	6060
accatgcaca ctggcttgaa gcaagaatgc tccttgacaa tatttacctc caagatggcc	6120
tcatagcctc gctctatcga cctgaggccg acaaagtagc agccattgag ggagagttca	6180
agcttaggac ggagcaaagg aagacctttg tggaactcat gaaaagagga gatcttcctg	6240
tttggtggc ctatcaggtt gcatctgccg gaataaccta cacagataga agatggtgct	6300
ttgatggcac gaccaacaac accataatgg aagacagtgt gccggcagag gtgtggacca	6360
gacacggaga gaaaagagtg ctcaaaccga ggtggatgga cgccagagtt tgttcagatc	6420
atgcggccct gaagtcattc aaggagtttg ccgctgggaa aagaggagcg gcttttgag	6480
tgatggaagc cctgggaaca ctgccaggac acatgacaga gagattccag gaagccattg	6540
acaacctcgc tgtgtcatg cgggcagaga ctggaagcag gccttacaaa gccgcggcgg	6600
cccaattgcc ggagacccta gagaccatta tgcttttggg gttgctggga acagtctcgc	6660
tggaatctt tttcgtcttg atgaggaaca agggcatagg gaagatgggc tttggaatgg	6720
tgactcttgg ggccagcgca tggctcatgt ggctctcgga aattgagcca gccagaattg	6780
catgtgtcct cattgttgtg ttctattgc tgggtggtgct catacctgag ccagaaaagc	6840
aaagatctcc ccaggacaac caaatggcaa tcatcatcat ggtagcagta ggtcttctgg	6900
gcttgattac cgccaatgaa ctcgatggg tggagagaac aaagagtgc ctaagccatc	6960
taatgggaag gagagaggag ggagcaacca taggattctc aatggacatt gacctgcggc	7020

cagcctcagc	ttggggccatc	tatgctgcct	tgacaacttt	cattacccca	gccgtccaac	7080
atgcagtgac	cacttcatac	aacaactact	ccttaatggc	gatggccacg	caagctggag	7140
tgttgtttgg	tatgggcaaa	gggatgccat	tctacgcatg	ggactttgga	gtcccgtgctg	7200
taatgatagg	ttgctactca	caattaacac	ccctgaccct	aatagtggcc	atcattttgc	7260
tcgtggcgca	ctacatgtac	ttgatcccag	ggctgcaggc	agcagctgcg	cgtgctgccc	7320
agaagagAAC	ggcagctggc	atcatgaaga	accctgttgt	ggatggaata	gtggtgactg	7380
acattgacac	aatgacaatt	gacccccaaG	tggagaaaaa	gatgggacag	gtgctactca	7440
tagcagtagc	agtctccagc	gccatactgt	cgcggaccgc	ctgggggtgg	ggggaggctg	7500
gggccctgat	cacagccgca	acttcactt	tgtgggaagg	ctctccgaac	aagtactgga	7560
actcctctac	agccacttca	ctgtgtaaca	tttttagggg	aagttacttg	gctggagctt	7620
ctctaattcta	catagtaaca	agaaacgctg	gcttgggtcaa	gagacgtggg	ggtggaacag	7680
gagagaccct	gggagagaaa	tggaaggccc	gcttgaacca	gatgtcggcc	ctggagttct	7740
actcctacaa	aaagtcaggc	atcaccgagg	tgtgcagaga	agaggcccgc	cgcgccctca	7800
aggatggtgt	ggcaacggga	ggccatgctg	tgtcccgagg	aagtgcaaag	ctgagatggt	7860
tggtggagcg	gggatacctg	cagccctatg	gaaagggtcat	tgatcttgga	tgtggcagag	7920
ggggctggag	ttactacgcc	gccaccatcc	gcaaagttca	agaagtgaAA	ggatacacaa	7980
aaggaggccc	tggtcatgaa	gaaccctgtg	tggtgcaaag	ctatgggtgg	aacatagtcc	8040
gtcttaagag	tgggggtggac	gtctttcata	tggcggctga	gccgtgtgac	acgttgctgt	8100
gtgacatagg	tgagtcatca	tctagtctctg	aagtggaaga	agcacggacg	ctcagagtcc	8160
tctccatggt	gggggattgg	cttgaaaaaa	gaccaggagc	cttttgtata	aaagtgttgt	8220
gcccatacac	cagcactatg	atggaaaccc	tggagcgact	gcagcgtagg	tatgggggag	8280
gactggtcag	agtgccactc	tcccgcaact	ctacacatga	gatgtactgg	gtctctggag	8340
cgaaaagcaa	caccataaaa	agtgtgtcca	ccacgagcca	gctcctcttg	gggcgcatgg	8400
acgggcctag	gaggccagtg	aaatatgagg	aggatgtgaa	tctcggctct	ggcacgcggg	8460
ctgtggtaaG	ctgcgctgaa	gctcccaaca	tgaagatcat	tggtAACgc	attgaaagga	8520
tccgcagtga	gcacgcggaa	acgtggttct	ttgacgagaa	ccaccatat	aggacatggg	8580
cttaccatgg	aagctatgag	gccccacac	aagggtcagc	gtcctctcta	ataaacgggg	8640
ttgtcaggct	cctgtcaaaa	ccctgggatg	tggtgactgg	agtcacagga	atagccatga	8700
ccgacaccac	accgtatggt	cagcaaagag	ttttcaagga	aaaagtggac	actagggtgc	8760

cagacccccca	agaaggcact	cgtcaggtta	tgagcatggt	ctcttcctgg	ttgtggaaag	8820
agctaggcaa	acacaaacgg	ccacgagtct	gtaccaaaga	agagttcatc	aacaagggtc	8880
gtagcaatgc	agcattaggg	gcaatatttg	aagaggaaaa	agagtggaaag	actgcagtgg	8940
aagctgtgaa	cgatccaagg	ttctgggctc	tagtggacaa	ggaaagagag	caccacctga	9000
gaggagagtg	ccagagttgt	gtgtacaaca	tgatgggaaa	aagagaaaag	aaacaagggg	9060
aatttgaaaa	ggccaagggc	agccgcgcca	tctggtatat	gtggctaggg	gctagatttc	9120
tagagttcga	agcccttgga	ttcttgaacg	aggatcactg	gatggggaga	gagaactcag	9180
gaggtggtgt	tgaagggctg	ggattacaaa	gactcggata	tgtcctagaa	gagatgagtc	9240
gcataccagg	aggaaggatg	tatgcagatg	acactgctgg	ctgggacacc	cgcatcagca	9300
ggttcgatct	ggagaatgaa	gctctaatac	ccaaccaaag	ggagaaaggg	catagggcct	9360
tggcattggc	cataatcaag	tacacatacc	aaaacaaagt	ggtaaagggtc	cttagaccag	9420
ctgaaaaagg	gaaaacagtt	atggacatta	tttcgagaca	agaccaaagg	gggagcggac	9480
aagttgtcac	ttacgctctt	aacacattta	ccaacctagt	ggtgcaactc	attcggaata	9540
tggaggctga	ggaagttcta	gagatgcaag	acttgtggct	gctgcggagg	tcagagaaaag	9600
tgaccaactg	gttgacagagc	aacggatggg	ataggctcaa	acgaatggca	gtcagtggag	9660
atgattgctg	tgtgaagcca	attgatgata	ggtttgcaca	tgccctcagg	ttcttgaatg	9720
atatgggaaa	agtttaggaag	gacacacaag	agtggaaacc	ctcaactgga	tgggacaact	9780
gggaagaagt	tccgttttgc	tcccaccact	tcaacaagct	ccatctcaag	gacgggaggt	9840
ccattgtggt	tccctgccgc	caccaagatg	aactgattgg	ccgggcccgc	gtctctccag	9900
gggcgggatg	gagcatccgg	gagactgctt	gcctagcaaa	atcatatgcg	caaagtgtggc	9960
agctccttta	tttccacaga	agggacctcc	gactgatggc	caatgccatt	tgttcatctg	10020
tgccagttga	ctgggttcca	actgggagaa	ctacctggtc	aatccatgga	aaggggagaat	10080
ggatgaccac	tgaagacatg	cttgtggtgt	ggaacagagt	gtggattgag	gagaacgacc	10140
acatggaaga	caagacccca	gttacgaaat	ggacagacat	tccctatttg	ggaaaaaggg	10200
aagacttgtg	gtgtggatct	ctcatagggc	acagaccgcg	caccacctgg	gctgagaaca	10260
ttaaaaacac	agtcaacatg	gtgcgcagga	tcataggtga	tgaagaaaag	tacatggact	10320
acctatccac	ccaagtctgc	tacttgggtg	aagaagggtc	tacacctgga	gtgctgtaag	10380
caccaatctt	aatgttgtca	ggcctgctag	tcagccacag	cttggggaaa	gctgtgcagc	10440
ctgtgacccc	cccaggagaa	gctgggaaac	caagcctata	gtcaggccga	gaacgccatg	10500

gcacggaaga agccatgctg cctgtgagcc cctcagagga cactgagtca aaaaacccca	10560
tgcgcttgga ggcgcaggat gggaaaagaa ggtggcgacc ttccccaccc ttcaatctgg	10620
ggcctgaact ggagatcagc tgtggatctc cagaagaggg actagtgggt agaggagacc	10680
ccccggaaaa cgcaaaacag catattgacg ctgggaaaga ccagagactc catgagtttc	10740
caccacgctg gccgccaggc acagatcgcc gaatagcggc ggccggtgtg gggaaatcca	10800
tgggtctt	10808

<210> 4
 <211> 10676
 <212> DNA
 <213> Zika virus strain Haiti/1225/2014, complete genome

<400> 4	
gttgttactg ttgctgactc agactgcgac agttcgagtt tgaagcgaaa gctagcaaca	60
gtatcaacag gttttatattg gatttggaag cgagagtttc tgggtcatgaa aaacccaaaa	120
aagaaatccg gaggattccg gattgtcaat atgctaaaac gcggagtagc ccgtgtgagc	180
ccctttgggg gcttgaagag gctgccagcc ggacttctgc tgggtcatgg gcccatcagg	240
atgggtcttg caattctagc ctttttgaga ttcacggcaa tcaagccatc actgggtctc	300
atcaatagat ggggttcagt ggggaaaaaa gaggctatgg aaataataaa gaagttcaag	360
aaagatctgg ctgccatgct gagaataatc aatgctagga aggagaagaa gagacgaggc	420
gcagatacta gtgtcggaat tgttggcctc ctgctgacca cagctatggc agcggaggtc	480
actagacgtg ggagtgcata ctatatgtac ttggacagaa acgatgctgg ggaggccata	540
tcttttccaa ccacattggg gatgaataag tggtatatac agatcatgga tcttggacac	600
atgtgtgatg ccaccatgag ctatgaatgc cctatgctgg atgagggggg ggaaccagat	660
gacgtcgatt gttggtgcaa cacgacgtca acttgggttg tgtacggaac ctgccatcac	720
aaaaaaggtg aagcacggag atctagaaga gctgtgacgc tcccctccca ttccactagg	780
aagctgcaaa cgcggtcgca aacctggttg gaatcaagag aatacacaaa gcacttgatt	840
agagtcgaaa attggatatt caggaaccct ggcttcgcgt tagcagcagc tgccatcgct	900
tggcttttgg gaagctcaac gagccaaaaa gtcataatac tgggtcatgat actgctgatt	960
gccccggcat acagcatcag gtgcatagga gtcagcaata gggactttgt ggaaggtatg	1020
tcaggtggga cttgggttga tgttgtcttg gaacatggag gttgtgtcac cgtaatggca	1080
caggacaaac cgactgtcga catagagctg gttacaacaa cagtcagcaa catggcggag	1140

gtaagatcct actgctatga ggcatacaata tcagacatgg cttcggacag ccgctgcccc	1200
acacaaggtg aagcctacct tgacaagcaa tcagacactc aatatgtctg caaaagaacg	1260
ttagtggaca gaggctgggg aaatggatgt ggactttttg gcaaagggag tctggtgaca	1320
tgcgctaagt ttgcatgctc caagaaaatg accgggaaga gcatccagcc agagaatctg	1380
gagtaccgga taatgctgtc agttcatggc tcccagcaca gtgggatgat cgtaaatgac	1440
acaggacatg aaactgatga gaatagagcg aaggttgaga taacgccccaa ttcaccaaga	1500
gccgaagcca ccctgggggg ttttggaagc ctaggacttg attgtgaacc gaggacaggc	1560
cttgactttt cagatttgta ttacttgact atgaataaca agcactgggtt gggttcacaag	1620
gagtggttcc acgacattcc attaccttg cagcgtgggg cagacaccgg aactccacac	1680
tggaacaaca aagaagcact ggtagagttc aaggacgcac atgccaaaag gcaaactgtc	1740
gtggttctag ggagtcaaga aggagcagtt cacacggccc ttgctggagc tctggaggct	1800
gagatggatg gtgcaaaggg aaggctgtcc tctggccact tgaaatgtcg cctgaaaatg	1860
gataaactta gattgaaggg cgtgtcatac tccttggtga ccgcagcgtt cacattcacc	1920
aagatcccgg ctgaaacact gcacgggaca gtcacagtgg aggtacagta cgcagggaca	1980
gatggacctt gcaagggttc agctcagatg gcggtggaca tgcaaactct gaccccagtt	2040
gggaggttga taaccgctaa ccccgtaatc actgaaagca ctgagaactc taagatgatg	2100
ctggaacttg atccaccatt tggggactct tacattgtca taggagtcgg ggagaagaag	2160
atcaccacc actggcacag gagtggcagc accattggaa aagcatttga agccactgtg	2220
agaggtgcca agagaatggc agtcttggga gacacagcct gggacttttg atcagttgga	2280
ggcgtctca actcattggg caagggcatc catcaaattt ttggagcagc tttcaaataca	2340
ttgtttggag gaatgtcctg gttctcaca attctcattg gaacgttgct gatgtggttg	2400
ggtctgaaca caaagaatgg atctatttcc cttatgtgct tggccttagg gggagtgttg	2460
atcttcttat ccacagccgt ctctgctgat gtgggggtgct cgggtggactt ctcaaagaag	2520
gagacgagat gcggtacagg ggtgttcgtc tataacgacg ttgaagcctg gagggacagg	2580
tacaagtacc atcctgactc cccccgtaga ttggcagcag cagtcaagca agcctgggaa	2640
gatggtatct gcgggatctc ctctgtttca agaattggaaa acatcatgtg gagatcagta	2700
gaaggggagc tcaacgcaat cctggaagag aatggagttc aactgacggc cgttgtggga	2760
tctgtaaaaa accccatgtg gagaggtcca cagagattgc ccgtgcctgt gaacgagctg	2820
ccccacggct ggaaggcttg ggggaaatcg cacttcgtca gagcagcaaa gacaaataac	2880

agctttgtcg	tggatggtga	cacactgaag	gaatgccac	tcaaacatag	agcatggaac	2940
agctttcttg	tggaggatca	tgggttcggg	gtatttcaca	ctagtgtctg	gctcaagggt	3000
agagaagatt	attcattaga	gtgtgatcca	gccgttattg	gaacagctgt	taagggaag	3060
gaggctgtac	acagtgatct	aggctactgg	attgagagtg	agaagaatga	cacatggagg	3120
ctgaagaggg	cccatctgat	cgagatgaaa	acatgtgaat	ggccaaagtc	ccacacattg	3180
tggacagatg	gaatagaaga	gagtgatctg	atcataccca	agtctttagc	tgggccactc	3240
agccatcaca	ataccagaga	gggctacagg	acccaaatga	aagggccatg	gcacagtga	3300
gagcttga	ttcggtttga	ggaatgccc	ggcactaagg	tccacgtgga	ggaaacatgt	3360
ggaacaagag	gaccatctct	gagatcaacc	actgcaagcg	gaagggtgat	cgaggaatgg	3420
tgctgcaggg	agtgcacaat	gccccactg	tcgttccggg	ctaaagatgg	ctgttggtat	3480
ggaatggaga	taaggcccag	gaaagaacca	gaaagcaact	tagtaagggtc	aatgggtgact	3540
gcaggatcaa	ctgatcacat	ggatcacttc	tcccttgagg	tgcttgatgat	tctgctcatg	3600
gtgcaggaag	ggctgaagaa	gagaatgacc	acaaagatca	tcataagcac	atcaatggca	3660
gtgctggtag	ctatgatcct	gggaggattt	tcaatgagtg	acctggctaa	gcttgcaatt	3720
ttgatgggtg	ccaccttcgc	ggaaatgaac	actggaggag	atgtagctca	tctggcgctg	3780
atagcggcat	tcaaagtcag	accagcgttg	ctggtatctt	tcattcttcag	agctaattgg	3840
acaccccgtg	aaagcatgct	gctggccttg	gcctcgtgtc	ttttgcaaac	tgcatctcc	3900
gccttggaag	gcgacctgat	ggttctcatc	aatggttttg	ctttggcctg	gttggaata	3960
cgagcgatgg	ttgttccacg	cactgataac	atcaccttgg	caatcctggc	tgctctgaca	4020
ccactggccc	ggggcacact	gcttgtggcg	tggagagcag	gccttgctac	ttgcgggggg	4080
tttatgctcc	tctctctgaa	gggaaaaggc	agtgtgaaga	agaacttacc	atttgtcatg	4140
gccctgggac	taaccgctgt	gaggctggtc	gaccccatca	acgtgggtggg	gctgctgttg	4200
ctcacaagga	gtgggaagcg	gagctggccc	cctagcgaag	tactcacagc	tggtggcctg	4260
atatgcgcat	tggctggagg	gttcgccaag	gcagatatag	agatggctgg	gcccattggc	4320
gcggtcggtc	tgctaattgt	cagttacgtg	gtctcaggaa	agagtgtgga	catgtacatt	4380
gaaagagcag	gtgacatcac	atgggaaaaa	gatgcggaag	tcactggaaa	cagtccccgg	4440
ctcgatgtgg	cgctagatga	gagtgggtgat	ttctccctgg	tggaggatga	cggtcccccc	4500
atgagagaga	tcataactcaa	ggtggtcctg	atgaccatct	gtggcatgaa	ccaatagcc	4560
ataccctttg	cagctggagc	gtggtacgta	tacgtgaaga	ctggaaaaag	gagtgggtgct	4620

ctatgggatg	tgcttgcctc	caaggaagta	aaaaaggggg	agaccacaga	tggagtgtac	4680
agagtaatga	ctcgtagact	gctaggttca	acacaagttg	gagtgggagt	tatgcaagag	4740
ggggtctttc	acactatgtg	gcacgtcaca	aaaggatccg	cgctgagaag	cggtgaaggg	4800
agacttgatc	catactgggg	agatgtcaag	caggatctgg	tgtcatactg	tgggtccatgg	4860
aagctagatg	ccgcctggga	cgggcacagc	gaggtgcagc	tcttggccgt	gcccccgga	4920
gagagagcga	ggaacatcca	gactctgccc	ggaatatatta	agacaaagga	tggggacatt	4980
ggagcggttg	cgctggatta	cccagcagga	acttcaggat	ctccaatcct	agacaagtgt	5040
gggagagtga	taggacttta	tggcaatggg	gtcgtgatca	aaaatgggag	ttatgttagt	5100
gccatcacc	aagggaggag	ggaggaagag	actcctgttg	agtgccttca	gccttcgatg	5160
ctgaagaaga	agcagctaac	tgtcttagac	ttgcatcctg	gagctgggaa	aaccaggaga	5220
gttcttcttg	aaatagtccg	tgaagccata	aaaacaagac	tccgtactgt	gatcttagct	5280
ccaaccaggg	ttgtcgtg	tgaaatggag	gaagccctta	gagggcttcc	agtgcgttat	5340
atgacaacag	cagtcaatgt	caccactct	ggaacagaaa	tcgtcgactt	aatgtgccat	5400
gccaccttca	cttcacgtct	actacagcca	atcagagtcc	ccaactataa	tctgtatatt	5460
atggatgagg	cccacttcac	agatccctca	agtatagcag	caagaggata	catttcaaca	5520
agggttgaga	tgggagaggc	ggctgccatc	ttcatgaccg	ccacgccacc	aggaaccggt	5580
gacgcatttc	cggactccaa	ctcaccaatt	atggacaccg	aagtggaagt	cccagagaga	5640
gcctggagct	caggctttga	ttgggtgacg	gattattctg	gaaaaacagt	ttggtttggt	5700
ccaagcgtga	ggaacggcaa	tgagatcgca	gcttgtctga	caaaggctgg	aaaacgggtc	5760
atacagctca	gcagaaagac	ttttgagaca	gagttccaga	aaacaaaaca	tcaagagtgg	5820
gactttgtcg	tgacaactga	catttcagag	atgggagcca	actttaagc	tgaccgtgtc	5880
atagattcca	ggagatgcct	aaagccggtc	atacttgatg	gagagagagt	cattctggct	5940
ggacccatgc	ctgtcacaca	tgccagcgct	gccagagga	gggggagcat	aggcaggaat	6000
ccaacaaac	ctggagatga	gtatctgtat	ggaggtgggt	gagcagagac	tgacgaagac	6060
catgcacact	ggcttgaagc	aagaatgctc	cttgacaata	tttacctcca	agatggcctc	6120
atagcctcgc	tctatcgacc	tgaggccgac	aaagtagcag	ccattgaggg	agagttcaag	6180
cttaggacgg	agcaaaggaa	gacctttgtg	gaactcatga	aaagaggaga	tcttctgtt	6240
tggctggcct	atcaggttgc	atctgccgga	ataacctaca	cagatagaag	atggtgcttt	6300
gatggcacga	ccaacaacac	cataatggaa	gacagtgtgc	cggcagaggt	gtggaccaga	6360

cacggagaga	aaagagtgct	caaaccgagg	tggatggacg	ccagagtttg	ttcagatcat	6420
gcggccctga	agtcattcaa	ggagtttgcc	gctgggaaaa	gaggagcggc	ttttggagtg	6480
atggaagccc	tgggaacact	gccaggacac	atgacagaga	gattccagga	agccattgac	6540
aacctcgctg	tgctcatgcg	ggcagagact	ggaagcaggc	cttaciaaagc	cgcggcggcc	6600
caattgccgg	agaccctaga	gaccattatg	cttttggggt	tgctgggaac	agtctcgctg	6660
ggaatctttt	tcgtcttgat	gaggaacaag	ggcataggga	agatgggctt	tggaatggtg	6720
actcttgggg	ccagcgcgatg	gctcatgtgg	ctctcggaaa	ttgagccagc	cagaattgca	6780
tgtgtcctca	ttgttgtggt	cctattgctg	gtgggtgctca	tacctgagcc	agaaaagcaa	6840
agatctcccc	aggacaacca	aatggcaatc	atcatcatgg	tagcagtagg	tcttctgggc	6900
ttgattaccg	ccaatgaact	cggatgggtg	gagagaacaa	agagtgacct	aagccatcta	6960
atgggaagga	gagaggaggg	ggcaaccatg	ggattctcaa	tggacattga	cctgcggcca	7020
gcctcagctt	gggccatcta	tgctgccttg	acaactttca	ttaccccagc	cgtccaacat	7080
gcagtgacca	cttcatacaa	caactactcc	ttaatggcga	tggccacgca	agctggagtg	7140
ttgtttggta	tgggcaaagg	gatgccattc	tacgcatggg	actttggagt	cccgctgcta	7200
atgatagggt	gctactcaca	attaacgccc	ctgaccctaa	tagtggccat	cattttgctc	7260
gtggcgcact	acatgtactt	gatcccaggg	ctgcaggcag	cagctgcgcg	tgctgccag	7320
aagagaacgg	cagctggcat	catgaagaac	cctgttgtgg	atggaatagt	ggtgactgac	7380
attgacacaa	tgacaattga	cccccaagtg	gagaaaaaga	tgggacaggt	gctactcatg	7440
gcagtagccg	tctccagcgc	catactgtcg	cggaccgcct	gggggtgggg	ggaggctggg	7500
gccctgatca	cagccgcaac	ttccactttg	tgggaaggct	ctccgaacaa	gtactggaac	7560
tcctctacag	ccacttcact	gtgtaacatt	tttaggggaa	gttacttggc	tggagcttct	7620
ctaactctaca	cagtaacaag	aaacgctggc	ttggtcaaga	gacgtggggg	tggaacagga	7680
gagaccctgg	gagagaaatg	gaaggcccg	ttgaaccaga	tgtcggccct	ggagttctac	7740
tcctacaaaa	agtcaggcat	caccgagggt	tgcagagaag	aggcccgcgc	cgcctcaag	7800
gacggtgtgg	caacgggagg	ccatgctgtg	tcccagggaa	gtgcaaagct	gagatggttg	7860
gtggagcggg	gataacctga	gccctatgga	aaggtcattg	atcttggatg	tggcagaggg	7920
ggctggagtt	actacgccgc	caccatccgc	aaagttcaag	aagtgaaagg	atacacaaaa	7980
ggaggccctg	gtcatgaaga	accctgtgtg	gtgcaaagct	atgggtggaa	catagtccgt	8040
cttaagagtg	gggtggacgt	ctttcatatg	gcggctgagc	cgtgtgacac	gttgctgtgt	8100

gacataggtg agtcatcatc tagtcctgaa gtggaagaag cacggacgct cagagtcctc	8160
tccatggtgg gggattggct tgaaaaaaga ccaggagcct tttgtataaa agtgttgtgc	8220
ccatacacca gcactatgat ggaaaccctg gagcgactgc agcgtaggta tgggggagga	8280
ctggtcagag tgccactctc ccgcaactct acacatgaga tgtactgggt ctctggagcg	8340
aaaagcaaca ccataaaaag tgtgtccacc acgagccagc tcctcttggg gcgcatggac	8400
gggcctagga ggccagtga atatgaggag gatgtgaatc tcggctcttg cacgcgggct	8460
gtggtaaagct gcgctgaagc tccaacatg aagatcattg gtaaccgcat tgaaaggatc	8520
cgcagtgagc acgcggaaac gtggttcttt gacgagaacc acccatatag gacatgggct	8580
taccatggaa gctatgaggc cccacacaa gggtcagcgt cctctctaataaacgggggtt	8640
gtcaggctcc tgtcaaaacc ctgggatgtg gtgactggag tcacaggaat agccatgacc	8700
gacaccacac cgtatggtca gcaaagagtt ttcaaggaaa aagtggacac tagggtgcca	8760
gacccccaag aaggcactcg tcaggttatg agcatggtct cttcctgggt gtggaaagag	8820
ctaggcaaac acaaacggcc acgagtctgt accaaagaag agttcatcaa caaggttcgt	8880
agcaatgcag cattaggggc aatatttgaa gaggaaaaag agtggaagac tgcagtggaa	8940
gctgtgaacg atccaagggt ctgggctcta gtggacaagg aaagagagca ccacctgaga	9000
ggagagtgcc agagttgtgt gtacaacatg atgggaaaaa gagaaaagaa acaaggggaa	9060
tttgaaaagg ccaagggcag ccgcgccatc tggatatatg ggctaggggc tagatttcta	9120
gagttcgaag cccttggtt cttgaacgag gatcactgga tggggagaga gaactcagga	9180
ggtggtgttg aagggtctgg attacaaaga ctcggatatg tcctagaaga gatgagtcgc	9240
ataccaggag gaaggatgta tgcagatgac actgctggct gggacacccg catcagcagg	9300
tttgatctgg agaatgaagc tctaatacacc aaccaaattg agaaagggca cagggccttg	9360
gcattggcca taatcaagta cacataccaa acaaagtgg taaaggctcct tagaccagct	9420
gaaaaaggga agacagttat ggacattatt tcgagacaag accaaagggg gagcggacaa	9480
gttgtcactt acgctcttaa cacatttacc aacctagtgg tgcaactcat tcggaatatg	9540
gaggctgagg aagttctaga gatgcaagac ttgtggctgc tgcggagggtc agagaaagtg	9600
accaactggt tgcagagcaa cggatgggat aggtcaaac gaatggcagt cagtggagat	9660
gattgcgttg tgaagccaat tgatgatagg tttgcacatg ccctcagggt cttgaatgat	9720
atgggaaaag ttaggaagga cacacaagag tggaaaccct caactggatg ggacaactgg	9780
gaagaagttc cgttttgctc ccaccacttc aacaagctcc atctcaagga cgggaggtcc	9840

attgtggttc cctgccgcca ccaagatgaa ctgattggcc gggcccgcgt ctctccaggg	9900
gcgggatgga gcatccggga gactgcttgc ctagcaaaat catatgcgca aatgtggcag	9960
ctcctttatt tccacagaag ggacctccga ctgatggcca atgccatttg ttcattctgtg	10020
ccagttgact gggttccaac tgggagaact acctgggtcaa tccatggaaa gggagaatgg	10080
atgaccactg aagacatgct tgtggtgtgg aacagagtgt ggattgagga gaacgaccac	10140
atggaagaca agaccccagt tacgaaatgg acagacattc cctatttggg aaaaaggga	10200
gacttgtggt gtggatctct catagggcac agaccgcgca ccacctgggc tgagaacatt	10260
aaaaacacag tcaacatggg gcgcaggatc ataggtgatg aagaaaagta catggactac	10320
ctatccaccc aagttcgcta cttgggtgaa gaagggtcta cacctggagt gctgtaagca	10380
ccaatcttaa tggtgtcagg cctgctagtc agccacagct tggggaaagc tgtgcagcct	10440
gtgaccccc caggagaagc tgggaaacca agcctatagt caggccgaga acgcatggc	10500
acggaagaag ccatgctgcc tgtgagcccc tcagaggaca ctgagtcaaa aaacccacg	10560
cgcttggagg cgcaggatgg gaaaagaagg tggcgacctt cccaccctt caatctggg	10620
cctgaactgg agatcagctg tggatctcca gaagagggac tagtggttag aggaga	10676

<210> 5
 <211> 10675
 <212> DNA
 <213> Zika virus strain PRVABC59

<400> 5	
gttgttgatc tgtgtgaatc agactgcgac agttcgagtt tgaagcgaaa gctagcaaca	60
gtatcaacag gttttatattt ggatttggaa acgagagttt ctgggtcatga aaaacccaaa	120
aaagaaatcc ggaggattcc ggattgtcaa tatgctaaaa cgcgagtag cccgtgtgag	180
cccctttggg ggcttgaaga ggctgccagc cggacttctg ctgggtcatg ggcccatcag	240
gatggtcttg gcgattctag cttttttgag attcacggca atcaagccat cactgggtct	300
catcaataga tggggttcag tggggaaaaa agaggctatg gaaacaataa agaagttcaa	360
gaaagatctg gctgccatgc tgagaataat caatgctagg aaggagaaga agagacgagg	420
cgcagatact agtgtcggaa ttgttggcct cctgctgacc acagctatgg cagcggaggt	480
cactagacgt gggagtgcac actatatgta cttggacaga aacgatgctg gggaggccat	540
atcttttcca accacattgg ggatgaataa gtgttatata cagatcatgg atcttggaca	600
catgtgtgat gccaccatga gctatgaatg ccctatgctg gatgaggggg tggaaccaga	660
tgacgtcgat tgttggtgca acacgacgtc aacttgggtt gtgtacggaa cctgccatca	720

caaaaaaggt gaagcacgga gatctagaag agctgtgacg ctccccctccc attccaccag	780
gaagctgcaa acgcgggtcgc aaacctgggtt ggaatcaaga gaatacacaa agcacttgat	840
tagagtcgaa aattggatat tcaggaaccc tggcttcgcg ttagcagcag ctgccatcgc	900
ttggcttttg ggaagctcaa cgagccaaaa agtcatatac ttgggtcatga tactgtctgat	960
tgccccggca tacagcatca ggtgcatagg agtcagcaat agggactttg tggaaggtat	1020
gtcaggtggg acttgggttg atgttgtctt ggaacatgga ggttgtgtca ccgtaatggc	1080
acaggacaaa ccgactgtcg acatagagct gggtacaaca acagtcagca acatggcgga	1140
ggtaagatcc tactgtctatg aggcattcaat atcagacatg gcttctgaca gccgctgcc	1200
aacacaaggt gaagcctacc ttgacaagca atcagacact caatatgtct gcaaaagaac	1260
gttagtggac agaggctggg gaaatggatg tggacttttt ggcaaaggga gcctggtgac	1320
atgcgctaag tttgcatgct ccaagaaaat gaccgggaag agcatccagc cagagaatct	1380
ggagtaccgg ataatgctgt cagttcatgg ctcccagcac agtgggatga tcgttaatga	1440
cacaggacat gaaactgatg agaatagagc gaaagttgag ataacgcca attcaccgag	1500
agccgaagcc accctggggg gttttggaag cctaggactt gattgtgaac cgaggacagg	1560
ccttgacttt tcagatttgt attacttgac tatgaataac aagcactggg ttggttcacaa	1620
ggagtgggtc cacgacattc cattaccttg gcacgctggg gcagacaccg gaactccaca	1680
ctggaacaac aaagaagcac tggtagagtt caaggacgca catgccaaaa ggcaaactgt	1740
cgtggttcta gggagtcaag aaggagcagt tcacacggcc cttgctggag ctctggaggc	1800
tgagatggat ggtgcaaagg gaaggctgtc ctctggccac ttgaaatgtc gcctgaaaat	1860
ggataaactt agattgaagg gcgtgtcata ctcccttgtgt actgcagcgt tcacattcac	1920
caagatcccc gctgaaacac tgcacgggac agtcacagtg gaggtacagt acgcagggac	1980
agatggacct tgcaaggttc cagctcagat ggcggtggac atgcaaactc tgaccccagt	2040
tgggaggttg ataaccgcta accccgtaat cactgaaagc actgagaact ctaagatgat	2100
gctggaactt gatccaccat ttggggactc ttacattgtc ataggagtcg gggagaagaa	2160
gatcaccac cactggcaca ggagtggcag caccattgga aaagcatttg aagccactgt	2220
gagaggtgcc aagagaatgg cagtcttggg agacacagcc tgggactttg gatcagttgg	2280
aggcgctctc aactcatttg gcaagggcat ccatcaaatt tttggagcag ctttcaaatc	2340
attgtttgga ggaatgtcct ggttctcaca aattctcatt ggaacgttgc tgatgtggtt	2400
gggtctgaac acaaagaatg gatctatttc ccttatgtgc ttggccttag ggggagtgtt	2460

gatcttctta tccacagccg tctctgctga tgtgggggtgc tcggtggact tctcaaagaa	2520
ggagacgaga tgcggtacag ggggtgttcgt ctataacgac gttgaagcct ggagggacag	2580
gtacaagtac catcctgact cccccgtag attggcagca gcagtcaagc aagcctggga	2640
agatggatc tgcgggatct cctctgtttc aagaatggaa aacatcatgt ggagatcagt	2700
agaaggggag ctcaacgcaa tcctggaaga gaatggagtt caactgacgg tcgttgtggg	2760
atctgtaaaa aaccccatgt ggagaggtcc acagagattg cccgtgcctg tgaacgagct	2820
gccccacggc tggaaggctt gggggaaatc gtatttcgtc agagcagcaa agacaaataa	2880
cagctttgtc gtggatgggtg acacactgaa ggaatgccca ctcaaacata gagcatggaa	2940
cagctttctt gtggaggatc atgggttcgg ggtatttcac actagtgtct ggctcaaggt	3000
tagagaagat tattcattag agtgtgatcc agccgttatt ggaacagctg ttaagggaaa	3060
ggaggctgta cacagtgatc taggctactg gattgagagt gagaagaatg acacatggag	3120
gctgaagagg gcccatctga tcgagatgaa aacatgtgaa tggccaaagt cccacacatt	3180
gtggacagat ggaatagaag agagtgatct gatcataccc aagtcttttag ctgggccact	3240
cagccatcac aataccagag agggctacag gacccaaatg aaagggccat ggcacagtga	3300
agagcttgaa attcggtttg aggaatgccc aggcactaag gtccacgtgg aggaaacatg	3360
tggaacaaga ggaccatctc tgagatcaac cactgcaagc ggaaggggtga tcgaggaatg	3420
gtgctgcagg gagtgcacaa tgccccact gtcgttccgg gctaaagatg gctgttggtg	3480
tggaatggag ataaggccca ggaaagaacc agaaagcaac ttagtaaggt caatggtgac	3540
tgcaggatca actgatcaca tggaccactt ctcccttgga gtgcttgtga tcctgctcat	3600
ggtgcaggaa gggctgaaga agagaatgac cacaagatc atcataagca catcaatggc	3660
agtgtgtgta gctatgatcc tgggaggatt ttcaatgagt gacctggcta agcttgcaat	3720
tttgatgggt gccaccttcg cggaatgaa cactggagga gatgtagctc atctggcgct	3780
gatagcggca ttcaaagtca gaccagcgtt gctggtatct ttcattctca gagctaattg	3840
gacaccccg taaagcatgc tgctggcctt ggcctcgtgt cttttgcaaa ctgcatctc	3900
cgccttgga ggcgacctga tggttctcat caatggtttt gctttggcct ggttggcaat	3960
acgagcgatg gttgttccac gactgataa catcaccttg gcaatcctgg ctgctctgac	4020
accactggcc cggggcacac tgcttgtggc gtggagagca ggccttgcta cttgcggggg	4080
gtttatgtc ctctctctga agggaaaagg cagtgtgaag aagaacttac catttgtcat	4140
ggccctggga ctaaccgctg tgaggctggc cgaccccatc aacgtgggtg gactgctgtt	4200

gctcacaagg agtgggaagc ggagctggcc ccctagcgaa gtactcacag ctgttggcct	4260
gatatgcgca ttggctggag ggttcgccaa ggcagatata gagatggctg ggcccatggc	4320
cgcggtcgggt ctgctaattg tcagttacgt ggtctcagga aagagtgtgg acatgtacat	4380
tgaaagagca ggtgacatca catgggaaaa agatgcggaa gtcactggaa acagtccccg	4440
gctcgatgtg gcgctagatg agagtggatg tttctccctg gtggaggatg acggtcccc	4500
catgagagag atcatactca aggtggctct gatgaccatc tgtggcatga acccaatagc	4560
catacccttt gcagctggag cgtggtagct atacgtgaag actggaaaaa ggagtggatgc	4620
tctatgggat gtgcctgctc ccaaggaagt aaaaaagggg gagaccacag atggagtgtg	4680
cagagtaatg actcgtagac tgctaggttc aacacaagtt ggagtgggag ttatgcaaga	4740
gggggtcttt cacactatgt ggcacgtcac aaaaggatcc gcgctgagaa gcggtgaagg	4800
gagacttgat ccatactggg gagatgtcaa gcaggatctg gtgtcatact gtggtccatg	4860
gaagctagat gccgcctggg atgggcacag cgaggtgcag ctcttggccg tgccccccg	4920
agagagagcg aggaacatcc agactctgcc cggaatatct aagacaaagg atggggacat	4980
tggagcgggt gcgctggatt acccagcagg aacttcagga tctccaatcc tagacaagtg	5040
tgggagagtg ataggacttt atggcaatgg ggtcgtgatc aaaaacggga gttatgttag	5100
tgccatcacc caaggagga gggaggaaga gactcctgtt gagtgcttcg agccctcgat	5160
gctgaagaag aagcagctaa ctgtcttaga cttgcatcct ggagctggga aaaccaggag	5220
agttcttcct gaaatagtcc gtgaagccat aaaaacaaga ctccgtactg tgatcttagc	5280
tccaaccagg gttgtcgctg ctgaaatgga ggaggccctt agagggttc cagtgcgtta	5340
tatgacaaca gcagtcaatg tcacccactc tggaacagaa atcgtcgact taatgtgcca	5400
tgccaccttc acttcacgtc tactacagcc aatcagagtc cccaactata atctgtatat	5460
tatggatgag gcccaactca cagatccctc aagtatagca gcaagaggat acatttcaac	5520
aagggttgag atgggcgagg cggtcgccat cttcatgacc gccacgccac caggaacccg	5580
tgacgcattt ccggactcca actcaccaat tatggacacc gaagtggaag tccagagag	5640
agcctggagc tcaggctttg attgggtgac ggatcattct ggaaaaacag tttggtttgt	5700
tccaagcgtg aggaacggca atgagatcgc agcttgtctg acaaaggctg gaaaacgggt	5760
catacagctc agcagaaaaga cttttgagac agagttccag aaaacaaaac atcaagagtg	5820
ggactttgtc gtgacaactg acatttcaga gatgggcgcc aactttaaag ctgaccgtgt	5880
catagattcc aggagatgcc taaagccggt catacttgat ggcgagagag tcattctggc	5940

tggacccatg cctgtcacac atgccagcgc tgcccagagg agggggcgca taggcaggaa	6000
tcccaacaaa cctggagatg agtatctgta tggagggtggg tgcgcgagaga ctgacgaaga	6060
ccatgcacac tggcttgaag caagaatgct ccttgacaat atttacctcc aagatggcct	6120
catagcctcg ctctatcgac ctgaggccga caaagtagca gccattgagg gagagttcaa	6180
gcttaggacg gagcaaagga agacctttgt ggaactcatg aaaagaggag atcttcctgt	6240
ttggctggcc tatcaggttg catctgccgg aataacctac acagatagaa gatgggtgctt	6300
tgatggcacg accaacaaca ccataatgga agacagtgtg ccggcagagg tgtggaccag	6360
acacggagag aaaagagtgc tcaaaccgag gtggatggac gccagagttt gttcagatca	6420
tgcggccctg aagtcattca aggagtttgc cgctgggaaa agaggagcgg cttttggagt	6480
gatggaagcc ctgggaacac tgccaggaca catgacagag agattccagg aagccattga	6540
caacctcgct gtgctcatgc gggcagagac tggaagcagg ccttaciaag ccgcggcggc	6600
ccaattgccg gagaccctag agaccataat gcttttgggg ttgctgggaa cagtctcgct	6660
gggaatcttc ttcgtcttga tgaggaacaa gggcataggg aagatgggct ttggaatggt	6720
gactcttggg gccagcgcat ggctcatgtg gctctcggaa attgagccag ccagaattgc	6780
atgtgtcctc attgtttgtg tcctattgct ggtggtgctc atacctgagc cagaaaagca	6840
aagatctccc caggacaacc aaatggcaat catcatcatg gtagcagtag gtcttctggg	6900
cttgattacc gccaatgaac tcggatgggt ggagagaaca aagagtgacc taagccatct	6960
aatgggaagg agagaggagg gggcaaccat aggattctca atggacattg acctgcggcc	7020
agcctcagct tgggccatct atgctgcctt gacaactttc attaccccag ccgtccaaca	7080
tgcaagtacc acctataca acaactactc cttaatggcg atggccacgc aagctggagt	7140
gttgtttggc atgggcaaag ggatgccatt ctacgcatgg gactttggag tcccgtgct	7200
aatgataggt tgctactcac aattaacacc cctgacccta atagtggcca tcattttgct	7260
cgtggcgcac tacatgtact tgatcccagg gctgcaggca gcagctgcgc gtgctgcca	7320
gaagagaacg gcagctggca tcatgaagaa ccctgttgtg gatggaatag tggtgactga	7380
cattgacaca atgacaattg accccaagt ggagaaaaag atgggacagg tgctactcat	7440
agcagtagcc gtctccagcg ccatactgtc gcggaccgcc tgggggtggg gggaggctgg	7500
ggctctgatc acagccgcaa cttccacttt gtgggaaggc tctccgaaca agtactggaa	7560
ctcctctaca gccacttcac tgtgtaacat ttttagggga agttacttgg ctggagcttc	7620
tctaacttac acagtaacaa gaaacgtgg cttggtcaag agacgtgggg gtggaacagg	7680

agagaccctg	ggagagaaat	ggaaggcccg	cttgaaccag	atgtcggccc	tggagtctta	7740
ctcctacaaa	aagtcaggca	tcaccgaggt	gtgcagagaa	gaggcccgcc	gcgcctcaa	7800
ggacggtgtg	gcaacgggag	gccatgctgt	gtcccagga	agtgcaaagc	tgagatggtt	7860
ggtggagcgg	ggatacctgc	agccctatgg	aaagggtcatt	gatcttggat	gtggcagagg	7920
gggctggagt	tactacgtcg	ccaccatccg	caaagttcaa	gaagtgaaag	gatacacaaa	7980
aggaggccct	ggtcatgaag	aaccctgtgt	ggtgcaaagc	tatgggtgga	acatagtccg	8040
tcttaagagt	ggggtggacg	tctttcatat	ggcggctgag	ccgtgtgaca	cgttgctgtg	8100
tgacataggt	gagtcatcat	ctagtcttga	agtggaagaa	gcacggacgc	tcagagtcct	8160
ctccatggtg	ggggattggc	ttgaaaaaag	accaggagcc	ttttgtataa	aagtgttgtg	8220
cccatacacc	agcactatga	tggaaacctt	ggagcgactg	cagcgtaggt	atgggggagg	8280
actggtcaga	gtgccactct	cccgcaactc	tacacatgag	atgtactggg	tctctggagc	8340
gaaaagcaac	accataaaaa	gtgtgtccac	cacgagccag	ctcctcttgg	ggcgcattga	8400
cgggcctagg	aggccagtga	aatatgagga	ggatgtgaat	ctcggctctg	gcacgcgggc	8460
tgttgtaagc	tgcgctgaag	ctcccaacat	gaagatcatt	ggtaaccgca	ttgaaaggat	8520
ccgcagtgag	cacgcggaaa	cgtggttctt	tgacgagaac	cacccatata	ggacatgggc	8580
ttaccatgga	agctatgagg	ccccacaca	agggtcagcg	tcctctctaa	taaacggggt	8640
tgtcaggctc	ctgtcaaaac	cctgggatgt	ggtgactgga	gtcacaggaa	tagccatgac	8700
cgacaccaca	ccgtatggtc	agcaaagagt	tttcaaggaa	aaagtggaca	ctaggggtgcc	8760
agacccccaa	gaaggcactc	gtcaggttat	gagcatggtc	tcttctctgg	tgtggaaaga	8820
gctaggcaaa	cacaaacggc	cacgagtctg	caccaaagaa	gagttcatca	acaaggttcg	8880
tagcaatgca	gcattagggg	caatatttga	agaggaaaaa	gagtgggaaga	ctgcagtgga	8940
agctgtgaac	gatccaaggt	tctgggctct	agtggacaag	gaaagagagc	accacctgag	9000
aggagagtgc	cagagctgtg	tgtacaacat	gatgggaaaa	agagaaaaga	aacaagggga	9060
atttgaaaag	gccaaaggga	gccgcgccat	ctggtatatg	tggctagggg	ctagatttct	9120
agagttcgaa	gcccttggat	tcttgaacga	ggatcactgg	atggggagag	agaactcagg	9180
aggtggtgtt	gaagggtctg	gattacaaag	actcggatat	gtcctagaag	agatgagtcg	9240
tataccagga	ggaaggatgt	atgcagatga	cactgctggc	tgggacaccc	gcattagcag	9300
gtttgatctg	gagaatgaag	ctctaatac	caaccaaagt	gagaaagggc	acagggcctt	9360
ggcattggcc	ataatcaagt	acacatacca	aaacaaagtg	gtaaagggtcc	ttagaccagc	9420

tgaaaaaggg aaaacagtta tggacattat ttcgagacaa gaccaaaggg ggagcggaca	9480
agttgtcact tacgctctta acacatttac caacctagtgtgtgcaactca ttcggaatat	9540
ggaggctgag gaagttctag agatgcaaga cttgtggctg ctgaggaggt cagagaaagt	9600
gaccaactgg ttgcagagca acggatggga taggctcaaa cgaatggcag tcagtggaga	9660
tgattgcgtt gtgaagccaa ttgatgatag gtttgcacat gccctcaggt tcttgaatga	9720
tatgggaaaa gttaggaagg acacacaaga gtggaaaccc tcaactggat gggacaactg	9780
ggaagaagtt ccgttttgct cccaccactt caacaagctc catctcaagg acgggaggtc	9840
cattgtggtt ccctgccgcc accaagatga actgattggc cgggcccgcg tctctccagg	9900
ggcgggatgg agcatccggg agactgcttg cctagcaaaa tcatatgcgc aaatgtggca	9960
gctcctttat ttccacagaa gggacctccg actgatggcc aatgccattt gttcatctgt	10020
gccagttgac tgggttccaa ctgggagaac tacctggtca atccatggaa agggagaatg	10080
gatgaccact gaagacatgc ttgtggtgtg gaacagagtgtggattgagg agaacgacca	10140
catggaagac aagaccccag ttacgaaatg gacagacatt ccctatttgg gaaaaaggga	10200
agacttgtgg tgtggatctc tcatagggca cagaccgcgc accacctggg ctgagaacat	10260
taaaaacaca gtcaacatgg tgcgcaggat cataggtgat gaagaaaagt acatggacta	10320
cctatccacc caagttcgct acttgggtga agaaggtct acacctggag tgctgtaagc	10380
accaatctta atgttgtcag gcctgctagt cagccacagc ttggggaaaag ctgtgcagcc	10440
tgtgaccccc ccaggagaag ctgggaaacc aagcctatag tcaggccgag aacgccatgg	10500
cacggaagaa gccatgctgc ctgtgagccc ctcagaggac actgagtcaa aaaacccac	10560
gcgcttgag gcgcaggatg ggaaaagaag gtggcgacct tccccacct tcaatctggg	10620
gcctgaactg gagatcagct gtggatctcc agaagaggga ctagtgggta gagga	10675

<210> 6
 <211> 10807
 <212> DNA
 <213> Zika virus genomic RNA, complete genome, strain: MR766-NIID

<400> 6	
agttgttgat ctgtgtgagt cagactgcga cagttcgagt ctgaagcgag agctaacaac	60
agtatcaaca ggtttaattt ggatttgga acgagagttt ctggatcatga aaaacccaaa	120
gaagaaatcc ggaggattcc ggattgtcaa tatgctaaaa cgcggagtag cccgtgtaaa	180
ccccttgga ggtttgaaga ggttgccagc cggacttctg ctgggtcatg gacccatcag	240

aatggttttg gcgatactag cctttttgag atttacagca atcaagccat cactgggcct	300
tatcaacaga tggggttccg tggggaaaaa agaggctatg gaaataataa agaagttcaa	360
gaaagatctt gctgccatgt tgagaataat caatgctagg aaagagagga agagacgtgg	420
cgcagacacc agcatcggaa tcattggcct cctgctgact acagccatgg cagcagagat	480
cactagacgc gggagtgcac actacatgta cttggatagg agcgatgccg ggaaggccat	540
ttcgtttgct accacattgg gagtgaacaa gtgccacgta cagatcatgg acctcgggca	600
catgtgtgac gccaccatga gttatgagtg ccctatgctg gatgagggag tggaaccaga	660
tgatgtcgat tgctgggtgca acacgacatc aacttgggtt gtgtacggaa cctgtcatca	720
caaaaaaggt gaggcacggc gatctagaag agccgtgacg ctcccttctc actctacaag	780
gaagttgcaa acgcgggtcgc agacctgggtt agaatcaaga gaatacacga agcacttgat	840
caaggttgaa aactggatat tcaggaaccc cgggtttgcg ctagtggccg ttgccattgc	900
ctggcttttg ggaagctcga cgagccaaaa agtcatatac ttgggtcatga tactgctgat	960
tgccccggca tacagtatca ggtgcattgg agtcagcaat agagacttcg tggagggcat	1020
gtcaggtggg acctgggttg atgttgtctt ggaacatgga ggctgcgtta ccgtgatggc	1080
acaggacaag ccaacagttg acatagagtt ggtcacgacg acggttagta acatggccga	1140
ggtaagatcc tattgctacg aggcacgat atcggacatg gcttcggaca gtcgttgccc	1200
aacacaaggt gaagcctacc ttgacaagca atcagacact caatatgtct gcaaaagaac	1260
attagtggac agaggttggg gaaacggttg tggacttttt ggcaaaggga gcttggtgac	1320
atgtgccaag ttacgtgtt ctaagaagat gaccgggaag agcattcaac cggaaaatct	1380
ggagtatcgg ataatgctat cagtgcattg ctcccagcat agcgggatga ctgtcaatga	1440
tataggatat gaaactgacg aaaatagagc gaaagtcgag gttacgccta attcaccaag	1500
agcggaagca accttgggag gctttggaag cttaggactt gactgtgaac caaggacagg	1560
ccttgacttt tcagatctgt attacctgac catgaacaat aagcattggg ttgtgcacaa	1620
agagtggttt catgacatcc cattgccttg gcatgctggg gcagacactg gaactccaca	1680
ctggaacaac aaagaggcat tggtagaatt caaggatgcc cacgccaaga ggcaaaccgt	1740
cgtcgttctg gggagccagg aaggagccgt tcacacggct ctcgctggag ctctagaggc	1800
tgagatggat ggtgcaaagg gaaagctgtt ctctggccat ttgaaatgcc gcctaaaaat	1860
ggacaagctt agattgaagg gcgtgtcata ttccttgtgc actgcggcat tcacattcac	1920
caaggtccca gctgaaacac tgcattggaac agtcacagtg gaggtgcagt atgcagggac	1980

agatggaccc	tgcaagatcc	cagtccagat	ggcgggtggac	atgcagaccc	tgaccccgagt	2040
tggaaggctg	ataaccgcca	accccgtgat	tactgaaagc	actgagaact	caaagatgat	2100
gttggagctt	gacccaccat	ttggggattc	ttacattgtc	ataggagttg	gggacaagaa	2160
aatcaccac	cactggcata	ggagtggtag	caccatcgga	aaggcatttg	aggccactgt	2220
gagaggcgcc	aagagaatgg	cagtcctggg	ggatacagcc	tgggacttcg	gatcagtcgg	2280
gggtgtgttc	aactcactgg	gtaagggcat	tcaccagatt	tttgagcag	ccttcaaate	2340
actgtttgga	ggaatgtcct	ggttctcaca	gatcctcata	ggcacgctgc	tagtgtgggt	2400
aggtttgaac	acaagaatg	gatctatctc	cctcacatgc	ttggccctgg	ggggagtgat	2460
gatcttcctc	tccacggctg	tttctgctga	cgtggggtgc	tcagtggact	tctcaaaaaa	2520
ggaaacgaga	tgtggcacgg	gggtattcat	ctataatgat	gttgaagcct	ggagggaccg	2580
gtacaagtac	catcctgact	ccccccgcag	attggcagca	gcagtcaagc	aggcctggga	2640
agaggggatc	tgtgggatct	catccgtttc	aagaatggaa	aacatcatgt	ggaaatcagt	2700
agaaggggag	ctcaatgcta	tcctagagga	gaatggagtt	caactgacag	ttgttgtggg	2760
atctgtaaaa	aaccccatgt	ggagagggtc	acaaagattg	ccagtgcctg	tgaatgagct	2820
gccccatggc	tggaagcct	gggggaaatc	gtattttgtt	agggcgga	agaccaacaa	2880
cagttttgtt	gtcgacggtg	acacactgaa	ggaatgtccg	cttgagcaca	gagcatggaa	2940
tagttttctt	gtggaggatc	acgggtttgg	agtcttcac	accagtgtct	ggcttaaggt	3000
cagagaagat	tactcattag	aatgtgaccc	agccgtcata	ggaacagctg	ttaagggaag	3060
ggaggccg	cacagtgatc	tgggctattg	gattgaaagt	gaaaagaatg	acacatggag	3120
gctgaagagg	gcccacctga	ttgagatgaa	aacatgtgaa	tggccaaagt	ctcacacatt	3180
gtggacagat	ggagtagaag	aaagtgatct	tatcataccc	aagtcttttag	ctggtccact	3240
cagccaccac	aacaccagag	agggttacag	aaccaagtg	aaagggccat	ggcacagtga	3300
agagcttgaa	atccggtttg	aggaatgtcc	aggcaccaag	gtttacgtgg	aggagacatg	3360
cggaactaga	ggaccatctc	tgagatcaac	tactgcaagt	ggaaggggtca	ttgaggaatg	3420
gtgctgtagg	gaatgcacaa	tgccccact	atcgtttcga	gcaaaagacg	gctgctggta	3480
tggaatggag	ataaggccca	ggaaagaacc	agagagcaac	ttagtgaggt	caatggtgac	3540
agcgggggtca	accgatcata	tggaccactt	ctctcttgga	gtgcttgtga	ttctactcat	3600
ggtgcaggag	gggttgaaga	agagaatgac	cacaaagatc	atcatgagca	catcaatggc	3660
agtgctggta	gtcatgatct	tgggaggatt	ttcaatgagt	gacctggcca	agcttgtgat	3720

cctgatgggt gctactttcg cagaaatgaa cactggagga gatgtagctc acttggcatt	3780
ggtagcggca tttaaagtca gaccagcctt gctgggtctcc ttcattttca gagccaattg	3840
gacaccccgt gagagcatgc tgctagccct ggcttcgtgt cttctgcaaa ctgcgatctc	3900
tgctcttgaa ggtgacttga tggtcctcat taatggattt gctttggcct ggttggcaat	3960
tcgagcaatg gccgtgccac gcactgacaa catcgctcta ccaatcttgg ctgctctaac	4020
accactagct cgaggcacac tgctcgtggc atggagagcg ggccctggcta cttgtggagg	4080
gatcatgctc ctctccctga aagggaaagg tagtgtgaag aagaacctgc catttgtcat	4140
ggccctggga ttgacagctg tgagggtagt agaccctatt aatgtggtag gactactgtt	4200
actcacaagg agtgggaagc ggagctggcc ccctagtga gttctcacag ccgttggcct	4260
gatatgtgca ctggccggag ggtttgccaa ggcagacatt gagatggctg gacccatggc	4320
tgcaagtaggc ttgctaattg tcagctatgt ggtctcggga aagagtgtgg acatgtacat	4380
tgaaagagca ggtgacatca catgggaaaa ggacgcggaa gtcactggaa acagtccctc	4440
gcttgacgtg gcactggatg agagtggtag tttctccttg gtagaggaag atggtccacc	4500
catgagagag atcataactta aggtggctct gatggccatc tgtggcatga acccaatagc	4560
tatacctttt gctgcaggag cgtgggtatgt gtatgtgaag actgggaaaa ggagtggcgc	4620
cctctgggac gtgcctgctc ccaaagaagt gaagaaagga gagaccacag atggagtgtg	4680
cagagtgatg actcgcagac tgctaggttc aacacagggt ggagtgggag tcatgcaaga	4740
gggagtcttc cacaccatgt ggcacgttac aaaaggagcc gcactgagga gcggtgaggg	4800
aagacttgat ccatactggg gggatgtcaa gcaggacttg gtgtcatact gtgggccttg	4860
gaagttggat gcagcttggg atggactcag cgaggtagag cttttggccg tacctcccgg	4920
agagagggcc agaaacattc agaccctgcc tggaaatattc aagacaaagg acggggacat	4980
cggagcagtt gctctggact accctgcagg gacctcagga tctccgatcc tagacaaatg	5040
tggaagagtg ataggactct atggcaatgg ggttgtgatc aagaatggaa gctatgttag	5100
tgctataacc cagggaaaga gggaggagga gactccggtt gaatgtttcg aaccctcgat	5160
gctgaagaag aagcagctaa ctgtcttgga tctgcatcca ggagccggaa aaaccaggag	5220
agttcttcct gaaatagtcc gtgaagccat aaaaaagaga ctccggacag tgatcttggc	5280
accaactagg gttgtcgctg ctgagatgga ggaggccttg agaggacttc cgggtgcgtta	5340
catgacaaca gcagtcaacg tcacccattc tgggacagaa atcgttgatt tgatgtgcca	5400
tgccactttc acttcacgct tactacaacc catcagagtc cctaattaca atctctacat	5460

catggatgaa gcccacttca cagacccctc aagtatagct gcaagaggat atatatcaac	5520
aagggttgaa atgggcgagg cggctgccat ttttatgact gccacaccac caggaacccg	5580
tgatgcgttt cctgactcta actcaccaat catggacaca gaagtggaag tcccagagag	5640
agcctggagc tcaggctttg attgggtgac agaccattct gggaaaacag tttggttcgt	5700
tccaagcgtg agaaacggaa atgaaatcgc agcctgtctg acaaaggctg gaaagcgggt	5760
catacagctc agcaggaaga cttttgagac agaatttcag aaaacaaaaa atcaagagt	5820
ggactttgtc ataacaactg acatctcaga gatgggcgcc aacttcaagg ctgaccgggt	5880
catagactct aggagatgcc taaaaccagt catacttgat ggtgagagag tcactttggc	5940
tgggcccatt cctgtcacgc atgctagtgc tgctcagagg agaggacgta taggcaggaa	6000
ccctaacaaa cctggagatg agtacatgta tggagggtgg tgtgcagaga ctgatgaagg	6060
ccatgcacac tggcttgaag caagaatgct tcttgacaac atctacctcc aggatggcct	6120
catagcctcg ctctatcggc ctgaggccga taaggtagcc gccattgagg gagagtttaa	6180
gctgaggaca gagcaaagga agaccttcgt ggaactcatg aagagaggag accttcccgt	6240
ctggctagcc tatcaggttg catctgccgg aataacttac acagacagaa gatggtgctt	6300
tgatggcaca accaacaaca ccataatgga agacagcgta ccagcagagg tgtggacaaa	6360
gtatggagag aagagagtgc tcaaaccgag atggatggat gctagggctt gttcagacca	6420
tgcggccctg aagtcgttca aagaattcgc cgctggaaaa agaggagcgg ctttgggagt	6480
aatggaggcc ctgggaacac tgccaggaca catgacagag aggtttcagg aagccattga	6540
caacctcgcc gtgctcatgc gagcagagac tggaagcagg ccttataagg cagcggcagc	6600
ccaactgccg gagaccctag agaccattat gctcttaggt ttgctgggaa cagtttcact	6660
ggggatcttc ttcgtcttga tgcggaataa gggcatcggg aagatgggct ttggaatggt	6720
aacccttggg gccagtgcatt ggctcatgtg gctttcggaa attgaaccag ccagaattgc	6780
atgtgtcctc attgtttgtg ttttattact ggtgggtgctc atacccgagc cagagaagca	6840
aagatctccc caagataacc agatggcaat tatcatcatg gtggcagtgg gccttctagg	6900
tttgataact gcaaacgaac ttggatggct ggaaagaaca aaaaatgaca tagctcatct	6960
aatgggaagg agagaagaag gagcaaccat gggattctca atggacattg atctgcggcc	7020
agcctccgcc tgggctatct atgccgcatt gacaactctc atcaccccag ctgtccaaca	7080
tgcggtaacc acttcataca acaactactc cttaatggcg atggccacac aagctggagt	7140
gctgtttggc atgggcaaag ggatgccatt ttatgcatgg gaccttggag tcccgtgct	7200

aatgatgggt	tgctattcac	aattaacacc	cctgactctg	atagtagcta	tcattctgct	7260
tgtggcgcac	tacatgtact	tgatcccagg	cctacaagcg	gcagcagcgc	gtgctgcca	7320
gaaaaggaca	gcagctggca	tcatgaagaa	tcccgttggt	gatggaatag	tggttaactga	7380
cattgacaca	atgacaatag	acccccaggt	ggagaagaag	atgggacaag	tgttactcat	7440
agcagtagcc	atctccagtg	ctgtgctgct	gcggaccgcc	tggggatggg	gggaggctgg	7500
agctctgata	acagcagcga	cctccacctt	gtgggaaggc	tctccaaaca	aatactggaa	7560
ctcctctaca	gccacctcac	tgtgcaacat	cttcagagga	agctatctgg	caggagcttc	7620
ccttatctat	acagtgcga	gaaacgctgg	cctgggttaag	agacgtggag	gtgggacggg	7680
agagactctg	ggagagaagt	ggaaagctcg	tctgaatcag	atgtcggccc	tggagtctta	7740
ctcttataaa	aagtcaggta	tcactgaagt	gtgtagagag	gaggctcgcc	gtgccctcaa	7800
ggatggagtg	gccacaggag	gacatgccgt	atcccgggga	agtgcaaagc	tcagatgggt	7860
ggtggagaga	ggatatctgc	agccctatgg	gaaggttggt	gacctcggat	gtggcagagg	7920
gggctggagc	tattatgccg	ccaccatccg	caaagtgcag	gaggtgagag	gatacacaaa	7980
gggaggtccc	ggtcatgaag	aacccatgct	ggtgcaaagc	tatgggtgga	acatagtctg	8040
tctcaagagt	ggagtggacg	tcttccacat	ggcggctgag	ccgtgtgaca	ctctgctgtg	8100
tgacataggt	gagtcatcat	ctagtccctga	agtggaaagag	acacgaacac	tcagagtgct	8160
ctctatggtg	ggggactggc	ttgaaaaaag	accagggggc	ttctgtataa	aggtgctgtg	8220
cccatacacc	agcactatga	tggaaccat	ggagcgactg	caacgtaggc	atgggggagg	8280
attagtcaga	gtgccattgt	ctcgcaactc	cacacatgag	atgtactggg	tctctggggc	8340
aaagagcaac	atcataaaaa	gtgtgtccac	cacaagtcag	ctcctcctgg	gacgcatgga	8400
tggccccagg	aggccagtga	aatatgagga	ggatgtgaac	ctcggctcgg	gtacacgagc	8460
tgtggcaagc	tgtgctgagg	ctcctaacat	gaaaatcatc	ggcaggcgca	ttgagagaat	8520
ccgcaatgaa	catgcagaaa	catggtttct	tgatgaaaac	caccataaca	ggacatgggc	8580
ctaccatggg	agctacgaag	ccccacgca	aggatcagcg	tcttcctcgg	tgaacggggg	8640
tgttagactc	ctgtcaaagc	cttgggacgt	ggtgactgga	gttacaggaa	tagccatgac	8700
tgacaccaca	ccatacggcc	aacaaagagt	cttcaaagaa	aaagtggaca	ccagggtgcc	8760
agatcccca	gaaggcactc	gccaggtaat	gaacatagtc	tcttcctggc	tgtggaagga	8820
gctggggaaa	cgcaagcggc	cacgcgtctg	caccaaagaa	gagtttatca	acaaggtgcg	8880
cagcaatgca	gcactgggag	caatatttga	agaggaaaaa	gaatggaaga	cggctgtgga	8940

agctgtgaat gatccaaggt tttgggccct agtggatagg gagagagaac accacctgag	9000
aggagagtgt cacagctgtg tgtacaacat gatgggaaaa agagaaaaga agcaaggaga	9060
gttcgggaaa gcaaaaggta gccgcgccat ctggtacatg tggttgggag ccagattctt	9120
ggagtttgaa gcccttggat tcttgaacga ggaccattgg atgggaagag aaaactcagg	9180
aggtggagtc gaagggttag gattgcaaag acttggatac attctagaag aaatgaatcg	9240
ggcaccagga ggaaagatgt acgcagatga cactgctggc tgggacaccc gcattagtaa	9300
gtttgatctg gagaatgaag ctctgattac caaccaaagtg gaggaagggc acagaactct	9360
ggcgttggcc gtgattaaat acacatacca aaacaaagtg gtgaagggtc tcagaccagc	9420
tgaaggagga aaaacagtta tggacatcat ttcaagacaa gaccagagag ggagtggaca	9480
agttgtcact tatgctctca acacattcac caacttggtg gtgcagctta tccggaacat	9540
ggaagctgag gaagtgttag agatgcaaga cttatggttg ttgaggaagc cagagaaagt	9600
gaccagatgg ttgcagagca atggatggga tagactcaaa cgaatggcgg tcagtggaga	9660
tgactgcgtt gtgaagccaa tcgatgatag gtttgcacat gccctcaggt tcttgaatga	9720
catgggaaaa gttaggaaag acacacagga gtggaaaccc tcgactggat ggagcaattg	9780
ggaagaagtc ccgttctgct cccaccactt caacaagctg tacctcaagg atgggagatc	9840
cattgtggtc ccttgccgcc accaagatga actgattggc cgagctcgcg tctcaccagg	9900
ggcaggatgg agcatccggg agactgcctg tcttgcaaaa tcatatgcgc agatgtggca	9960
gctcctttat ttccacagaa gagaccttcg actgatggct aatgccattt gctcggctgt	10020
gccagttgac tgggtaccaa ctgggagaaac cacctggcca atccatggaa agggagaatg	10080
gatgaccact gaggacatgc tcatggtgtg gaatagagtg tggattgagg agaacgacca	10140
tatggaggac aagactcctg taacaaaatg gacagacatt ccctatctag gaaaaaggga	10200
ggacttatgg tgtggatccc ttatagggca cagaccccgcc accacttggg ctgaaaacat	10260
caaagacaca gtcaacatgg tgcgcaggat cataggtgat gaagaaaagt acatggacta	10320
tctatccacc caagtccgct acttgggtga ggaaggggcc acaccggag tgttgtaagc	10380
accaatttta gtgttgctcag gcctgctagt cagccacagt ttggggaaaag ctgtgcagcc	10440
tgtaaccccc ccaggagaag ctgggaaacc aagctcatag tcaggccgag aacgccatgg	10500
cacggaagaa gccatgctgc ctgtgagccc ctcagaggac actgagtcaa aaaacccac	10560
gcgcttgga gcgcaggatg ggaaaagaag gtggcgacct tccccaccct tcaatctggg	10620
gcctgaactg gagactagct gtgaatctcc agcagaggga ctagtgggta gaggagaccc	10680

cccgaaaaac gcaaaacagc atattgacgc tgggaaagac cagagactcc atgagtttcc	10740
accacgctgg ccgccaggca cagatcgccg aacagcggcg gccggtgtgg ggaaatccat	10800
ggttttct	10807

<210> 7
 <211> 10794
 <212> DNA
 <213> Zika virus, NCBI Reference Sequence: NC_012532.1

<400> 7	
agttgttgat ctgtgtgagt cagactgcga cagttcgagt ctgaagcgag agctaacaac	60
agtatcaaca ggtttaattt ggatttgga aacgagagttt ctgggtcatga aaaaccccaa	120
agaagaaatc cggaggatcc ggattgtcaa tatgctaaaa cgcgagtag cccgtgtaaa	180
ccccttggga ggtttgaaga ggttgccagc cggacttctg ctgggtcatg gacccatcag	240
aatggttttg gcgatactag cttttttgag atttacagca atcaagccat cactgggcct	300
tatcaacaga tggggttccg tggggaaaaa agaggctatg gaaataataa agaagttcaa	360
gaaagatctt gctgccatgt tgagaataat caatgctagg aaagagagga agagacgtgg	420
cgcagacacc agcatcgga tcattggcct cctgctgact acagccatgg cagcagagat	480
cactagacgc gggagtgcac actacatgta cttggatagg agcgatgccg ggaaggccat	540
ttcgtttgct accacattgg gagtgaacaa gtgccacgta cagatcatgg acctcgggca	600
catgtgtgac gccaccatga gttatgagt ccctatgctg gatgagggag tggaaccaga	660
tgatgtcgat tgctgggtgca acacgacatc aacttgggtt gtgtacggaa cctgtcatca	720
caaaaaaggt gaggcacggc gatctagaag agccgtgacg ctcccttctc actctacaag	780
gaagttgcaa acgcggtcgc agacctgggtt agaatacaaga gaatacacga agcattgat	840
caaggttgaa aactggatat tcaggaaccc cgggtttgcg ctagtggccg ttgccattgc	900
ctggcttttg ggaagctcga cgagccaaaa agtcatatac ttgggtcatga tactgctgat	960
tgccccggca tacagtatca ggtgcattgg agtcagcaat agagacttcg tggagggcat	1020
gtcaggtggg acctgggttg atgttgtctt ggaacatgga ggctgcgtta ccgtgatggc	1080
acaggacaag ccaacagtcg acatagagtt ggtcacgacg acggtttagta acatggccga	1140
ggtaagatcc tattgctacg aggcacgat atcggacatg gcttcggaca gtcgttgccc	1200
aacacaaggt gaagcctacc ttgacaagca atcagacact caatatgtct gcaaaagaac	1260
attagtggac agaggttggg gaaacggttg tggacttttt ggcaaaggga gcttgggtgac	1320
atgtgccaag ttacgtgtt ctaagaagat gaccgggaag agcattcaac cggaaaatct	1380

ggagtatcgg	ataatgctat	cagtgcattg	ctcccagcat	agcgggatga	ttggatatga	1440
aactgacgaa	gatagagcga	aagtcgaggt	tacgcctaata	tcaccaagag	cggaagcaac	1500
cttgggaggc	tttggaaagct	taggacttga	ctgtgaacca	aggacaggcc	ttgacttttc	1560
agatctgtat	tacctgacca	tgaacaataa	gcattgggtg	gtgcacaaaag	agtggtttca	1620
tgacatccca	ttgccttggc	atgctggggc	agacaccgga	actccacact	ggaacaacaa	1680
agaggcattg	gtagaattca	aggatgcccc	cgccaagagg	caaaccgtcg	tcgttctggg	1740
gagccaggaa	ggagccgttc	acacggctct	cgctggagct	ctagaggctg	agatggatgg	1800
tgcaaaggga	aggctgttct	ctggccattt	gaaatgccgc	ctaaaaatgg	acaagcttag	1860
attgaagggc	gtgtcatatt	ccttgtgcac	tgccggcattc	acattcacca	aggtcccagc	1920
tgaaacactg	catggaacag	tcacagtgga	ggtgcagtat	gcagggacag	atggaccctg	1980
caagatccca	gtccagatgg	cggtggacat	gcagaccctg	accccagttg	gaaggctgat	2040
aaccgccaac	cccgtgatta	ctgaaagcac	tgagaactca	aagatgatgt	tggagcttga	2100
cccaccattt	ggggattctt	acattgtcat	aggagttggg	gacaagaaaa	tcaccaccca	2160
ctggcatagg	agtggtagca	ccatcggaag	ggcatttgag	gccactgtga	gaggcgccaa	2220
gagaatggca	gtcctggggg	atacagcctg	ggacttcgga	tcagtcgggg	gtgtgttcaa	2280
ctcactgggt	aagggcattc	accagatttt	tggagcagcc	ttcaaatcac	tgtttggagg	2340
aatgtcctgg	ttctcacaga	tcctcatagg	cacgctgcta	gtgtgggttag	gtttgaacac	2400
aaagaatgga	tctatctccc	tcacatgctt	ggccctgggg	ggagtgatga	tcttctcttc	2460
cacggctgtt	tctgctgacg	tggggtgctc	agtggacttc	tcaaaaaagg	aaacgagatg	2520
tggcacgggg	gtattcatct	ataatgatgt	tgaagcctgg	agggaccggg	acaagtacca	2580
tcctgactcc	ccccgcagat	tggcagcagc	agtcaagcag	gcctgggaag	aggggatctg	2640
tgggatctca	tccgtttcaa	gaatggaaaa	catcatgtgg	aatcagtag	aaggggagct	2700
caatgctatc	ctagaggaga	atggagttca	actgacagtt	gttgtgggat	ctgtaaaaaa	2760
ccccatgtgg	agaggccac	aaagattgcc	agtgccctgtg	aatgagctgc	cccatggctg	2820
gaaagcctgg	gggaaatcgt	atthttgttag	ggcggcaaag	accaacaaca	gttttgttgt	2880
cgacggtgac	acactgaagg	aatgtccgct	tgagcacaga	gcatggaata	gttttcttgt	2940
ggaggatcac	gggtttggag	tcttccacac	cagtgtctgg	cttaagggtca	gagaagatta	3000
ctcattagaa	tgtgaccag	ccgtcatagg	aacagctgtt	aaggggaagg	agggcgcgca	3060
cagtgatctg	ggctattgga	ttgaaagtga	aaagaatgac	acatggaggc	tgaagagggc	3120

ccacctgatt	gagatgaaaa	catgtgaatg	gccaaagtct	cacacattgt	ggacagatgg	3180
agtagaagaa	agtgatctta	tcatacccaa	gtcttttagct	ggtcactca	gccaccacaa	3240
caccagagag	ggttacagaa	cccaagtga	agggccatgg	cacagtgaag	agcttgaaat	3300
ccggtttgag	gaatgtccag	gcaccaaggt	ttacgtggag	gagacatgcg	gaactagagg	3360
accatctctg	agatcaacta	ctgcaagtgg	aagggtcatt	gaggaatggg	gctgtaggga	3420
atgcacaatg	ccccactat	cgtttcgagc	aaaagacggc	tgctgggatg	gaatggagat	3480
aaggcccagg	aaagaaccag	agagcaactt	agtgagggtca	atggtgacag	cgggggtcaac	3540
cgatcatatg	gaccacttct	ctcttgaggt	gcttgtgatt	ctactcatgg	tgaggagggg	3600
gttgaagaag	agaatgacca	caaagatcat	catgagcaca	tcaatggcag	tgctggtagt	3660
catgatcttg	ggaggatttt	caatgagtga	cctggccaag	cttgtgatcc	tgatgggtgc	3720
tactttcgca	gaaatgaaca	ctggaggaga	tgtagctcac	ttggcattgg	tagcggcatt	3780
taaagtcaga	ccagccttgc	tggtctcctt	cattttcaga	gccaattgga	caccccgtga	3840
gagcatgctg	ctagccctgg	cttcgtgtct	tctgcaaact	gcgatctctg	ctcttgaagg	3900
tgacttgatg	gtcctcatta	atggatttgc	tttggcctgg	ttggcaattc	gagcaatggc	3960
cgtgccacgc	actgacaaca	tcgctctacc	aatcttggct	gctctaacac	cactagctcg	4020
aggcacactg	ctcgtggcat	ggagagcggg	cctggctact	tgtggaggga	tcatgctcct	4080
ctccctgaaa	gggaaaggta	gtgtgaagaa	gaacctgcca	tttgtcatgg	ccctgggatt	4140
gacagctgtg	agggtagtag	accctattaa	tgtggtagga	ctactgttac	tcacaaggag	4200
tggggaagcg	agctggcccc	ctagtgaagt	tctcacagcc	gttggcctga	tatgtgcact	4260
ggccggaggg	tttgccaagg	cagacattga	gatggctgga	cccatggctg	cagtaggctt	4320
gctaattgtc	agctatgtgg	tctcgggaaa	gagtgtggac	atgtacattg	aaagagcagg	4380
tgacatcaca	tgggaaaagg	acgcggaagt	cactggaaac	agtcctcggc	ttgacgtggc	4440
actggatgag	agtggtgact	tctccttggg	agaggaagat	ggtcaccca	tgagagagat	4500
catactcaag	gtggctctga	tggccatctg	tggcatgaac	ccaatagcta	taccttttgc	4560
tgaggagcg	tggtatgtgt	atgtgaagac	tgggaaaagg	agtggcgccc	tctgggacgt	4620
gcctgctccc	aaagaagtga	agaaaggaga	gaccacagat	ggagtgtaca	gagtgatgac	4680
tcgcagactg	ctaggttcaa	cacaggttgg	agtgggagtc	atgcaagagg	gagtcttcca	4740
caccatgtgg	cacgttacao	aaggagccgc	actgaggagc	ggtgagggaa	gacttgatcc	4800
atactggggg	gatgtcaagc	aggacttggg	gtcatactgt	gggccttggg	agttggatgc	4860

agcttgggat	ggactcagcg	aggtacagct	tttggccgta	cctcccggag	agagggccag	4920
aaacattcag	accctgcctg	gaatattcaa	gacaaaggac	ggggacatcg	gagcagttgc	4980
tctggactac	cctgcaggga	cctcaggatc	tccgataccta	gacaaatgtg	gaagagtgat	5040
aggactctat	ggcaatgggg	ttgtgatcaa	gaatggaagc	tatgttagtg	ctataaccca	5100
gggaaagagg	gaggaggaga	ctccggttga	atgtttcgaa	ccctcgatgc	tgaagaagaa	5160
gcagctaact	gtcttggatc	tgcattccagg	agccggaaaa	accaggagag	ttcttcctga	5220
aatagtccgt	gaagccataa	aaaagagact	ccggacagtg	atcttggcac	caactagggt	5280
tgtcgctgct	gagatggagg	aggccttgag	aggacttccg	gtgcggttaca	tgacaacagc	5340
agtcaacgtc	acccattctg	ggacagaaat	cgttgatttg	atgtgccatg	ccactttcac	5400
ttcacgctta	ctacaaccca	tcagagtccc	taattacaat	ctcaacatca	tggatgaagc	5460
ccacttcaca	gacccctcaa	gtatagctgc	aagaggatac	atatcaacaa	gggttgaaat	5520
gggcgaggcg	gctgccatth	ttatgactgc	cacaccacca	ggaacccgtg	atgcgtttcc	5580
tgactctaac	tcaccaatca	tggacacaga	agtggaagtc	ccagagagag	cctggagctc	5640
aggctttgat	tgggtgacag	accattctgg	gaaaacagtt	tggttcgttc	caagcgtgag	5700
aaacggaaat	gaaatcgag	cctgtctgac	aaaggctgga	aagcgggtca	tacagctcag	5760
caggaagact	tttgagacag	aatttcagaa	aacaaaaaat	caagagtggg	actttgtcat	5820
aacaactgac	atctcagaga	tgggcgcaa	cttcaaggct	gaccgggtca	tagactctag	5880
gagatgccta	aaaccagtca	tacttgatgg	tgagagagtc	atcttggctg	ggcccatgcc	5940
tgtcacgcat	gctagtgtg	ctcagaggag	aggacgtata	ggcaggaacc	ctaacaacc	6000
tggagatgag	tacatgtatg	gaggtgggtg	tgcagagact	gatgaaggcc	atgcacactg	6060
gcttgaagca	agaatgcttc	ttgacaacat	ctacctccag	gatggcctca	tagcctcgct	6120
ctatcggcct	gaggccgata	aggtagccgc	cattgaggga	gagtttaagc	tgaggacaga	6180
gcaaaggaag	accttcgtgg	aactcatgaa	gagaggagac	cttcccgtct	ggctagccta	6240
tcaggttgca	tctgccggaa	taacttacac	agacagaaga	tgggtgctttg	atggcacaac	6300
caacaacacc	ataatggaag	acagtgtacc	agcagagggt	tggacaaagt	atggagagaa	6360
gagagtgtc	aaaccgagat	ggatggatgc	tagggctctgt	tcagaccatg	cggccctgaa	6420
gtcgttcaaa	gaattcgccg	ctggaaaaag	aggagcggct	ttgggagtaa	tggaggccct	6480
gggaacactg	ccaggacaca	tgacagagag	gtttcaggaa	gccattgaca	acctcgccgt	6540
gctcatgcga	gcagagactg	gaagcaggcc	ttataaggca	gcggcagccc	aactgccgga	6600

gaccctagag accattatgc tcttaggttt gctgggaaca gtttcactgg ggatcttctt	6660
cgtcttgatg cggaataagg gcatcgggaa gatgggcttt ggaatggtaa cccttggggc	6720
cagtgcattg ctcatgtggc tttcggaaat tgaaccagcc agaattgcat gtgtcctcat	6780
tgttggtgtt ttattactgg tgggtgctcat acccgagcca gagaagcaaa gatctcccca	6840
agataaccag atggcaatta tcatcatggt ggcagtgggc cttctagggt tgataactgc	6900
aaacgaactt ggatggctgg aaagaacaaa aaatgacata gctcatctaa tgggaaggag	6960
agaagaagga gcaaccatgg gattctcaat ggacattgat ctgcggccag cctccgcctg	7020
ggctatctat gccgcattga caactctcat caccacagct gtccaacatg cggtaccac	7080
ttcatacaac aactactcct taatggcgat ggccacacaa gctggagtgc tgtttggcat	7140
gggcaaagg atgccattta tgcattggga ccttgagtc ccgctgctaa tgatgggttg	7200
ctattcaciaa ttaacacccc tgactctgat agtagctatc attctgcttg tggcgacta	7260
catgtacttg atcccaggcc tacaagcggc agcagcgcgt gctgcccaga aaaggacagc	7320
agctggcatc atgaagaatc ccgttggtga tggaaatagt gtaactgaca ttgacacaat	7380
gacaatagac cccaggtgg agaagaagat gggacaagtg ttactcatag cagtagccat	7440
ctccagtgtg gtgctgctgc ggaccgcctg gggatggggg gaggctggag ctctgatcac	7500
agcagcgacc tccaccttgt gggaaggctc tccaaacaaa tactggaact cctctacagc	7560
cacctcactg tgcaacatct tcagaggaag ctatctggca ggagcttccc ttatctatac	7620
agtgacgaga aacgctggcc tggtaagag acgtggaggt gggacgggag agactctggg	7680
agagaagtgg aaagctcgtc tgaatcagat gtcggccctg gagttctact cttataaaaa	7740
gtcaggtatc actgaagtgt gtagagagga ggctcgccgt gccctcaagg atggagtggc	7800
cacaggagga catgccgtat cccggggaag tgcaaagatc agatgggttg aggagagagg	7860
atatctgcag ccctatggga aggttggtga cctcggatgt ggcagagggg gctggagcta	7920
ttatgccgcc accatccgca aagtgcagga ggtgagagga tacacaaagg gaggtcccgg	7980
tcatgaagaa cccatgctgg tgcaaagcta tgggtggaac atagtctgct tcaagagtgg	8040
agtggacgtc ttccacatgg cggtgagcc gtgtgacact ctgctgtgtg acataggtga	8100
gtcatcatct agtcctgaag tggaagagac acgaacactc agagtgtct ctatggtggg	8160
ggactggctt gaaaaaagac caggggcctt ctgtataaag gtgctgtgcc catacaccag	8220
cactatgatg gaaaccatgg agcgactgca acgtaggcat gggggaggat tagtcagagt	8280
gccattgtgt cgcaactcca cacatgagat gtactgggtc tctggggcaa agagcaacat	8340

cataaaaagt	gtgtccacca	caagtcagct	cctcctggga	cgcatggatg	gccccaggag	8400
gccagtga	atgaggagg	atgtgaacct	cggctcgggt	acacgagctg	tggcaagctg	8460
tgctgaggct	cctaacatga	aatcatcgg	caggcgcatt	gagagaatcc	gcaatgaaca	8520
tgcagaaaca	tggtttcttg	atgaaaacca	cccatacagg	acatgggcct	accatgggag	8580
ctacgaagcc	cccacgcaag	gatcagcgtc	ttccctcgtg	aacgggggtg	ttagactcct	8640
gtcaaagcct	tgggacgtgg	tgactggagt	tacaggaata	gccatgactg	acaccacacc	8700
atacggccaa	caaagagtct	tcaaagaaaa	agtggacacc	agggtgccag	atccccaaga	8760
aggcactcgc	caggtaatga	acatagtctc	ttcctggctg	tggaaggagc	tggggaaacg	8820
caagcggcca	cgcgctctgca	caaagaaga	gtttatcaac	aaggtgcgca	gcaatgcagc	8880
actgggagca	atatttgaag	agaaaaaga	atggaagacg	gctgtggaag	ctgtgaatga	8940
tccaaggttt	tgggcccctag	tggataggga	gagagaacac	cacctgagag	gagagtgtca	9000
cagctgtgtg	tacaacatga	tgggaaaaag	agaaaagaag	caaggagagt	tcgggaaagc	9060
aaaaggtagc	cgcgccatct	gttacatgtg	gttgggagcc	agattcttgg	agtttgaagc	9120
ccttggattc	ttgaacgagg	accattggat	gggaagagaa	aactcaggag	gtggagtcga	9180
agggttagga	ttgcaaagac	ttggatacat	tctagaagaa	atgaatcggg	caccaggagg	9240
aaagatgtac	gcagatgaca	ctgctggctg	ggacacccgc	attagtaagt	ttgatctgga	9300
gaatgaagct	ctgattacca	accaaagga	ggaagggcac	agaactctgg	cgttggccgt	9360
gattaaatac	acataccaaa	acaagtgggt	gaaggttctc	agaccagctg	aaggaggaaa	9420
aacagttatg	gacatcattt	caagacaaga	ccagagaggg	agtggacaag	ttgtcactta	9480
tgctctcaac	acattcacca	acttgggtgg	gcagcttata	cggaacatgg	aagctgagga	9540
agtgttagag	atgcaagact	tatggttggt	gaggaagcca	gagaaagtga	ccagatgggt	9600
gcagagcaat	ggatgggata	gactcaaacg	aatggcggtc	agtggagatg	actgcgttgt	9660
gaagccaatc	gatgataggt	ttgcacatgc	cctcagggtc	ttgaatgaca	tgggaaaagt	9720
taggaaagac	acacaggagt	ggaaaccctc	gactggatgg	agcaattggg	aagaagtccc	9780
gttctgctcc	caccacttca	acaagctgta	cctcaaggat	gggagatcca	tttgtgtccc	9840
ttgccgccac	caagatgaac	tgattggccg	agctcgcgtc	tcaccagggg	caggatggag	9900
catccgggag	actgcctgtc	ttgcaaaatc	atatgcgcag	atgtggcagc	tcctttattt	9960
ccacagaaga	gaccttcgac	tgatggctaa	tgccatttgc	tcggctgtgc	cagttgactg	10020
ggtaccaact	gggagaacca	cctggtcaat	ccatggaaag	ggagaatgga	tgaccactga	10080

ggacatgctc atggtgtgga atagagtgtg gattgaggag aacgaccata tggaggacaa	10140
gactcctgta acaaaatgga cagacattcc ctatctagga aaaagggagg acttatggtg	10200
tggatccctt atagggcaca gaccccgcac cacttgggct gaaaacatca aagacacagt	10260
caacatggtg cgcaggatca taggtgatga agaaaagtac atggactatc tatccacca	10320
agtccgctac ttgggtgagg aagggccac acccggagtg ttgtaagcac caattttagt	10380
gttgtcaggc ctgctagtca gccacagttt ggggaaagct gtgcagcctg taaccccccc	10440
aggagaagct gggaaaccaa gctcatagtc aggccgagaa cgccatggca cggaagaagc	10500
catgctgcct gtgagcccct cagaggacac tgagtcaaaa aaccccacgc gcttgaagc	10560
gcaggatggg aaaagaaggt ggcgacctc cccaccctc aatctggggc ctgaactgga	10620
gactagctgt gaatctccag cagagggact agtggttaga ggagaccccc cggaacacgc	10680
aaaacagcat attgacgtgg gaaagaccag agactccatg agtttccacc acgctggccg	10740
ccaggcacag atcgccgaac ttcggcggcc ggtgtgggga aatccatggt ttct	10794

<210> 8
 <211> 10676
 <212> DNA
 <213> Zika virus strain ZikaSPH2015

<400> 8	
gttgttactg ttgctgactc agactgcgac agttcgagtt tgaagcgaaa gctagcaaca	60
gtatcaacag gttttatattg gatttggaaa cgagagtttc tggatcatgaa aaacccaaaa	120
aagaaatccg gaggattccg gattgtcaat atgctaaaac gcggagtagc ccgtgtgagc	180
ccctttgggg gcttgaagag gctgccagcc ggacttctgc tgggtcatgg gcccatcagg	240
atgggtcttg caattctagc ctttttgaga ttcacggcaa tcaagccatc actgggtctc	300
atcaatagat ggggttcagt ggggaaaaaa gaggctatgg aaataataaa gaagttcaag	360
aaagatctgg ctgccatgct gagaataatc aatgctagga aggagaagaa gagacggggc	420
gcagatacta gtgtcggaat tggtggcctc ctgctgacca cagctatggc agcggaggtc	480
actagacgtg ggagtgcata ctatatgtac ttggacagaa acgatgctgg ggaggccata	540
tcttttccaa ccacattggg gatgaataag tggtatatac agatcatgga tcttggacac	600
atgtgtgatg ccaccatgag ctatgaatgc cctatgctgg atgagggggg ggaaccagat	660
gacgtcgatt gttggtgcaa cacgacgtca acttgggttg tgtacggaac ctgccatcac	720
aaaaaagggtg aagcacggag atctagaaga gctgtgacgc tcccctccca ttccactagg	780

aagctgcaaa	cgcggtcgca	aacctgggtg	gaatcaagag	aatacacaaa	gcacttgatt	840
agagtcgaaa	attggatatt	caggaaccct	ggcttcgcgt	tagcagcagc	tgccatcgct	900
tggcttttgg	gaagctcaac	gagccaaaaa	gtcatatact	tggtcatgat	actgctgatt	960
gccccggcat	acagcatcag	gtgcatagga	gtcagcaata	gggactttgt	ggaaggtatg	1020
tcagggtgga	cttgggttga	tattgtcttg	gaacatggag	gttgtgtcac	cgtaatggca	1080
caggacaaac	cgactgtcga	catagagctg	gttacaacaa	cagtcagcaa	catggcggag	1140
gtaagatcct	actgctatga	ggcatcaata	tcagacatgg	cttcggacag	ccgctgcca	1200
acacaaggtg	aagcctacct	tgacaagcaa	tcagacactc	aatatgtctg	caaaagaacg	1260
ttagtggaca	gaggctgggg	aaatggatgt	ggactttttg	gcaaagggag	tctggtgaca	1320
tgcgctaagt	ttgcatgctc	caagaaaatg	accggaaga	gcatccagcc	agagaatctg	1380
gagtaccgga	taatgctgtc	agttcatggc	tcccagcaca	gtgggatgat	cgtaaatgac	1440
acaggacatg	aaactgatga	gaatagagcg	aaggttgaga	taacgcccaa	ttcaccaaga	1500
gccgaagcca	ccctgggggg	ttttggaagc	ctaggacttg	attgtgaacc	gaggacaggc	1560
cttgactttt	cagatttgta	ttacttgact	atgaataaca	agcactgggt	ggttcacaag	1620
gagtggttcc	acgacattcc	attaccttgg	cacgctgggg	cagacaccgg	aactccacac	1680
tggaacaaca	aagaagcact	ggtagagttc	aaggacgcac	atgccaaaag	gcaaactgtc	1740
gtggttctag	ggagtcaaga	aggagcagtt	cacacggccc	ttgctggagc	tctggaggct	1800
gagatggatg	gtgcaaaggg	aaggctgtcc	tctggccact	tgaaatgtcg	cctgaaaatg	1860
gataaactta	gattgaaggg	cgtgtcatac	tccttgtgta	ccgcagcggt	cacattcacc	1920
aagatcccgg	ctgaaacact	gcacgggaca	gtcacagtgg	aggtacagta	cgcagggaca	1980
gatggacctt	gcaaggttcc	agctcagatg	gcggtggaca	tgcaaactct	gaccccagtt	2040
gggaggttga	taaccgctaa	ccccgtaatc	actgaaagca	ctgagaactc	taagatgatg	2100
ctggaacttg	atccaccatt	tggggactct	tacattgtca	taggagtcgg	ggagaagaag	2160
atcaccacc	actggcacag	gagtggcagc	accattggaa	aagcatttga	agccactgtg	2220
agaggtgcca	agagaatggc	agtcttggga	gacacagcct	gggactttgg	atcagttgga	2280
ggcgctctca	actcattggg	caagggcatc	catcaaattt	ttggagcagc	tttcaaata	2340
ttgtttggag	gaatgtcctg	gttctcacia	attctcattg	gaacgttgct	gatgtggttg	2400
ggtctgaaca	caaagaatgg	atctatttcc	cttatgtgct	tggccttagg	gggagtgttg	2460
atcttcttat	ccacagccgt	ctctgctgat	gtggggtgct	cggtggactt	ctcaaagaag	2520

gagacgagat gcggtacagg ggtgttcgtc tataacgacg ttgaagcctg gagggacagg	2580
tacaagtacc atcctgactc cccccgtaga ttggcagcag cagtcaagca agcctgggaa	2640
gatggtatct gcgggatctc ctctgtttca agaatggaaa acatcatgtg gagatcagta	2700
gaaggggagc tcaacgcaat cctggaagag aatggagttc aactgacggc cgttgtggga	2760
tctgtaaaaa accccatgtg gagaggtcca cagagattgc ccgtgcctgt gaacgagctg	2820
ccccacggct ggaaggcttg ggggaaatcg cacttcgtca gagcagcaaa gacaaataac	2880
agctttgtcg tggatggtga cacactgaag gaatgccac tcaaacatag agcatggaac	2940
agctttcttg tggaggatca tgggttcggg gtatttcaca ctagtgtctg gctcaagggt	3000
agagaagatt attcattaga gtgtgatcca gccgttattg gaacagctgt taagggaag	3060
gaggctgtac acagtgatct aggctactgg attgagagtg agaagaatga cacatggagg	3120
ctgaagaggg cccatctgat cgagatgaaa acatgtgaat ggccaaagtc ccacacattg	3180
tggacagatg gaatagaaga gagtgatctg atcataccca agtctttagc tgggccactc	3240
agccatcaca ataccagaga gggctacagg acccaaataa aagggccatg gcacagtga	3300
gagcttgaaa ttcggtttga ggaatgccca ggcactaagg tccacgtgga ggaaacatgt	3360
ggaacaagag gaccatctct gagatcaacc actgcaagcg gaagggtgat cgaggaatgg	3420
tgctgcaggg agtgcacaat gccccactg tcgttccggg ctaaagatgg ctgttggtat	3480
ggaatggaga taaggcccag gaaagaacca gaaagcaact tagtaaggtc aatggtgact	3540
gcaggatcaa ctgatcacat ggatcacttc tcccttgagg tgcttgatgat tctgctcatg	3600
gtgcaggaag ggctgaagaa gagaatgacc acaaagatca tcataagcac atcaatggca	3660
gtgctggtag ctatgatcct gggaggatth tcaatgagtg acctggctaa gcttgcaatt	3720
ttgatgggtg ccaccttcgc ggaaatgaac actggaggag atgtagctca tctggcgctg	3780
atagcggcat tcaaagtcag accagcgttg ctggtatctt tcactttcag agctaattgg	3840
acaccccgtg aaagcatgct gctggccttg gcctcgtgtc ttttgcaaac tgcgatctcc	3900
gccttggaag gcgacctgat ggttctcatc aatggttttg ctttggcctg gttggcaata	3960
cgagcgatgg ttgttccacg cactgataac atcaccttgg caatcctggc tgctctgaca	4020
ccactggccc ggggcacact gcttgtggcg tggagagcag gccttgctac ttgcgggggg	4080
tttatgctcc tctctctgaa gggaaaaggc agtgtgaaga agaacttacc atttgtcatg	4140
gccctgggac taaccgctgt gaggtgggtc gaccccatca acgtgggtggg gctgctgttg	4200
ctcacaagga gtgggaagcg gagctggccc cctagcgaag tactcacagc tgttggcctg	4260

atatgcgcat	tggtctggagg	gttcgccaag	gcagatatag	agatggctgg	gcccatggcc	4320
gcggtcggtc	tgctaattgt	cagttacgtg	gtctcaggaa	agagtgtgga	catgtacatt	4380
gaaagagcag	gtgacatcac	atgggaaaaa	gatgcggaag	tcactggaaa	cagtccccgg	4440
ctcgatgtgg	cgctagatga	gagtgggtgat	ttctccctgg	tggaggatga	cggtcccccc	4500
atgagagaga	tcataactcaa	ggtggctcctg	atgaccatct	gtggcatgaa	cccaatagcc	4560
ataccctttg	cagctggagc	gtgggtacgta	tacgtgaaga	ctggaaaaag	gagtgggtgct	4620
ctatgggatg	tgcttgctcc	caaggaagta	aaaaaggggg	agaccacaga	tggagtgtac	4680
agagtaatga	ctcgtagact	gctaggttca	acacaagttg	gagtgggagt	tatgcaagag	4740
ggggtctttc	acactatgtg	gcacgtcaca	aaaggatccg	cgctgagaag	cggtgaaggg	4800
agacttgatc	catactgggg	agatgtcaag	caggatctgg	tgtcatactg	tgggtccatgg	4860
aagctagatg	ccgcctggga	cgggcacagc	gaggtgcagc	tcttggccgt	gcccccgga	4920
gagagagcga	ggaacatcca	gactctgccc	ggaatattta	agacaaagga	tggggacatt	4980
ggagcggttg	cgctggatta	cccagcagga	acttcaggat	ctccaatcct	agacaagtgt	5040
gggagagtga	taggacttta	tggcaatggg	gtcgtgatca	aaaatgggag	ttatgttagt	5100
gccatcacc	aaggaggag	ggaggaagag	actcctgttg	agtgccttca	gccttcgatg	5160
ctgaagaaga	agcagctaac	tgtcttagac	ttgcatcctg	gagctgggaa	aaccaggaga	5220
gttcttcctg	aaatagtccg	tgaagccata	aaaacaagac	tccgtactgt	gatcttagct	5280
ccaaccagg	ttgtcgctgc	tgaaatggag	gaagccctta	gagggcttcc	agtgcgttat	5340
atgacaacag	cagtcaatgt	caccactct	ggaacagaaa	tcgtcgactt	aatgtgccat	5400
gccaccttca	cttcacgtct	actacagcca	atcagagtcc	ccaactataa	tctgtatatt	5460
atggatgagg	cccacttcac	agatccctca	agtatagcag	caagaggata	catttcaaca	5520
agggttgaga	tgggagaggc	ggctgccatc	ttcatgaccg	ccacgccacc	aggaaccggt	5580
gacgcatttc	cggactccaa	ctcaccaatt	atggacaccg	aagtggaagt	cccagagaga	5640
gcctggagct	caggctttga	ttgggtgacg	gattattctg	gaaaaacagt	ttggtttgtt	5700
ccaagcgtga	ggaacggcaa	tgagatcgca	gcttgtctga	caaaggctgg	aaaacgggtc	5760
atacagctca	gcagaaagac	ttttgagaca	gagttccaga	aaacaaaaca	tcaagagtgg	5820
gactttgtcg	tgacaactga	catttcagag	atgggcgcca	actttaaaagc	tgaccgtgtc	5880
atagattcca	ggagatgcct	aaagccggtc	atacttgatg	gcgagagagt	cattctggct	5940
ggacccatgc	ctgtcacaca	tgccagcgct	gcccagagga	gggggcgcat	aggcaggaat	6000

cccaacaaac	ctggagatga	gtatctgtat	ggaggtgggt	gcgagagac	tgacgaagac	6060
catgcacact	ggcttgaagc	aagaatgctc	cttgacaata	ttacctcca	agatggcctc	6120
atagcctcgc	tctatcgacc	tgaggccgac	aaagtagcag	ccattgaggg	agagttcaag	6180
cttaggacgg	agcaaaggaa	gacctttgtg	gaactcatga	aaagaggaga	tcttcctggt	6240
tggctggcct	atcaggttgc	atctgccgga	ataacctaca	cagatagaag	atggtgcttt	6300
gatggcacga	ccaacaacac	cataatggaa	gacagtgtgc	cggcagaggt	gtggaccaga	6360
cacggagaga	aaagagtgtc	caaaccgagg	tggatggacg	ccagagtttg	ttcagatcat	6420
gcggccctga	agtcattcaa	ggagtttgcc	gctgggaaaa	gaggagcggc	ttttggagtg	6480
atggaagccc	tgggaacact	gccaggacac	atgacagaga	gattccagga	agccattgac	6540
aacctcgctg	tgctcatgcg	ggcagagact	ggaagcaggc	cttacaagc	cgcggcggcc	6600
caattgccgg	agaccctaga	gaccattatg	cttttggggt	tgctgggaac	agtctcgctg	6660
ggaatctttt	tcgtcttgat	gaggaacaag	ggcataggga	agatgggctt	tggaatggtg	6720
actcttgggg	ccagcgcgatg	gctcatgtgg	ctctcggaac	ttgagccagc	cagaattgca	6780
tgtgtcctca	ttgttgtggt	cctattgctg	gtggtgctca	tacctgagcc	agaaaagcaa	6840
agatctcccc	aggacaacca	aatggcaatc	atcatcatgg	tagcagtagg	tcttctgggc	6900
ttgattaccg	ccaatgaact	cggatggttg	gagagaacaa	agagtgacct	aagccatcta	6960
atgggaagga	gagaggaggg	ggcaaccatg	ggattctcaa	tggacattga	cctgcggcca	7020
gcctcagctt	gggccatcta	tgctgccttg	acaactttca	ttacccagc	cgtccaacat	7080
gcagtgacca	cttcatacaa	caactactcc	ttaatggcga	tggccacgca	agctggagtg	7140
ttgtttggta	tgggcaaagg	gatgccattc	tacgcatggg	actttggagt	cccgtgcta	7200
atgatagggt	gctactcaca	attaacgccc	ctgaccctaa	tagtggccat	cattttgctc	7260
gtggcgact	acatgtactt	gatcccaggg	ctgcaggcag	cagctgcgcg	tgctgccag	7320
aagagaacgg	cagctggcat	catgaagaac	cctgttgtgg	atggaatagt	ggtgactgac	7380
attgacacaa	tgacaattga	cccccaagtg	gagaaaaaga	tgggacaggt	gctactcatg	7440
gcagtagccg	tctccagcgc	catactgtcg	cggaccgcct	gggggtgggg	ggaggctggg	7500
gccctgatca	cagccgcaac	ttccactttg	tgggaaggct	ctccgaacaa	gtactggaac	7560
tcctctacag	ccacttcact	gtgtaacatt	tttaggggaa	gttacttggc	tggagcttct	7620
ctaacttaca	cagtaacaag	aaacgctggc	ttggtcaaga	gacgtggggg	tggaacagga	7680
gagaccctgg	gagagaaatg	gaaggcccg	ttgaaccaga	tgctggccct	ggagttctac	7740

tcctacaaaa	agtcaggcat	caccgaggtg	tgcagagaag	aggccccgccg	cgccctcaag	7800
gacggtgtgg	caacgggagg	ccatgctgtg	tcccgaggaa	gtgcaaagct	gagatggttg	7860
gtggagcggg	gatacctgca	gccctatgga	aaggctcattg	atcttggaatg	tggcagaggg	7920
ggctggagtt	actacgccgc	caccatccgc	aaagttcaag	aagtgaaagg	atacacaaaa	7980
ggaggccctg	gtcatgaaga	accctgtttg	gtgcaaagct	atgggtggaa	catagtccgt	8040
cttaagagtg	gggtggacgt	ctttcatatg	gcggctgagc	cgtgtgacac	gttgctgtgt	8100
gacataggtg	agtcatcatc	tagtcctgaa	gtggaagaag	cacggacgct	cagagtcctc	8160
tccatggtgg	gggattggct	tgaaaaaaga	ccaggagcct	tttgataaaa	agtgttgtgc	8220
ccatacacca	gcactatgat	ggaaaccctg	gagcgactgc	agcgtaggta	tgggggagga	8280
ctggtcagag	tgccactctc	ccgcaactct	acacatgaga	tgtactgggt	ctctggagcg	8340
aaaagcaaca	ccataaaaag	tgtgtccacc	acgagccagc	tcctcttggg	gcgcatggac	8400
gggcctagga	ggccagtga	atatgaggag	gatgtgaatc	tcggctctgg	cacgcgggct	8460
gtggtaaagct	gcgctgaagc	tccaacatg	aagatcattg	gtaaccgcat	tgaaaggatc	8520
cgcagtgagc	acgcggaaac	gtggttcttt	gacgagaacc	acccatatag	gacatgggct	8580
taccatggaa	gctatgaggc	ccccacacaa	gggtcagcgt	cctctctaata	aaacgggggt	8640
gtcaggctcc	tgtcaaaaacc	ctgggatgtg	gtgactggag	tcacaggaat	agccatgacc	8700
gacaccacac	cgtatggtca	gcaaagagtt	ttcaaggaaa	aagtggacac	tagggtgcca	8760
gacccccaa	aaggtactcg	tcaggttatg	agcatggtct	cttcttggtt	gtggaaagag	8820
ctaggcaaac	acaaacggcc	acgagtctgt	accaaagaag	agttcatcaa	caaggttcgt	8880
agcaatgcag	cattaggggc	aatatttgaa	gaggaaaaag	agtggaagac	tgcagtggaa	8940
gctgtgaacg	atccaagggt	ctgggctcta	gtggacaagg	aaagagagca	ccacctgaga	9000
ggagagtgcc	agagtttgtg	gtacaacatg	atgggaaaaa	gagaaaagaa	acaaggggaa	9060
tttggaagg	ccaagggcag	ccgcgccatc	tggtatatgt	ggctaggggc	tagatttcta	9120
gagttcgaag	cccttggtt	cttgaacgag	gatcactgga	tggggagaga	gaactcagga	9180
ggtggtgttg	aagggtctgg	attacaaaga	ctcggatatg	tcctagaaga	gatgagtcgc	9240
ataccaggag	gaaggatgta	tgcagatgac	actgctggct	gggacacccg	catcagcagg	9300
tttgatctgg	agaatgaagc	tctaatacacc	aaccaaagtgg	agaaagggca	cagggccttg	9360
gcattggcca	taatcaagta	cacataccaa	aacaaagtgg	taaaggtcct	tagaccagct	9420
gaaaaaggga	aaacagttat	ggacattatt	tcgagacaag	accaaagggg	gagcggacaa	9480

gttgctcactt acgctcttaa cacatttacc aacctagtgg tgcaactcat tcggaatatg	9540
gaggctgagg aagtcctaga gatgcaagac ttgtggctgc tgcggagggtc agagaaagtg	9600
accaactggt tgcagagcaa cggatgggat aggctcaaac gaatggcagt cagtggagat	9660
gattgcgttg tgaagccaat tgatgatagg tttgcacatg ccctcagggtt cttgaatgat	9720
atgggaaaag ttaggaagga cacacaagag tggaaaccct caactggatg ggacaactgg	9780
gaagaagttc cgttttgctc ccaccacttc aacaagctcc atctcaagga cgggagggtcc	9840
attgtggttc cctgccgcca ccaagatgaa ctgattggcc gggcccgcgt ctctccaggg	9900
gcgggatgga gcatccggga gactgcttgc ctagcaaaat catatgcgca aatgtggcag	9960
ctcctttatt tccacagaag ggacctcca ctgatggcca atgccatttg ttcattctgtg	10020
ccagttgact gggttccaac tgggagaact acctggtcaa tccatggaaa gggagaatgg	10080
atgaccactg aagacatgct tgtggtgtgg aacagagtgt ggattgagga gaacgaccac	10140
atggaagaca agaccccagt tacgaaatgg acagacattc cctatttggg aaaaaggga	10200
gacttgtggt gtggatctct catagggcac agaccgcgca ccacctgggc tgagaacatt	10260
aaaaacacag tcaacatggt gcgcaggatc ataggtgatg aagaaaagta catggactac	10320
ctatccaccc aagttcgcta cttgggtgaa gaagggctca cacctggagt gctgtaagca	10380
ccaatcttaa tgttgtcagg cctgctagtc agccacagct tggggaaagc tgtgcagcct	10440
gtgaccccc caggagaagc tgggaaacca agcctatagt caggccgaga acgcatggc	10500
acggaagaag ccatgctgcc tgtgagcccc tcagaggaca ctgagtcaaa aaacccacg	10560
cgcttgagg cgcaggatgg gaaaagaagg tggcgacctt cccacacctt caatctgggg	10620
cctgaactgg agatcagctg tggatctcca gaagagggtac tagtgggttag aggaga	10676

<210> 9
 <211> 10794
 <212> DNA
 <213> Zika virus strain MR 766

<400> 9	
agttgttgat ctgtgtgagt cagactgcga cagttcgagt ctgaagcgag agctaacaac	60
agtatcaaca ggtttaattt ggatttggaa acgagagttt ctggatcatga aaaaccccaa	120
agaagaaatc cggaggatcc ggattgtcaa tatgctaaaa cgcggagtag cccgtgtaaa	180
ccccttggga ggtttgaaga ggttgccagc cggacttctg ctgggtcatg gacccatcag	240
aatggttttg gcgatactag cttttttgag atttacagca atcaagccat cactgggcct	300
tatcaacaga tggggttccg tggggaaaaa agaggctatg gaaataataa agaagttcaa	360

gaaagatctt gctgccatgt tgagaataat caatgctagg aaagagagga agagacgtgg	420
cgcagacacc agcatcggaa tcattggcct cctgctgact acagccatgg cagcagagat	480
cactagacgc gggagtgcac actacatgta cttggatagg agcgatgccg ggaaggccat	540
ttcgtttgct accacattgg gagtgaacaa gtgccacgta cagatcatgg acctcgggca	600
catgtgtgac gccaccatga gttatgagtg ccctatgctg gatgagggag tggaaccaga	660
tgatgtcgat tgctgggtgca acacgacatc aacttggggt gtgtacggaa cctgtcatca	720
caaaaaaggt gaggcacggc gatctagaag agccgtgacg ctcccttctc actctacaag	780
gaagttgcaa acgcggtcgc agacctgggt agaatacaaga gaatacacga agcacttgat	840
caaggttgaa aactggatat tcaggaaccc cgggtttgcg ctagtggccg ttgccattgc	900
ctggcttttg ggaagctcga cgagccaaaa agtcatatac ttgggtcatga tactgctgat	960
tgccccggca tacagtatca ggtgcattgg agtcagcaat agagacttcg tggagggcat	1020
gtcaggtggg acctgggttg atgttgtctt ggaacatgga ggctgcgtta ccgtgatggc	1080
acaggacaag ccaacagtcg acatagagtt ggtcacgacg acggttagta acatggccga	1140
ggtaagatcc tattgctacg aggcacgat atcggacatg gcttcggaca gtcgttgccc	1200
aacacaaggt gaagcctacc ttgacaagca atcagacact caatatgtct gcaaaagaac	1260
attagtggac agaggttggg gaaacggttg tggacttttt ggcaaaggga gcttggtgac	1320
atgtgccaag ttacgtgtt ctaagaagat gaccgggaag agcattcaac cggaaaatct	1380
ggagtatcgg ataatgctat cagtgcattg ctcccagcat agcgggatga ttggatatga	1440
aactgacgaa gatagagcga aagtcgaggt tacgcctaata tcaccaagag cggaagcaac	1500
cttgggaggc tttggaagct taggacttga ctgtgaacca aggacaggcc ttgacttttc	1560
agatctgtat tacctgacca tgaacaataa gcattggttg gtgcacaaag agtggtttca	1620
tgacatccca ttgccttggc atgctggggc agacaccgga actccacact ggaacaacaa	1680
agaggcattg gtagaattca aggatgcca cgccaagagg caaacgctcg tcgttctggg	1740
gagccaggaa ggagccgttc acacggctct cgctggagct ctagaggctg agatggatgg	1800
tgcaaaggga aggctgttct ctggccattt gaaatgccgc ctaaaaatgg acaagcttag	1860
attgaagggc gtgtcatatt ccttgtgcac tgcggcattc acattcacca aggtcccagc	1920
tgaaacactg catggaacag tcacagtgga ggtgcagtat gcagggacag atggaccctg	1980
caagatccca gtccagatgg cggtggacat gcagaccctg accccagttg gaaggctgat	2040
aaccgccaac cccgtgatta ctgaaagcac tgagaactca aagatgatgt tggagcttga	2100

cccaccattt	ggggattctt	acattgtcat	aggagttggg	gacaagaaaa	tcaccaccca	2160
ctggcatagg	agtggtagca	ccatcgga	ggcatttgag	gccactgtga	gaggcgccaa	2220
gagaatggca	gtcctggggg	atacagcctg	ggacttcgga	tcagtcgggg	gtgtgttcaa	2280
ctcactgggt	aagggcattc	accagatttt	tggagcagcc	ttcaaatac	tgtttggagg	2340
aatgtcctgg	ttctcacaga	tcctcatagg	cacgctgcta	gtgtgggttag	gtttgaacac	2400
aaagaatgga	tctatctccc	tcacatgctt	ggccctgggg	ggagtgatga	tcttctctc	2460
cacggctgtt	tctgctgacg	tggggtgctc	agtggacttc	tcaaaaaagg	aaacgagatg	2520
tggcacgggg	gtattcatct	ataatgatgt	tgaagcctgg	agggaccggt	acaagtacca	2580
tcctgactcc	ccccgcagat	tggcagcagc	agtcaagcag	gcctgggaag	aggggatctg	2640
tgggatctca	tccgtttcaa	gaatggaaaa	catcatgtgg	aatcagtag	aaggggagct	2700
caatgctatc	ctagaggaga	atggagttca	actgacagtt	gttgtgggat	ctgtaaaaaa	2760
ccccatgtgg	agaggtccac	aaagattgcc	agtgcctgtg	aatgagctgc	cccatggctg	2820
gaaagcctgg	gggaaatcgt	attttggttag	ggcggcaaag	accaacaaca	gttttggtgt	2880
cgacggtgac	acactgaagg	aatgtccgct	tgagcacaga	gcatggaata	gttttcttgt	2940
ggaggatcac	gggtttggag	tcttccacac	cagtgtctgg	cttaagggtca	gagaagatta	3000
ctcattagaa	tgtgaccag	ccgtcatagg	aacagctgtt	aaggggaagg	aggccgcgca	3060
cagtgatctg	ggctattgga	ttgaaagtga	aaagaatgac	acatggaggc	tgaagagggc	3120
ccacctgatt	gagatgaaaa	catgtgaatg	gccaaagtct	cacacattgt	ggacagatgg	3180
agtagaagaa	agtgatctta	tcatacccaa	gtcttttagct	ggtccactca	gccaccacaa	3240
caccagagag	ggttacagaa	ccaagtga	agggccatgg	cacagtgaag	agcttgaaat	3300
ccggtttgag	gaatgtccag	gcaccaaggt	ttacgtggag	gagacatgcg	gaactagagg	3360
accatctctg	agatcaacta	ctgcaagtgg	aagggtcatt	gaggaatggt	gctgtaggga	3420
atgcacaatg	ccccactat	cgtttcgagc	aaaagacggc	tgctggtatg	gaatggagat	3480
aaggcccagg	aaagaaccag	agagcaactt	agtgaggtca	atggtgacag	cggggtcaac	3540
cgatcatatg	gaccacttct	ctcttgaggt	gcttgtgatt	ctactcatgg	tgcaggaggg	3600
gttgaagaag	agaatgacca	caaagatcat	catgagcaca	tcaatggcag	tgctggtagt	3660
catgatcttg	ggaggatttt	caatgagtga	cctggccaag	cttgtgatcc	tgatgggtgc	3720
tactttcgca	gaaatgaaca	ctggaggaga	tgtagctcac	ttggcattgg	tagcggcatt	3780
taaagtcaga	ccagccttgc	tggctctcct	cattttcaga	gccaatggga	caccccgtga	3840

gagcatgctg	ctagccctgg	cttcgtgtct	tctgcaaact	gcgatctctg	ctcttgaagg	3900
tgacttgatg	gtcctcatta	atggatttgc	tttggcctgg	ttggcaattc	gagcaatggc	3960
cgtgccacgc	actgacaaca	tcgctctacc	aatcttggct	gctctaacac	cactagctcg	4020
aggcacactg	ctcgtggcat	ggagagcggg	cctggctact	tgtggaggga	tcatgctcct	4080
ctccctgaaa	gggaaaggta	gtgtgaagaa	gaacctgcca	tttgtcatgg	ccctgggatt	4140
gacagctgtg	agggtagtag	accctattaa	tgtggtagga	ctactgttac	tcacaaggag	4200
tgggaagcgg	agctggcccc	ctagtgaagt	tctcacagcc	gttggcctga	tatgtgcact	4260
ggccggaggg	tttgccaagg	cagacattga	gatggctgga	cccatggctg	cagtaggctt	4320
gctaattgtc	agctatgtgg	tctcgggaaa	gagtgtggac	atgtacattg	aaagagcagg	4380
tgacatcaca	tgggaaaagg	acgcggaagt	cactggaaac	agtcctcggc	ttgacgtggc	4440
actggatgag	agtggtgact	tctccttggg	agaggaagat	gggccaccca	tgagagagat	4500
catactcaag	gtggctcctga	tggccatctg	tggcatgaac	ccaatagcta	taccttttgc	4560
tgcaggagcg	tggatatgtgt	atgtgaagac	tgggaaaagg	agtggcgccc	tctgggacgt	4620
gcctgctccc	aaagaagtga	agaaaggaga	gaccacagat	ggagtgtaca	gagtgatgac	4680
tcgcagactg	ctaggttcaa	cacaggttgg	agtgggagtc	atgcaagagg	gagtcttcca	4740
caccatgtgg	cacgttacaa	aaggagccgc	actgaggagc	ggtgagggaa	gacttgatcc	4800
atactggggg	gatgtcaagc	aggacttggg	gtcatactgt	gggccttgga	agttggatgc	4860
agcttgggat	ggactcagcg	aggtacagct	tttggccgta	cctcccggag	agagggccag	4920
aaacattcag	accctgcctg	gaatattcaa	gacaaaggac	ggggacatcg	gagcagttgc	4980
tctggactac	cctgcaggga	cctcaggatc	tccgatccta	gacaaatgtg	gaagagtgat	5040
aggactctat	ggcaatgggg	ttgtgatcaa	gaatggaagc	tatgttagtg	ctataaccca	5100
gggaaagagg	gaggaggaga	ctccggttga	atgtttcgaa	ccctcgatgc	tgaagaagaa	5160
gcagctaact	gtcttggatc	tgcatccagg	agccggaaaa	accaggagag	ttcttcctga	5220
aatagtccgt	gaagccataa	aaaagagact	ccggacagtg	atcttggcac	caactagggt	5280
tgtcgctgct	gagatggagg	aggccttgag	aggacttccg	gtgcgttaca	tgacaacagc	5340
agtcaacgtc	acccattctg	ggacagaaat	cgttgatttg	atgtgccatg	ccactttcac	5400
ttcacgctta	ctacaaccca	tcagagtccc	taattacaat	ctcaacatca	tggtatgaagc	5460
ccacttcaca	gacccctcaa	gtatagctgc	aagaggatac	atatcaacaa	gggttgaaat	5520
gggcgaggcg	gctgccatth	ttatgactgc	cacaccacca	ggaacccgtg	atgcgtttcc	5580

tgactctaac	tcaccaatca	tggacacaga	agtggaagtc	ccagagagag	cctggagctc	5640
aggctttgat	tgggtgacag	accattctgg	gaaaacagtt	tggttcgttc	caagcgtgag	5700
aaacggaaat	gaaatcgcag	cctgtctgac	aaaggctgga	aagcgggtca	tacagctcag	5760
caggaagact	tttgagacag	aatttcagaa	aacaaaaaat	caagagtggg	actttgtcat	5820
aacaactgac	atctcagaga	tgggcgcaa	cttcaaggct	gaccgggtca	tagactctag	5880
gagatgccta	aaaccagtca	tacttgatgg	tgagagagtc	atcttggctg	ggcccatgcc	5940
tgtcacgcat	gctagtgtctg	ctcagaggag	aggacgtata	ggcaggaacc	ctaacaacc	6000
tggagatgag	tacatgtatg	gaggtgggtg	tgcagagact	gatgaaggcc	atgcacactg	6060
gcttgaagca	agaatgcttc	ttgacaacat	ctacctcag	gatggcctca	tagcctcgct	6120
ctatcggcct	gaggccgata	aggtagccgc	cattgaggga	gagtttaagc	tgaggacaga	6180
gcaaaggaag	accttcgtgg	aactcatgaa	gagaggagac	cttcccgtct	ggctagccta	6240
tcaggttgca	tctgccggaa	taacttacac	agacagaaga	tggtgctttg	atggcacaac	6300
caacaacacc	ataatggaag	acagtgtacc	agcagagggt	tggacaaagt	atggagagaa	6360
gagagtgtc	aaaccgagat	ggatggatgc	taggggtctgt	tcagaccatg	cggccctgaa	6420
gtcgttcaaa	gaattcgccg	ctggaaaaag	aggagcggct	ttgggagtaa	tggaggccct	6480
gggaacactg	ccaggacaca	tgacagagag	gtttcaggaa	gccattgaca	acctcgccgt	6540
gctcatgcga	gcagagactg	gaagcaggcc	ttataaggca	gcggcagccc	aactgccgga	6600
gaccctagag	accattatgc	tcttaggttt	gctgggaaca	gtttcactgg	ggatcttctt	6660
cgtcttgatg	cggaataagg	gcacgggaa	gatgggcttt	ggaatggtaa	cccttggggc	6720
cagtgcattg	ctcatgtggc	tttcggaaat	tgaaccagcc	agaattgcat	gtgtcctcat	6780
tgttggtgtt	ttattactgg	tggtgctcat	acccgagcca	gagaagcaaa	gatctcccca	6840
agataaccag	atggcaatta	tcacatgggt	ggcagtgggc	cttctagggt	tgataactgc	6900
aaacgaactt	ggatggctgg	aaagaacaaa	aatgacata	gctcatctaa	tgggaaggag	6960
agaagaagga	gcaaccatgg	gattctcaat	ggacattgat	ctgcggccag	cctccgcctg	7020
ggctatctat	gccgcattga	caactctcat	caccccagct	gtccaacatg	cggtaaccac	7080
ttcatacaac	aactactcct	taatggcgat	ggccacacaa	gctggagtgc	tgtttggcat	7140
gggcaaaggg	atgccattta	tgcatgggga	ccttggagtc	ccgctgctaa	tgatgggttg	7200
ctattcacia	ttaacacccc	tgactctgat	agtagctatc	attctgcttg	tggcgacta	7260
catgtacttg	atcccaggcc	tacaagcggc	agcagcgcgt	gctgcccaga	aaaggacagc	7320

agctggcatc atgaagaatc ccgttgtgga tggaatagtg gtaactgaca ttgacacaat	7380
gacaatagac ccccaggtgg agaagaagat gggacaagtg ttactcatag cagtagccat	7440
ctccagtgct gtgctgctgc ggaccgcctg gggatggggg gaggctggag ctctgatcac	7500
agcagcgacc tccaccttgt gggaaggctc tccaaacaaa tactggaact cctctacagc	7560
cacctcactg tgcaacatct tcagaggaag ctatctggca ggagcttccc ttatctatac	7620
agtgacgaga aacgctggcc tggtaagag acgtggaggt gggacgggag agactctggg	7680
agagaagtgg aaagctcgtc tgaatcagat gtcggccctg gagttctact cttataaaaa	7740
gtcaggatc actgaagtgt gtagagagga ggctcgccgt gccctcaagg atggagtggc	7800
cacaggagga catgccgtat cccggggaag tgcaaagatc agatggttgg aggagagagg	7860
atatctgcag ccctatggga aggttgttga cctcggatgt ggcagagggg gctggagcta	7920
ttatgccgcc accatccgca aagtgcagga ggtgagagga tacacaaagg gaggtcccgg	7980
tcatgaagaa cccatgctgg tgcaaagcta tgggtggaac atagtctgctc tcaagagtgg	8040
agtggacgtc ttccacatgg cggctgagcc gtgtgacact ctgctgtgtg acataggtga	8100
gtcatcatct agtcctgaag tggaagagac acgaacactc agagtgctct ctatggtggg	8160
ggactggctt gaaaaaagac caggggcctt ctgtataaag gtgctgtgcc catacaccag	8220
cactatgatg gaaaccatgg agcgactgca acgtaggcat gggggaggat tagtcagagt	8280
gccatttgtt cgcaactcca cacatgagat gtactgggtc tctggggcaa agagcaacat	8340
cataaaaagt gtgtccacca caagtcagct cctcctggga cgcattggatg gccccaggag	8400
gccagtgaat tatgaggagg atgtgaacct cggctcgggt acacgagctg tggcaagctg	8460
tgctgaggct cctaacatga aaatcatcgg caggcgcatt gagagaatcc gcaatgaaca	8520
tgcagaaaca tggtttcttg atgaaaacca cccatacagg acatgggcct accatgggag	8580
ctacgaagcc cccacgcaag gatcagcgtc ttccctcgtg aacgggggtg ttagactcct	8640
gtcaaagcct tgggacgtgg tgactggagt tacaggaata gccatgactg acaccacacc	8700
atacggccaa caaagagtct tcaaagaaaa agtggaacac agggtgccag atccccaaga	8760
aggcactcgc caggtaatga acatagtctc ttccctggctg tggaaggagc tggggaaacg	8820
caagcggcca cgcgtctgca ccaaagaaga gtttatcaac aaggtgcgca gcaatgcagc	8880
actgggagca atatttgaag aggaaaaaga atggaagacg gctgtggaag ctgtgaatga	8940
tccaaggttt tgggccctag tggataggga gagagaacac cacctgagag gagagtgtca	9000
cagctgtgtg tacaacatga tgggaaaaag agaaaagaag caaggagagt tcgggaaagc	9060

aaaaggtagc	cgcgccatct	ggtacatgtg	gttgggagcc	agattcttgg	agtttgaagc	9120
ccttggattc	ttgaacgagg	accattggat	gggaagagaa	aactcaggag	gtggagtcga	9180
agggttagga	ttgcaaagac	ttggatacat	tctagaagaa	atgaatcggg	caccaggagg	9240
aaagatgtac	gcagatgaca	ctgctggctg	ggacacccgc	attagtaagt	ttgatctgga	9300
gaatgaagct	ctgattacca	accaaagtga	ggaagggcac	agaactctgg	cgttggccgt	9360
gattaaatac	acataccaaa	acaaagtggg	gaaggttctc	agaccagctg	aaggaggaaa	9420
aacagttatg	gacatcattt	caagacaaga	ccagagaggg	agtggacaag	ttgtcactta	9480
tgctctcaac	acattcacca	acttgggtgg	gcagcttata	cggaacatgg	aagctgagga	9540
agtgttagag	atgcaagact	tatggttggt	gaggaagcca	gagaaagtga	ccagatgggt	9600
gcagagcaat	ggatgggata	gactcaaacg	aatggcggtc	agtggagatg	actgcgttgt	9660
gaagccaatc	gatgataggt	ttgcacatgc	cctcagggtc	ttgaatgaca	tgggaaaagt	9720
taggaaagac	acacaggagt	ggaaaccctc	gactggatgg	agcaattggg	aagaagtccc	9780
gttctgctcc	caccacttca	acaagctgta	cctcaaggat	gggagatcca	tttgtgtccc	9840
ttgccgccac	caagatgaac	tgattggccg	agctcgcgtc	tcaccagggg	caggatggag	9900
catccgggag	actgcctgtc	ttgcaaaatc	atatgcgcag	atgtggcagc	tcctttattt	9960
ccacagaaga	gaccttcgac	tgatggctaa	tgccatttgc	tcggctgtgc	cagttgactg	10020
ggtaccaact	gggagaacca	cctggtcaat	ccatggaaaag	ggagaatgga	tgaccactga	10080
ggacatgctc	atggtgtgga	atagagtgtg	gattgaggag	aacgaccata	tggaggacaa	10140
gactcctgta	acaaaatgga	cagacattcc	ctatctagga	aaaagggagg	acttatggtg	10200
tggatccctt	atagggcaca	gaccccgcac	cacttgggct	gaaaacatca	aagacacagt	10260
caacatggtg	cgcaggatca	taggtgatga	agaaaagtac	atggactatc	tatccacca	10320
agtccgctac	ttgggtgagg	aagggccac	acccgagtg	ttgtaagcac	caattttagt	10380
gttgtcaggc	ctgctagtca	gccacagttt	ggggaaagct	gtgcagcctg	taaccccccc	10440
aggagaagct	gggaaaccaa	gctcatagtc	aggccgagaa	cgccatggca	cggaagaagc	10500
catgctgcct	gtgagcccct	cagaggacac	tgagtcaaaa	aaccccacgc	gcttgaagc	10560
gcaggatggg	aaaagaaggt	ggcgaccttc	cccacccttc	aatctggggc	ctgaactgga	10620
gactagctgt	gaatctccag	cagagggact	agtggttaga	ggagaccccc	cgaaaaacgc	10680
aaaacagcat	attgacgtgg	gaaagaccag	agactccatg	agtttccacc	acgctggccg	10740
ccaggcacag	atcgccgaac	ttcggcgggc	ggtgtgggga	aatccatggt	ttct	10794

<210> 10
 <211> 10662
 <212> DNA
 <213> Zika virus strain BeH815744 polyprotein gene

<400> 10
 gtgaatcaga ctgcgacagt tcgagtttga agcgaaagct agcaacagta tcaacaggtt 60
 ttatttttgga tttggaaacg agagtttctg gtcattgaaaa acccaaaaaa gaaatccgga 120
 ggattccgga ttgtcaatat gctaaaacgc ggagtagccc gtgtgagccc ctttgggggc 180
 ttgaagaggc tgccagccgg acttctgctg ggtcatgggc ccatcaggat ggtcttggcg 240
 attctagcct ttttgagatt cacggcaatc aagccatcac tgggtctcat caatagatgg 300
 ggttcagtgg ggaaaaaaga ggctatggaa ataataaaga agttcaagaa agatctggct 360
 gccatgctga gaataatcaa tgctaggaag gagaagaaga gacgaggcgc agatactagt 420
 gtcggaattg ttggcctcct gctgaccaca gctatggcag cggagggtcac tagacgtggg 480
 agtgcatact atatgtactt ggacagaaac gatgctgggg aggccatatac ttttccaacc 540
 acattgggga tgaataagtg ttatatacag atcatggatc ttggacacat gtgtgatgcc 600
 accatgagct atgaatgccc tatgctggat gaggggggtgg aaccagatga cgtcgattgt 660
 tgggtgcaaca cgacgtcaac ttgggttgtg tacggaacct gccatcaciaa aaaaggtgaa 720
 gcacggagat ctagaagagc tgtgacgctc ccctccatt ccactaggaa gctgcaaacg 780
 cggtcgcaaa cctgggttga atcaagagaa tacacaaagc acttgattag agtcgaaaat 840
 tggatattta ggaaccctgg cttcgcgtta gcagcagctg ccatcgcttg gcttttggga 900
 agctcaacga gccaaaaagt catatacttg gtcattgatac tgctgattgc cccggcatac 960
 agcatcaggt gcataggagt cagcaatagg gactttgtgg aaggatatgtc aggtgggacc 1020
 tgggttgatg ttgtcttga acatggaggt tgtgtcaccg taatggcaca ggacaaaccg 1080
 actgtcgaca tagagctggg tacaacaaca gtcagcaaca tggcggaggt aagatcctac 1140
 tgctatgagg catcaatatac agacatggct tcggacagcc gctgccaac acaaggtgaa 1200
 gcctaccttg acaagcaatc agacactcaa tatgtctgca aaagaacgtt agtggacaga 1260
 ggctggggaa atggatgtgg actttttggc aaaggagacc tggtgacatg cgctaagttt 1320
 gcatgctcca agaaaatgac cgggaagagc atccagccag agaattctgga gtaccggata 1380
 atgctgtcag ttcattggctc ccagcacagt gggatgattg ttaatgacac aggacatgaa 1440
 actgatgaga atagagcgaa agttgagata acgccaatt caccaagagc cgaagccacc 1500

ctgggggggtt	ttggaagcct	aggacttgat	tgtgaaccga	ggacaggcct	tgacttttca	1560
gatttgtatt	acttgactat	gaataacaag	cactgggttg	ttcacaagga	gtggttccac	1620
gacattccat	taccttggca	cgctggggca	gacaccggaa	ctccacactg	gaacaacaaa	1680
gaagcactgg	tagagttcaa	ggacgcacat	gccaaaaggc	aaactgtcgt	ggttctaggg	1740
agtcaagaag	gagcagttca	cacggccctt	gctggagctc	tggaggctga	gatggatggt	1800
gcaaagggaa	ggctgtcctc	tggccacttg	aaatgtcgcc	tgaaaatgga	taaacttaga	1860
ttgaagggcg	tgtcatactc	cttgtgtact	gcagcgttca	cattcaccaa	gatcccggct	1920
gaaacactgc	acgggacagt	cacagtggag	gtacagtacg	cagggacaga	tggaccttgc	1980
aaggttccag	ctcagatggc	ggtggacatg	caaactctga	cccagttgg	gaggttgata	2040
accgctaacc	ccgtaatcac	tgaaagcact	gagaactcta	agatgatgct	ggaacttgat	2100
ccaccatttg	gggactctta	cattgtcata	ggagtcgggg	agaagaagat	caccaccac	2160
tggcacagga	gtggcagcac	cattggaaaa	gcatttgaag	ccactgtgag	aggtgccaa	2220
agaatggcag	tcttgggaga	cacagcctgg	gactttggat	cagttggagg	cgctctcaac	2280
tcattgggca	agggcatcca	tcaaattttt	ggagcagctt	tcaaatacatt	gtttggagga	2340
atgtcctgg	tctcaciaaat	tctcattgga	acgttgctga	tgtgggtggg	tctgaacaca	2400
aagaatggat	ctatttccct	tatgtgcttg	gccttagggg	gagtgttgat	cttcttatcc	2460
acagccgtct	ctgctgatgt	ggggtgctcg	gtggacttct	caaagaagga	gacgagatgc	2520
ggtacagggg	tgttcgtcta	taacgacgtt	gaagcctgga	gggacaggta	caagtaccat	2580
cctgactccc	cccgtagatt	ggcagcagca	gtcaagcaag	cctgggaaga	tggatatctgc	2640
gggatctcct	ctgtttcaag	aatggaaaac	atcatgtgga	gatcagtaga	aggggagctc	2700
aacgcaatcc	tggaagagaa	tggagttcaa	ctgacggtcg	ttgtgggatc	tgtaaaaaac	2760
cccatgtgga	gaggtccaca	gagattgccc	gtgcctgtga	acgagctgcc	ccacggctgg	2820
aaggcttggg	ggaaatcgta	cttcgtcaga	gcagcaaaga	caaataacag	ctttgtcgtg	2880
gatggtgaca	cactgaagga	atgcccactc	aaacatagag	catggaacag	ctttcttgtg	2940
gaggatcatg	ggttcggggg	atttcacact	agtgtctggc	tcaaggttag	agaagattat	3000
tcattagagt	gtgatccagc	cgttattgga	acagctgtta	agggaaagga	ggctgtacac	3060
agtgatctag	gctactggat	tgagagtgag	aagaatgaca	catggaggct	gaagagggcc	3120
catctgatcg	agatgaaaac	atgtgaatgg	ccaaagtccc	acacattgtg	gacagatgga	3180
atagaagaga	gtgatctgat	catacccaag	tcttttagctg	ggccactcag	ccatcacaat	3240

accagagagg	gctacaggac	ccaaatgaaa	gggccatggc	acagtgaaga	gcttgaatt	3300
cggtttgagg	aatgcccagg	cactaaggtc	cacgtggagg	aaacatgtgg	aacaagagga	3360
ccatctctga	gatcaaccac	tgcaagcgga	agggatgatcg	aggaatgggtg	ctgcagggag	3420
tgcacaatgc	ccccactgtc	gttccgggct	aaagatggct	gttggtatgg	aatggagata	3480
aggcccagga	aagaaccaga	aagcaactta	gtaagggtcaa	tggtgactgc	aggatcaact	3540
gatcacatgg	accacttctc	ccttggagtg	cttgtgattc	tgctcatggg	gcaggaaggg	3600
ctgaagaaga	gaatgaccac	aaagatcatc	ataagcacat	caatggcagt	gctggtagct	3660
atgatcctgg	gaggattttc	aatgagtgc	ctggctaagc	ttgcaatttt	gatgggtgcc	3720
accttcgcgg	aaatgaacac	tggaggagat	gtagctcatc	tggcgctgat	agcggcattc	3780
aaagtgcagc	cagcgttgct	ggtatctttc	atcttcagag	ctaattggac	accccgtaga	3840
agcatgctgc	tggccttggc	ctcgtgtctt	ttgcaaactg	cgatctccgc	cttgaaggc	3900
gacctgatgg	ttctcatcaa	tggttttgct	ttggcctggg	tggcaatacg	agcgatgggt	3960
gttccacgca	ctgataacat	caccttggca	atcctggctg	ctctgacacc	actggcccgg	4020
ggcacactgc	ttgtggcgtg	gagagcaggc	cttgctactt	gcgggggggt	tatgctcctc	4080
tctctgaagg	gaaaaggcag	tgtgaagaag	aacttaccat	ttgtcatggc	cctgggacta	4140
accgctgtga	ggctggtcga	ccccatcaac	gtgggtgggac	tgctgttgct	cacaaggagt	4200
gggaagcggg	gctggccccc	tagcgaagta	ctcacagctg	ttggcctgat	atgcgcattg	4260
gctggagggg	tcgccaaggc	agatatagag	atggctgggc	ccatggccgc	ggtcgggtctg	4320
ctaattgtca	gttacgtggg	ctcaggaaaag	agtgtggaca	tgtacattga	aagagcagggt	4380
gacatcacat	gggaaaaaga	tgcggaagtc	actggaaaca	gtccccggct	cgatgtggcg	4440
ctagatgaga	gtgggtgattt	ctccctgggtg	gaggatgacg	gtccccccat	gagagagatc	4500
atactcaagg	tggtcctgat	gaccatctgt	ggcatgaacc	caatagccat	accctttgca	4560
gctggagcgt	ggtacgtata	cgtgaagact	ggaaaaagga	gtgggtgctct	atgggatgtg	4620
cctgctccca	aggaagtaaa	aaagggggag	accacagatg	gagtgtacag	agtaatgact	4680
cgtagactgc	taggttcaac	acaagttgga	gtgggagtta	tgcaagaggg	ggtctttcac	4740
actatgtggc	acgtcacaaa	aggatccgcg	ctgagaagcg	gtgaaggag	acttgatcca	4800
tactggggag	atgtcaagca	ggatctgggtg	tcatactgtg	gtccatggaa	gctagatgcc	4860
gcctgggacg	ggcacagcga	ggtgcagctc	ttggccgtgc	cccccgaga	gagagcgagg	4920
aacatccaga	ctctgcccgg	aatatttaag	acaaaggatg	gggacattgg	agcggttgcg	4980

ctggattacc	cagcaggaac	ttcaggatct	ccaatcctag	acaagtgtgg	gagagtgata	5040
ggactttatg	gcaatggggg	cgatgatcaa	aatgggagtt	atgttagtgc	catcacccaa	5100
gggaggaggg	aggaagagac	tcctgttgag	tgcttcgagc	cttcgatgct	gaagaagaag	5160
cagctaactg	tcttagactt	gcattcctga	gctgggaaaa	ccaggagagt	tcttcctgaa	5220
atagtccgtg	aagccataaa	aacaagactc	cgcaccgtga	tcttagctcc	aaccagggtt	5280
gtcgctgctg	aaatggagga	ggcccttaga	gggcttccag	tgcgttatat	gacaacagca	5340
gtcaatgtca	cccactctgg	aacagaaaac	gtcgacttaa	tgtgccatgc	caccttcact	5400
tcacgtctac	tacagccaat	cagagtcccc	aactataatc	tgtatattat	ggatgaggcc	5460
cacttcacag	atccctcaag	tatagcagca	agaggataca	tttcaacaag	ggttgagatg	5520
ggcgaggcgg	ctgccatctt	catgaccgcc	acgccaccag	gaaccctgtg	cgcatttccg	5580
gactccaact	caccaattat	ggacaccgaa	gtggaagtcc	cagagagagc	ctggagctca	5640
ggctttgatt	gggtgacgga	tcattctgga	aaaacagttt	ggtttgttcc	aagcgtgagg	5700
aacggcaatg	agatcgcagc	ttgtctgaca	aaggctggaa	aacgggtcat	acagctcagc	5760
agaaagactt	ttgagacaga	gttccagaaa	acaaaacatc	aagagtggga	ctttgtcgtg	5820
acaactgaca	tttcagagat	ggcgcccaac	tttaaagctg	accgtgtcat	agattccagg	5880
agatgcctaa	agccgggtcat	acttgatggc	gagagagtca	ttctggctgg	acctatgcct	5940
gtcacacatg	ccagcgtctg	ccagaggagg	ggcgcatag	gcaggaatcc	caacaaacct	6000
ggagatgagt	atctgtatgg	aggtgggtgc	gcagagactg	acgaagacca	tgcacactgg	6060
cttgaagcaa	gaatgctcct	tgacaatatt	tacctccaag	atggcctcat	agcctcgtct	6120
tatcgacctg	aggccgacaa	agtagcagcc	attgaggagg	agttcaagct	taggacggag	6180
caaaggaaga	cctttgtgga	actcatgaaa	agaggagatc	ttcctgtttg	gctggcctat	6240
caggttgcac	ctgccggaat	aacctacaca	gatagaagat	ggtgctttga	tggcacgacc	6300
aacaacacca	taatggaaga	cagtgtgccg	gcagaggtgt	ggaccagaca	cggagagaaa	6360
agagtgtctc	aaccgaggtg	gatggacgcc	agagtttggt	cagatcatgc	ggccctgaag	6420
tcattcaagg	agtttgccgc	tgggaaaaga	ggagcggctt	ttggagtgat	ggaagccctg	6480
ggaacactgc	caggacacat	gacagagaga	ttccaggaag	ccattgacaa	cctcgtgtgt	6540
ctcatgcggg	cagagactgg	aagcaggcct	tacaaagccg	cggcggccca	attgccggag	6600
accctagaga	ccattatgct	tttgggggtg	ctgggaacag	tctcgtggg	aatcttcttc	6660
gtcttgatga	ggaacaaggg	catagggaag	atgggctttg	gaatgggtgac	tcttggggcc	6720

agcgcacatggc	tcatgtggct	ctcggaaatt	gagccagcca	gaattgcatg	tgtcctcatt	6780
gttgtgtttc	tattgctggt	ggtgctcata	cctgagccag	aaaagcaaag	atctccccag	6840
gacaacaaaa	tggaatcat	catcatggta	gcagtaggtc	ttctgggctt	gattaccgcc	6900
aatgaactcg	gatggttgga	gagaacaaag	agtgacctaa	gccatctaata	gggaaggaga	6960
gaggaggggg	caaccatagg	attctcaatg	gacattgacc	tgcgggccagc	ctcagcttgg	7020
gccatctatg	ctgccttgac	aactttcatt	accccagccg	tccaacatgc	agtgaccact	7080
tcatacaaca	actactcctt	aatggcgatg	gccacgcaag	ctggagtggt	gtttggtatg	7140
ggcaaaggga	tgccattcta	cgcatgggac	tttgaggtcc	cgctgctaata	gataggttgc	7200
tactcacaat	taacacccct	gaccctaata	gtggccatca	ttttgctcgt	ggcgactac	7260
atgtacttga	tcccagggct	gcaggcagca	gctgcgcgtg	ctgcccagaa	gagaacggca	7320
gctggcatca	tgaagaaccc	tgttgtggat	ggaatagtgg	tgactgacat	tgacacaatg	7380
acaattgacc	cccaagtgga	gaaaaagatg	ggacaggtgc	tactcatagc	agtagccgtc	7440
tccagcgcca	tactgtcgcg	gaccgcctgg	gggtgggggg	aggctggggc	cctgatcaca	7500
gccgcaactt	ccactttgtg	ggaaggctct	ccgaacaagt	actggaactc	ctctacagcc	7560
acttcactgt	gtaacatfff	taggggaagt	tacttggtg	gagcttctct	aatctacaca	7620
gtaacaagaa	acgctggctt	gtcaagaga	cgtgggggtg	gaacaggaga	gaccctggga	7680
gagaaatgga	aggcccgctt	gaaccagatg	tcggccctgg	agttctactc	ctacaaaaag	7740
tcaggcatca	ccgaggtgtg	cagagaagag	gcccgcgcg	ccctcaagga	cgtgtgtgga	7800
acgggaggcc	atgctgtgtc	ccgaggaagt	gcaaagctga	gatggtttgt	ggagcgggga	7860
tacctgcagc	cctatggaaa	gtcattgat	cttggtgtg	gcagaggggg	ctggagttac	7920
tacgccgcca	ccatccgcaa	agttcaagaa	gtgaaaggat	acacaaaagg	aggccctggt	7980
catgaagaac	ccgtgttggt	gcaaagctat	gggtggaaca	tagtccgtct	taagagtggg	8040
gtggacgtct	ttcatatggc	ggctgagccg	tgtgacacgt	tgctgtgtga	cataggtgag	8100
tcatcatcta	gtcctgaagt	ggaagaagca	cggacgctca	gagtcctctc	catggtgggg	8160
gattggcttg	aaaaaagacc	aggagccttt	tgtataaagg	tgttgtgccc	atacaccagc	8220
actatgatgg	aaaccctgga	gcgactgcag	cgtaggtatg	ggggaggact	ggtcagagtg	8280
ccactctccc	gcaactctac	acatgagatg	tattgggtct	ctggagcgaa	aagcaacacc	8340
ataaaaagtg	tgtccaccac	gagccagctc	ctcttggggc	gcatggacgg	gcctaggagg	8400
ccagtgaaat	atgaggagga	tgtggtctc	ggctctggca	cgcgggctgt	ggtaagctgc	8460

gctgaagctc ccaacatgaa gatcattggt aaccgcattg aaaggatccg cagtgaagcac	8520
gcggaaacgt ggttctttga cgagaaccac ccatatagga catgggctta ccatggaagc	8580
tatgaggccc ccacacaagg gtcagcgctc tctctaataa acggggttgt caggctcctg	8640
tcaaaaccct gggatgtggt gactggagtc acaggaatag ccatgaccga caccacaccg	8700
tatggtcagc aaagagtttt caaggaaaaa gtggacacta gggtgccaga cccccaagaa	8760
ggcactcgtc aggttatgag catggtctct tcctggttgt ggaaagagct aggcaaacac	8820
aaacggccac gagtctgtac caaagaagag ttcatacaaa aggttcgtag caatgcagca	8880
ttaggggcaa tatttgaaga ggaaaaagag tggaagactg cagtggaagc tgtgaacgat	8940
ccaaggttct gggctctagt ggataaggaa agagagcacc acctgagagg agagtgccag	9000
agttgtgtgt acaacatgat gggaaaaaga gaaaagaaac aaggggaatt tggaaaggcc	9060
aagggcagcc gcgccatctg gtatatgtgg ctaggggcta gatttctaga gttcgaagcc	9120
cttggttct tgaacgagga tctctggatg gggagagaga actcaggagg tgggtgtgaa	9180
gggctgggat taaaagact cgatatgtc ctagaagaga tgagtcgtat accaggagga	9240
aggatgtatg cagatgacac tgctggctgg gacacccgca tcagcagggt tgatctggag	9300
aatgaagctc taatcaccaa ccaaatggaa aaagggcaca gggccttggc attggccata	9360
atcaagtaca catacaaaaa caaagtggta aaggtcctta gaccagctga aaaagggaaa	9420
acagttatgg acattatttc gagacaagac caaaggggga gcggacaagt tgtcacttac	9480
gctcttaaca catttaccaa ctagtggtg caactcattc ggaatatgga ggctgaggaa	9540
gttctagaga tgcaagactt gtggctgctg cggaggtcag agaaagtgac caactggttg	9600
cagagcaacg gatgggatag gctcaaacga atggcagtc gtggagatga ttgcgttgtg	9660
aagccaattg atgatagggt tgcacatgcc ctcaggttct tgaatgatat gggaaaagtt	9720
aggaaggaca cacaagagtg gaaaccctca actggatggg acaactggga agaagttccg	9780
ttttgctccc accacttcaa caagctccat ctcaaggacg ggaggtccat tgtggttccc	9840
tgccgccacc aagatgaact gattggccgg gcccgctct ctccaggggc gggatggagc	9900
atccgggaga ctgcttgctt agcaaaatca tatgcgcaaa tgtggcagct cttttatttc	9960
cacagaaggg acctccgact gatggccaat gccatttggt catctgtgcc agttgactgg	10020
gttccaactg ggagaactac ctggtcaatc catggaaagg gagaatggat gaccactgaa	10080
gacatgcttg tgggtgtggaa cagagtgtgg attgaggaga acgaccacat ggaagacaag	10140
accccagtta cgaaatggac agacattccc tatttgggaa aaagggaaga cttgtggtgt	10200

ggatctctca tagggcacag accgcgacac accctgggctg agaacattaa aaacacagtc	10260
aacatggtgc gcaggatcat aggtgatgaa gaaaagtaca tggactacct atccacccaa	10320
gttcgctact tgggtgaaga agggctctaca cctggagtg gcagcctgt gacccccag	10380
ttgtcaggcc tgctagtcag ccacagcttg gggaaagctg tgcagcctgt gacccccag	10440
gagaagctgg gaaaccaagc ctatagtcag gccgagaacg ccatggcacg gaagaagcca	10500
tgctgcctgt gagccccctca gaggacactg agtcaaaaaa cccacgcgc ttggaggcgc	10560
aggatgggaa aagaaggtgg cgaccttccc cacccttcaa tctggggcct gaactggaga	10620
tcagctgtgg atctccagaa gagggactag tggtagagg ag	10662

<210> 11

<211> 10662

<212> DNA

<213> Zika virus strain BeH819966 polyprotein gene

<400> 11

gtgaatcaga ctgacagct tcgagtttga agcgaaagct agcaacagta tcaacaggtt	60
ttattttga tttggaaacg agagtttctg gtcattgaaaa acccaaaaaa gaaatccgga	120
ggattccgga ttgtcaatat gctaaaacgc ggagtagccc gtgtgagccc ctttgggggc	180
ttgaagaggc tgccagccgg acttctgctg ggtcatgggc ccatcaggat ggtcttggcg	240
attctagcct ttttgagatt cacggcaatc aagccatcac tgggtctcat caatagatgg	300
ggttcagtgg ggaaaaaaga ggctatggaa ataataaaga agttcaagaa agatctggct	360
gccatgctga gaataatcaa tgctaggaag gagaagaaga gacgaggcgc agatactagt	420
gtcgggaattg ttggcctcct gctgaccaca gctatggcag cggagggtcac tagacgtggg	480
agtgcatact atatgtactt ggacagaaac gatgctgggg aggccatatac ttttccaacc	540
acattgggga tgaataagtg ttatatacag atcatggatc ttggacacat gtgtgatgcc	600
accatgagct atgaatgccc tatgctggat gaggggggtgg aaccagatga cgtcgattgt	660
tggtgcaaca cgacgtcaac ttgggttgtg tacggaacct gccatcacia aaaaggtgaa	720
gcacggagat ctagaagagc tgtgacgctc ccctccatt ccactaggaa gctgcaaacg	780
cggtcgcaaa cctgggttga atcaagagaa tacacaaagc acttgattag agtcgaaaat	840
tggaatttca ggaaccctgg cttcgcttta gcagcagctg ccatcgcttg gcttttggga	900
agctcaacga gccaaaaagt catatacttg gtcattgatac tgctgattgc cccggcatac	960
agcatcaggt gcataggagt cagcaatagg gactttgtgg aaggatgtc aggtgggacc	1020
tggttggatg ttgtcttga acatggaggt tgtgtcaccg taatggcaca ggacaaaccg	1080

actgtcgaca tagagctggt tacaacaaca gtcagcaaca tggcggaggt aagatcctac	1140
tgctatgagg catcaatatc agacatggct tcggacagcc gctgccaac acaaggtgaa	1200
gcctaccttg acaagcaatc agacactcaa tatgtctgca aaagaacggt agtggacaga	1260
ggctggggaa atggatgtgg actttttggc aaagggagcc tggtgacatg cgctaagttt	1320
gcatgctcca agaaaatgac cgggaagagc atccagccag agaactctgga gtaccggata	1380
atgctgtcag ttcattggctc ccagcacagt gggatgattg ttaatgacac aggacatgaa	1440
actgatgaga atagagcgaa agttgagata acgccaatt caccaagagc cgaagccacc	1500
ctgggggggtt ttggaagcct aggacttgat tgtgaaccga ggacaggcct tgacttttca	1560
gatttgtatt acttgactat gaataacaag cactgggttg ttcacaagga gtggttccac	1620
gacattccat taccttggca cgctggggca gacaccggaa ctccacactg gaacaacaaa	1680
gaagcactgg tagagttcaa ggacgcacat gccaaaaggc aaactgtcgt ggttctaggg	1740
agtcaagaag gagcagttca cacggccctt gctggagctc tggaggctga gatggatggt	1800
gcaaagggaa ggctgtcctc tggccacttg aaatgtcgcc tgaaaatgga taaacttaga	1860
ttgaagggcg tgtcatactc cttgtgtact gcagcgttca cattcaccaa gatcccggct	1920
gaaacactgc acgggacagt cacagtggag gtacagtacg cagggacaga tggaccttgc	1980
aaggttccag ctcatatggc ggtggacatg caaactctga cccagttgg gaggttgata	2040
accgctaacc ccgtaatcac tgaaagcact gagaactcta agatgatgct ggaacttgat	2100
ccaccatttg gggactctta cattgtcata ggagtcgggg agaagaagat caccaccac	2160
tggcacagga gtggcagcac cattggaaaa gcatttgaag ccactgtgag aggtgccaag	2220
agaatggcag tcttgggaga cacagcctgg gactttggat cagttggagg cgctctcaac	2280
tcattgggca agggcatcca tcaaattttt ggagcagctt tcaaattcatt gtttggagga	2340
atgtcctggt tctcaciaat tctcattgga acgttgctga tgtggttggg tctgaacaca	2400
aagaatggat ctatttccct tatgtgcttg gccttagggg gagtgttgat cttcttatcc	2460
acagccgtct ctgctgatgt ggggtgctcg gtggacttct caaagaagga gacgagatgc	2520
ggtacagggg tgttcgtcta taacgacgtt gaagcctgga gggacaggta caagtaccat	2580
cctgactccc cccgtagatt ggcagcagca gtcaagcaag cctgggaaga tggatatctgc	2640
gggatctcct ctgtttcaag aatggaaaac atcatgtgga gatcagtaga aggggagctc	2700
aacgcaatcc tggaagagaa tggagttcaa ctgacggtcg ttgtgggatc tgtaaaaaac	2760
cccatgtgga gaggtccaca gagattgccc gtgcctgtga acgagctgcc ccacggctgg	2820

aaggcttggg	ggaaatcgta	cttcgtcaga	gcagcaaaga	caaataacag	ctttgtcgtg	2880
gatggtgaca	cactgaagga	atgcccactc	aaacatagag	catggaacag	ctttcttgtg	2940
gaggatcatg	ggttcggggg	atttcacact	agtgtctggc	tcaaggttag	agaagattat	3000
tcattagagt	gtgatccagc	cgttattgga	acagctgtta	agggaaagga	ggctgtacac	3060
agtgatctag	gctactggat	tgagagtgag	aagaatgaca	catggaggct	gaagagggcc	3120
catctgatcg	agatgaaaac	atgtgaatgg	ccaaagtccc	acacattgtg	gacagatgga	3180
atagaagaga	gtgatctgat	catacccaag	tcttttagctg	ggccactcag	ccatcacaat	3240
accagagagg	gctacaggac	ccaaatgaaa	gggccatggc	acagtgaaga	gcttgaaatt	3300
cggtttgagg	aatgcccagg	cactaaggtc	cacgtggagg	aaacatgtgg	aacaagagga	3360
ccatctctga	gatcaaccac	tgcaagcgga	agggtgatcg	aggaatgggtg	ctgcagggag	3420
tgcacaatgc	ccccactgtc	gttccggggc	aaagatggct	gttggtatgg	aatggagata	3480
aggcccagga	aagaaccaga	aagcaactta	gtaaggtcaa	tggtgactgc	aggatcaact	3540
gatcacatgg	accacttctc	ccttgaggatg	cttgtgattc	tgctcatggg	gcaggaaggg	3600
ctgaagaaga	gaatgaccac	aaagatcatc	ataagcacat	caatggcagt	gctggtagct	3660
atgatcctgg	gaggattttc	aatgagtgac	ctggctaagc	ttgcaatttt	gatgggtgcc	3720
accttcgcgg	aaatgaacac	tggaggagat	gtagctcatc	tggcgctgat	agcggcattc	3780
aaagtcagac	cagcgttgct	ggtatctttc	atcttcagag	ctaattggac	accccgtaga	3840
agcatgctgc	tggccttggc	ctcgtgtctt	ttgcaaactg	cgatctccgc	cttggaaggc	3900
gacctgatgg	ttctcatcaa	tggttttgct	ttggcctggg	tggcaatacg	agcgatgggt	3960
gttccacgca	ctgataacat	caccttggca	atcctggctg	ctctgacacc	actggcccgg	4020
ggcacactgc	ttgtggcgtg	gagagcaggc	cttgctactt	gcgggggggt	tatgctcctc	4080
tctctgaagg	gaaaaggcag	tgtgaagaag	aacttaccat	ttgtcatggc	cctgggacta	4140
accgctgtga	ggctggtcga	ccccatcaac	gtgggtgggac	tgctgttgct	cacaaggagt	4200
gggaagcgga	gctggccccc	tagcgaagta	ctcacagctg	ttggcctgat	atgcgcattg	4260
gctggagggg	tcgccaaggc	agatatagag	atggctgggc	ccatggccgc	ggtcggtctg	4320
ctaattgtca	gttacgtggg	ctcaggaaag	agtgtggaca	tgtacattga	aagagcaggt	4380
gacatcacat	gggaaaaaga	tgcggaagtc	actggaaaca	gtccccggct	cgatgtggcg	4440
ctagatgaga	gtgggtgattt	ctccctgggtg	gaggatgacg	gtccccccat	gagagagatc	4500
atactcaagg	tggtcctgat	gaccatctgt	ggcatgaacc	caatagccat	accctttgca	4560

gctggagcgt ggtacgtata cgtgaagact ggaaaaagga gtggtgctct atgggatgtg	4620
cctgctccca aggaagtaaa aaagggggag accacagatg gagtgtacag agtaatgact	4680
cgtagactgc taggttcaac acaagttgga gtgggagtta tgcaagaggg ggtctttcac	4740
actatgtggc acgtcacaaa aggatccgcg ctgagaagcg gtgaagggag acttgatcca	4800
tactggggag atgtcaagca ggatctggtg tcatactgtg gtccatggaa gctagatgcc	4860
gcctgggacg ggcacagcga ggtgcagctc ttggccgtgc cccccggaga gagagcgagg	4920
aacatccaga ctctgcccgg aatatttaag acaaaggatg gggacattgg agcggttgcg	4980
ctggattacc cagcaggaac ttcaggatct ccaatcctag acaagtgtgg gagagtgata	5040
ggactttatg gcaatggggg cgtgatcaaa aatgggagtt atgttagtgc catcacccaa	5100
gggaggaggg aggaagagac tcctgttgag tgcttcgagc cttcgatgct gaagaagaag	5160
cagctaactg tcttagactt gcacccctga gctgggaaaa ccaggagagt tcttcctgaa	5220
atagtccgtg aagccataaa aacaagactc cgtactgtga tcttagctcc aaccagggtt	5280
gtcgctgctg aaatggagga ggcccttaga gggcttccag tgcgttatat gacaacagca	5340
gtcaatgtca cccactctgg aacagaaaac gtcgacttaa tgtgccatgc caccttcact	5400
tcacgtctac tacagccaat cagagtcccc aactataatc tgtatattat ggatgaggcc	5460
cacttcacag atccctcaag tatagcagca agaggataca tttcaacaag ggttgagatg	5520
ggcgaggcgg ctgccatctt catgaccgcc acgccaccag gaaccctga cgcatttccg	5580
gactccaact caccaattat ggacaccgaa gtggaagtcc cagagagagc ctggagctca	5640
ggctttgatt gggtgacgga tcattctgga aaaacagttt ggtttgttcc aagcgtgagg	5700
aacggcaatg agatcgcagc ttgtctgaca aaggctggaa aacgggtcat acagctcagc	5760
agaaagactt ttgagacaga gttccagaaa acaaaacatc aagagtggga ctttgtcgtg	5820
acaactgaca tttcagagat gggcgccaac tttaaagctg accgtgtcat agattccagg	5880
agatgcctaa agccgggtcat acttgatggc gagagagtca ttctggctgg acccatgcct	5940
gtcacacatg ccagcgctgc ccagaggagg gggcgcatag gcaggaatcc caacaaacct	6000
ggagatgagt atctgtatgg aggtgggtgc gcagagactg acgaagacca tgcacactgg	6060
cttgaagcaa gaatgctcct tgacaatatt tacctccaag atggcctcat agcctcgtc	6120
tatcgacctg aggccgacaa agtagcagcc attgaggag agttcaagct taggacggag	6180
caaaggaaga cttttgtgga actcatgaaa agaggagatc ttctgtttg gctggcctat	6240
caggttgcac ctgccggaat aacctacaca gatagaagat ggtgctttga tggcacgacc	6300

aacaacacca	taatggaaga	cagtgtgccg	gcagaggtgt	ggaccagaca	cggagagaaa	6360
agagtgtca	aaccgaggtg	gatggacgcc	agagtttggt	cagatcatgc	ggccctgaag	6420
tcattcaagg	agtttgccgc	tgggaaaaga	ggagcggctt	ttggagtgat	ggaagccctg	6480
ggaacactgc	caggacacat	gacagagaga	ttccaggaag	ccattgacaa	cctcgctgtg	6540
ctcatgcggg	cagagactgg	aagcaggcct	tacaaagccg	cggcggccca	attgccggag	6600
accctagaga	ccattatgct	tttgggggtg	ctgggaacag	tctcgctggg	aatcttcttc	6660
gtcttgatga	ggaacaaggg	cataggaag	atgggctttg	gaatggtgac	tcttggggcc	6720
agcgcattgg	tcatgtggct	ctcgaaatt	gagccagcca	gaattgcatg	tgtcctcatt	6780
gttgtgtttc	tattgctggt	ggtgctcata	cctgagccag	aaaagcaaag	atctcccag	6840
gacaaccaa	tggcaatcat	catcatggta	gcagtaggtc	ttctgggctt	gattaccgcc	6900
aatgaactcg	gatggttgga	gagaacaaag	agtgacctaa	gccatcta	gggaaggaga	6960
gaggaggggg	caaccatagg	attctcaatg	gacattgacc	tgcgccagc	ctcagcttgg	7020
gccatctatg	ctgccttgac	aactttcatt	acccagccg	tccaacatgc	agtgaccact	7080
tcatacaaca	actactcctt	aatggcgatg	gccacgcaag	ctggagtgtt	gtttggtatg	7140
ggcaaaggga	tgccattcta	cgcatgggac	tttgaggtcc	cgctgcta	gataggttgc	7200
tactcacaat	taacacccct	gaccctaata	gtggccatca	ttttgctcgt	ggcgactac	7260
atgtacttga	tcccagggct	gcaggcagca	gctgcgcgtg	ctgccagaa	gagaacggca	7320
gctggcatca	tgaagaacct	tggtgtggat	ggaatagtgg	tgactgacat	tgacacaatg	7380
acaattgacc	ccaagtgga	gaaaaagatg	ggacaggtgc	tactcatagc	agtagccgtc	7440
tccagcgcca	tactgtcgcg	gaccgcctgg	gggtgggggg	aggctggggc	cctgatcaca	7500
gccgcaactt	ccactttgtg	ggaaggctct	ccgaacaagt	actggaactc	ctctacagcc	7560
acttactgt	gtaacat	taggggaagt	tacttggtg	gagcttctct	aatctacaca	7620
gtaacaagaa	acgctggctt	ggtcaagaga	cgtgggggtg	gaacaggaga	gaccctggga	7680
gagaaatgga	aggcccgctt	gaaccagatg	tcggccctgg	agttctactc	ctacaaaag	7740
tcaggcatca	ccgaggtgtg	cagagaagag	gcccgcgcg	ccctcaagga	cgggtgtggca	7800
acgggaggcc	atgctgtgtc	ccgaggaagt	gcaaagctga	gatggttggt	ggagcgggga	7860
tacctgcagc	cctatggaaa	ggtcattgat	cttgatgtg	gcagaggggg	ctggagttac	7920
tacgccgcca	ccatccgcaa	agttcaagaa	gtgaaaggat	acacaaaagg	aggccctggt	7980
catgaagaac	ccgtgttggt	gcaaagctat	gggtggaaca	tagtccgtct	taagagtggg	8040

gtggacgtct	ttcatatggc	ggctgagccg	tgtgacacgt	tgctgtgtga	cataggtgag	8100
tcatcatcta	gtcctgaagt	ggaagaagca	cggacgctca	gagtcctctc	catggtgggg	8160
gattggcttg	aaaaaagacc	aggagccttt	tgtataaagg	tgttggtgcc	atacaccagc	8220
actatgatgg	aaaccctgga	gcgactgcag	cgtaggtatg	ggggaggact	ggtcagagtg	8280
ccactctccc	gcaactctac	acatgagatg	tattgggtct	ctggagcgaa	aagcaacacc	8340
ataaaaagtg	tgtccaccac	gagccagctc	ctcttggggc	gcatggacgg	gcctaggagg	8400
ccagtgaat	atgaggagga	tgtgaatctc	ggctctggca	cgcgggctgt	ggtaagctgc	8460
gctgaagctc	ccaacatgaa	gatcattggt	aaccgcattg	aaaggatccg	cagtgagcac	8520
gcggaaacgt	ggttctttga	cgagaaccac	ccatatagga	catgggctta	ccatggaagc	8580
tatgaggccc	ccacacaagg	gtcagcgtcc	tctctaataa	acggggttgt	caggctcctg	8640
tcaaaaccct	gggatgtggt	gactggagtc	acaggaatag	ccatgaccga	caccacaccg	8700
tatggtcagc	aaagagtttt	caaggaaaaa	gtggacacta	gggtgccaga	cccccaagaa	8760
ggcactcgtc	aggttatgag	catggtctct	tcctggttgt	ggaaagagct	aggcaaacac	8820
aaacggccac	gagtctgtac	caaagaagag	ttcatcaaca	aggttcgtag	caatgcagca	8880
ttaggggcaa	tatttgaaga	ggaaaaagag	tggaagactg	cagtgggaagc	tgtgaacgat	8940
ccaaggttct	gggctctagt	ggataaggaa	agagagcacc	acctgagagg	agagtgccag	9000
agttgtgtgt	acaacatgat	gggaaaaaga	gaaaagaaac	aaggggaatt	tggaaaggcc	9060
aagggcagcc	gcgccatctg	gtatatgtgg	ctaggggcta	gatttctaga	gttcgaagcc	9120
cttggattct	tgaacgagga	tactggatg	gggagagaga	actcaggagg	tggtgttgaa	9180
gggctgggat	tacaaagact	cggatatgtc	ctagaagaga	tgagtcgtat	accaggagga	9240
aggatgtatg	cagatgacac	tgctggctgg	gacacccgca	tcagcagggt	tgatctggag	9300
aatgaagctc	taatcaccaa	ccaaatggaa	aaagggcaca	gggccttggc	attggccata	9360
atcaagtaca	cataccaaaa	caaagtggta	aaggtcctta	gaccagctga	aaaagggaaa	9420
acagttatgg	acattatttc	gagacaagac	caaaggggga	gcggacaagt	tgtcacttac	9480
gctcttaaca	catttaccaa	cctagtgggtg	caactcattc	ggaatatgga	ggctgaggaa	9540
gttctagaga	tgcaagactt	gtggctgctg	cggaggtcag	agaaagtgac	caactggttg	9600
cagagcaacg	gatgggatag	gctcaaacga	atggcagtca	gtggagatga	ttgcgttgtg	9660
aagccaattg	atgatagggt	tgcacatgcc	ctcaggttct	tgaatgatat	gggaaaagtt	9720
aggaaggaca	cacaagagtg	gaaaccctca	actggatggg	acaactggga	agaagttccg	9780

ttttgctccc accacttcaa caagctccat ctcaaggacg ggaggtccat tgtgggtccc	9840
tgccgccacc aagatgaact gattggccgg gcccgcgtct ctccaggggc gggatggagc	9900
atccgggaga ctgcttgctt agcaaaatca tatgcgcaaa tgtggcagct cctttatttc	9960
cacagaaggg acctccgact gatggccaat gccatttgtt catctgtgcc agttgactgg	10020
gttccaactg ggagaactac ctgggtcaatc catggaaagg gagaatggat gaccactgaa	10080
gacatgcttg tgggtgtggaa cagagtgtgg attgaggaga acgaccacat ggaagacaag	10140
accccagtta cgaaatggac agacatcccc tatttgggaa aaaggggaaga cttgtgggtgt	10200
ggatctctca tagggcacag accgcgccacc acctgggctg agaacattaa aaacacagtc	10260
aacatggtgc gcaggatcat aggtgatgaa gaaaagtaca tggactacct atccacccaa	10320
gttcgctact tgggtgaaga aggggtctaca cctggagtgc tgtaagcacc agtcttaatg	10380
ttgtcaggcc tgctagtcag ccacagcttg gggaaagctg tgcagcctgt gacccccag	10440
gagaagctgg gaaaccaagc ctatagtcag gccgagaacg ccatggcacg gaagaagcca	10500
tgctgcctgt gagccctca gaggacactg agtcaaaaaa cccacgcgc ttggaggcgc	10560
aggatgggaa aagaaggtgg cgaccttccc cacccttcaa tctggggcct gaactggaga	10620
tcagctgtgg atctccagaa gagggactag tgggttagagg ag	10662

<210> 12

<211> 10727

<212> DNA

<213> Zika virus strain BeH819015 polyprotein gene

<400> 12

tgtgaatcag actgcgacag ttcgagtttg aagcgaaagc tagcaacagt atcaacaggt	60
tttatTTTTGG atttgGaaac gagagtttct ggtcatgaaa aacccaaaaa agaatccgg	120
aggattccgg attgtcaata tgctaaaacg cggagtagcc cgtgtgagcc ctttggggg	180
cttgaagagg ctgccagccg gacttctgct ggggtcatggg cccatcagga tggctctggc	240
gattctagcc tttttgagat tcacggcaat caagccatca ctgggtctca tcaatagatg	300
gggttcagtt gggaaaaaag aggctatgga aataataaag aagttcaaga aagatctggc	360
tgccatgctg agaataatca atgctaggaa ggagaagaag agacgaggcg cagatactag	420
tgtcggaatt gttggcctcc tgctgaccac agctatggca gcggagggtca ctagacgtgg	480
gagtgcatac tatatgtact tggacagaaa cgatgctggg gaggccatat cttttccaac	540
cacattgggg atgaataagt gttatataca gatcatggat cttggacaca tgtgtgatgc	600

caccatgagc	tatgaatgcc	ctatgctgga	tgagggggtg	gaaccagatg	acgtcgattg	660
ttggtgcaac	acgacgtcaa	cttgggttgt	gtacggaacc	tgccatcaca	aaaaaggtga	720
agcacggaga	tctagaagag	ctgtgacgct	cccctcccat	tccactagga	agctgcaaac	780
gcggtcgcaa	acctggtttg	aatcaagaga	atacacaaag	cacttgatta	gagtcgaaaa	840
ttggatattc	aggaaccctg	gcttcgcgtt	agcagcagct	gccatcgctt	ggcttttggg	900
aagctcaacg	agccaaaaag	tcatatactt	ggcatgata	ctgctgattg	ccccggcata	960
cagcatcagg	tgcataggag	tcagcaatag	ggactttgtg	gaaggatatgt	caggtgggac	1020
ttgggttgat	gttgtcttgg	aacatggagg	ttgtgtcacc	gtaatggcac	aggacaaacc	1080
gactgtcgac	atagagctgg	ttacaacaac	agtcagcaac	atggcggagg	taagatccta	1140
ctgctatgag	gcatcaatat	cagacatggc	ttcggacagc	cgctgcccaa	cacaaggtga	1200
agcctacctt	gacaagcaat	cagacactca	atatgtctgc	aaaagaacgt	tagtggacag	1260
aggctgggga	aatggatgtg	gacttttttg	caaagggagc	ctggtgacat	gcgctaagtt	1320
tgcatgctcc	aagaaaatga	ccgggaagag	catccagcca	gagaatctgg	agtaccggat	1380
aatgctgtca	gttcatggct	cccagcacag	tgggatgadc	gttaatgaca	caggacatga	1440
aactgatgag	aatagagcga	aagttgagat	aacgccaat	tcaccaagag	ccgaagccac	1500
cctggggggg	tttggaaagg	taggacttga	ttgtgaaccg	aggacaggcc	ttgacttttc	1560
agatttgtat	tacttgacta	tgaataacaa	gcactggttg	gttcacaagg	agtggttcca	1620
cgacattcca	ttaccttggc	acgctggggc	agacaccgga	actccacact	ggaacaacaa	1680
agaagcactg	gtagagttca	aggacgcaca	tgccaaaagg	caaactgtcg	tggttctagg	1740
gagtcaagaa	ggagcagttc	acacggccct	tgctggagct	ctggaggctg	agatggatgg	1800
tgcaaaggga	aggctgtcct	ctggccactt	gaaatgtcgc	ctgaaaatgg	ataaacttag	1860
attgaagggc	gtgtcatact	ccttgtgtac	tgacgcgttc	acattcacca	agatcccggc	1920
tgaaacactg	cacgggacag	tcacagtgga	ggtacagtac	gcagggacag	atggaccttg	1980
caaggttcca	gctcagatgg	cggtggacat	gcaaactctg	accccagttg	ggaggttgat	2040
aaccgctaac	cccgtaatca	ctgaaagcac	tgagaactct	aagatgatgc	tggaacttga	2100
tccaccattt	ggggactctt	acattgtcat	aggagtcggg	gagaagaaga	tcaccaccca	2160
ctggcacagg	agtggcagca	ccattggaaa	agcatttgaa	gccactgtga	gaggtgccaa	2220
gagaatggca	gtcttgggag	acacagcctg	ggactttgga	tcagttggag	gcgctctcaa	2280
ctcattgggc	aagggcatcc	atcaaatttt	tggagcagct	ttcaaatcat	tgtttggagg	2340

aatgtcctgg	ttctcacaaa	ttctcattgg	aacgttgctg	atgtgggttg	gtctgaacac	2400
aaagaatgga	tctatttccc	ttatgtgctt	ggccttaggg	ggggtggtga	tcttcttctc	2460
cacagccgtc	tctgctgatg	tggggtgctc	ggtggacttc	tcaaagaagg	agacgagatg	2520
cggtacaggg	gtgttcgtct	ataacgacgt	tgaagcctgg	agggacaggt	acaagtacca	2580
tcctgactcc	ccccgtagat	tggcagcagc	agtcaagcaa	gcctgggaag	atggtatctg	2640
cgggatctcc	tctgtttcaa	gaatggaaaa	catcatgtgg	agatcagtag	aaggggagct	2700
caacgcaatc	ctggaagaga	atggagttca	actgacggtc	gttgtgggat	ctgtaaaaaa	2760
ccccatgtgg	agaggtccac	agagattgcc	cgtgcctgtg	aacgagctgc	cccacggctg	2820
gaaggcttgg	gggaaatcgt	acttcgtcag	agcagcaaag	acaaataaca	gctttgtcgt	2880
ggatggtgac	acactgaagg	aatgcccact	caaacataga	gcatggaaca	gctttcttgt	2940
ggaggatcat	gggttcgggg	tatttcacac	tagtgtctgg	ctcaaggtta	gagaagatta	3000
ttcattagag	tgtgatccag	ccgttattgg	aacagctgtt	aagggaaagg	aggctgtaca	3060
cagtgatcta	ggctactgga	ttgagagtga	gaagaatgac	acatggaggc	tgaagagggc	3120
ccatctgata	gagatgaaaa	catgtgaatg	gccaaagtcc	cacacattgt	ggacagatgg	3180
aatagaagag	agtgatctga	tcatacccaa	gtcttttagct	gggccactca	gccatcacia	3240
taccagagag	ggctacagga	cccaaataaa	agggccatgg	cacagtgaag	agcttgaaat	3300
tcggtttgag	gaatgcccag	gcactaaggt	ccacgtggag	gaaacatgtg	gaacaagagg	3360
accatctctg	agatcaacca	ctgcaagcgg	aagggtgatc	gaggaatggg	gctgcaggga	3420
gtgcacaatg	ccccactgt	cgttccgggc	taaagatggc	tgttggtatg	gaatggagat	3480
aaggcccagg	aaagaaccag	aaagcaactt	agtaagggtc	atggtgactg	caggatcaac	3540
tgatcacatg	gaccacttct	cccttgaggt	gcttgtgatc	ctgctcatgg	tgcaggaagg	3600
gctgaagaag	agaatgacca	caaagatcat	cataagcaca	tcaatggcag	tgctggtagc	3660
tatgatcctg	ggaggatttt	caatgagtga	cctggctaag	cttgcaattt	tgatgggtgc	3720
caccttcgcg	gaaatgaaca	ctggaggaga	tgtagctcat	ctggcgctga	tagcggcatt	3780
caaagtcaga	ccagcgttgc	tggtatcttt	catcttcaga	gctaattgga	caccccgtga	3840
aagcatgctg	ctggccttgg	cctcgtgtct	tttgcaaact	gcatctccg	ccttgaagg	3900
cgacctgatg	gttctcatca	atggttttgc	tttgccctgg	ttggcaatac	gagcgtgggt	3960
tgttccacgc	actgataaca	tcaccttggc	aatcctgggt	gctctgacac	cactggcccg	4020
gggcacactg	cttgtggcgt	ggagagcagg	ccttgctact	tgccgggggt	ttatgctcct	4080

ctctctgaag ggaaaaggca gtgtgaagaa gaacttacca tttgtcatgg ccctgggact	4140
aaccgctgtg aggctggtcg accccatcaa cgtgggtggga ctgctgttac tcacaaggag	4200
tgggaagcgg agctggcccc ctagcgaagt actcacagct gttggcctga tatgcgcatt	4260
ggctggaggg ttcgccaagg cagatataga gatggctggg cccatggccg cggtcggctct	4320
gctaattgtc agttacgtgg tctcaggaaa gagtgtggac atgtacattg aaagagcagg	4380
tgacatcaca tgggaaaaaag atgcggaagt cactggaaac agtccccggc tcgatgtggc	4440
gctagatgag agtggtgatt tctccctggg ggaggatgac ggtcccccca tgagagagat	4500
catactcaag gtggtcctga tgaccatctg tggcatgaat ccaatagcca taccctttgc	4560
agctggagcg tggtagctat acgtgaagac tggaaaaagg agtggtgctc tatgggatgt	4620
gcctgctccc aaggaagtaa aaaaggggga gaccacagat ggagtgtaca gagtaatgac	4680
tcgtagactg ctaggttcaa cacaagttgg agtgggagtt atgcaagagg gggctcttca	4740
cactatgtgg cacgtcacia aaggatccgc gctgagaagc ggtgaaggga gacttgatcc	4800
atactgggga gatgtcaagc aggatctggg gtcatactgt ggtccatgga agctagatgc	4860
cgcttgggac gggcacagcg aggtgcagct cttggccgtg cccccggag agagagcgag	4920
gaacatccag actctgcccc gaatatTTaa gacaaaggat ggggacattg gagcggttgc	4980
gctggattac ccagcaggaa cttcaggatc tccaatccta gacaagtgtg ggagagtgat	5040
aggactttat ggcaatgggg tcgtgatcaa aaatgggagt tatgttagtg ccatcaccca	5100
agggaggagg gaagaagaga ctctgttga gtgcttcgag ccctcgatgc tgaagaagaa	5160
gcagctaact gtcttagact tgcattctgg agctgggaaa accaggagag ttcttctga	5220
aatagtccgt gaagccataa aaacaagact ccgtactgtg atcttagctc caaccagggt	5280
tgtcgctgct gaaatggagg aggcccttag agggcttcca gtgcgttata tgacaacagc	5340
agtcaatgtc acccactctg gaacagaaat cgtcgactta atgtgccatg ccaccttcac	5400
ttcacgtcta ctacagccaa tcagagtccc caactataat ctgtatatta tggatgaggc	5460
ccacttcaca gatccctcaa gtatagcagc aagaggatac atttcaacaa gggttgagat	5520
gggcgaggcg gctgccatct tcatgaccgc cacgccacca ggaaccctg acgcatttcc	5580
ggactccaac tcaccaatta tggacaccga agtggaagtc ccagagagag cctggagctc	5640
aggctttgat tgggtgacgg atcattctgg aaaaacagtt tggtttggtc caagcgtgag	5700
gaacggcaat gagatcgag cttgtctgac aaaggctgga aaacgggtca tacagctcag	5760
cagaaagact tttgagacag agttccagaa aacaaaacat caagagtggg actttgtcgt	5820

gacaactgac atttcagaga tgggcgccaa ctttaaagct gaccgtgtca tagattccag	5880
gagatgccta aagccgggtca tacttgatgg cgagagagtc attctggctg gacccatgcc	5940
tgtcacacat gccagcgctg cccagaggag ggggcgcata ggcaggaatc ccaacaaacc	6000
tggagatgag tatctgtatg gaggtgggtg cgcagagact gacgaagacc atgcacactg	6060
gcttgaagca agaatgctcc ttgacaatat ttacctcaa gatggcctca tagcctcgct	6120
ctatcgacct gaggccgaca aagtagcagc cattgaggga gagttcaagc ttaggacgga	6180
gcaaaggaag acctttgtgg aactcatgaa aagaggagat cttcctgttt ggctggccta	6240
tcaggttgca tctgccggaa taacctacac agatagaaga tggtgctttg atggcacgac	6300
caacaacacc ataatggaag atagtgtgcc ggcagagggtg tggaccagac acggagagaa	6360
aagagtgtc aaaccgaggt ggatggacgc cagagtttgt tcagatcatg cggccctgaa	6420
gtcattcaag gagtttgccg ctgggaaaag aggagcggct tttggagtga tggaaagcct	6480
gggaacactg ccaggacaca tgacagagag attccaggaa gccattgaca acctcgctgt	6540
gctcatgcg gacagagactg gaagcaggcc ttacaaagcc gcggcgggccc aattgccgga	6600
gaccctagag accataatgc ttttgggggt gctgggaaca gtctcgctgg gaatcttctt	6660
cgtcttgatg aggaacaagg gcatagggaa gatgggcttt ggaatgggtga ctcttggggc	6720
cagcgcatgg ctcatgtggc tctcgaaat tgagccagcc agaattgcat gtgtcctcat	6780
tgttgtgttc ctattgctgg tggtgctcat acctgagcca gaaaagcaaa gatctcccca	6840
ggacaaccaa atggcaatca tcatcatggt agcagtaggt cttctgggct tgattaccgc	6900
caatgaactc ggatggttgg agagaacaaa gagtgaccta agccatctaa tgggaaggag	6960
agaggagggg gcaaccatag gattctcaat ggacattgac ctgcggccag cctcagcttg	7020
ggccatctat gctgccttga caactttcat taccacagcc gtccaacatg cagtgaccac	7080
ctcatacaac aactactcct taatggcgat ggccacgcaa gctggagtgt tgtttggtat	7140
gggcaaaggg atgccattct acgcatggga ctttgagtc ccgctgctaa tgataggttg	7200
ctactcacia ttaacacccc tgaccctaag agtggccatc attttgctcg tggcgacta	7260
catgtacttg atcccagggc tgcaggcagc agctgcgcgt gctgcccaga agagaacggc	7320
agctggcatc atgaagaacc ctgttgtgga tggaaatagt gtgactgaca ttgacacaat	7380
gacaattgac cccaagtgg agaaaaagat gggacagggt ctactcatag cagtagccgt	7440
ctccagcgcc atactgtcgc ggaccgctg ggggtggggg gaggctgggg ccctgatcac	7500
agccgcaact tccactttgt gggaaggctc tccgaacaag tactggaact cctctacagc	7560

cacttcactg	tgtaacat	ttaggggaag	ttacttggct	ggagcttctc	taatctacac	7620
agtaacaaga	aacgctggct	tggtcaagag	acgtgggggt	ggaacaggag	agaccctggg	7680
agagaaatgg	aaggcccgc	tgaaccagat	gtcggccctg	gagttctact	cctacaaaaa	7740
gtcaggcatc	accgaggtgt	gcagagaaga	ggcccgcgc	gccctcaagg	acggtgtggc	7800
aacgggaggc	catgctgtgt	cccgaggaag	tgcaaagctg	agatggttgg	tggagcgggg	7860
atacctgcag	ccctatggaa	aggtcattga	tcttggatgt	ggcagagggg	gctggagtta	7920
ctacgccgcc	accatccgca	aagttcaaga	agtgaaagga	tacacaaaag	gaggccctgg	7980
tcatgaagaa	cccgtgttgg	tgcaaagcta	tgggtggaac	atagtccgtc	ttaagagtgg	8040
ggtggacgtc	tttcatatgg	cggctgagcc	gtgtgacacg	ctgctgtgtg	acataggtga	8100
gtcatcatct	agtccctgaag	tggaagaagc	acggacgctc	agagtcctct	ccatggtggg	8160
ggattggctt	gaaaaaagac	caggagcctt	ttgtataaaa	gtgttgtgcc	catacaccag	8220
cactatgatg	gaaaccctgg	agcgactgca	gcgtaggtat	gggggaggac	tggtcagagt	8280
gccactctcc	cgcaactcta	cacatgagat	gtactgggtc	tctggagcga	aaagcaacac	8340
cataaaaagt	gtgtccacca	cgagccagct	cctcttgggg	cgcattggacg	ggcctaggag	8400
gccagtgaag	tatgaggagg	atgtgaatct	cggctctggc	acgcgggctg	tggtaagctg	8460
cgctgaagct	cccaacatga	agatcattgg	taaccgcatt	gaaaggatcc	gcagtgagca	8520
cgcggaaacg	tggttctttg	acgagaacca	cccatatagg	acatgggctt	accatggaag	8580
ctatgaggcc	cccacacaag	ggtcagcgtc	ctctctaata	aacggggttg	tcaggctcct	8640
gtcaaaaccc	tgggatgtgg	tgactggagt	cacaggaata	gccatgaccg	acaccacacc	8700
gtatggtcag	caaagagttt	tcaaggaaaa	agtggacact	agggtgccag	acccccaaga	8760
aggcactcgt	caggttatga	gcatggtctc	ttcctggttg	tggaaagagc	taggcaaaca	8820
caaacggcca	cgagtctgta	ccaagaaga	gttcatcaac	aaggttcgta	gcaatgcagc	8880
attaggggca	atatttgaag	aggaaaaaga	gtggaagact	gcagtggaag	ctgtgaacga	8940
tccaaggttc	tgggctctag	tggacaagga	aagagagcac	cacctgagag	gagagtgcca	9000
gagttgtgtg	tataacatga	tgggaaaaag	agaaaagaaa	caaggggaat	ttggaaaggc	9060
caagggcagc	cgcgccatct	ggtatatgtg	gctaggggct	agatttctag	agttcgaagc	9120
ccttggattc	ttgaacgagg	atcactggat	ggggagagag	aactcaggag	gtggtgttga	9180
agggctggga	ttacaaagac	tcggatatgt	cctagaagag	atgagtcgta	taccaggagg	9240
aaggatgtat	gcagatgaca	ctgctggctg	ggacacccgc	attagcaggt	ttgatctgga	9300

gaatgaagct ctaatcacca accaaatgga gaaagggcac agggccttgg cattggccat	9360
aatcaagtac acataccaaa acaaagtggg aaaggtcctt agaccagctg aaaaagggaa	9420
aacagttatg gacattattt cgagacaaga ccaaaggggg agcggacaag ttgtcactta	9480
cgctcttaac acattttacca acctagtggg gcaactcatt cggaatatgg aggctgagga	9540
agttctagag atgcaagact tgtgggtgct gcggagggtca gagaaagtga ccaactgggt	9600
gcagagcaac ggatgggata ggctcaaacg aatggcagtc agtggagatg attgcgttgt	9660
gaagccaatt gatgatagggt ttgcacatgc cctcagggtc ttgaatgata tgggaaaagt	9720
tagaaaggac acacaagagt ggaaaccctc aactggatgg gacaactggg aagaagttcc	9780
gttttgctcc caccacttca acaagctcca tctcaaggac gggagggtcca ttgtgggtcc	9840
ctgccgccac caagatgaac tgattggccg ggcccgctc tctccagggg cgggatggag	9900
catccgggag actgcttgcc tagcaaaatc atatgcgcag atgtggcagc tcctttat	9960
ccacagaagg gacctccgac tgatggccaa tgccatttgt tcatctgtgc cagttgactg	10020
ggttccaact gggagaacta cctgggtcaat ccatggaaag ggagaatgga tgaccactga	10080
agacatgctt gtggtgtgga acagagtgtg gattgaggag aacgaccaca tggaagacaa	10140
gacccagtt acgaaatgga cagacattcc ctatttgga aaaaggggaag acttgtggtg	10200
tggatctctc atagggcaca gaccgcgcac cacctgggct gagaacatta aaaacacagt	10260
caacatggtg cgcaggatca taggtgatga agaaaagtac atggactacc tatccacca	10320
agttcgctac ttgggtgaag aagggtctac acctggagtg ctgtaagcac caatctta	10380
gttgtcaggc ctgctagtca gccacagctt ggggaaagct gtgcagcctg tgacccccca	10440
ggagaagctg ggaaaccaag cctatagtca ggccgagaac gccatggcac ggaagaagcc	10500
atgctgcctg tgagcccctc agaggatact gagtcaaaaa accccacgcg cttggaggcg	10560
caggatggga aaagaagggtg gcgaccttcc ccacccttca atctggggcc tgaactggag	10620
atcagctgtg gatccccaga agagggacta gtgggttagag gagaccccc ggaaaacgca	10680
aaacagcata ttgacgctgg gaaagaccag agactccatg agtttcc	10727

<210> 13
 <211> 10374
 <212> DNA
 <213> Zika virus isolate Z1106033 polyprotein gene

<400> 13	
acaggtttta ttttggattt ggaaacgaga gtttctggtc atgaaaaacc caaaaaagaa	60
atccggagga ttccggattg tcaatatgct aaaacgcgga gtagcccggtg tgagcccctt	120

tgggggcttg	aagaggctgc	cagccggact	tctgctgggt	catgggcca	tcaggatggt	180
cttggcgatt	ctagcctttt	tgagattcac	ggcaatcaag	ccatcactgg	gtctcatcaa	240
tagatggggt	tcagtgggga	aaaaagaggc	tatggaaata	ataaagaagt	tcaagaaaga	300
tctggctgcc	atgctgagaa	taatcaatgc	taggaaggag	aagaagagac	gaggcgcaga	360
tactagtgtc	ggaattgttg	gcctcctgct	gaccacagct	atggcagcgg	aggtcactag	420
acgtgggagt	gcatactata	tgtacttgga	cagaaacgat	gctggggagg	ccatatcttt	480
tccaaccaca	ttgggggatga	ataagtgtta	tatacagatc	atggatcttg	gacacacgtg	540
tgatgccacc	atgagctatg	aatgccctat	gctggatgag	ggggtggaac	cagatgacgt	600
cgattgttgg	tgcaacacga	cgtcaacttg	ggttgtgtac	ggaacctgcc	atcacaaaaa	660
aggtgaagca	cggagatcta	gaagagctgt	gacgctcccc	tcccattcca	ctaggaagct	720
gcaaacgcgg	tcgcaaacct	ggttggaatc	aagagaatac	acaaagcact	tgattagagt	780
cgaaaattgg	atattcagga	accctggctt	cgcgtagca	gcagctgcca	tcgcttggct	840
tttggaagc	tcaacgagcc	aaaaagtcac	atacttggtc	atgatactgc	tgattgcccc	900
ggcatacagc	atcaggtgca	taggagtcag	caatagggac	tttgtggaag	gtatgtcagg	960
tgggacttgg	gttgatgttg	tcttgaaca	tggaggttgt	gtcactgtaa	tggcacagga	1020
caaaccgact	gtcgacatag	agctggttac	aacaacagtc	agcaacatgg	cggaggtaag	1080
atcctactgc	tatgagggcat	caatatcaga	catggcttcg	gacagccgct	gccaacaca	1140
aggtgaagcc	taccttgaca	agcaatcaga	cactcaatat	gtctgcaaaa	gaacgttagt	1200
ggacagaggc	tggggaaatg	gatgtggact	ttttggcaaa	gggagcctgg	tgacatgcgc	1260
taagtttgca	tgctccaaga	aatgaccgg	gaagagcatc	cagccagaga	atctggagta	1320
ccggataatg	ctgtcagttc	atggctccca	gcacagtggg	atgatcggtta	atgacacagg	1380
acatgaaact	gatgagaata	gagcgaaagt	tgagataacg	cccaattcac	caagagccga	1440
agccaccctg	gggggggttg	gaagcctagg	acttgattgt	gaaccgagga	caggccttga	1500
cttttcagat	ttgtattact	tgactatgaa	taacaagcac	tggctgggtc	acaaggagtg	1560
gttccacgac	attccattac	cttggcacgc	tggggcagac	accggaactc	cacactggaa	1620
caacaaagaa	gcactggtag	agttcaagga	cgcacatgcc	aaaaggcaaa	ctgtcgtggt	1680
tctagggagt	caagaaggag	cagttcacac	ggcccttgct	ggagctctgg	aggctgagat	1740
ggatggtgca	aagggaaggc	tgtcctctgg	ccacttgaaa	tgtcgccctga	aatggataa	1800
acttagattg	aagggcgtgt	catactcctt	gtgtactgca	gcgttcacat	tcaccaagat	1860

cccggtgtaa	acactgcacg	ggacagtcac	agtggaggta	cagtacgcag	ggacagatgg	1920
accttgcaag	gttccagctc	agatggcggt	ggacatgcaa	actctgaccc	cagttgggag	1980
gttgataacc	gctaaccccc	taatcactga	aagcactgag	aactctaaga	tgatgctgga	2040
acttgatcca	ccatttgggg	actcttacat	tgtcatagga	gtcggggaga	agaagatcac	2100
ccaccactgg	cacaggagtg	gcagcaccat	tggaaaagca	tttgaagcca	ctgtgagagg	2160
tgccaagaga	atggcagtct	tgggagacac	agcctgggac	tttggatcag	ttggaggcgc	2220
tctcaactca	ttgggcaagg	gcattccatca	aatcttttga	gcagctttca	aatcattggt	2280
tggaggaatg	tcctggttct	cacaaattct	cattggaacg	ttgctgatgt	ggttgggtct	2340
gaacgcaaag	aatggatcta	tttcccttat	gtgcttggcc	ttagggggag	tgttgatctt	2400
cttatccaca	gccgtctctg	ctgatgtggg	gtgctcgggt	gacttctcaa	agaaggagac	2460
gagatgcggt	acaggggtgt	tcgtctataa	cgacgttgaa	gcctggaggg	acaggtacaa	2520
gtaccatcct	gactcccccc	gtagattggc	agcagcagtc	aagcaagcct	gggaagatgg	2580
tatctgcggg	atctcctctg	tttcaagaat	ggaaaacatc	atgtggagat	cagtagaagg	2640
ggagctcaac	gcaatcctgg	aagagaatgg	agttcaactg	acggtcggtg	tgggatctgt	2700
aaaaaacccc	atgtggagag	gtccacagag	attgcccgtg	cctgtgaacg	agctgccccca	2760
cggctggaag	gcttggggga	aatcgactct	cgtcagagca	gcaaagacaa	ataacagctt	2820
tgctcgtggat	ggtgacacac	tgaaggaatg	cccactcaaa	catagagcat	ggaacagctt	2880
tcttgtggag	gatcatgggt	tcgggggtatt	tcacactagt	gtctgggtca	aggttagaga	2940
agattattca	ttagagtgtg	atccagccgt	tattggaaca	gctgttaagg	gaaaggaggc	3000
tgtacacagt	gatctaggct	actggattga	gagtgagaag	aatgacacat	ggaggctgaa	3060
gagggcccat	ctgatcgaga	tgaaaacatg	tgaatggcca	aagtcccaca	cattgtggac	3120
agatggaata	gaagagagtg	atctgatcat	acccaagtct	ttagctgggc	cactcagcca	3180
tcacaatacc	agagagggct	acaggaccca	aatgaaaggg	ccatggcaca	gtgaagagct	3240
tgaaattcgg	tttgaggaat	gcccaggcac	taagggtccac	gtggaggaaa	catgtggaac	3300
gagaggacca	tctctgagat	caaccactgc	aagcggaagg	gtgatcgagg	aatggtgctg	3360
cagggagtgc	acaatgcccc	cactgtcgtt	ccgggctaaa	gatggctggt	ggtatggaat	3420
ggagataagg	cccaggaaaag	aaccagaaaag	caacttagta	aggtcaatgg	tgactgcagg	3480
atcaactgat	cacatggacc	acttctccct	tggagtgctt	gtgattctgc	tcatggtgca	3540
ggaaggggtg	aagaagagaa	tgaccacaaa	gatcatcata	agcacatcaa	tggcagtgct	3600

ggtagctatg atcctgggag gattttcaat gaggtagcctg gctaagcttg caattttgat	3660
gggtgccacc ttcgcggaaa tgaacactgg aggagatgta gctcatcttg cgctgatagc	3720
ggcattcaaa gtcagaccag cggtgctggg atctttcatc ttcagagcta attggacacc	3780
ccgtgaaagc atgctgctgg ccttggcctc gtgtcttttg caaactgcga tctccgcctt	3840
ggaaggcgac ctgatgggtc tcatcaatgg ttttgctttg gcctgggttg caatacgagc	3900
gatggttgtt ccacgcactg ataacatcac cttggcaatc ctggctgctc tgacaccact	3960
ggcccggggc aactgcttg tggcgtggag agcaggcctt gctacttgcg gggggtttat	4020
gctcctctct ctgaaggga aaggcagtgt gaagaagaac ttaccatttg tcatggcctt	4080
gggactaacc gctgtgaggc tggtcgacct catcaacgtg gtgggactgc tgttgctcac	4140
aaggagtggg aagcggagct ggccccctag cgaagtactc acagctgttg gcctgatatg	4200
cgcattggct ggaggggttcg ccaaggcaga tatagagatg gctgggcca tggccgcggt	4260
cggctctgcta attgtcagtt acgtggtctc aggaaagagt gtggacatgt acattgaaag	4320
agcaggtgac atcacatggg aaaaagatgc ggaagtcact ggaaacagtc cccggctcga	4380
tgtggcgcta gatgagagtg gtgatttctc cctgggtggag gatgacggtc ccccatgag	4440
agagatcata ctcaagggtg tctgatgac catctgtggc atgaacccaa tagccatacc	4500
ctttgcagct ggagcgtggg acgtatacgt gaagactgga aaaaggagtg gtgctctatg	4560
ggatgtgcct gctcccaagg aagtaaaaaa gggggagacc acagatggag tgtacagagt	4620
aatgactcgt agactgctag gttcaacaca agttggagtg ggagttatgc aagagggggg	4680
ctttcacact atgtggcacg tcacaaaagg atccgcgctg agaagcggtg aaggagact	4740
tgatccatac tggggagatg tcaagcagga tctggtgtca tactgtggtc catggaagct	4800
agatgccgcc tgggacgggc acagcgaggt gcagctcttg gccgtgcccc ccggagagag	4860
agcgaggaac atccagactc tgcccgaat atttaagaca aaggatgggg acattggagc	4920
ggttgcgctg gattaccag caggaacttc aggatctcct atcctagaca agtgtgggag	4980
agtgatagga ctttatggca atggggctgt gatcaaaaat gggagttatg ttagtgccat	5040
caccaaggg aggagggagg aagagactcc tgttgagtgc ttcgagcctt cgatgctgaa	5100
gaagaagcag ctaactgtct tagacttgca tcctggagct gggaaaacca ggagagttct	5160
tcctgaaata gtccgtgaag ccataaaaac aagactccgt actgtgatct tagctccaac	5220
cagggttgtc gctgctgaaa tggaggaggc ccttagaggg cttccagtgc gttatatgac	5280
aacagcagtc aatgtcacc actctggaac agaaatcgtc gacttaatgt gccatgccac	5340

cttcacttcg	cgtctactac	agccaatcag	agtccccaac	tataatctgt	atattatgga	5400
tgaggccac	ttcacagatc	cctcaagtat	agcagcaaga	ggatacattt	caacaagggg	5460
tgagatgggc	gaggcggccg	ccatcttcat	gaccgccacg	ccaccaggaa	cccgtgacgc	5520
atttccggac	tccaactcac	caattatgga	caccgaagtg	gaagtcccag	agagagcctg	5580
gagctcaggc	tttgattggg	tgacggatca	ttctggaaaa	acagtttggt	ttgttccaag	5640
cgtgaggaac	ggcaatgaga	tcgcagcttg	tctgacaaag	gctggaaaac	gggtcataca	5700
gctcagcaga	aagacttttg	agacagagtt	ccagaaaaca	aaacatcaag	agtgggactt	5760
tgctcgtgaca	actgacattt	cagagatggg	cgccaacttt	aaagctgacc	gtgtcataga	5820
ttccaggaga	tgccctaaagc	cggtcatact	tgatggcgag	agagtcattc	tggctggacc	5880
catgcctgtc	acacatgcca	gcgctgccca	gaggaggggg	cgcataggca	ggaatcccaa	5940
caaacctgga	gatgagtatc	tgtatggagg	tgggtgcgca	gagactgacg	aagaccatgc	6000
acactggctt	gaagcaagaa	tgctccttga	caatattttac	ctccaagatg	gcctcatagc	6060
ctcgctctat	cgacctgagg	ccgacaaaagt	agcagccatt	gaggagagag	tcaagcttag	6120
gacggagcaa	aggaagacct	ttgtggaact	catgaaaaga	ggagatcttc	ctgtttggct	6180
ggcctatcag	gttgcatctg	ccggaataac	ctacacagat	agaagatggg	gctttgatgg	6240
cacgaccaac	aacaccataa	tggaagacag	tgtgccggca	gaagtgtgga	ccagacacgg	6300
agagaaaaga	gtgctcaaac	cgaggtggat	ggacgccaga	gtttgttcag	atcatgcggc	6360
cctgaagtca	ttcaaggagt	ttgccgctgg	gaaaagagga	gcggcttttg	gagtgatgga	6420
agccctggga	acactgccag	gacacatgac	agagagattc	caggaagcca	ttgacaacct	6480
cgctgtgctc	atgcgggcag	agactggaag	caggccttac	aaagccgcgg	cggcccaatt	6540
gccggagacc	ctagagacca	ttatgctttt	ggggttgctg	ggaacagtct	cgctgggaat	6600
cttcttcgtc	ttgatgagga	acaagggcat	agggaaagatg	ggctttggaa	tggtgactct	6660
tggggccagc	gcatggctca	tgtggctctc	ggaaattgag	ccagccagaa	ttgcatgtgt	6720
cctcattgtt	gtgttcctat	tgctgggtgg	gctcatacct	gagccagaaa	agcaaagatc	6780
tccccaggac	aaccaaattg	caatcatcat	catggtagca	gtaggtcttc	tgggcttgat	6840
taccgccaat	gaactcggat	ggttgagag	aacaaagagt	gacctaagcc	atctaattggg	6900
aaggagagag	gagggggcaa	ccataggatt	ctcaatggac	attgacctgc	ggccagcctc	6960
agcttgggcc	atctatgctg	ccttgacaac	tttcattacc	ccagccgtcc	aacatgcagt	7020
gaccacctca	tacaacaact	actccttaat	ggcgatggcc	acgcaagctg	gagtgttggt	7080

tggtatgggc aaagggatgc cattctacgc atgggacttt ggagtccccg tgctaattgat	7140
aggttgctac tcacaattaa caccctgac cctaatagtg gccatcattt tgctcgtggc	7200
gcactacatg tacttgatcc cagggctgca ggcagcagct gcgctgctg cccagaagag	7260
aacggcagct ggcacatga agaaccctgt tgtggatgga atagtgggtga ctgacattga	7320
cacaatgaca attgaccccc aagtggagaa aaagatggga caggtgctac tcatagcagt	7380
agccgtctcc agcgccatac tgtcgcgac cgcctggggg tggggggagg ctggggccct	7440
gatcacagcc gcaacttcca ctttgtggga aggctctccg aacaagtact ggaactcctc	7500
tacagccact tcaactgtgta acatttttag ggggaagttac ttggctggag cttctcta	7560
ctacacagta acaagaaacg ctggcttggg caagagacgt gggggtggaa caggagagac	7620
cctgggagag aaatggaagg cccgcttgaa ccagatgtcg gccctggagt tctactccta	7680
caaaaagtca ggcacaccg aggtgtgcag agaagaggcc cgccgcgcc tcaaggacgg	7740
tgtggcaacg ggaggccatg ctgtgtcccg aggaagtgca aagctgagat ggttgggtgga	7800
gcggggatac ctgcagccct atggaaaggt cattgatctt ggatgtggca gagggggctg	7860
gagttactac gccgccacca tccgcaaagt tcaagaagtg aaaggataca caaaaggagg	7920
ccctggtcat gaagaacccg tggtgtgca aagctatggg tggaacatag tccgtcttaa	7980
gagtggggtg gacgtctttc atatggcggc tgagccgtgt gacacgttgc tgtgtgacat	8040
aggtgagtca tcatctagtc ctgaagtgga agaagcacgg acgctcagag tcctctccat	8100
ggtgggggat tggcttgaaa aaagaccagg agccttttgt ataaaagtgt tgtgcccata	8160
caccagcact atgatggaaa ccctggagcg actgcagcgt aggtatgggg gaggactggt	8220
cagagtgcca ctctcccgca actctacaca tgagatgtac tgggtctctg gagcgaaaag	8280
caacaccata aaaagtgtgt ccaccacgag ccagctcctc ttggggcgca tggacggggc	8340
taggaggcca gtgaaatatg aggaggatgt gaatctcggc tctggcacgc gggctgtggt	8400
aagctgcgct gaagctccca acatgaagat cattggtaac cgcattgaaa ggatccgcag	8460
tgagcacgcg gaaacgtggt tctttgacga gaaccacca tataggacat gggcttacca	8520
tggaagctat gaggccccca cacaagggtc agcgtcctct ctaataaacg gggttgtcag	8580
gctcctgtca aaaccctggg atgtggtgac tggagtcaca ggaatagcca tgaccgacac	8640
cacaccgtat ggtcagcaaa gagttttcaa ggaaaaagtg gacactaggg tgccagaccc	8700
ccaagaaggc actcgtcagg ttatgagcat ggtctcttcc tggttgtgga aagagctagg	8760
caaacacaaa cggccacgag tctgtaccaa agaagagttc atcaacaagg ttcgtagcaa	8820

tgcagcatta	ggggcaatat	ttgaagagga	aaaagagtgg	aagactgcag	tggaagctgt	8880
gaacgatcca	aggttcttggg	ctctagtggg	caaggaaaga	gagcaccacc	tgagaggaga	8940
gtgccagagt	tgtgtgtaca	acatgatggg	aaaaagagaa	aagaaacaag	gggaatttgg	9000
aaaggccaag	ggcagccgcg	ccatctggta	tatgtggcta	ggggctagat	ttctagagtt	9060
cgaagccctt	ggattcttga	acgaggatca	ctggatgggg	agagagaact	caggaggtgg	9120
tgttgaaggg	ctgggattac	aaagactcgg	atatgtccta	gaagagatga	gtcgtatacc	9180
aggaggaagg	atgtatgcag	atgacactgc	tggctgggac	acccgcatta	gcaggtttga	9240
tctggagaat	gaagctctaa	tcaccaacca	aatggagaaa	gggcacaggg	ccttggcatt	9300
ggccataatc	aagtacacat	acaaaaacaa	agtggtaaag	gtccttagac	cagctgaaaa	9360
agggaaaaca	gttatggaca	ttatttcgag	acaagaccaa	agggggagcg	gacaagttgt	9420
cacttacgct	cttaacacat	ttaccaacct	agtggtgcaa	ctcattcgga	atatggaggc	9480
tgaggaagtt	ctagagatgc	aagacttgtg	gctgctgcgg	aggtcagaga	aagtgactaa	9540
ctggttgcag	agcaacggat	gggataggct	caaacgaatg	gcagtcagtg	gagatgattg	9600
cgttgtgaag	ccaattgatg	ataggtttgc	acatgccctc	aggttcttga	atgatatggg	9660
aaaagttagg	aaggacacac	aagagtggaa	accctcaact	ggatgggaca	actgggaaga	9720
agttccgttt	tgctcccacc	acttcaacaa	gtcccatctc	aaggacggga	ggtccattgt	9780
ggttccctgc	cgccaccaag	atgaactgat	tggccggggc	cgcgctctctc	caggggcggg	9840
atggagcatc	cgggagactg	cttgcctagc	aaaatcatat	gcgcaaagt	ggcagctcct	9900
ttatttccac	agaagggacc	tccgactgat	ggccaatgcc	atttgttcat	ctgtgccagt	9960
tgactgggtt	ccaactggga	gaactacctg	gtcaatccat	ggaaaggag	aatggatgac	10020
cactgaagac	atgcttgtgg	tgtggaacag	agtgtggatt	gaggagaacg	accacatgga	10080
agacaagacc	ccagttacga	aatggacaga	cattccctat	ttgggaaaaa	gggaagactt	10140
gtggtgtgga	tctctcatag	ggcacagacc	gcgcaccacc	tgggctgaga	acattaaaaa	10200
cacagtcaac	atggtgcgca	ggatcatagg	tgatgaagaa	aagtacatgg	actacctatc	10260
caccaagtt	cgctacttgg	gtgaagaagg	gtctacacct	ggagtgctgt	aagcaccaat	10320
cttaatgttg	tcaggcctgc	tagtcagcca	cagcttgggg	aaagctgtgc	agcc	10374

<210> 14

<211> 3423

<212> PRT

<213> Zika virus strain BeH818995 polyprotein

<400> 14

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
195 200 205

Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
210 215 220

Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr
 225 230 235 240

Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly
 245 250 255

Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr
 260 265 270

Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
 275 280 285

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
 290 295 300

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
 305 310 315 320

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
 325 330 335

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
 340 345 350

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
 355 360 365

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
 370 375 380

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
 385 390 395 400

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
 405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
 420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
 435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro

450		455		460											
Arg	Ala	Glu	Ala	Thr	Leu	Gly	Gly	Phe	Gly	Ser	Leu	Gly	Leu	Asp	Cys
465					470					475					480
Glu	Pro	Arg	Thr	Gly	Leu	Asp	Phe	Ser	Asp	Leu	Tyr	Tyr	Leu	Thr	Met
				485					490					495	
Asn	Asn	Lys	His	Trp	Leu	Val	His	Lys	Glu	Trp	Phe	His	Asp	Ile	Pro
			500					505					510		
Leu	Pro	Trp	His	Ala	Gly	Ala	Asp	Thr	Gly	Thr	Pro	His	Trp	Asn	Asn
		515					520					525			
Lys	Glu	Ala	Leu	Val	Glu	Phe	Lys	Asp	Ala	His	Ala	Lys	Arg	Gln	Thr
	530					535					540				
Val	Val	Val	Leu	Gly	Ser	Gln	Glu	Gly	Ala	Val	His	Thr	Ala	Leu	Ala
545					550					555					560
Gly	Ala	Leu	Glu	Ala	Glu	Met	Asp	Gly	Ala	Lys	Gly	Arg	Leu	Ser	Ser
				565					570					575	
Gly	His	Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Arg	Leu	Lys	Gly
			580					585					590		
Val	Ser	Tyr	Ser	Leu	Cys	Thr	Ala	Ala	Phe	Thr	Phe	Thr	Lys	Ile	Pro
		595					600						605		
Ala	Glu	Thr	Leu	His	Gly	Thr	Val	Thr	Val	Glu	Val	Gln	Tyr	Ala	Gly
	610					615					620				
Thr	Asp	Gly	Pro	Cys	Lys	Val	Pro	Ala	Gln	Met	Ala	Val	Asp	Met	Gln
625					630					635					640
Thr	Leu	Thr	Pro	Val	Gly	Arg	Leu	Ile	Thr	Ala	Asn	Pro	Val	Ile	Thr
				645					650					655	
Glu	Ser	Thr	Glu	Asn	Ser	Lys	Met	Met	Leu	Glu	Leu	Asp	Pro	Pro	Phe
			660					665					670		
Gly	Asp	Ser	Tyr	Ile	Val	Ile	Gly	Val	Gly	Glu	Lys	Lys	Ile	Thr	His
		675					680					685			

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
770 775 780

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val

915	920	925
Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp 930 935 940		
Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser 945 950 955 960		
Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala 965 970 975		
Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu 980 985 990		
Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg 995 1000 1005		
Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His 1010 1015 1020		
Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro 1025 1030 1035		
Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly 1040 1045 1050		
Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu 1055 1060 1065		
Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu 1070 1075 1080		
Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser 1085 1090 1095		
Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro 1100 1105 1110		
Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu 1115 1120 1125		
Ile Arg Pro Arg Lys Glu Pro Glu Ser Asn Leu Val Arg Ser Met 1130 1135 1140		

Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg

1355						1360						1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val	
1370						1375					1380				
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile	
1385						1390					1395				
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser	
1400						1405					1410				
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala	
1415						1420					1425				
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser	
1430						1435					1440				
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu	
1445						1450					1455				
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val	
1460						1465					1470				
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe	
1475						1480					1485				
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser	
1490						1495					1500				
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly	
1505						1510					1515				
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu	
1520						1525					1530				
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe	
1535						1540					1545				
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly	
1550						1555					1560				
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu	
1565						1570					1575				

Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile

1790						1795						1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	
1805						1810					1815				
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser	
1820						1825					1830				
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser	
1835						1840					1845				
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp	
1850						1855					1860				
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu	
1865						1870					1875				
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	
1880						1885					1890				
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val	
1895						1900					1905				
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp	
1910						1915					1920				
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp	
1925						1930					1935				
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala	
1940						1945					1950				
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys	
1955						1960					1965				
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp	
1970						1975					1980				
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn	
1985						1990					1995				
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu	
2000						2005					2010				

Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu

2225		2230		2235
Ile Pro Glu Pro Glu Lys	Gln Arg Ser Pro Gln Asp	Asn Gln Met		
2240	2245	2250		
Ala Ile Ile Ile Met Val	Ala Val Gly Leu Leu Gly	Leu Ile Thr		
2255	2260	2265		
Ala Asn Glu Leu Gly Trp	Leu Glu Arg Thr Lys Ser	Asp Leu Ser		
2270	2275	2280		
His Leu Met Gly Arg Arg	Glu Glu Gly Ala Thr Ile	Gly Phe Ser		
2285	2290	2295		
Met Asp Ile Asp Leu Arg	Pro Ala Ser Ala Trp Ala	Ile Tyr Ala		
2300	2305	2310		
Ala Leu Thr Thr Phe Ile	Thr Pro Ala Val Gln His	Ala Val Thr		
2315	2320	2325		
Thr Ser Tyr Asn Asn Tyr	Ser Leu Met Ala Met Ala	Thr Gln Ala		
2330	2335	2340		
Gly Val Leu Phe Gly Met	Gly Lys Gly Met Pro Phe	Tyr Ala Trp		
2345	2350	2355		
Asp Phe Gly Val Pro Leu	Leu Met Ile Gly Cys Tyr	Ser Gln Leu		
2360	2365	2370		
Thr Pro Leu Thr Leu Ile	Val Ala Ile Ile Leu Leu	Val Ala His		
2375	2380	2385		
Tyr Met Tyr Leu Ile Pro	Gly Leu Gln Ala Ala Ala	Ala Arg Ala		
2390	2395	2400		
Ala Gln Lys Arg Thr Ala	Ala Gly Ile Met Lys Asn	Pro Val Val		
2405	2410	2415		
Asp Gly Ile Val Val Thr	Asp Ile Asp Thr Met Thr	Ile Asp Pro		
2420	2425	2430		
Gln Val Glu Lys Lys Met	Gly Gln Val Leu Leu Ile	Ala Val Ala		
2435	2440	2445		

Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
	2450					2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
	2465					2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
	2480					2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
	2495					2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
	2510					2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
	2525					2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
	2540					2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
	2555					2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
	2570					2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
	2585					2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
	2600					2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
	2615					2620					2625			
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
	2630					2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
	2645					2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser

2660		2665		2670
Pro Glu Val Glu Glu Ala Arg Thr Leu Arg Val Leu Ser Met Val				
2675		2680		2685
Gly Asp Trp Leu Glu Lys Arg Pro Gly Ala Phe Cys Ile Lys Val				
2690		2695		2700
Leu Cys Pro Tyr Thr Ser Thr Met Met Glu Thr Leu Glu Arg Leu				
2705		2710		2715
Gln Arg Arg Tyr Gly Gly Gly Leu Val Arg Val Pro Leu Ser Arg				
2720		2725		2730
Asn Ser Thr His Glu Met Tyr Trp Val Ser Gly Ala Lys Ser Asn				
2735		2740		2745
Thr Ile Lys Ser Val Ser Thr Thr Ser Gln Leu Leu Leu Gly Arg				
2750		2755		2760
Met Asp Gly Pro Arg Arg Pro Val Lys Tyr Glu Glu Asp Val Asp				
2765		2770		2775
Leu Gly Ser Gly Thr Arg Ala Val Val Ser Cys Ala Glu Ala Pro				
2780		2785		2790
Asn Met Lys Ile Ile Gly Asn Arg Ile Glu Arg Ile Arg Ser Glu				
2795		2800		2805
His Ala Glu Thr Trp Phe Phe Asp Glu Asn His Pro Tyr Arg Thr				
2810		2815		2820
Trp Ala Tyr His Gly Ser Tyr Glu Ala Pro Thr Gln Gly Ser Ala				
2825		2830		2835
Ser Ser Leu Ile Asn Gly Val Val Arg Leu Leu Ser Lys Pro Trp				
2840		2845		2850
Asp Val Val Thr Gly Val Thr Gly Ile Ala Met Thr Asp Thr Thr				
2855		2860		2865
Pro Tyr Gly Gln Gln Arg Val Phe Lys Glu Lys Val Asp Thr Arg				
2870		2875		2880

Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly

3095							3100						3105
Lys Thr Val Met Asp Ile Ile Ser Arg Gln Asp Gln Arg Gly Ser													
3110							3115						3120
Gly Gln Val Val Thr Tyr Ala Leu Asn Thr Phe Thr Asn Leu Val													
3125							3130						3135
Val Gln Leu Ile Arg Asn Met Glu Ala Glu Glu Val Leu Glu Met													
3140							3145						3150
Gln Asp Leu Trp Leu Leu Arg Arg Ser Glu Lys Val Thr Asn Trp													
3155							3160						3165
Leu Gln Ser Asn Gly Trp Asp Arg Leu Lys Arg Met Ala Val Ser													
3170							3175						3180
Gly Asp Asp Cys Val Val Lys Pro Ile Asp Asp Arg Phe Ala His													
3185							3190						3195
Ala Leu Arg Phe Leu Asn Asp Met Gly Lys Val Arg Lys Asp Thr													
3200							3205						3210
Gln Glu Trp Lys Pro Ser Thr Gly Trp Asp Asn Trp Glu Glu Val													
3215							3220						3225
Pro Phe Cys Ser His His Phe Asn Lys Leu His Leu Lys Asp Gly													
3230							3235						3240
Arg Ser Ile Val Val Pro Cys Arg His Gln Asp Glu Leu Ile Gly													
3245							3250						3255
Arg Ala Arg Val Ser Pro Gly Ala Gly Trp Ser Ile Arg Glu Thr													
3260							3265						3270
Ala Cys Leu Ala Lys Ser Tyr Ala Gln Met Trp Gln Leu Leu Tyr													
3275							3280						3285
Phe His Arg Arg Asp Leu Arg Leu Met Ala Asn Ala Ile Cys Ser													
3290							3295						3300
Ser Val Pro Val Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser													
3305							3310						3315

Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val
 3320 3325 3330

Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp
 3335 3340 3345

Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
 3350 3355 3360

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg
 3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 15
 <211> 3423
 <212> PRT
 <213> Zika virus isolate SSABR1 polyprotein

<400> 15

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

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

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
 325 330 335

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
 340 345 350

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
 355 360 365

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
 370 375 380

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
 385 390 395 400

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
 405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
 420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
 435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
 450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
 465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
 485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
 500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
 515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
 530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
 545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
770 775 780

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr	Leu	Trp	Thr	Asp	Gly	Ile	Glu	Glu	Ser	Asp	Leu	Ile	Ile	Pro
1025						1030					1035			
Lys	Ser	Leu	Ala	Gly	Pro	Leu	Ser	His	His	Asn	Thr	Arg	Glu	Gly
1040						1045					1050			
Tyr	Arg	Thr	Gln	Met	Lys	Gly	Pro	Trp	His	Ser	Glu	Glu	Leu	Glu
1055						1060					1065			
Ile	Arg	Phe	Glu	Glu	Cys	Pro	Gly	Thr	Lys	Val	His	Val	Glu	Glu
1070						1075					1080			
Thr	Cys	Gly	Thr	Arg	Gly	Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser
1085						1090					1095			
Gly	Arg	Val	Ile	Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro
1100						1105					1110			
Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu
1115						1120					1125			
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met
1130						1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			

Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			

Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
1460						1465					1470			
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			

Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
	1670					1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
	1685					1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
	1700					1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
	1715					1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
	1730					1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
	1745					1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
	1760					1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
	1775					1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
	1790					1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
	1805					1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
	1820					1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
	1835					1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
	1850					1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
	1865					1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
	1880					1885					1890			

Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			

Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			

Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
2510						2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
2525						2530					2535			

Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			

Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
	2765					2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
	2780					2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
	2795					2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
	2810					2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
	2825					2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
	2840					2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
	2855					2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
	2870					2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
	2885					2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
	2900					2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
	2915					2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
	2930					2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
	2945					2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
	2960					2965					2970			

Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			

Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			
Ser	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3305						3310					3315			
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Val
3320						3325					3330			
Val	Trp	Asn	Arg	Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp
3335						3340					3345			
Lys	Thr	Pro	Val	Thr	Lys	Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys
3350						3355					3360			
Arg	Glu	Asp	Leu	Trp	Cys	Gly	Ser	Leu	Ile	Gly	His	Arg	Pro	Arg
3365						3370					3375			
Thr	Thr	Trp	Ala	Glu	Asn	Ile	Lys	Asn	Thr	Val	Asn	Met	Val	Arg
3380						3385					3390			
Arg	Ile	Ile	Gly	Asp	Glu	Glu	Lys	Tyr	Met	Asp	Tyr	Leu	Ser	Thr
3395						3400					3405			

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 16

<211> 3423

<212> PRT

<213> Zika virus strain Natal RGN polyprotein

<400> 16

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
 100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
 130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
 145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
 165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
 180 185 190

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

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

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
770 775 780

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln

885	890	895
Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp		
900	905	910
Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val		
915	920	925
Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Glu His Arg Ala Trp		
930	935	940
Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser		
945	950	955
Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala		
965	970	975
Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu		
980	985	990
Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg		
995	1000	1005
Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His		
1010	1015	1020
Thr Leu Trp Ala Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro		
1025	1030	1035
Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly		
1040	1045	1050
Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu		
1055	1060	1065
Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu		
1070	1075	1080
Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser		
1085	1090	1095
Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro		
1100	1105	1110

Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu
	1115					1120					1125			
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Val
	1130					1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
	1145					1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
	1160					1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
	1175					1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
	1190					1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
	1205					1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
	1220					1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
	1235					1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
	1250					1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
	1265					1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
	1280					1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
	1295					1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
	1310					1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys

1325						1330						1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg	
1340						1345					1350				
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg	
1355						1360					1365				
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val	
1370						1375					1380				
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile	
1385						1390					1395				
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser	
1400						1405					1410				
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala	
1415						1420					1425				
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser	
1430						1435					1440				
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu	
1445						1450					1455				
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val	
1460						1465					1470				
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe	
1475						1480					1485				
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser	
1490						1495					1500				
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly	
1505						1510					1515				
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu	
1520						1525					1530				
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe	
1535						1540					1545				

His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
	1550					1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
	1565					1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
	1580					1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
	1595					1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
	1610					1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
	1625					1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
	1640					1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
	1655					1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
	1670					1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
	1685					1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
	1700					1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
	1715					1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
	1730					1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
	1745					1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu

1760						1765						1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu	
1775						1780					1785				
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	
1790						1795					1800				
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	
1805						1810					1815				
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser	
1820						1825					1830				
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser	
1835						1840					1845				
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp	
1850						1855					1860				
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu	
1865						1870					1875				
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	
1880						1885					1890				
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val	
1895						1900					1905				
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp	
1910						1915					1920				
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp	
1925						1930					1935				
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala	
1940						1945					1950				
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys	
1955						1960					1965				
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp	
1970						1975					1980				

Glu 1985	Asp	His	Ala	His	Trp	Leu 1990	Glu	Ala	Arg	Met	Leu 1995	Leu	Asp	Asn
Ile 2000	Tyr	Leu	Gln	Asp	Gly	Leu 2005	Ile	Ala	Ser	Leu	Tyr 2010	Arg	Pro	Glu
Ala 2015	Asp	Lys	Val	Ala	Ala	Ile 2020	Glu	Gly	Glu	Phe	Lys 2025	Leu	Arg	Thr
Glu 2030	Gln	Arg	Lys	Thr	Phe	Val 2035	Glu	Leu	Met	Lys	Arg 2040	Gly	Asp	Leu
Pro 2045	Val	Trp	Leu	Ala	Tyr	Gln 2050	Val	Ala	Ser	Ala	Gly 2055	Ile	Thr	Tyr
Thr 2060	Asp	Arg	Arg	Trp	Cys	Phe 2065	Asp	Gly	Thr	Thr	Asn 2070	Asn	Thr	Ile
Met 2075	Glu	Asp	Ser	Val	Pro	Ala 2080	Glu	Val	Trp	Thr	Arg 2085	His	Gly	Glu
Lys 2090	Arg	Val	Leu	Lys	Pro	Arg 2095	Trp	Met	Asp	Ala	Arg 2100	Val	Cys	Ser
Asp 2105	His	Ala	Ala	Leu	Lys	Ser 2110	Phe	Lys	Glu	Phe	Ala 2115	Ala	Gly	Lys
Arg 2120	Gly	Ala	Ala	Phe	Gly	Val 2125	Met	Glu	Ala	Leu	Gly 2130	Thr	Leu	Pro
Gly 2135	His	Met	Thr	Glu	Arg	Phe 2140	Gln	Glu	Ala	Ile	Asp 2145	Asn	Leu	Ala
Val 2150	Leu	Met	Arg	Ala	Glu	Thr 2155	Gly	Ser	Arg	Pro	Tyr 2160	Lys	Ala	Ala
Ala 2165	Ala	Gln	Leu	Pro	Glu	Thr 2170	Leu	Glu	Thr	Ile	Met 2175	Leu	Leu	Gly
Leu 2180	Leu	Gly	Thr	Val	Ser	Leu 2185	Gly	Ile	Phe	Phe	Val 2190	Leu	Met	Arg
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly

2195		2200		2205
Ala Ser 2210	Ala Trp Leu Met	Trp Leu Ser Glu Ile 2215	Glu Pro Ala Arg 2220	
Ile Ala 2225	Cys Val Leu Ile	Val Val Phe Leu Leu 2230	Leu Val Val Leu 2235	
Ile Pro 2240	Glu Pro Glu Lys	Gln Arg Ser Pro Gln 2245	Asp Asn Gln Met 2250	
Ala Ile 2255	Ile Ile Met Val	Ala Val Gly Leu Leu 2260	Gly Leu Ile Thr 2265	
Ala Asn 2270	Glu Leu Gly Trp	Leu Glu Arg Thr Lys 2275	Ser Asp Leu Ser 2280	
His Leu 2285	Met Gly Arg Arg	Glu Glu Gly Ala Thr 2290	Ile Gly Phe Ser 2295	
Met Asp 2300	Ile Asp Leu Arg	Pro Ala Ser Ala Trp 2305	Ala Ile Tyr Ala 2310	
Ala Leu 2315	Thr Thr Phe Ile	Thr Pro Ala Val Gln 2320	His Ala Val Thr 2325	
Thr Ser 2330	Tyr Asn Asn Tyr	Ser Leu Met Ala Met 2335	Ala Thr Gln Ala 2340	
Gly Val 2345	Leu Phe Gly Met	Gly Lys Gly Met Pro 2350	Phe Tyr Ala Trp 2355	
Asp Phe 2360	Gly Val Pro Leu	Leu Met Ile Gly Cys 2365	Tyr Ser Gln Leu 2370	
Thr Pro 2375	Leu Thr Leu Ile	Val Ala Ile Ile Leu 2380	Leu Val Ala His 2385	
Tyr Met 2390	Tyr Leu Ile Pro	Gly Leu Gln Ala Ala 2395	Ala Ala Arg Ala 2400	
Ala Gln 2405	Lys Arg Thr Ala	Ala Gly Ile Met Lys 2410	Asn Pro Val Val 2415	

Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			
Ile	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
2510						2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
2525						2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile

2630						2635						2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu	
2645						2650					2655				
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser	
2660						2665					2670				
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val	
2675						2680					2685				
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val	
2690						2695					2700				
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu	
2705						2710					2715				
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg	
2720						2725					2730				
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn	
2735						2740					2745				
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg	
2750						2755					2760				
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn	
2765						2770					2775				
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro	
2780						2785					2790				
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu	
2795						2800					2805				
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr	
2810						2815					2820				
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala	
2825						2830					2835				
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp	
2840						2845					2850				

Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met

3065		3070		3075
Glu Lys Gly His Arg Ala Leu Ala Leu Ala Ile Ile Lys Tyr Thr	3080	3085		3090
Tyr Gln Asn Lys Val Val Lys Val Leu Arg Pro Ala Glu Lys Gly	3095	3100		3105
Lys Thr Val Met Asp Ile Ile Ser Arg Gln Asp Gln Arg Gly Ser	3110	3115		3120
Gly Gln Val Val Thr Tyr Ala Leu Asn Thr Phe Thr Asn Leu Val	3125	3130		3135
Val Gln Leu Ile Arg Asn Met Glu Ala Glu Glu Val Leu Glu Met	3140	3145		3150
Gln Asp Leu Trp Leu Leu Arg Arg Ser Glu Lys Val Thr Asn Trp	3155	3160		3165
Leu Gln Ser Asn Gly Trp Asp Arg Leu Lys Arg Met Ala Val Ser	3170	3175		3180
Gly Asp Asp Cys Val Val Lys Pro Ile Asp Asp Arg Phe Ala His	3185	3190		3195
Ala Leu Arg Phe Leu Asn Asp Met Gly Lys Val Arg Lys Asp Thr	3200	3205		3210
Gln Glu Trp Lys Pro Ser Thr Gly Trp Asp Asn Trp Glu Glu Val	3215	3220		3225
Pro Phe Cys Ser His His Phe Asn Lys Leu His Leu Lys Asp Gly	3230	3235		3240
Arg Ser Ile Val Val Pro Cys Arg His Gln Asp Glu Leu Ile Gly	3245	3250		3255
Arg Ala Arg Val Ser Pro Gly Ala Gly Trp Ser Ile Arg Glu Thr	3260	3265		3270
Ala Cys Leu Ala Lys Ser Tyr Ala Gln Met Trp Gln Leu Leu Tyr	3275	3280		3285

Phe His Arg Arg Asp Leu Arg Leu Met Ala Asn Ala Ile Cys Ser
 3290 3295 3300

Ser Val Pro Val Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser
 3305 3310 3315

Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val
 3320 3325 3330

Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp
 3335 3340 3345

Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
 3350 3355 3360

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg
 3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 17

<211> 3423

<212> PRT

<213> Zika virus strain Haiti/1225/2014 polyprotein

<400> 17

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
195 200 205

Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
210 215 220

Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr
225 230 235 240

Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly
245 250 255

Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr
260 265 270

Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
275 280 285

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

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
770 775 780

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser His Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro
1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
1040 1045 1050

Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu
1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
1100 1105 1110

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu
1115 1120 1125

Ile Arg Pro Arg Lys Glu Pro Glu Ser Asn Leu Val Arg Ser Met
1130 1135 1140

Val Thr Ala Gly Ser Thr Asp His Met Asp His Phe Ser Leu Gly
1145 1150 1155

Val Leu Val Ile Leu Leu Met Val Gln Glu Gly Leu Lys Lys Arg
1160 1165 1170

Met Thr Thr Lys Ile Ile Ile Ser Thr Ser Met Ala Val Leu Val
1175 1180 1185

Ala Met Ile Leu Gly Gly Phe Ser Met Ser Asp Leu Ala Lys Leu
1190 1195 1200

Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			

Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
1460						1465					1470			
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			

Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	Tyr	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			

Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			

Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Met	Gly	Phe	Ser
2285						2290					2295			

Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Met	Ala	Val	Ala
2435						2440					2445			
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			

Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
2510						2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
2525						2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			

Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			

Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			

Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			
Ser	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3305						3310					3315			
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Val
3320						3325					3330			
Val	Trp	Asn	Arg	Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp
3335						3340					3345			
Lys	Thr	Pro	Val	Thr	Lys	Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys
3350						3355					3360			
Arg	Glu	Asp	Leu	Trp	Cys	Gly	Ser	Leu	Ile	Gly	His	Arg	Pro	Arg
3365						3370					3375			

Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg
 3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 18
 <211> 3423
 <212> PRT
 <213> Zika virus strain PRVABC59 polyprotein
 <400> 18

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Thr
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
 100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
 130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
 145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
195 200 205

Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
210 215 220

Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr
225 230 235 240

Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly
245 250 255

Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr
260 265 270

Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
275 280 285

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
290 295 300

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
305 310 315 320

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
325 330 335

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
340 345 350

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
355 360 365

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
370 375 380

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys

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

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
770 775 780

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser

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

Thr	Cys	Gly	Thr	Arg	Gly	Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser
1085						1090					1095			
Gly	Arg	Val	Ile	Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro
1100						1105					1110			
Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu
1115						1120					1125			
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met
1130						1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala

1295		1300		1305
Arg Gly Thr Leu Leu Val	Ala Trp Arg Ala Gly Leu	Ala Thr Cys		
1310	1315	1320		
Gly Gly Phe Met Leu Leu	Ser Leu Lys Gly Lys Gly	Ser Val Lys		
1325	1330	1335		
Lys Asn Leu Pro Phe Val	Met Ala Leu Gly Leu Thr	Ala Val Arg		
1340	1345	1350		
Leu Val Asp Pro Ile Asn	Val Val Gly Leu Leu Leu	Leu Thr Arg		
1355	1360	1365		
Ser Gly Lys Arg Ser Trp	Pro Pro Ser Glu Val Leu	Thr Ala Val		
1370	1375	1380		
Gly Leu Ile Cys Ala Leu	Ala Gly Gly Phe Ala Lys	Ala Asp Ile		
1385	1390	1395		
Glu Met Ala Gly Pro Met	Ala Ala Val Gly Leu Leu	Ile Val Ser		
1400	1405	1410		
Tyr Val Val Ser Gly Lys	Ser Val Asp Met Tyr Ile	Glu Arg Ala		
1415	1420	1425		
Gly Asp Ile Thr Trp Glu	Lys Asp Ala Glu Val Thr	Gly Asn Ser		
1430	1435	1440		
Pro Arg Leu Asp Val Ala	Leu Asp Glu Ser Gly Asp	Phe Ser Leu		
1445	1450	1455		
Val Glu Asp Asp Gly Pro	Pro Met Arg Glu Ile Ile	Leu Lys Val		
1460	1465	1470		
Val Leu Met Thr Ile Cys	Gly Met Asn Pro Ile Ala	Ile Pro Phe		
1475	1480	1485		
Ala Ala Gly Ala Trp Tyr	Val Tyr Val Lys Thr Gly	Lys Arg Ser		
1490	1495	1500		
Gly Ala Leu Trp Asp Val	Pro Ala Pro Lys Glu Val	Lys Lys Gly		
1505	1510	1515		

Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val

1730						1735						1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu	
1745						1750					1755				
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu	
1760						1765					1770				
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu	
1775						1780					1785				
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	
1790						1795					1800				
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	
1805						1810					1815				
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser	
1820						1825					1830				
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser	
1835						1840					1845				
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp	
1850						1855					1860				
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu	
1865						1870					1875				
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	
1880						1885					1890				
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val	
1895						1900					1905				
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp	
1910						1915					1920				
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp	
1925						1930					1935				
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala	
1940						1945					1950				

Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly

2165		2170		2175
Leu 2180	Leu 2185	Gly 2190	Thr 2195	Val 2200
Val 2205	Ser 2210	Met 2215	Gly 2220	Ile 2225
Phe 2230	Phe 2235	Val 2240	Leu 2245	Met 2250
Asn 2195	Lys 2200	Gly 2205	Ile 2210	Gly 2215
Lys 2220	Met 2225	Gly 2230	Phe 2235	Gly 2240
Met 2245	Val 2250	Thr 2255	Leu 2260	Gly 2265
Ala 2210	Ser 2215	Ala 2220	Trp 2225	Leu 2230
Trp 2235	Leu 2240	Ser 2245	Glu 2250	Ile 2255
Glu 2260	Pro 2265	Ala 2270	Arg 2275	Leu 2280
Ile 2285	Val 2290	Val 2295	Phe 2300	Leu 2305
Val 2310	Val 2315	Leu 2320	Val 2325	Leu 2330
Ile 2335	Pro 2340	Glu 2345	Lys 2350	Gln 2355
Asn 2360	Gln 2365	Met 2370	Leu 2375	Gly 2380
Ala 2255	Ile 2260	Ile 2265	Ile 2270	Met 2275
Val 2280	Ala 2285	Val 2290	Gly 2295	Leu 2300
Leu 2305	Gly 2310	Leu 2315	Leu 2320	Gly 2325
Ala 2270	Asn 2275	Glu 2280	Leu 2285	Gly 2290
Trp 2295	Leu 2300	Glu 2305	Arg 2310	Thr 2315
Lys 2320	Ser 2325	Asp 2330	Leu 2335	Ser 2340
His 2285	Leu 2290	Met 2295	Gly 2300	Arg 2305
Arg 2310	Glu 2315	Glu 2320	Gly 2325	Ala 2330
Thr 2335	Ile 2340	Gly 2345	Phe 2350	Ser 2355
Met 2360	Ala 2365	Trp 2370	Ile 2375	Ala 2380
Ala 2385	Ile 2390	Tyr 2395	Ser 2400	Gln 2405
Leu 2410	Thr 2415	Ala 2420	Val 2425	Thr 2430
Ala 2435	Val 2440	Ala 2445	Val 2450	Thr 2455
Met 2460	Ala 2465	Ser 2470	Ala 2475	Trp 2480
Pro 2485	Ala 2490	Val 2495	Gln 2500	His 2505
Thr 2510	Pro 2515	Ala 2520	Val 2525	Gln 2530
His 2535	Leu 2540	Met 2545	Ala 2550	Trp 2555
Gly 2560	Val 2565	Leu 2570	Phe 2575	Gly 2580
Met 2585	Gly 2590	Met 2595	Pro 2600	Phe 2605
Tyr 2610	Ser 2615	Gln 2620	Leu 2625	His 2630
Ala 2635	Val 2640	Thr 2645	Ala 2650	Val 2655
Thr 2660	Pro 2665	Leu 2670	Thr 2675	Leu 2680
Ile 2685	Val 2690	Ala 2695	Ile 2700	Ile 2705
Leu 2710	Leu 2715	Leu 2720	Leu 2725	Leu 2730

Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
	2390					2395						2400		
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
	2405					2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
	2420					2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
	2435					2440					2445			
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
	2450					2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
	2465					2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
	2480					2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
	2495					2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
	2510					2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
	2525					2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
	2540					2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
	2555					2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
	2570					2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
	2585					2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Val	Ala	Thr

2600		2605		2610
Ile Arg Lys Val Gln Glu Val Lys Gly Tyr Thr Lys Gly Gly Pro				
2615		2620		2625
Gly His Glu Glu Pro Val Leu Val Gln Ser Tyr Gly Trp Asn Ile				
2630		2635		2640
Val Arg Leu Lys Ser Gly Val Asp Val Phe His Met Ala Ala Glu				
2645		2650		2655
Pro Cys Asp Thr Leu Leu Cys Asp Ile Gly Glu Ser Ser Ser Ser				
2660		2665		2670
Pro Glu Val Glu Glu Ala Arg Thr Leu Arg Val Leu Ser Met Val				
2675		2680		2685
Gly Asp Trp Leu Glu Lys Arg Pro Gly Ala Phe Cys Ile Lys Val				
2690		2695		2700
Leu Cys Pro Tyr Thr Ser Thr Met Met Glu Thr Leu Glu Arg Leu				
2705		2710		2715
Gln Arg Arg Tyr Gly Gly Gly Leu Val Arg Val Pro Leu Ser Arg				
2720		2725		2730
Asn Ser Thr His Glu Met Tyr Trp Val Ser Gly Ala Lys Ser Asn				
2735		2740		2745
Thr Ile Lys Ser Val Ser Thr Thr Ser Gln Leu Leu Leu Gly Arg				
2750		2755		2760
Met Asp Gly Pro Arg Arg Pro Val Lys Tyr Glu Glu Asp Val Asn				
2765		2770		2775
Leu Gly Ser Gly Thr Arg Ala Val Val Ser Cys Ala Glu Ala Pro				
2780		2785		2790
Asn Met Lys Ile Ile Gly Asn Arg Ile Glu Arg Ile Arg Ser Glu				
2795		2800		2805
His Ala Glu Thr Trp Phe Phe Asp Glu Asn His Pro Tyr Arg Thr				
2810		2815		2820

Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly

3035		3040		3045
Gly Arg Met Tyr Ala Asp Asp Thr Ala Gly Trp Asp Thr Arg Ile				
3050		3055		3060
Ser Arg Phe Asp Leu Glu Asn Glu Ala Leu Ile Thr Asn Gln Met				
3065		3070		3075
Glu Lys Gly His Arg Ala Leu Ala Leu Ala Ile Ile Lys Tyr Thr				
3080		3085		3090
Tyr Gln Asn Lys Val Val Lys Val Leu Arg Pro Ala Glu Lys Gly				
3095		3100		3105
Lys Thr Val Met Asp Ile Ile Ser Arg Gln Asp Gln Arg Gly Ser				
3110		3115		3120
Gly Gln Val Val Thr Tyr Ala Leu Asn Thr Phe Thr Asn Leu Val				
3125		3130		3135
Val Gln Leu Ile Arg Asn Met Glu Ala Glu Glu Val Leu Glu Met				
3140		3145		3150
Gln Asp Leu Trp Leu Leu Arg Arg Ser Glu Lys Val Thr Asn Trp				
3155		3160		3165
Leu Gln Ser Asn Gly Trp Asp Arg Leu Lys Arg Met Ala Val Ser				
3170		3175		3180
Gly Asp Asp Cys Val Val Lys Pro Ile Asp Asp Arg Phe Ala His				
3185		3190		3195
Ala Leu Arg Phe Leu Asn Asp Met Gly Lys Val Arg Lys Asp Thr				
3200		3205		3210
Gln Glu Trp Lys Pro Ser Thr Gly Trp Asp Asn Trp Glu Glu Val				
3215		3220		3225
Pro Phe Cys Ser His His Phe Asn Lys Leu His Leu Lys Asp Gly				
3230		3235		3240
Arg Ser Ile Val Val Pro Cys Arg His Gln Asp Glu Leu Ile Gly				
3245		3250		3255

Arg Ala Arg Val Ser Pro Gly Ala Gly Trp Ser Ile Arg Glu Thr
3260 3265 3270

Ala Cys Leu Ala Lys Ser Tyr Ala Gln Met Trp Gln Leu Leu Tyr
3275 3280 3285

Phe His Arg Arg Asp Leu Arg Leu Met Ala Asn Ala Ile Cys Ser
3290 3295 3300

Ser Val Pro Val Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser
3305 3310 3315

Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val
3320 3325 3330

Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp
3335 3340 3345

Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
3350 3355 3360

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg
3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
3410 3415 3420

<210> 19

<211> 3423

<212> PRT

<213> Zika virus strain: MR766-NIID polyprotein

<400> 19

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Asn Pro Leu Gly Gly Leu Lys Arg
20 25 30

161

Phe Ala Leu Val Ala Val Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr
260 265 270
Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
275 280 285
Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
290 295 300
Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
305 310 315 320
Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
325 330 335
Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
340 345 350
Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
355 360 365
Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
370 375 380
Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
385 390 395 400
Gly Ser Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr
405 410 415
Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
420 425 430
Val His Gly Ser Gln His Ser Gly Met Thr Val Asn Asp Ile Gly Tyr
435 440 445
Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro
450 455 460
Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
465 470 475 480
Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
485 490 495

Asn	Asn	Lys	His	Trp	Leu	Val	His	Lys	Glu	Trp	Phe	His	Asp	Ile	Pro	
			500					505					510			
Leu	Pro	Trp	His	Ala	Gly	Ala	Asp	Thr	Gly	Thr	Pro	His	Trp	Asn	Asn	
		515					520					525				
Lys	Glu	Ala	Leu	Val	Glu	Phe	Lys	Asp	Ala	His	Ala	Lys	Arg	Gln	Thr	
	530					535					540					
Val	Val	Val	Leu	Gly	Ser	Gln	Glu	Gly	Ala	Val	His	Thr	Ala	Leu	Ala	
545					550					555					560	
Gly	Ala	Leu	Glu	Ala	Glu	Met	Asp	Gly	Ala	Lys	Gly	Lys	Leu	Phe	Ser	
				565					570					575		
Gly	His	Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Arg	Leu	Lys	Gly	
			580					585					590			
Val	Ser	Tyr	Ser	Leu	Cys	Thr	Ala	Ala	Phe	Thr	Phe	Thr	Lys	Val	Pro	
		595					600					605				
Ala	Glu	Thr	Leu	His	Gly	Thr	Val	Thr	Val	Glu	Val	Gln	Tyr	Ala	Gly	
	610					615					620					
Thr	Asp	Gly	Pro	Cys	Lys	Ile	Pro	Val	Gln	Met	Ala	Val	Asp	Met	Gln	
625					630					635					640	
Thr	Leu	Thr	Pro	Val	Gly	Arg	Leu	Ile	Thr	Ala	Asn	Pro	Val	Ile	Thr	
				645					650					655		
Glu	Ser	Thr	Glu	Asn	Ser	Lys	Met	Met	Leu	Glu	Leu	Asp	Pro	Pro	Phe	
			660					665					670			
Gly	Asp	Ser	Tyr	Ile	Val	Ile	Gly	Val	Gly	Asp	Lys	Lys	Ile	Thr	His	
		675					680					685				
His	Trp	His	Arg	Ser	Gly	Ser	Thr	Ile	Gly	Lys	Ala	Phe	Glu	Ala	Thr	
	690					695					700					
Val	Arg	Gly	Ala	Lys	Arg	Met	Ala	Val	Leu	Gly	Asp	Thr	Ala	Trp	Asp	
705					710					715					720	

Phe	Gly	Ser	Val	Gly	Gly	Val	Phe	Asn	Ser	Leu	Gly	Lys	Gly	Ile	His	
				725					730					735		
Gln	Ile	Phe	Gly	Ala	Ala	Phe	Lys	Ser	Leu	Phe	Gly	Gly	Met	Ser	Trp	
			740					745					750			
Phe	Ser	Gln	Ile	Leu	Ile	Gly	Thr	Leu	Leu	Val	Trp	Leu	Gly	Leu	Asn	
		755					760					765				
Thr	Lys	Asn	Gly	Ser	Ile	Ser	Leu	Thr	Cys	Leu	Ala	Leu	Gly	Gly	Val	
	770					775					780					
Met	Ile	Phe	Leu	Ser	Thr	Ala	Val	Ser	Ala	Asp	Val	Gly	Cys	Ser	Val	
785					790					795					800	
Asp	Phe	Ser	Lys	Lys	Glu	Thr	Arg	Cys	Gly	Thr	Gly	Val	Phe	Ile	Tyr	
			805						810					815		
Asn	Asp	Val	Glu	Ala	Trp	Arg	Asp	Arg	Tyr	Lys	Tyr	His	Pro	Asp	Ser	
		820						825					830			
Pro	Arg	Arg	Leu	Ala	Ala	Ala	Val	Lys	Gln	Ala	Trp	Glu	Glu	Gly	Ile	
		835					840					845				
Cys	Gly	Ile	Ser	Ser	Val	Ser	Arg	Met	Glu	Asn	Ile	Met	Trp	Lys	Ser	
	850					855					860					
Val	Glu	Gly	Glu	Leu	Asn	Ala	Ile	Leu	Glu	Glu	Asn	Gly	Val	Gln	Leu	
865					870					875				880		
Thr	Val	Val	Val	Gly	Ser	Val	Lys	Asn	Pro	Met	Trp	Arg	Gly	Pro	Gln	
				885					890					895		
Arg	Leu	Pro	Val	Pro	Val	Asn	Glu	Leu	Pro	His	Gly	Trp	Lys	Ala	Trp	
			900					905					910			
Gly	Lys	Ser	Tyr	Phe	Val	Arg	Ala	Ala	Lys	Thr	Asn	Asn	Ser	Phe	Val	
		915					920					925				
Val	Asp	Gly	Asp	Thr	Leu	Lys	Glu	Cys	Pro	Leu	Glu	His	Arg	Ala	Trp	
	930					935					940					
Asn	Ser	Phe	Leu	Val	Glu	Asp	His	Gly	Phe	Gly	Val	Phe	His	Thr	Ser	
945					950					955					960	

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Arg Glu Ala Ala His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Val Glu Glu Ser Asp Leu Ile Ile Pro
1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
1040 1045 1050

Tyr Arg Thr Gln Val Lys Gly Pro Trp His Ser Glu Glu Leu Glu
1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val Tyr Val Glu Glu
1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
1100 1105 1110

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu
1115 1120 1125

Ile Arg Pro Arg Lys Glu Pro Glu Ser Asn Leu Val Arg Ser Met
1130 1135 1140

Val Thr Ala Gly Ser Thr Asp His Met Asp His Phe Ser Leu Gly
1145 1150 1155

Val Leu Val Ile Leu Leu Met Val Gln Glu Gly Leu Lys Lys Arg
1160 1165 1170

Met	Thr	Thr	Lys	Ile	Ile	Met	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Val	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Val	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Ala	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Ala	Leu	Pro	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Ile	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Val	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			

Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Lys	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Lys	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			

Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	Asn	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Ile	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Met	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Gly	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			

Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Lys	Tyr	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Leu	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			

Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Asn	Asp	Ile	Ala
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Met	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Leu	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Leu	Gly	Val	Pro	Leu	Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Ile	Ser	Ser	Ala	Val	Leu	Leu	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			

Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
	2480					2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
	2495					2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
	2510					2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
	2525					2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
	2540					2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
	2555					2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
	2570					2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Val
	2585					2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
	2600					2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Arg	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
	2615					2620					2625			
Gly	His	Glu	Glu	Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
	2630					2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
	2645					2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
	2660					2665					2670			
Pro	Glu	Val	Glu	Glu	Thr	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
	2675					2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
	2690					2695					2700			

Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Met	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	His	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Ile	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Arg	Arg	Ile	Glu	Arg	Ile	Arg	Asn	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Leu	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Val	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Asn	Ile	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg
2900						2905					2910			

Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Arg
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Ile	Leu	Glu	Glu	Met	Asn	Arg	Ala	Pro	Gly
3035						3040					3045			
Gly	Lys	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Lys	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Glu	Gly	His	Arg	Thr	Leu	Ala	Leu	Ala	Val	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Gly	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			

Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Lys	Val	Thr	Arg	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	Tyr	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			
Ala	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3305						3310					3315			
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Met
3320						3325					3330			
Val	Trp	Asn	Arg	Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp
3335						3340					3345			

Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
 3350 3355 3360

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asp Thr Val Asn Met Val Arg
 3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 20
 <211> 3419
 <212> PRT
 <213> Zika virus NC_012532.1 polyprotein

<400> 20

Met Lys Asn Pro Lys Glu Glu Ile Arg Arg Ile Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Asn Pro Leu Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

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

Ile Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Ile Thr Arg Arg
 115 120 125

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

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

Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu Thr Leu
595 600 605

His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro
610 615 620

Cys Lys Ile Pro Val Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro
625 630 635 640

Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu
645 650 655

Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr
660 665 670

Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp His Arg
675 680 685

Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala
690 695 700

Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val
705 710 715 720

Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly
725 730 735

Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile
740 745 750

Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys Asn Gly
755 760 765

Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile Phe Leu
770 775 780

Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val Asp Phe Ser Lys
785 790 795 800

Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Ile Tyr Asn Asp Val Glu
805 810 815

Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser Pro Arg Arg Leu

820	825	830
Ala Ala Ala Val Lys Gln Ala Trp Glu Glu Gly Ile Cys Gly Ile Ser		
835	840	845
Ser Val Ser Arg Met Glu Asn Ile Met Trp Lys Ser Val Glu Gly Glu		
850	855	860
Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu Thr Val Val Val		
865	870	875
Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln Arg Leu Pro Val		
	885	890
Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp Gly Lys Ser Tyr		
	900	905
Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val Val Asp Gly Asp		
	915	920
Thr Leu Lys Glu Cys Pro Leu Glu His Arg Ala Trp Asn Ser Phe Leu		
	930	935
Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser Val Trp Leu Lys		
945	950	955
Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala Val Ile Gly Thr		
	965	970
Ala Val Lys Gly Arg Glu Ala Ala His Ser Asp Leu Gly Tyr Trp Ile		
	980	985
Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg Ala His Leu Ile		
	995	1000
Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His Thr Leu Trp Thr		
1010	1015	1020
Asp Gly Val Glu Glu Ser Asp Leu Ile Ile Pro Lys Ser Leu Ala		
1025	1030	1035
Gly Pro Leu Ser His His Asn Thr Arg Glu Gly Tyr Arg Thr Gln		
1040	1045	1050

Val	Lys	Gly	Pro	Trp	His	Ser	Glu	Glu	Leu	Glu	Ile	Arg	Phe	Glu
1055						1060					1065			
Glu	Cys	Pro	Gly	Thr	Lys	Val	Tyr	Val	Glu	Glu	Thr	Cys	Gly	Thr
1070						1075					1080			
Arg	Gly	Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser	Gly	Arg	Val	Ile
1085						1090					1095			
Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro	Pro	Leu	Ser	Phe
1100						1105					1110			
Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu	Ile	Arg	Pro	Arg
1115						1120					1125			
Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met	Val	Thr	Ala	Gly
1130						1135					1140			
Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly	Val	Leu	Val	Ile
1145						1150					1155			
Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg	Met	Thr	Thr	Lys
1160						1165					1170			
Ile	Ile	Met	Ser	Thr	Ser	Met	Ala	Val	Leu	Val	Val	Met	Ile	Leu
1175						1180					1185			
Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu	Val	Ile	Leu	Met
1190						1195					1200			
Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly	Asp	Val	Ala	His
1205						1210					1215			
Leu	Ala	Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro	Ala	Leu	Leu	Val
1220						1225					1230			
Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg	Glu	Ser	Met	Leu
1235						1240					1245			
Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala	Ile	Ser	Ala	Leu
1250						1255					1260			
Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe	Ala	Leu	Ala	Trp

1265						1270						1275			
Leu	Ala	Ile	Arg	Ala	Met	Ala	Val	Pro	Arg	Thr	Asp	Asn	Ile	Ala	
1280						1285					1290				
Leu	Pro	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala	Arg	Gly	Thr	Leu	
1295						1300					1305				
Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys	Gly	Gly	Ile	Met	
1310						1315					1320				
Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys	Lys	Asn	Leu	Pro	
1325						1330					1335				
Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg	Val	Val	Asp	Pro	
1340						1345					1350				
Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg	Ser	Gly	Lys	Arg	
1355						1360					1365				
Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val	Gly	Leu	Ile	Cys	
1370						1375					1380				
Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile	Glu	Met	Ala	Gly	
1385						1390					1395				
Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser	Tyr	Val	Val	Ser	
1400						1405					1410				
Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala	Gly	Asp	Ile	Thr	
1415						1420					1425				
Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser	Pro	Arg	Leu	Asp	
1430						1435					1440				
Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu	Val	Glu	Glu	Asp	
1445						1450					1455				
Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val	Val	Leu	Met	Ala	
1460						1465					1470				
Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe	Ala	Ala	Gly	Ala	
1475						1480					1485				

Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser	Gly	Ala	Leu	Trp
1490						1495					1500			
Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly	Glu	Thr	Thr	Asp
1505						1510					1515			
Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu	Gly	Ser	Thr	Gln
1520						1525					1530			
Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe	His	Thr	Met	Trp
1535						1540					1545			
His	Val	Thr	Lys	Gly	Ala	Ala	Leu	Arg	Ser	Gly	Glu	Gly	Arg	Leu
1550						1555					1560			
Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu	Val	Ser	Tyr	Cys
1565						1570					1575			
Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly	Leu	Ser	Glu	Val
1580						1585					1590			
Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala	Arg	Asn	Ile	Gln
1595						1600					1605			
Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly	Asp	Ile	Gly	Ala
1610						1615					1620			
Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly	Ser	Pro	Ile	Leu
1625						1630					1635			
Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly	Asn	Gly	Val	Val
1640						1645					1650			
Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr	Gln	Gly	Lys	Arg
1655						1660					1665			
Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro	Ser	Met	Leu	Lys
1670						1675					1680			
Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro	Gly	Ala	Gly	Lys
1685						1690					1695			
Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu	Ala	Ile	Lys	Lys

1700		1705		1710
Arg Leu 1715	Arg Thr Val Ile	Leu Ala Pro Thr Arg 1720	Val Val Ala Ala 1725	
Glu Met 1730	Glu Glu Ala Leu	Arg Gly Leu Pro Val 1735	Arg Tyr Met Thr 1740	
Thr Ala 1745	Val Asn Val Thr	His Ser Gly Thr Glu 1750	Ile Val Asp Leu 1755	
Met Cys 1760	His Ala Thr Phe	Thr Ser Arg Leu Leu 1765	Gln Pro Ile Arg 1770	
Val Pro 1775	Asn Tyr Asn Leu	Asn Ile Met Asp Glu 1780	Ala His Phe Thr 1785	
Asp Pro 1790	Ser Ser Ile Ala	Ala Arg Gly Tyr Ile 1795	Ser Thr Arg Val 1800	
Glu Met 1805	Gly Glu Ala Ala	Ala Ile Phe Met Thr 1810	Ala Thr Pro Pro 1815	
Gly Thr 1820	Arg Asp Ala Phe	Pro Asp Ser Asn Ser 1825	Pro Ile Met Asp 1830	
Thr Glu 1835	Val Glu Val Pro	Glu Arg Ala Trp Ser 1840	Ser Gly Phe Asp 1845	
Trp Val 1850	Thr Asp His Ser	Gly Lys Thr Val Trp 1855	Phe Val Pro Ser 1860	
Val Arg 1865	Asn Gly Asn Glu	Ile Ala Ala Cys Leu 1870	Thr Lys Ala Gly 1875	
Lys Arg 1880	Val Ile Gln Leu	Ser Arg Lys Thr Phe 1885	Glu Thr Glu Phe 1890	
Gln Lys 1895	Thr Lys Asn Gln	Glu Trp Asp Phe Val 1900	Ile Thr Thr Asp 1905	
Ile Ser 1910	Glu Met Gly Ala	Asn Phe Lys Ala Asp 1915	Arg Val Ile Asp 1920	

Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp	Gly	Glu	Arg	Val
1925						1930					1935			
Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala	Ser	Ala	Ala	Gln
1940						1945					1950			
Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys	Pro	Gly	Asp	Glu
1955						1960					1965			
Tyr	Met	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp	Glu	Gly	His	Ala
1970						1975					1980			
His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn	Ile	Tyr	Leu	Gln
1985						1990					1995			
Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu	Ala	Asp	Lys	Val
2000						2005					2010			
Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr	Glu	Gln	Arg	Lys
2015						2020					2025			
Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu	Pro	Val	Trp	Leu
2030						2035					2040			
Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr	Thr	Asp	Arg	Arg
2045						2050					2055			
Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile	Met	Glu	Asp	Ser
2060						2065					2070			
Val	Pro	Ala	Glu	Val	Trp	Thr	Lys	Tyr	Gly	Glu	Lys	Arg	Val	Leu
2075						2080					2085			
Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser	Asp	His	Ala	Ala
2090						2095					2100			
Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys	Arg	Gly	Ala	Ala
2105						2110					2115			
Leu	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro	Gly	His	Met	Thr
2120						2125					2130			
Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala	Val	Leu	Met	Arg

2135		2140		2145
Ala Glu Thr Gly Ser Arg	Pro Tyr Lys Ala Ala	Ala Ala Gln Leu		
2150	2155	2160		
Pro Glu Thr Leu Glu Thr	Ile Met Leu Leu Gly	Leu Leu Gly Thr		
2165	2170	2175		
Val Ser Leu Gly Ile Phe	Phe Val Leu Met Arg	Asn Lys Gly Ile		
2180	2185	2190		
Gly Lys Met Gly Phe Gly	Met Val Thr Leu Gly	Ala Ser Ala Trp		
2195	2200	2205		
Leu Met Trp Leu Ser Glu	Ile Glu Pro Ala Arg	Ile Ala Cys Val		
2210	2215	2220		
Leu Ile Val Val Phe Leu	Leu Leu Val Val Leu	Ile Pro Glu Pro		
2225	2230	2235		
Glu Lys Gln Arg Ser Pro	Gln Asp Asn Gln Met	Ala Ile Ile Ile		
2240	2245	2250		
Met Val Ala Val Gly Leu	Leu Gly Leu Ile Thr	Ala Asn Glu Leu		
2255	2260	2265		
Gly Trp Leu Glu Arg Thr	Lys Asn Asp Ile Ala	His Leu Met Gly		
2270	2275	2280		
Arg Arg Glu Glu Gly Ala	Thr Met Gly Phe Ser	Met Asp Ile Asp		
2285	2290	2295		
Leu Arg Pro Ala Ser Ala	Trp Ala Ile Tyr Ala	Ala Leu Thr Thr		
2300	2305	2310		
Leu Ile Thr Pro Ala Val	Gln His Ala Val Thr	Thr Ser Tyr Asn		
2315	2320	2325		
Asn Tyr Ser Leu Met Ala	Met Ala Thr Gln Ala	Gly Val Leu Phe		
2330	2335	2340		
Gly Met Gly Lys Gly Met	Pro Phe Met His Gly	Asp Leu Gly Val		
2345	2350	2355		

Pro	Leu	Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu	Thr	Pro	Leu	Thr
	2360					2365					2370			
Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His	Tyr	Met	Tyr	Leu
	2375					2380					2385			
Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala	Ala	Gln	Lys	Arg
	2390					2395					2400			
Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val	Asp	Gly	Ile	Val
	2405					2410					2415			
Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro	Gln	Val	Glu	Lys
	2420					2425					2430			
Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala	Ile	Ser	Ser	Ala
	2435					2440					2445			
Val	Leu	Leu	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu	Ala	Gly	Ala	Leu
	2450					2455					2460			
Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly	Ser	Pro	Asn	Lys
	2465					2470					2475			
Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys	Asn	Ile	Phe	Arg
	2480					2485					2490			
Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr	Thr	Val	Thr	Arg
	2495					2500					2505			
Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly	Thr	Gly	Glu	Thr
	2510					2515					2520			
Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln	Met	Ser	Ala	Leu
	2525					2530					2535			
Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr	Glu	Val	Cys	Arg
	2540					2545					2550			
Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val	Ala	Thr	Gly	Gly
	2555					2560					2565			
His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Ile	Arg	Trp	Leu	Glu	Glu

2570							2575						2580			
Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Val	Asp	Leu	Gly	Cys		
2585						2590					2595					
Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr	Ile	Arg	Lys	Val		
2600						2605					2610					
Gln	Glu	Val	Arg	Gly	Tyr	Thr	Lys	Gly	Gly	Pro	Gly	His	Glu	Glu		
2615						2620					2625					
Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile	Val	Arg	Leu	Lys		
2630						2635					2640					
Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu	Pro	Cys	Asp	Thr		
2645						2650					2655					
Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser	Pro	Glu	Val	Glu		
2660						2665					2670					
Glu	Thr	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val	Gly	Asp	Trp	Leu		
2675						2680					2685					
Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val	Leu	Cys	Pro	Tyr		
2690						2695					2700					
Thr	Ser	Thr	Met	Met	Glu	Thr	Met	Glu	Arg	Leu	Gln	Arg	Arg	His		
2705						2710					2715					
Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Cys	Arg	Asn	Ser	Thr	His		
2720						2725					2730					
Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn	Ile	Ile	Lys	Ser		
2735						2740					2745					
Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg	Met	Asp	Gly	Pro		
2750						2755					2760					
Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn	Leu	Gly	Ser	Gly		
2765						2770					2775					
Thr	Arg	Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro	Asn	Met	Lys	Ile		
2780						2785					2790					

Ile	Gly	Arg	Arg	Ile	Glu	Arg	Ile	Arg	Asn	Glu	His	Ala	Glu	Thr
	2795					2800					2805			
Trp	Phe	Leu	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr	Trp	Ala	Tyr	His
	2810					2815					2820			
Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala	Ser	Ser	Leu	Val
	2825					2830					2835			
Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp	Asp	Val	Val	Thr
	2840					2845					2850			
Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr	Pro	Tyr	Gly	Gln
	2855					2860					2865			
Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg	Val	Pro	Asp	Pro
	2870					2875					2880			
Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Asn	Ile	Val	Ser	Ser	Trp	Leu
	2885					2890					2895			
Trp	Lys	Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg	Val	Cys	Thr	Lys
	2900					2905					2910			
Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala	Ala	Leu	Gly	Ala
	2915					2920					2925			
Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	Val	Glu	Ala	Val
	2930					2935					2940			
Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Arg	Glu	Arg	Glu	His
	2945					2950					2955			
His	Leu	Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr	Asn	Met	Met	Gly
	2960					2965					2970			
Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys	Ala	Lys	Gly	Ser
	2975					2980					2985			
Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg	Phe	Leu	Glu	Phe
	2990					2995					3000			
Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp	Met	Gly	Arg	Glu

3005						3010						3015			
Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu	Gln	Arg	Leu	Gly	
3020						3025					3030				
Tyr	Ile	Leu	Glu	Glu	Met	Asn	Arg	Ala	Pro	Gly	Gly	Lys	Met	Tyr	
3035						3040					3045				
Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile	Ser	Lys	Phe	Asp	
3050						3055					3060				
Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met	Glu	Glu	Gly	His	
3065						3070					3075				
Arg	Thr	Leu	Ala	Leu	Ala	Val	Ile	Lys	Tyr	Thr	Tyr	Gln	Asn	Lys	
3080						3085					3090				
Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Gly	Gly	Lys	Thr	Val	Met	
3095						3100					3105				
Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser	Gly	Gln	Val	Val	
3110						3115					3120				
Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val	Val	Gln	Leu	Ile	
3125						3130					3135				
Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met	Gln	Asp	Leu	Trp	
3140						3145					3150				
Leu	Leu	Arg	Lys	Pro	Glu	Lys	Val	Thr	Arg	Trp	Leu	Gln	Ser	Asn	
3155						3160					3165				
Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser	Gly	Asp	Asp	Cys	
3170						3175					3180				
Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His	Ala	Leu	Arg	Phe	
3185						3190					3195				
Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr	Gln	Glu	Trp	Lys	
3200						3205					3210				
Pro	Ser	Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val	Pro	Phe	Cys	Ser	
3215						3220					3225				

His His Phe Asn Lys Leu Tyr Leu Lys Asp Gly Arg Ser Ile Val
 3230 3235 3240
 Val Pro Cys Arg His Gln Asp Glu Leu Ile Gly Arg Ala Arg Val
 3245 3250 3255
 Ser Pro Gly Ala Gly Trp Ser Ile Arg Glu Thr Ala Cys Leu Ala
 3260 3265 3270
 Lys Ser Tyr Ala Gln Met Trp Gln Leu Leu Tyr Phe His Arg Arg
 3275 3280 3285
 Asp Leu Arg Leu Met Ala Asn Ala Ile Cys Ser Ala Val Pro Val
 3290 3295 3300
 Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser Ile His Gly Lys
 3305 3310 3315
 Gly Glu Trp Met Thr Thr Glu Asp Met Leu Met Val Trp Asn Arg
 3320 3325 3330
 Val Trp Ile Glu Glu Asn Asp His Met Glu Asp Lys Thr Pro Val
 3335 3340 3345
 Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys Arg Glu Asp Leu
 3350 3355 3360
 Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg Thr Thr Trp Ala
 3365 3370 3375
 Glu Asn Ile Lys Asp Thr Val Asn Met Val Arg Arg Ile Ile Gly
 3380 3385 3390
 Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr Gln Val Arg Tyr
 3395 3400 3405
 Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415

<210> 21
 <211> 3423
 <212> PRT
 <213> Zika virus strain ZikaSPH2015 polyprotein

<400> 21

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
195 200 205

Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
210 215 220

Arg	Lys	Leu	Gln	Thr	Arg	Ser	Gln	Thr	Trp	Leu	Glu	Ser	Arg	Glu	Tyr	225	230	235	240
Thr	Lys	His	Leu	Ile	Arg	Val	Glu	Asn	Trp	Ile	Phe	Arg	Asn	Pro	Gly	245	250	255	
Phe	Ala	Leu	Ala	Ala	Ala	Ala	Ile	Ala	Trp	Leu	Leu	Gly	Ser	Ser	Thr	260	265	270	
Ser	Gln	Lys	Val	Ile	Tyr	Leu	Val	Met	Ile	Leu	Leu	Ile	Ala	Pro	Ala	275	280	285	
Tyr	Ser	Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	290	295	300	
Met	Ser	Gly	Gly	Thr	Trp	Val	Asp	Ile	Val	Leu	Glu	His	Gly	Gly	Cys	305	310	315	320
Val	Thr	Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val	325	330	335	
Thr	Thr	Thr	Val	Ser	Asn	Met	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Glu	340	345	350	
Ala	Ser	Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	Gly	355	360	365	
Glu	Ala	Tyr	Leu	Asp	Lys	Gln	Ser	Asp	Thr	Gln	Tyr	Val	Cys	Lys	Arg	370	375	380	
Thr	Leu	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	385	390	395	400
Gly	Ser	Leu	Val	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Lys	Lys	Met	Thr	405	410	415	
Gly	Lys	Ser	Ile	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu	Ser	420	425	430	
Val	His	Gly	Ser	Gln	His	Ser	Gly	Met	Ile	Val	Asn	Asp	Thr	Gly	His	435	440	445	
Glu	Thr	Asp	Glu	Asn	Arg	Ala	Lys	Val	Glu	Ile	Thr	Pro	Asn	Ser	Pro	450	455	460	

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
 465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
 485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
 500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
 515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
 530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
 545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
 565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
 580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
 595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
 610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
 625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
 645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
 660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
 675 680 685

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

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
 930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
 945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
 965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu
 980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
 995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
 1010 1015 1020

Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro
 1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
 1040 1045 1050

Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu
 1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
 1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
 1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
 1100 1105 1110

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu
 1115 1120 1125

Ile Arg Pro Arg Lys Glu Pro Glu Ser Asn Leu Val Arg Ser Met
 1130 1135 1140

Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			

Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
1460						1465					1470			
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			

Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			

Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	Tyr	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			

Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			

Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Met	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Met	Ala	Val	Ala
2435						2440					2445			

Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
2510						2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
2525						2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			

Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			

Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			

Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			
Ser	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3305						3310					3315			

Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val
 3320 3325 3330

Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp
 3335 3340 3345

Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
 3350 3355 3360

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg
 3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 22
 <211> 3419
 <212> PRT
 <213> Zika virus strain MR 766 polyprotein
 <400> 22

Met Lys Asn Pro Lys Glu Glu Ile Arg Arg Ile Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Asn Pro Leu Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

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

Ile Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Ile Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Ser Asp Ala Gly Lys Ala
 130 135 140

Ile Ser Phe Ala Thr Thr Leu Gly Val Asn Lys Cys His Val Gln Ile
 145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
 165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
 180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
 195 200 205

Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
 210 215 220

Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr
 225 230 235 240

Thr Lys His Leu Ile Lys Val Glu Asn Trp Ile Phe Arg Asn Pro Gly
 245 250 255

Phe Ala Leu Val Ala Val Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr
 260 265 270

Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
 275 280 285

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
 290 295 300

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
 305 310 315 320

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val

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

Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His Leu Lys
565 570 575

Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser
580 585 590

Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu Thr Leu
595 600 605

His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro
610 615 620

Cys Lys Ile Pro Val Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro
625 630 635 640

Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu
645 650 655

Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr
660 665 670

Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp His Arg
675 680 685

Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala
690 695 700

Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val
705 710 715 720

Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly
725 730 735

Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile
740 745 750

Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys Asn Gly
755 760 765

Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile Phe Leu
770 775 780

Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val Asp Phe Ser Lys

Asp	Gly	Val	Glu	Glu	Ser	Asp	Leu	Ile	Ile	Pro	Lys	Ser	Leu	Ala
1025						1030					1035			
Gly	Pro	Leu	Ser	His	His	Asn	Thr	Arg	Glu	Gly	Tyr	Arg	Thr	Gln
1040						1045					1050			
Val	Lys	Gly	Pro	Trp	His	Ser	Glu	Glu	Leu	Glu	Ile	Arg	Phe	Glu
1055						1060					1065			
Glu	Cys	Pro	Gly	Thr	Lys	Val	Tyr	Val	Glu	Glu	Thr	Cys	Gly	Thr
1070						1075					1080			
Arg	Gly	Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser	Gly	Arg	Val	Ile
1085						1090					1095			
Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro	Pro	Leu	Ser	Phe
1100						1105					1110			
Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu	Ile	Arg	Pro	Arg
1115						1120					1125			
Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met	Val	Thr	Ala	Gly
1130						1135					1140			
Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly	Val	Leu	Val	Ile
1145						1150					1155			
Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg	Met	Thr	Thr	Lys
1160						1165					1170			
Ile	Ile	Met	Ser	Thr	Ser	Met	Ala	Val	Leu	Val	Val	Met	Ile	Leu
1175						1180					1185			
Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu	Val	Ile	Leu	Met
1190						1195					1200			
Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly	Asp	Val	Ala	His
1205						1210					1215			
Leu	Ala	Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro	Ala	Leu	Leu	Val
1220						1225					1230			
Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg	Glu	Ser	Met	Leu

1235	1240	1245
Leu Ala 1250	Leu Ala Ser Cys 1255	Leu Leu Gln Thr Ala Ile Ser Ala Leu 1260
Glu Gly 1265	Asp Leu Met Val 1270	Leu Ile Asn Gly Phe Ala Leu Ala Trp 1275
Leu Ala 1280	Ile Arg Ala Met 1285	Ala Val Pro Arg Thr Asp Asn Ile Ala 1290
Leu Pro 1295	Ile Leu Ala Ala 1300	Leu Thr Pro Leu Ala Arg Gly Thr Leu 1305
Leu Val 1310	Ala Trp Arg Ala 1315	Gly Leu Ala Thr Cys Gly Gly Ile Met 1320
Leu Leu 1325	Ser Leu Lys Gly 1330	Lys Gly Ser Val Lys Lys Asn Leu Pro 1335
Phe Val 1340	Met Ala Leu Gly 1345	Leu Thr Ala Val Arg Val Val Asp Pro 1350
Ile Asn 1355	Val Val Gly Leu 1360	Leu Leu Thr Arg Ser Gly Lys Arg 1365
Ser Trp 1370	Pro Pro Ser Glu 1375	Val Leu Thr Ala Val Gly Leu Ile Cys 1380
Ala Leu 1385	Ala Gly Gly Phe 1390	Ala Lys Ala Asp Ile Glu Met Ala Gly 1395
Pro Met 1400	Ala Ala Val Gly 1405	Leu Leu Ile Val Ser Tyr Val Val Ser 1410
Gly Lys 1415	Ser Val Asp Met 1420	Tyr Ile Glu Arg Ala Gly Asp Ile Thr 1425
Trp Glu 1430	Lys Asp Ala Glu 1435	Val Thr Gly Asn Ser Pro Arg Leu Asp 1440
Val Ala 1445	Leu Asp Glu Ser 1450	Gly Asp Phe Ser Leu Val Glu Glu Asp 1455

Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val	Val	Leu	Met	Ala
1460						1465					1470			
Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe	Ala	Ala	Gly	Ala
1475						1480					1485			
Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser	Gly	Ala	Leu	Trp
1490						1495					1500			
Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly	Glu	Thr	Thr	Asp
1505						1510					1515			
Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu	Gly	Ser	Thr	Gln
1520						1525					1530			
Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe	His	Thr	Met	Trp
1535						1540					1545			
His	Val	Thr	Lys	Gly	Ala	Ala	Leu	Arg	Ser	Gly	Glu	Gly	Arg	Leu
1550						1555					1560			
Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu	Val	Ser	Tyr	Cys
1565						1570					1575			
Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly	Leu	Ser	Glu	Val
1580						1585					1590			
Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala	Arg	Asn	Ile	Gln
1595						1600					1605			
Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly	Asp	Ile	Gly	Ala
1610						1615					1620			
Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly	Ser	Pro	Ile	Leu
1625						1630					1635			
Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly	Asn	Gly	Val	Val
1640						1645					1650			
Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr	Gln	Gly	Lys	Arg
1655						1660					1665			
Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro	Ser	Met	Leu	Lys

1670						1675						1680			
Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro	Gly	Ala	Gly	Lys	
1685						1690					1695				
Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu	Ala	Ile	Lys	Lys	
1700						1705					1710				
Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg	Val	Val	Ala	Ala	
1715						1720					1725				
Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val	Arg	Tyr	Met	Thr	
1730						1735					1740				
Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu	Ile	Val	Asp	Leu	
1745						1750					1755				
Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu	Gln	Pro	Ile	Arg	
1760						1765					1770				
Val	Pro	Asn	Tyr	Asn	Leu	Asn	Ile	Met	Asp	Glu	Ala	His	Phe	Thr	
1775						1780					1785				
Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	Ser	Thr	Arg	Val	
1790						1795					1800				
Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	Ala	Thr	Pro	Pro	
1805						1810					1815				
Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser	Pro	Ile	Met	Asp	
1820						1825					1830				
Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser	Ser	Gly	Phe	Asp	
1835						1840					1845				
Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp	Phe	Val	Pro	Ser	
1850						1855					1860				
Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu	Thr	Lys	Ala	Gly	
1865						1870					1875				
Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	Glu	Thr	Glu	Phe	
1880						1885					1890				

Gln	Lys	Thr	Lys	Asn	Gln	Glu	Trp	Asp	Phe	Val	Ile	Thr	Thr	Asp
1895						1900					1905			
Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp	Arg	Val	Ile	Asp
1910						1915					1920			
Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp	Gly	Glu	Arg	Val
1925						1930					1935			
Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala	Ser	Ala	Ala	Gln
1940						1945					1950			
Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys	Pro	Gly	Asp	Glu
1955						1960					1965			
Tyr	Met	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp	Glu	Gly	His	Ala
1970						1975					1980			
His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn	Ile	Tyr	Leu	Gln
1985						1990					1995			
Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu	Ala	Asp	Lys	Val
2000						2005					2010			
Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr	Glu	Gln	Arg	Lys
2015						2020					2025			
Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu	Pro	Val	Trp	Leu
2030						2035					2040			
Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr	Thr	Asp	Arg	Arg
2045						2050					2055			
Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile	Met	Glu	Asp	Ser
2060						2065					2070			
Val	Pro	Ala	Glu	Val	Trp	Thr	Lys	Tyr	Gly	Glu	Lys	Arg	Val	Leu
2075						2080					2085			
Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser	Asp	His	Ala	Ala
2090						2095					2100			
Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys	Arg	Gly	Ala	Ala

2105		2110		2115
Leu Gly Val Met Glu Ala	Leu Gly Thr Leu Pro	Gly His Met Thr		
2120	2125	2130		
Glu Arg Phe Gln Glu Ala	Ile Asp Asn Leu Ala	Val Leu Met Arg		
2135	2140	2145		
Ala Glu Thr Gly Ser Arg	Pro Tyr Lys Ala Ala	Ala Ala Gln Leu		
2150	2155	2160		
Pro Glu Thr Leu Glu Thr	Ile Met Leu Leu Gly	Leu Leu Gly Thr		
2165	2170	2175		
Val Ser Leu Gly Ile Phe	Phe Val Leu Met Arg	Asn Lys Gly Ile		
2180	2185	2190		
Gly Lys Met Gly Phe Gly	Met Val Thr Leu Gly	Ala Ser Ala Trp		
2195	2200	2205		
Leu Met Trp Leu Ser Glu	Ile Glu Pro Ala Arg	Ile Ala Cys Val		
2210	2215	2220		
Leu Ile Val Val Phe Leu	Leu Leu Val Val Leu	Ile Pro Glu Pro		
2225	2230	2235		
Glu Lys Gln Arg Ser Pro	Gln Asp Asn Gln Met	Ala Ile Ile Ile		
2240	2245	2250		
Met Val Ala Val Gly Leu	Leu Gly Leu Ile Thr	Ala Asn Glu Leu		
2255	2260	2265		
Gly Trp Leu Glu Arg Thr	Lys Asn Asp Ile Ala	His Leu Met Gly		
2270	2275	2280		
Arg Arg Glu Glu Gly Ala	Thr Met Gly Phe Ser	Met Asp Ile Asp		
2285	2290	2295		
Leu Arg Pro Ala Ser Ala	Trp Ala Ile Tyr Ala	Ala Leu Thr Thr		
2300	2305	2310		
Leu Ile Thr Pro Ala Val	Gln His Ala Val Thr	Thr Ser Tyr Asn		
2315	2320	2325		

Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala	Gly	Val	Leu	Phe
2330						2335					2340			
Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Met	His	Gly	Asp	Leu	Gly	Val
2345						2350					2355			
Pro	Leu	Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu	Thr	Pro	Leu	Thr
2360						2365					2370			
Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His	Tyr	Met	Tyr	Leu
2375						2380					2385			
Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala	Ala	Gln	Lys	Arg
2390						2395					2400			
Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val	Asp	Gly	Ile	Val
2405						2410					2415			
Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro	Gln	Val	Glu	Lys
2420						2425					2430			
Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala	Ile	Ser	Ser	Ala
2435						2440					2445			
Val	Leu	Leu	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu	Ala	Gly	Ala	Leu
2450						2455					2460			
Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly	Ser	Pro	Asn	Lys
2465						2470					2475			
Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys	Asn	Ile	Phe	Arg
2480						2485					2490			
Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr	Thr	Val	Thr	Arg
2495						2500					2505			
Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly	Thr	Gly	Glu	Thr
2510						2515					2520			
Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln	Met	Ser	Ala	Leu
2525						2530					2535			
Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr	Glu	Val	Cys	Arg

2540		2545		2550
Glu Glu Ala Arg Arg Ala Leu Lys Asp Gly Val Ala Thr Gly Gly	2555	2560	2565	
His Ala Val Ser Arg Gly Ser Ala Lys Ile Arg Trp Leu Glu Glu	2570	2575	2580	
Arg Gly Tyr Leu Gln Pro Tyr Gly Lys Val Val Asp Leu Gly Cys	2585	2590	2595	
Gly Arg Gly Gly Trp Ser Tyr Tyr Ala Ala Thr Ile Arg Lys Val	2600	2605	2610	
Gln Glu Val Arg Gly Tyr Thr Lys Gly Gly Pro Gly His Glu Glu	2615	2620	2625	
Pro Met Leu Val Gln Ser Tyr Gly Trp Asn Ile Val Arg Leu Lys	2630	2635	2640	
Ser Gly Val Asp Val Phe His Met Ala Ala Glu Pro Cys Asp Thr	2645	2650	2655	
Leu Leu Cys Asp Ile Gly Glu Ser Ser Ser Ser Pro Glu Val Glu	2660	2665	2670	
Glu Thr Arg Thr Leu Arg Val Leu Ser Met Val Gly Asp Trp Leu	2675	2680	2685	
Glu Lys Arg Pro Gly Ala Phe Cys Ile Lys Val Leu Cys Pro Tyr	2690	2695	2700	
Thr Ser Thr Met Met Glu Thr Met Glu Arg Leu Gln Arg Arg His	2705	2710	2715	
Gly Gly Gly Leu Val Arg Val Pro Leu Cys Arg Asn Ser Thr His	2720	2725	2730	
Glu Met Tyr Trp Val Ser Gly Ala Lys Ser Asn Ile Ile Lys Ser	2735	2740	2745	
Val Ser Thr Thr Ser Gln Leu Leu Leu Gly Arg Met Asp Gly Pro	2750	2755	2760	

Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn	Leu	Gly	Ser	Gly
2765						2770					2775			
Thr	Arg	Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro	Asn	Met	Lys	Ile
2780						2785					2790			
Ile	Gly	Arg	Arg	Ile	Glu	Arg	Ile	Arg	Asn	Glu	His	Ala	Glu	Thr
2795						2800					2805			
Trp	Phe	Leu	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr	Trp	Ala	Tyr	His
2810						2815					2820			
Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala	Ser	Ser	Leu	Val
2825						2830					2835			
Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp	Asp	Val	Val	Thr
2840						2845					2850			
Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr	Pro	Tyr	Gly	Gln
2855						2860					2865			
Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg	Val	Pro	Asp	Pro
2870						2875					2880			
Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Asn	Ile	Val	Ser	Ser	Trp	Leu
2885						2890					2895			
Trp	Lys	Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg	Val	Cys	Thr	Lys
2900						2905					2910			
Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala	Ala	Leu	Gly	Ala
2915						2920					2925			
Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	Val	Glu	Ala	Val
2930						2935					2940			
Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Arg	Glu	Arg	Glu	His
2945						2950					2955			
His	Leu	Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr	Asn	Met	Met	Gly
2960						2965					2970			
Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys	Ala	Lys	Gly	Ser

2975		2980		2985
Arg Ala Ile Trp Tyr Met	Trp Leu Gly Ala Arg Phe	Leu Glu Phe		
2990	2995	3000		
Glu Ala Leu Gly Phe Leu	Asn Glu Asp His Trp Met	Gly Arg Glu		
3005	3010	3015		
Asn Ser Gly Gly Gly Val	Glu Gly Leu Gly Leu Gln	Arg Leu Gly		
3020	3025	3030		
Tyr Ile Leu Glu Glu Met	Asn Arg Ala Pro Gly Gly	Lys Met Tyr		
3035	3040	3045		
Ala Asp Asp Thr Ala Gly	Trp Asp Thr Arg Ile Ser	Lys Phe Asp		
3050	3055	3060		
Leu Glu Asn Glu Ala Leu	Ile Thr Asn Gln Met Glu	Glu Gly His		
3065	3070	3075		
Arg Thr Leu Ala Leu Ala	Val Ile Lys Tyr Thr Tyr	Gln Asn Lys		
3080	3085	3090		
Val Val Lys Val Leu Arg	Pro Ala Glu Gly Gly Lys	Thr Val Met		
3095	3100	3105		
Asp Ile Ile Ser Arg Gln	Asp Gln Arg Gly Ser Gly	Gln Val Val		
3110	3115	3120		
Thr Tyr Ala Leu Asn Thr	Phe Thr Asn Leu Val Val	Gln Leu Ile		
3125	3130	3135		
Arg Asn Met Glu Ala Glu	Glu Val Leu Glu Met Gln	Asp Leu Trp		
3140	3145	3150		
Leu Leu Arg Lys Pro Glu	Lys Val Thr Arg Trp Leu	Gln Ser Asn		
3155	3160	3165		
Gly Trp Asp Arg Leu Lys	Arg Met Ala Val Ser Gly	Asp Asp Cys		
3170	3175	3180		
Val Val Lys Pro Ile Asp	Asp Arg Phe Ala His Ala	Leu Arg Phe		
3185	3190	3195		

Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr	Gln	Glu	Trp	Lys
3200						3205					3210			
Pro	Ser	Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val	Pro	Phe	Cys	Ser
3215						3220					3225			
His	His	Phe	Asn	Lys	Leu	Tyr	Leu	Lys	Asp	Gly	Arg	Ser	Ile	Val
3230						3235					3240			
Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly	Arg	Ala	Arg	Val
3245						3250					3255			
Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr	Ala	Cys	Leu	Ala
3260						3265					3270			
Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr	Phe	His	Arg	Arg
3275						3280					3285			
Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser	Ala	Val	Pro	Val
3290						3295					3300			
Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser	Ile	His	Gly	Lys
3305						3310					3315			
Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Met	Val	Trp	Asn	Arg
3320						3325					3330			
Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp	Lys	Thr	Pro	Val
3335						3340					3345			
Thr	Lys	Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys	Arg	Glu	Asp	Leu
3350						3355					3360			
Trp	Cys	Gly	Ser	Leu	Ile	Gly	His	Arg	Pro	Arg	Thr	Thr	Trp	Ala
3365						3370					3375			
Glu	Asn	Ile	Lys	Asp	Thr	Val	Asn	Met	Val	Arg	Arg	Ile	Ile	Gly
3380						3385					3390			
Asp	Glu	Glu	Lys	Tyr	Met	Asp	Tyr	Leu	Ser	Thr	Gln	Val	Arg	Tyr
3395						3400					3405			
Leu	Gly	Glu	Glu	Gly	Ser	Thr	Pro	Gly	Val	Leu				

3410

3415

<210> 23

<211> 3423

<212> PRT

<213> Zika virus strain BeH815744 polyprotein

<400> 23

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
 100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
 130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
 145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
 165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
 180 185 190

Thr	Thr	Ser	Thr	Trp	Val	Val	Tyr	Gly	Thr	Cys	His	His	Lys	Lys	Gly
		195					200					205			
Glu	Ala	Arg	Arg	Ser	Arg	Arg	Ala	Val	Thr	Leu	Pro	Ser	His	Ser	Thr
	210					215					220				
Arg	Lys	Leu	Gln	Thr	Arg	Ser	Gln	Thr	Trp	Leu	Glu	Ser	Arg	Glu	Tyr
225					230					235					240
Thr	Lys	His	Leu	Ile	Arg	Val	Glu	Asn	Trp	Ile	Phe	Arg	Asn	Pro	Gly
				245					250					255	
Phe	Ala	Leu	Ala	Ala	Ala	Ala	Ile	Ala	Trp	Leu	Leu	Gly	Ser	Ser	Thr
			260					265					270		
Ser	Gln	Lys	Val	Ile	Tyr	Leu	Val	Met	Ile	Leu	Leu	Ile	Ala	Pro	Ala
		275					280					285			
Tyr	Ser	Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly
	290					295					300				
Met	Ser	Gly	Gly	Thr	Trp	Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys
305					310					315					320
Val	Thr	Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val
				325					330					335	
Thr	Thr	Thr	Val	Ser	Asn	Met	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Glu
			340					345					350		
Ala	Ser	Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	Gly
		355				360						365			
Glu	Ala	Tyr	Leu	Asp	Lys	Gln	Ser	Asp	Thr	Gln	Tyr	Val	Cys	Lys	Arg
	370					375					380				
Thr	Leu	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys
385					390					395					400
Gly	Ser	Leu	Val	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Lys	Lys	Met	Thr
				405					410					415	
Gly	Lys	Ser	Ile	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu	Ser
			420					425					430		

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
770 775 780

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro
1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
1040 1045 1050

Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu
1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
1100 1105 1110

Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu
	1115					1120					1125			
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met
	1130					1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
	1145					1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
	1160					1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
	1175					1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
	1190					1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
	1205					1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
	1220					1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
	1235					1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
	1250					1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
	1265					1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
	1280					1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
	1295					1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
	1310					1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
	1325					1330					1335			

Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
1460						1465					1470			
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			

His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			

Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			

Glu 1985	Asp	His	Ala	His	Trp	Leu 1990	Glu	Ala	Arg	Met	Leu 1995	Leu	Asp	Asn
Ile 2000	Tyr	Leu	Gln	Asp	Gly	Leu 2005	Ile	Ala	Ser	Leu	Tyr 2010	Arg	Pro	Glu
Ala 2015	Asp	Lys	Val	Ala	Ala	Ile 2020	Glu	Gly	Glu	Phe	Lys 2025	Leu	Arg	Thr
Glu 2030	Gln	Arg	Lys	Thr	Phe	Val 2035	Glu	Leu	Met	Lys	Arg 2040	Gly	Asp	Leu
Pro 2045	Val	Trp	Leu	Ala	Tyr	Gln 2050	Val	Ala	Ser	Ala	Gly 2055	Ile	Thr	Tyr
Thr 2060	Asp	Arg	Arg	Trp	Cys	Phe 2065	Asp	Gly	Thr	Thr	Asn 2070	Asn	Thr	Ile
Met 2075	Glu	Asp	Ser	Val	Pro	Ala 2080	Glu	Val	Trp	Thr	Arg 2085	His	Gly	Glu
Lys 2090	Arg	Val	Leu	Lys	Pro	Arg 2095	Trp	Met	Asp	Ala	Arg 2100	Val	Cys	Ser
Asp 2105	His	Ala	Ala	Leu	Lys	Ser 2110	Phe	Lys	Glu	Phe	Ala 2115	Ala	Gly	Lys
Arg 2120	Gly	Ala	Ala	Phe	Gly	Val 2125	Met	Glu	Ala	Leu	Gly 2130	Thr	Leu	Pro
Gly 2135	His	Met	Thr	Glu	Arg	Phe 2140	Gln	Glu	Ala	Ile	Asp 2145	Asn	Leu	Ala
Val 2150	Leu	Met	Arg	Ala	Glu	Thr 2155	Gly	Ser	Arg	Pro	Tyr 2160	Lys	Ala	Ala
Ala 2165	Ala	Gln	Leu	Pro	Glu	Thr 2170	Leu	Glu	Thr	Ile	Met 2175	Leu	Leu	Gly
Leu 2180	Leu	Gly	Thr	Val	Ser	Leu 2185	Gly	Ile	Phe	Phe	Val 2190	Leu	Met	Arg
Asn 2195	Lys	Gly	Ile	Gly	Lys	Met 2200	Gly	Phe	Gly	Met	Val 2205	Thr	Leu	Gly

Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			

Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
2510						2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
2525						2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			

Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asp
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			

Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			

Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			

Phe His Arg Arg Asp Leu Arg Leu Met Ala Asn Ala Ile Cys Ser
 3290 3295 3300

Ser Val Pro Val Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser
 3305 3310 3315

Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val
 3320 3325 3330

Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp
 3335 3340 3345

Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
 3350 3355 3360

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg
 3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 24

<211> 3423

<212> PRT

<213> Zika virus strain BeH819966 polyprotein

<400> 24

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
195 200 205

Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
210 215 220

Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr
225 230 235 240

Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly
245 250 255

Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr
260 265 270

Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
275 280 285

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly

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

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn

755					760					765					
Thr	Lys	Asn	Gly	Ser	Ile	Ser	Leu	Met	Cys	Leu	Ala	Leu	Gly	Gly	Val
	770					775					780				
Leu	Ile	Phe	Leu	Ser	Thr	Ala	Val	Ser	Ala	Asp	Val	Gly	Cys	Ser	Val
785					790					795					800
Asp	Phe	Ser	Lys	Lys	Glu	Thr	Arg	Cys	Gly	Thr	Gly	Val	Phe	Val	Tyr
				805					810					815	
Asn	Asp	Val	Glu	Ala	Trp	Arg	Asp	Arg	Tyr	Lys	Tyr	His	Pro	Asp	Ser
			820					825					830		
Pro	Arg	Arg	Leu	Ala	Ala	Ala	Val	Lys	Gln	Ala	Trp	Glu	Asp	Gly	Ile
			835				840					845			
Cys	Gly	Ile	Ser	Ser	Val	Ser	Arg	Met	Glu	Asn	Ile	Met	Trp	Arg	Ser
	850					855					860				
Val	Glu	Gly	Glu	Leu	Asn	Ala	Ile	Leu	Glu	Glu	Asn	Gly	Val	Gln	Leu
865					870					875					880
Thr	Val	Val	Val	Gly	Ser	Val	Lys	Asn	Pro	Met	Trp	Arg	Gly	Pro	Gln
				885					890					895	
Arg	Leu	Pro	Val	Pro	Val	Asn	Glu	Leu	Pro	His	Gly	Trp	Lys	Ala	Trp
			900					905					910		
Gly	Lys	Ser	Tyr	Phe	Val	Arg	Ala	Ala	Lys	Thr	Asn	Asn	Ser	Phe	Val
		915					920					925			
Val	Asp	Gly	Asp	Thr	Leu	Lys	Glu	Cys	Pro	Leu	Lys	His	Arg	Ala	Trp
	930					935					940				
Asn	Ser	Phe	Leu	Val	Glu	Asp	His	Gly	Phe	Gly	Val	Phe	His	Thr	Ser
945					950					955					960
Val	Trp	Leu	Lys	Val	Arg	Glu	Asp	Tyr	Ser	Leu	Glu	Cys	Asp	Pro	Ala
				965					970					975	
Val	Ile	Gly	Thr	Ala	Val	Lys	Gly	Lys	Glu	Ala	Val	His	Ser	Asp	Leu
			980					985					990		

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro
1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
1040 1045 1050

Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu
1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
1100 1105 1110

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu
1115 1120 1125

Ile Arg Pro Arg Lys Glu Pro Glu Ser Asn Leu Val Arg Ser Met
1130 1135 1140

Val Thr Ala Gly Ser Thr Asp His Met Asp His Phe Ser Leu Gly
1145 1150 1155

Val Leu Val Ile Leu Leu Met Val Gln Glu Gly Leu Lys Lys Arg
1160 1165 1170

Met Thr Thr Lys Ile Ile Ile Ser Thr Ser Met Ala Val Leu Val
1175 1180 1185

Ala Met Ile Leu Gly Gly Phe Ser Met Ser Asp Leu Ala Lys Leu
1190 1195 1200

Ala Ile Leu Met Gly Ala Thr Phe Ala Glu Met Asn Thr Gly Gly

1205						1210						1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro	
1220						1225					1230				
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg	
1235						1240					1245				
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala	
1250						1255					1260				
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe	
1265						1270					1275				
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr	
1280						1285					1290				
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala	
1295						1300					1305				
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys	
1310						1315					1320				
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys	
1325						1330					1335				
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg	
1340						1345					1350				
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg	
1355						1360					1365				
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val	
1370						1375					1380				
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile	
1385						1390					1395				
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser	
1400						1405					1410				
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala	
1415						1420					1425				

Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
1460						1465					1470			
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly

1640						1645						1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr	
1655						1660					1665				
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro	
1670						1675					1680				
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro	
1685						1690					1695				
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu	
1700						1705					1710				
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg	
1715						1720					1725				
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val	
1730						1735					1740				
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu	
1745						1750					1755				
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu	
1760						1765					1770				
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu	
1775						1780					1785				
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	
1790						1795					1800				
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	
1805						1810					1815				
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser	
1820						1825					1830				
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser	
1835						1840					1845				
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp	
1850						1855					1860				

Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu

2075	2080	2085
Lys Arg Val Leu Lys Pro 2090	Arg Trp Met Asp Ala 2095	Arg Val Cys Ser 2100
Asp His Ala Ala Leu Lys 2105	Ser Phe Lys Glu Phe 2110	Ala Ala Gly Lys 2115
Arg Gly Ala Ala Phe Gly 2120	Val Met Glu Ala Leu 2125	Gly Thr Leu Pro 2130
Gly His Met Thr Glu Arg 2135	Phe Gln Glu Ala Ile 2140	Asp Asn Leu Ala 2145
Val Leu Met Arg Ala Glu 2150	Thr Gly Ser Arg Pro 2155	Tyr Lys Ala Ala 2160
Ala Ala Gln Leu Pro Glu 2165	Thr Leu Glu Thr Ile 2170	Met Leu Leu Gly 2175
Leu Leu Gly Thr Val Ser 2180	Leu Gly Ile Phe Phe 2185	Val Leu Met Arg 2190
Asn Lys Gly Ile Gly Lys 2195	Met Gly Phe Gly Met 2200	Val Thr Leu Gly 2205
Ala Ser Ala Trp Leu Met 2210	Trp Leu Ser Glu Ile 2215	Glu Pro Ala Arg 2220
Ile Ala Cys Val Leu Ile 2225	Val Val Phe Leu Leu 2230	Leu Val Val Leu 2235
Ile Pro Glu Pro Glu Lys 2240	Gln Arg Ser Pro Gln 2245	Asp Asn Gln Met 2250
Ala Ile Ile Ile Met Val 2255	Ala Val Gly Leu Leu 2260	Gly Leu Ile Thr 2265
Ala Asn Glu Leu Gly Trp 2270	Leu Glu Arg Thr Lys 2275	Ser Asp Leu Ser 2280
His Leu Met Gly Arg Arg 2285	Glu Glu Gly Ala Thr 2290	Ile Gly Phe Ser 2295

Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly

2510						2515						2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln	
2525						2530					2535				
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr	
2540						2545					2550				
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val	
2555						2560					2565				
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg	
2570						2575					2580				
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile	
2585						2590					2595				
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr	
2600						2605					2610				
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro	
2615						2620					2625				
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile	
2630						2635					2640				
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu	
2645						2650					2655				
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser	
2660						2665					2670				
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val	
2675						2680					2685				
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val	
2690						2695					2700				
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu	
2705						2710					2715				
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg	
2720						2725					2730				

Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys

2945						2950						2955			
Glu Arg	Glu His	His Leu	Arg	Gly Glu	Cys Gln	Ser	Cys Val	Tyr							
2960				2965		2970									
Asn Met	Met Gly	Lys Arg	Glu	Lys Lys	Gln Gly	Glu	Phe Gly	Lys							
2975				2980		2985									
Ala Lys	Gly Ser	Arg Ala	Ile	Trp Tyr	Met Trp	Leu	Gly Ala	Arg							
2990				2995		3000									
Phe Leu	Glu Phe	Glu Ala	Leu	Gly Phe	Leu Asn	Glu	Asp His	Trp							
3005				3010		3015									
Met Gly	Arg Glu	Asn Ser	Gly	Gly Gly	Val Glu	Gly	Leu Gly	Leu							
3020				3025		3030									
Gln Arg	Leu Gly	Tyr Val	Leu	Glu Glu	Met Ser	Arg	Ile Pro	Gly							
3035				3040		3045									
Gly Arg	Met Tyr	Ala Asp	Asp	Thr Ala	Gly Trp	Asp	Thr Arg	Ile							
3050				3055		3060									
Ser Arg	Phe Asp	Leu Glu	Asn	Glu Ala	Leu Ile	Thr	Asn Gln	Met							
3065				3070		3075									
Glu Lys	Gly His	Arg Ala	Leu	Ala Leu	Ala Ile	Ile	Lys Tyr	Thr							
3080				3085		3090									
Tyr Gln	Asn Lys	Val Val	Lys	Val Leu	Arg Pro	Ala	Glu Lys	Gly							
3095				3100		3105									
Lys Thr	Val Met	Asp Ile	Ile	Ser Arg	Gln Asp	Gln	Arg Gly	Ser							
3110				3115		3120									
Gly Gln	Val Val	Thr Tyr	Ala	Leu Asn	Thr Phe	Thr	Asn Leu	Val							
3125				3130		3135									
Val Gln	Leu Ile	Arg Asn	Met	Glu Ala	Glu Glu	Val	Leu Glu	Met							
3140				3145		3150									
Gln Asp	Leu Trp	Leu Leu	Arg	Arg Ser	Glu Lys	Val	Thr Asn	Trp							
3155				3160		3165									

Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			
Ser	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3305						3310					3315			
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Val
3320						3325					3330			
Val	Trp	Asn	Arg	Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp
3335						3340					3345			
Lys	Thr	Pro	Val	Thr	Lys	Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys
3350						3355					3360			
Arg	Glu	Asp	Leu	Trp	Cys	Gly	Ser	Leu	Ile	Gly	His	Arg	Pro	Arg
3365						3370					3375			
Thr	Thr	Trp	Ala	Glu	Asn	Ile	Lys	Asn	Thr	Val	Asn	Met	Val	Arg

3380 3385 3390
 Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

 Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

 <210> 25
 <211> 3423
 <212> PRT
 <213> Zika virus strain BeH819015 polyprotein

 <400> 25

 Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

 Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

 Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

 Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

 Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

 Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

 Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
 100 105 110

 Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
 115 120 125

 Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
 130 135 140

 Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
 145 150 155 160

Met	Asp	Leu	Gly	His	Met	Cys	Asp	Ala	Thr	Met	Ser	Tyr	Glu	Cys	Pro	
				165					170					175		
Met	Leu	Asp	Glu	Gly	Val	Glu	Pro	Asp	Asp	Val	Asp	Cys	Trp	Cys	Asn	
			180					185					190			
Thr	Thr	Ser	Thr	Trp	Val	Val	Tyr	Gly	Thr	Cys	His	His	Lys	Lys	Gly	
		195					200					205				
Glu	Ala	Arg	Arg	Ser	Arg	Arg	Ala	Val	Thr	Leu	Pro	Ser	His	Ser	Thr	
	210					215					220					
Arg	Lys	Leu	Gln	Thr	Arg	Ser	Gln	Thr	Trp	Leu	Glu	Ser	Arg	Glu	Tyr	
225					230					235					240	
Thr	Lys	His	Leu	Ile	Arg	Val	Glu	Asn	Trp	Ile	Phe	Arg	Asn	Pro	Gly	
				245					250					255		
Phe	Ala	Leu	Ala	Ala	Ala	Ala	Ile	Ala	Trp	Leu	Leu	Gly	Ser	Ser	Thr	
			260					265					270			
Ser	Gln	Lys	Val	Ile	Tyr	Leu	Val	Met	Ile	Leu	Leu	Ile	Ala	Pro	Ala	
		275					280					285				
Tyr	Ser	Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	
	290					295					300					
Met	Ser	Gly	Gly	Thr	Trp	Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys	
305					310					315					320	
Val	Thr	Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val	
				325					330					335		
Thr	Thr	Thr	Val	Ser	Asn	Met	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Glu	
			340					345					350			
Ala	Ser	Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	Gly	
		355					360					365				
Glu	Ala	Tyr	Leu	Asp	Lys	Gln	Ser	Asp	Thr	Gln	Tyr	Val	Cys	Lys	Arg	
	370					375					380					
Thr	Leu	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	
385					390					395					400	

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
770 775 780

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro
1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
1040 1045 1050

Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu
1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
1070 1075 1080

Thr	Cys	Gly	Thr	Arg	Gly	Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser
1085						1090					1095			
Gly	Arg	Val	Ile	Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro
1100						1105					1110			
Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu
1115						1120					1125			
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met
1130						1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			

Arg Gly	Thr Leu Leu Val	Ala	Trp Arg Ala Gly	Leu	Ala Thr Cys
1310		1315		1320	
Gly Gly	Phe Met Leu Leu Ser	Leu Lys Gly Lys	Gly	Ser Val Lys	
1325		1330		1335	
Lys Asn	Leu Pro Phe Val Met	Ala Leu Gly Leu Thr	Ala Val Arg		
1340		1345		1350	
Leu Val	Asp Pro Ile Asn Val	Val Gly Leu Leu Leu	Leu Thr Arg		
1355		1360		1365	
Ser Gly	Lys Arg Ser Trp Pro	Pro Ser Glu Val Leu	Thr Ala Val		
1370		1375		1380	
Gly Leu	Ile Cys Ala Leu Ala	Gly Gly Phe Ala Lys	Ala Asp Ile		
1385		1390		1395	
Glu Met	Ala Gly Pro Met Ala	Ala Val Gly Leu Leu	Ile Val Ser		
1400		1405		1410	
Tyr Val	Val Ser Gly Lys Ser	Val Asp Met Tyr Ile	Glu Arg Ala		
1415		1420		1425	
Gly Asp	Ile Thr Trp Glu Lys	Asp Ala Glu Val Thr	Gly Asn Ser		
1430		1435		1440	
Pro Arg	Leu Asp Val Ala Leu	Asp Glu Ser Gly Asp	Phe Ser Leu		
1445		1450		1455	
Val Glu	Asp Asp Gly Pro Pro	Met Arg Glu Ile Ile	Leu Lys Val		
1460		1465		1470	
Val Leu	Met Thr Ile Cys Gly	Met Asn Pro Ile Ala	Ile Pro Phe		
1475		1480		1485	
Ala Ala	Gly Ala Trp Tyr Val	Tyr Val Lys Thr Gly	Lys Arg Ser		
1490		1495		1500	
Gly Ala	Leu Trp Asp Val Pro	Ala Pro Lys Glu Val	Lys Lys Gly		
1505		1510		1515	

Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			

Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			

Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			

Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			

Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
2510						2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
2525						2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			

Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			

Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
3035						3040					3045			

Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			

Arg Ala Arg Val Ser Pro Gly Ala Gly Trp Ser Ile Arg Glu Thr
3260 3265 3270

Ala Cys Leu Ala Lys Ser Tyr Ala Gln Met Trp Gln Leu Leu Tyr
3275 3280 3285

Phe His Arg Arg Asp Leu Arg Leu Met Ala Asn Ala Ile Cys Ser
3290 3295 3300

Ser Val Pro Val Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser
3305 3310 3315

Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val
3320 3325 3330

Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp
3335 3340 3345

Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
3350 3355 3360

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg
3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
3410 3415 3420

<210> 26

<211> 3423

<212> PRT

<213> Zika virus isolate Z1106033 polyprotein

<400> 26

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
 100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
 130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
 145 150 155 160

Met Asp Leu Gly His Thr Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
 165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
 180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
 195 200 205

Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
 210 215 220

Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr
 225 230 235 240

Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly
 245 250 255

Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr

260	265	270
Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala		
275	280	285
Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly		
290	295	300
Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys		
305	310	320
Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val		
325	330	335
Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu		
340	345	350
Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly		
355	360	365
Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg		
370	375	380
Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys		
385	390	400
Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr		
405	410	415
Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser		
420	425	430
Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His		
435	440	445
Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro		
450	455	460
Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys		
465	470	475
Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met		
485	490	495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His

725								730				735			
Gln	Ile	Phe	Gly	Ala	Ala	Phe	Lys	Ser	Leu	Phe	Gly	Gly	Met	Ser	Trp
			740						745				750		
Phe	Ser	Gln	Ile	Leu	Ile	Gly	Thr	Leu	Leu	Met	Trp	Leu	Gly	Leu	Asn
		755					760					765			
Ala	Lys	Asn	Gly	Ser	Ile	Ser	Leu	Met	Cys	Leu	Ala	Leu	Gly	Gly	Val
	770					775					780				
Leu	Ile	Phe	Leu	Ser	Thr	Ala	Val	Ser	Ala	Asp	Val	Gly	Cys	Ser	Val
785					790				795						800
Asp	Phe	Ser	Lys	Lys	Glu	Thr	Arg	Cys	Gly	Thr	Gly	Val	Phe	Val	Tyr
			805						810					815	
Asn	Asp	Val	Glu	Ala	Trp	Arg	Asp	Arg	Tyr	Lys	Tyr	His	Pro	Asp	Ser
		820							825				830		
Pro	Arg	Arg	Leu	Ala	Ala	Ala	Val	Lys	Gln	Ala	Trp	Glu	Asp	Gly	Ile
		835					840					845			
Cys	Gly	Ile	Ser	Ser	Val	Ser	Arg	Met	Glu	Asn	Ile	Met	Trp	Arg	Ser
	850					855					860				
Val	Glu	Gly	Glu	Leu	Asn	Ala	Ile	Leu	Glu	Glu	Asn	Gly	Val	Gln	Leu
865					870					875					880
Thr	Val	Val	Val	Gly	Ser	Val	Lys	Asn	Pro	Met	Trp	Arg	Gly	Pro	Gln
				885					890					895	
Arg	Leu	Pro	Val	Pro	Val	Asn	Glu	Leu	Pro	His	Gly	Trp	Lys	Ala	Trp
			900						905				910		
Gly	Lys	Ser	Tyr	Phe	Val	Arg	Ala	Ala	Lys	Thr	Asn	Asn	Ser	Phe	Val
		915					920					925			
Val	Asp	Gly	Asp	Thr	Leu	Lys	Glu	Cys	Pro	Leu	Lys	His	Arg	Ala	Trp
	930					935					940				
Asn	Ser	Phe	Leu	Val	Glu	Asp	His	Gly	Phe	Gly	Val	Phe	His	Thr	Ser
945					950					955					960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro
1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
1040 1045 1050

Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu
1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
1100 1105 1110

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu
1115 1120 1125

Ile Arg Pro Arg Lys Glu Pro Glu Ser Asn Leu Val Arg Ser Met
1130 1135 1140

Val Thr Ala Gly Ser Thr Asp His Met Asp His Phe Ser Leu Gly
1145 1150 1155

Val Leu Val Ile Leu Leu Met Val Gln Glu Gly Leu Lys Lys Arg
1160 1165 1170

Met Thr Thr Lys Ile Ile Ile Ser Thr Ser Met Ala Val Leu Val

1175		1180		1185
Ala Met Ile Leu Gly Gly Phe Ser Met Ser Asp Leu Ala Lys Leu				
1190		1195		1200
Ala Ile Leu Met Gly Ala Thr Phe Ala Glu Met Asn Thr Gly Gly				
1205		1210		1215
Asp Val Ala His Leu Ala Leu Ile Ala Ala Phe Lys Val Arg Pro				
1220		1225		1230
Ala Leu Leu Val Ser Phe Ile Phe Arg Ala Asn Trp Thr Pro Arg				
1235		1240		1245
Glu Ser Met Leu Leu Ala Leu Ala Ser Cys Leu Leu Gln Thr Ala				
1250		1255		1260
Ile Ser Ala Leu Glu Gly Asp Leu Met Val Leu Ile Asn Gly Phe				
1265		1270		1275
Ala Leu Ala Trp Leu Ala Ile Arg Ala Met Val Val Pro Arg Thr				
1280		1285		1290
Asp Asn Ile Thr Leu Ala Ile Leu Ala Ala Leu Thr Pro Leu Ala				
1295		1300		1305
Arg Gly Thr Leu Leu Val Ala Trp Arg Ala Gly Leu Ala Thr Cys				
1310		1315		1320
Gly Gly Phe Met Leu Leu Ser Leu Lys Gly Lys Gly Ser Val Lys				
1325		1330		1335
Lys Asn Leu Pro Phe Val Met Ala Leu Gly Leu Thr Ala Val Arg				
1340		1345		1350
Leu Val Asp Pro Ile Asn Val Val Gly Leu Leu Leu Leu Thr Arg				
1355		1360		1365
Ser Gly Lys Arg Ser Trp Pro Pro Ser Glu Val Leu Thr Ala Val				
1370		1375		1380
Gly Leu Ile Cys Ala Leu Ala Gly Gly Phe Ala Lys Ala Asp Ile				
1385		1390		1395

1610						1615						1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly	
1625						1630					1635				
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly	
1640						1645					1650				
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr	
1655						1660					1665				
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro	
1670						1675					1680				
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro	
1685						1690					1695				
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu	
1700						1705					1710				
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg	
1715						1720					1725				
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val	
1730						1735					1740				
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu	
1745						1750					1755				
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu	
1760						1765					1770				
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu	
1775						1780					1785				
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	
1790						1795					1800				
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	
1805						1810					1815				
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser	
1820						1825					1830				

Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr

2045	2050	2055
Thr Asp Arg Arg Trp Cys Phe 2060 2065	Asp Gly Thr Thr Asn 2070	Asn Thr Ile
Met Glu Asp Ser Val Pro Ala 2075 2080	Glu Val Trp Thr Arg 2085	His Gly Glu
Lys Arg Val Leu Lys Pro Arg 2090 2095	Trp Met Asp Ala Arg 2100	Val Cys Ser
Asp His Ala Ala Leu Lys Ser 2105 2110	Phe Lys Glu Phe Ala 2115	Ala Gly Lys
Arg Gly Ala Ala Phe Gly Val 2120 2125	Met Glu Ala Leu Gly 2130	Thr Leu Pro
Gly His Met Thr Glu Arg Phe 2135 2140	Gln Glu Ala Ile Asp 2145	Asn Leu Ala
Val Leu Met Arg Ala Glu Thr 2150 2155	Gly Ser Arg Pro Tyr 2160	Lys Ala Ala
Ala Ala Gln Leu Pro Glu Thr 2165 2170	Leu Glu Thr Ile Met 2175	Leu Leu Gly
Leu Leu Gly Thr Val Ser Leu 2180 2185	Gly Ile Phe Phe Val 2190	Leu Met Arg
Asn Lys Gly Ile Gly Lys Met 2195 2200	Gly Phe Gly Met Val 2205	Thr Leu Gly
Ala Ser Ala Trp Leu Met Trp 2210 2215	Leu Ser Glu Ile Glu 2220	Pro Ala Arg
Ile Ala Cys Val Leu Ile Val 2225 2230	Val Phe Leu Leu Leu 2235	Val Val Leu
Ile Pro Glu Pro Glu Lys Gln 2240 2245	Arg Ser Pro Gln Asp 2250	Asn Gln Met
Ala Ile Ile Ile Met Val Ala 2255 2260	Val Gly Leu Leu Gly 2265	Leu Ile Thr

Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys

2480		2485		2490
Asn Ile Phe Arg Gly Ser Tyr Leu Ala Gly Ala Ser Leu Ile Tyr				
2495		2500		2505
Thr Val Thr Arg Asn Ala Gly Leu Val Lys Arg Arg Gly Gly Gly				
2510		2515		2520
Thr Gly Glu Thr Leu Gly Glu Lys Trp Lys Ala Arg Leu Asn Gln				
2525		2530		2535
Met Ser Ala Leu Glu Phe Tyr Ser Tyr Lys Lys Ser Gly Ile Thr				
2540		2545		2550
Glu Val Cys Arg Glu Glu Ala Arg Arg Ala Leu Lys Asp Gly Val				
2555		2560		2565
Ala Thr Gly Gly His Ala Val Ser Arg Gly Ser Ala Lys Leu Arg				
2570		2575		2580
Trp Leu Val Glu Arg Gly Tyr Leu Gln Pro Tyr Gly Lys Val Ile				
2585		2590		2595
Asp Leu Gly Cys Gly Arg Gly Gly Trp Ser Tyr Tyr Ala Ala Thr				
2600		2605		2610
Ile Arg Lys Val Gln Glu Val Lys Gly Tyr Thr Lys Gly Gly Pro				
2615		2620		2625
Gly His Glu Glu Pro Val Leu Val Gln Ser Tyr Gly Trp Asn Ile				
2630		2635		2640
Val Arg Leu Lys Ser Gly Val Asp Val Phe His Met Ala Ala Glu				
2645		2650		2655
Pro Cys Asp Thr Leu Leu Cys Asp Ile Gly Glu Ser Ser Ser Ser				
2660		2665		2670
Pro Glu Val Glu Glu Ala Arg Thr Leu Arg Val Leu Ser Met Val				
2675		2680		2685
Gly Asp Trp Leu Glu Lys Arg Pro Gly Ala Phe Cys Ile Lys Val				
2690		2695		2700

Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala

2915						2920						2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	
2930						2935					2940				
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys	
2945						2950					2955				
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr	
2960						2965					2970				
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys	
2975						2980					2985				
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg	
2990						2995					3000				
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp	
3005						3010					3015				
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu	
3020						3025					3030				
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly	
3035						3040					3045				
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile	
3050						3055					3060				
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met	
3065						3070					3075				
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr	
3080						3085					3090				
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly	
3095						3100					3105				
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser	
3110						3115					3120				
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val	
3125						3130					3135				

Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			
Ser	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3305						3310					3315			
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Val
3320						3325					3330			
Val	Trp	Asn	Arg	Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp
3335						3340					3345			
Lys	Thr	Pro	Val	Thr	Lys	Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys

3350 3355 3360
 Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375
 Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg
 3380 3385 3390
 Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405
 Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

 <210> 27
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:1/14

 <400> 27
 Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15
 Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30
 Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45
 Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60
 Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80
 Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95
 Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110
 Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser

<210> 28
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:2/15

<400> 28

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr

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

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser

<210> 29
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:3/16

<400> 29

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser

<210> 30

<211> 403

<212> PRT

<213> sE of SEQ ID NO:4/17

<400> 30

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser

<210> 31

<211> 403
 <212> PRT
 <213> sE of SEQ ID NO:5/18

<400> 31

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
 180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
 195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
 210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
 225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
 245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser

<210> 32

<211> 403

<212> PRT

<213> sE of SEQ ID NO:6/19

<400> 32

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

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

Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu
260 265 270

Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His Leu Lys Cys Arg
275 280 285

Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys
290 295 300

Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu Thr Leu His Gly
305 310 315 320

Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys
325 330 335

Ile Pro Val Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly
340 345 350

Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser
355 360 365

Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val
370 375 380

Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp His Arg Ser
385 390 395

<210> 34

<211> 403

<212> PRT

<213> sE of SEQ ID NO:8/21

<400> 34

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Ile Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser

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

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser

<210> 35
 <211> 399
 <212> PRT
 <213> sE of SEQ ID NO:9/22

<400> 35

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

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

Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu Thr Leu His Gly
 305 310 315 320

Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys
 325 330 335

Ile Pro Val Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly
 340 345 350

Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser
 355 360 365

Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val
 370 375 380

Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp His Arg Ser
 385 390 395

<210> 36
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:10/23

<400> 36

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser

<210> 38
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:12/25

<400> 38

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr

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

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser

<210> 39
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:13/26

<400> 39

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser

<210> 40

<211> 504

<212> PRT

<213> E protein + stem-anchor of SEQ ID NO:1/14

<400> 40

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly

420 425 430
 Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
 435 440 445
 Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
 450 455 460
 Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
 465 470 475 480
 Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
 485 490 495
 Phe Leu Ser Thr Ala Val Ser Ala
 500

 <210> 41
 <211> 504
 <212> PRT
 <213> E protein + stem-anchor of SEQ ID NO:2/15

 <400> 41

 Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

 Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

 Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

 Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

 Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

 Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

 Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
 180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
 195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
 210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
 225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
 245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
 435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
 450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
 465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
 485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
 500

<210> 42
 <211> 504
 <212> PRT
 <213> E protein + stem-anchor of SEQ ID NO:3/16

<400> 42

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr

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

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
 435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
 450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
 465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
 485 490 495

Phe Leu Ser Thr Ala Val Ser Ala

500

<210> 43
<211> 504
<212> PRT
<213> E protein + stem-anchor of SEQ ID NO:4/17

<400> 43

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
 195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
 210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
 225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
 245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 44

<211> 504

<212> PRT

<213> E protein + stem-anchor of SEQ ID NO:5/18

<400> 44

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys

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

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 45

<211> 504

<212> PRT

<213> E protein + stem-anchor of SEQ ID NO:6/19

<400> 45

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

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

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Lys Leu Phe Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Ile Pro Val Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
420 425 430

Ser Val Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Ile His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 46
 <211> 500
 <212> PRT
 <213> E protein + stem-anchor of SEQ ID NO:7/20

<400> 46

Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Met	Ser
1				5					10					15	

Gly	Gly	Thr	Trp	Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys	Val	Thr
			20					25					30		

Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val	Thr	Thr
		35					40					45			

Thr	Val	Ser	Asn	Met	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Glu	Ala	Ser
	50					55					60				

Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Ala
65					70				75						80

Tyr	Leu	Asp	Lys	Gln	Ser	Asp	Thr	Gln	Tyr	Val	Cys	Lys	Arg	Thr	Leu
			85					90						95	

Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser
			100					105					110		

Leu	Val	Thr	Cys	Ala	Lys	Phe	Thr	Cys	Ser	Lys	Lys	Met	Thr	Gly	Lys
		115					120					125			

Ser	Ile	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu	Ser	Val	His
	130					135					140				

Gly	Ser	Gln	His	Ser	Gly	Met	Ile	Gly	Tyr	Glu	Thr	Asp	Glu	Asp	Arg
145					150					155					160

Ala	Lys	Val	Glu	Val	Thr	Pro	Asn	Ser	Pro	Arg	Ala	Glu	Ala	Thr	Leu
			165						170					175	

Gly	Gly	Phe	Gly	Ser	Leu	Gly	Leu	Asp	Cys	Glu	Pro	Arg	Thr	Gly	Leu
			180					185					190		

Asp	Phe	Ser	Asp	Leu	Tyr	Tyr	Leu	Thr	Met	Asn	Asn	Lys	His	Trp	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

195					200					205					
Val	His	Lys	Glu	Trp	Phe	His	Asp	Ile	Pro	Leu	Pro	Trp	His	Ala	Gly
210					215					220					
Ala	Asp	Thr	Gly	Thr	Pro	His	Trp	Asn	Asn	Lys	Glu	Ala	Leu	Val	Glu
225					230					235					240
Phe	Lys	Asp	Ala	His	Ala	Lys	Arg	Gln	Thr	Val	Val	Val	Leu	Gly	Ser
				245					250					255	
Gln	Glu	Gly	Ala	Val	His	Thr	Ala	Leu	Ala	Gly	Ala	Leu	Glu	Ala	Glu
			260					265					270		
Met	Asp	Gly	Ala	Lys	Gly	Arg	Leu	Phe	Ser	Gly	His	Leu	Lys	Cys	Arg
		275					280					285			
Leu	Lys	Met	Asp	Lys	Leu	Arg	Leu	Lys	Gly	Val	Ser	Tyr	Ser	Leu	Cys
		290					295					300			
Thr	Ala	Ala	Phe	Thr	Phe	Thr	Lys	Val	Pro	Ala	Glu	Thr	Leu	His	Gly
305					310					315					320
Thr	Val	Thr	Val	Glu	Val	Gln	Tyr	Ala	Gly	Thr	Asp	Gly	Pro	Cys	Lys
				325					330					335	
Ile	Pro	Val	Gln	Met	Ala	Val	Asp	Met	Gln	Thr	Leu	Thr	Pro	Val	Gly
			340					345					350		
Arg	Leu	Ile	Thr	Ala	Asn	Pro	Val	Ile	Thr	Glu	Ser	Thr	Glu	Asn	Ser
		355					360					365			
Lys	Met	Met	Leu	Glu	Leu	Asp	Pro	Pro	Phe	Gly	Asp	Ser	Tyr	Ile	Val
		370				375					380				
Ile	Gly	Val	Gly	Asp	Lys	Lys	Ile	Thr	His	His	Trp	His	Arg	Ser	Gly
385					390					395					400
Ser	Thr	Ile	Gly	Lys	Ala	Phe	Glu	Ala	Thr	Val	Arg	Gly	Ala	Lys	Arg
				405					410					415	
Met	Ala	Val	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Val	Gly	Gly
			420					425						430	

Val Phe Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala
435 440 445

Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile
450 455 460

Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile
465 470 475 480

Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile Phe Leu Ser Thr
485 490 495

Ala Val Ser Ala
500

<210> 47
<211> 504
<212> PRT
<213> E protein + stem-anchor of SEQ ID NO:8/21

<400> 47

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Ile Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 48

<211> 500

<212> PRT

<213> E protein + stem-anchor of SEQ ID NO:9/22

<400> 48

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

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

275		280		285
Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys	290	295	300	
Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu Thr Leu His Gly	305	310	315	320
Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys	325	330	335	
Ile Pro Val Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly	340	345	350	
Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser	355	360	365	
Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val	370	375	380	
Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp His Arg Ser Gly	385	390	395	400
Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg	405	410	415	
Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly	420	425	430	
Val Phe Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala	435	440	445	
Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile	450	455	460	
Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile	465	470	475	480
Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile Phe Leu Ser Thr	485	490	495	
Ala Val Ser Ala	500			

<210> 49
 <211> 504
 <212> PRT
 <213> E protein + stem-anchor of SEQ ID NO:10/23

<400> 49

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
 180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
 195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
 210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
 225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
 245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 50

<211> 504

<212> PRT

<213> E protein + stem-anchor of SEQ ID NO:11/24

<400> 50

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser

355 360 365
 Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380
 Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400
 His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415
 Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430
 Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
 435 440 445
 Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
 450 455 460
 Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
 465 470 475 480
 Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
 485 490 495
 Phe Leu Ser Thr Ala Val Ser Ala
 500
 <210> 51
 <211> 504
 <212> PRT
 <213> E protein + stem-anchor of SEQ ID NO:12/25
 <400> 51
 Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15
 Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30
 Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

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

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
 435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
 450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
 465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
 485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
 500

<210> 52
 <211> 504
 <212> PRT
 <213> E protein + stem-anchor of SEQ ID NO:13/26

<400> 52

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
 180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
 195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
 210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
 225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
 245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile

435

440

445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
 450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Ala Lys
 465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
 485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
 500

<210> 53
 <211> 1773
 <212> DNA
 <213> Insert sE no codon optimization

<400> 53
 agacgaggcg cagatactag tgtcgggaatt gttggcctcc tgctgaccac agctatggca 60
 gcggagggtca ctagacgtgg gagtgcatac tatatgtact tggacagaaa cgatgctggg 120
 gaggccatat cttttccaac cacattgggg atgaataagt gttatataca gatcatggat 180
 cttggacaca tgttgtgatgc caccatgagc tatgaatgcc ctatgctgga tgaggggggtg 240
 gaaccagatg acgtcgattg ttggtgcaac acgacgtcaa cttgggttgt gtacggaacc 300
 tgccatcaca aaaaagggtga agcacggaga tctagaagag ctgtgacgct cccctcccat 360
 tccactagga agctgcaaac gcggtcgcaa acctgggttg aatcaagaga atacacaaag 420
 cacttgatta gagtcgaaaa ttggatat tt aggaaccctg gcttcgcgtt agcagcagct 480
 gccatcgctt ggcttttggg aagctcaacg agccaaaaag tcatatactt ggtcatgata 540
 ctgctgattg ccccggcata cagcatcagg tgcataaggag tcagcaatag ggactttgtg 600
 gaaggtatgt cagggtgggac ctgggttgat gttgtcttgg aacatggagg ttgtgtcacc 660
 gtaatggcac aggacaaacc gactgtcgac atagagctgg ttacaacaac agtcagcaac 720
 atggcggagg taagatccta ctgctatgag gcatcaatat cagacatggc ttcggacagc 780
 cgctgcccaa cacaagggtga agcctacctt gacaagcaat cagacactca atatgtctgc 840
 aaaagaacgt tagtggacag aggctgggga aatggatgtg gacttttttg caaagggagc 900
 ctggtgacat gcgctaagtt tgcattgctcc aagaaaatga ccgggaagag catccagcca 960
 gagaatctgg agtaccggat aatgctgtca gttcatggct cccagcacag tgggatgatt 1020

gttaatgaca caggacatga aactgatgag aatagagcga aagttgagat aacgccaat	1080
tcaccaagag ccgaagccac cctgggggggt tttggaagcc taggacttga ttgtgaaccg	1140
aggacaggcc ttgacttttc agatttgtat tacttgacta tgaataacaa gacttggttg	1200
gttcacaagg agtggttcca cgacattcca ttaccttggc acgctggggc agacaccgga	1260
actccacact ggaacaacaa agaagcactg gtagagttca aggacgcaca tgccaaaagg	1320
caaactgtcg tggttctagg gagtcaagaa ggagcagttc acacggccct tgctggagct	1380
ctggaggctg agatggatgg tgcaaaggga aggctgtcct ctggccactt gaaatgtcgc	1440
ctgaaaatgg ataaacttag attgaagggc gtgtcatact ccttgtgtac tgcagcgttc	1500
acattcacca agatcccggc tgaaacactg cacgggacag tcacagtgga ggtacagtac	1560
gcagggacag atggaccttg caaggttcca gctcagatgg cgggtggacat gcaaactctg	1620
accccagttg ggaggttgat aaccgctaac cccgtaatca ctgaaagcac tgagaactct	1680
aagatgatgc tggaacttga tccaccatth ggggactctt acattgtcat aggagtcggg	1740
gagaagaaga tcaccaccca ctggcacagg agt	1773

<210> 54
 <211> 2076
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Insert RSP no codon optimization L107D

<400> 54	
agacgaggcg cagatactag tgtcggaatt gttggcctcc tgctgaccac agctatggca	60
gcggaggtca ctagacgtgg gagtgcatac tatatgtact tggacagaaa cgatgctggg	120
gaggccatat cttttccaac cacattgggg atgaataagt gttatataca gatcatggat	180
cttggacaca tgtgtgatgc caccatgagc tatgaatgcc ctatgctgga tgaggggggtg	240
gaaccagatg acgtcgattg ttggtgcaac acgacgtcaa cttgggttgt gtacggaacc	300
tgccatcaca aaaaaggtga agcacggaga tctagaagag ctgtgacgct cccctcccat	360
tccactagga agctgcaaac gcggtcgcaa acctgggttg aatcaagaga atacacaaag	420
cacttgatta gagtcgaaaa ttggatatth aggaaccctg gcttcgcggt agcagcagct	480
gccatcgctt ggcttttggg aagctcaacg agccaaaaag tcatatactt ggtcatgata	540
ctgctgattg ccccggcata cagcatcagg tgcataggag tcagcaatag ggactttgtg	600
gaaggtatgt caggtgggac ctgggttgat gttgtcttgg aacatggagg ttgtgtcacc	660

gtaatggcac aggacaaacc gactgtcgac atagagctgg ttacaacaac agtcagcaac	720
atggcggagg taagatccta ctgctatgag gcatcaatat cagacatggc ttcggacagc	780
cgctgcccac cacaaggtga agcctacctt gacaagcaat cagacactca atatgtctgc	840
aaaagaacgt tagtggacag aggctgggga aatggatgtg gagacttttg caaagggagc	900
ctggtgacat gcgctaagtt tgcattgtcc aagaaaatga ccgggaagag catccagcca	960
gagaatctgg agtaccggat aatgctgtca gttcatggct ccagcacag tgggatgatt	1020
gttaatgaca caggacatga aactgatgag aatagagcga aagttgagat aacgccaat	1080
tcaccaagag ccgaagccac cctggggggg tttggaagcc taggacttga ttgtgaaccg	1140
aggacaggcc ttgacttttc agatttgtat tacttgacta tgaataacaa gcactgggtg	1200
gttcacaagg agtggttcca cgacattcca ttaccttggc acgctggggc agacaccgga	1260
actccacact ggaacaacaa agaagcactg gtagagtcca aggacgcaca tgccaaaagg	1320
caaactgtcg tggttctagg gagtcaagaa ggagcagttc acacggccct tgctggagct	1380
ctggaggctg agatggatgg tgcaaagga aggctgtcct ctggccactt gaaatgtcgc	1440
ctgaaaatgg ataaacttag attgaagggc gtgtcactac ccttgtgtac tgcagcgttc	1500
acattcacca agatcccggc tgaaacactg cacgggacag tcacagtgga ggtacagtac	1560
gcagggacag atggaccttg caaggttcca gctcagatgg cgggtggacat gcaaactctg	1620
accccagttg ggaggttgat aaccgctaac cccgtaatca ctgaaagcac tgagaactct	1680
aagatgatgc tggaacttga tccaccattt ggggactctt acattgtcat aggagtcggg	1740
gagaagaaga tcaccaccca ctggcacagg agtggcagca ccattggaaa agcatttgaa	1800
gccactgtga gaggtgccaa gagaatggca gtcttgggag acacagcctg ggactttgga	1860
tcagttggag gcgctctcaa ctcatggggc aagggcatcc atcaaatttt tggagcagct	1920
ttcaaatacat tgtttggagg aatgtcctgg ttctcacaaa ttctcattgg aacgttgctg	1980
atgtggttgg gtctgaacac aaagaatgga tctatttccc ttatgtgctt ggccttaggg	2040
ggagtgttga tcttcttata cacagccgtc tctgct	2076

<210> 55
 <211> 1773
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Insert sE codon optimization (human)

<400> 55

cgcagaggag cggatacgtc agttggcatt gtgggcttgc tcctcaccac cgctatggcc	60
gcagaagtta caagaagagg gtctgcctac tacatgtatc tggacaggaa cgatgctggc	120
gaagccatct cttttccac aaccctgggg atgaacaagt gctacattca gatcatggat	180
cttggtcaca tgtgcatgc cacaatgtcc tatgagtgtc ccatgctcga tgagggcgtc	240
gagcctgacg acgttgattg ctggtgtaac accaccagca cctgggtggg ctatggcact	300
tgccatcaca agaaggggtga agcacggagg tcacgacggg cagtgcatt gccaaagtc	360
agcactagga aactgcagac tcgctccag acctggcttg aatcccagaga gtacacgaaa	420
cacctcattc gtgtggagaa ctggatcttc cggaatcccg ggtttgccct ggctgctgcc	480
gctattgcct ggttgctcgg ctctagcaca tcacagaaag tcatctacct ggtgatgatc	540
ttgctcattg ctccagccta ctctatcaga tgcacggag tttccaatcg tgactttgtc	600
gaagggatgt ccggaggcac ctgggttgac gtggtgcttg agcatgggtg ctgcgtaacg	660
gtaatggctc aggacaaacc cacggttgac atagaactgg tgaccacgac tgtcagtaat	720
atggccgaag tgcgaagcta ctgctatgag gcctctatct ctgacatggc atcagacagc	780
cgggtgtcaa ctcaaggcga agcttatctg gacaagcaat ccgatacaca gtacgtgtgc	840
aagcggactc tcgtggatag aggttggggc aatgggtgtg gtctgtttgg gaaaggcagt	900
ctggtaacat gcgcaaagtt cgcatgttcc aagaaaatga caggaaagag cattcagccg	960
gaaaatctgg agtataggat tatgctcagc gtgcatggga gccagcacag tggcatgatt	1020
gtcaatgata caggccacga aaccgacgag aacagagcga aggttgagat cactcccaat	1080
tcacctcgcg cagaggccac tctgggaggg tttggaagtc tcggtctgga ctgtgaacct	1140
cgcactggcc tggacttcag cgatctgtat tacctgacga tgaacaacaa gcattggctg	1200
gtccataagg agtggttcca tgatattccg cttccttggc atgccggagc cgataccgga	1260
acacccact ggaacaacaa agaggctttg gtggagtcca aagatgcaca cgctaagcgc	1320
caaaccgtcg tggctctggg tagccaagaa ggagcggttc aactgcgct tgccggagcc	1380
ctggaggcgg aaatggatgg ggccaaaggg cgcctttcca gtggacacct gaagtgtcgg	1440
ctgaaaatgg acaagctgag actgaaaggt gtgtcttaca gcctgtgcac cgcagccttc	1500
actttcacca aaatccctgc tgaaaccttg cacggaacag tgacagtaga ggtgcagtat	1560
gcaggcacag atggcccatg taagggtgcca gctcagatgg cagtggacat gcagaccctg	1620
actccagtgg gaaggctcat aactgccaat ccggtcatca cagagtctac cgagaactca	1680
aagatgatgc tggagctgga ccctcccttt ggggactctt acatagtcac aggggtaggc	1740

gagaagaaaa tcacccatca ctggcacagg agc

1773

<210> 56

<211> 2076

<212> DNA

<213> Artificial sequence

<220>

<223> Insert RSP codon optimization (human) L107D

<400> 56

cgcagaggcg ctgatacctc agttggtata gtgggattgc tgttgacaac cgccatggcc	60
gcagaagtga cgagaagggg ttctgcctac tatatgtacc ttgatcggaa tgacgctgga	120
gaggcaatct cattcccgac caccttgggc atgaacaaat gctacatcca gattatggac	180
ctgggacata tgtgcatgac cactatgagc tatgagtggc ccatgctgga tgaggagta	240
gagcctgacg atgttgactg ctggtgtaac accactagta catgggtggg gtacggaacg	300
tgccaccaca agaaaggaga agctcgaaga tcccgctcgc cggttactct tccctcccat	360
tccacaagga aactccaaac ccgtagccag acatggcttg aaagccgaga atacactaaa	420
cacttgatac gggtagagaa ctggattttc cgcaatcccg ggtttgctct tgcagctgcg	480
gcaattgctt ggctcctcgc gtcaagcaca tcccagaagg tgatctacct ggtgatgac	540
ctgctgattg caccagccta ttcaatccgc tgtatcgggt tctcaaactc tgacttcgtc	600
gaggggatga gtggcgggac ctgggtggat gtcgttcttg aacatggagg ctgtgtaacg	660
gtgatggctc aagacaagcc aaccgttgac atcgaaactg taacgacgac agtcagcaat	720
atggccgaag tccgctctta ctgctatgaa gccagcatca gcgatatggc cagcgatagt	780
cgatgtccga ctcaaggcga agcctatctc gacaaacagt ctgacacca gtacgtgtgc	840
aagaggactc tcgtggatag aggggtgggc aatggttgtg gggatttcgc caaggggtca	900
ctggtaacct gtgcaaagtt cgcctgctct aagaagatga ctgggaagag tatccagccc	960
gagaatctgg agtataggat catgctgagc gttcatggat cccagcatag cgggatgac	1020
gtgaatgata cgggtcacga aacagacgag aaccgcgcaa aggtcgagat tactcccaat	1080
tcccctaggg ccgaagccac actcggaggc tttggcagtc tcggcctgga ttgagcct	1140
cgcactggac tggatttctc cgacctgtac tacctgacta tgaacaacaa acattggctg	1200
gtgcacaagg aatggtttca cgacattccc ctgccttggc acgctggggc tgacactggt	1260
acacctcatt ggaacaacaa agaggctctg gtggagttca aagatgcaca tgccaagaga	1320
caaaccgtgg tggttctggg atcacaggaa ggcgccgtgc ataccgcgct tgccggagca	1380

ctggaagcag agatggacgg tgctaaaggc cggttgagct ctggccacct taagtgtcgg	1440
ctgaagatgg acaagctgag attgaaagga gtctcctata gtctgtgtac agccgcgttt	1500
acctttacga aaatccccgc tgagacactg cacggaacag tgaccgtgga ggtgcaatat	1560
gcagggactg atggcccatg taagggtgcca gcacagatgg ctgttgacat gcagactctc	1620
accccgatcg gcaggccttat tactgccaat ccggtcataa ccgagagtac agagaatagc	1680
aagatgatgc tggagcttga ccctccattc ggagactcct acattgtcat tggcgtcggg	1740
gagaagaaga ttaccacacca ctggcacagg tctggctcca caatcggtaa agccttcgaa	1800
gcgacagtga gaggagccaa acggatggcg gtactcggag acacagcctg ggatttcggg	1860
agcgttggtg gcgctctgaa ctctctcggg aaaggtatcc accagatatt tggggcagcc	1920
tttaaatacac tctttggcgg catgagctgg ttttctcaga tcctgattgg gaccctcctg	1980
atgtggctgg ggctgaacac caagaacggc tctataagcc tgatgtgctt ggccctgggc	2040
ggggtgttga ttttcctgtc caccgctgtg agtgcc	2076

<210> 57
 <211> 20896
 <212> DNA
 <213> Artificial sequence

<220>
 <223> MV Zika sE codon optimization (human)

<400> 57	
tcatgaacgc ggccgctaata acgactcact atagggccaa ctttgtttgg tctgatgagt	60
ccgtgaggac gaaacccgga gtcccgggtc accaaacaaa gttgggtaag gatagttcaa	120
tcaatgatca tcttctagtg cacttaggat tcaagatcct attatcaggg acaagagcag	180
gattagggat atccgagatg gccacacttt taaggagctt agcattgttc aaaagaaaca	240
aggacaaacc acccattaca tcaggatccg gtggagccat cagaggaatc aaacacatta	300
ttatagtacc aatccctgga gattcctcaa ttaccactcg atccagactt ctggaccggt	360
tggtgagggt aattggaaac ccggatgtga gcggggccaa actaacaggg gcactaatag	420
gtatattatc cttatttgtg gagtctccag gtcaattgat tcagaggatc accgatgacc	480
ctgacgttag cataaggctg ttagaggttg tccagagtga ccagtcacaa tctggcctta	540
ccttcgcatac aagagggtacc aacatggagg atgaggcgga ccaatacttt tcacatgatg	600
atccaattag tagtgatcaa tccaggttcg gatggttcgg gaacaaggaa atctcagata	660
ttgaagtgca agaccctgag ggattcaaca tgattctggg taccatccta gcccaaattt	720

gggtcttgct	cgcaaaggcg	gttacggccc	cagacacggc	agctgattcg	gagctaagaa	780
ggtggataaa	gtacacccaa	caaagaaggg	tagttggtga	atttagattg	gagagaaaat	840
ggttggatgt	ggtgaggaac	aggattgccg	aggacctctc	cttacgccga	ttcatggtcg	900
ctctaadcct	ggatatcaag	agaacacccg	gaaacaaacc	caggattgct	gaaatgatat	960
gtgacattga	tacatatatc	gtagaggcag	gattagccag	ttttatcctg	actattaagt	1020
ttgggataga	aactatgtat	cctgctcttg	gactgcatga	atttgctggg	gagttatcca	1080
cacttgagtc	cttgatgaac	ctttaccagc	aaatggggga	aactgcaccc	tacatggtaa	1140
tcctggagaa	ctcaattcag	aacaagttca	gtgcaggatc	ataccctctg	ctctggagct	1200
atgccatggg	agtaggagtg	gaacttgaaa	actccatggg	aggtttgaac	tttggccgat	1260
cttactttga	tccagcatat	tttagattag	ggcaagagat	ggtaaggagg	tcagctggaa	1320
aggtcagttc	cacattggca	tctgaactcg	gtatcactgc	cgaggatgca	aggcttgttt	1380
cagagattgc	aatgcatact	actgaggaca	agatcagtag	agcggttgga	cccagacaag	1440
cccaagtatc	atctctacac	ggtgatcaaa	gtgagaatga	gctaccgaga	ttggggggca	1500
aggaagatag	gaggggtcaaa	cagagtcgag	gagaagccag	ggagagctac	agagaaaccg	1560
ggcccagcag	agcaagtgat	gcgagagctg	cccatcttcc	aaccggcaca	cccctagaca	1620
ttgacactgc	aacggagttc	agccaagatc	cgcaggacag	tcgaagggtca	gctgacgccc	1680
tgcttaggct	gcaagccatg	gcaggaatct	cggagaagaa	aggctcagac	acggacaccc	1740
ctatagtgtg	caatgacaga	aatcttctag	actaggtgcg	agaggccgag	ggccagaaca	1800
acatccgcct	accatccatc	attgttataa	aaaacttagg	aaccagggtc	acacagccgc	1860
cagcccatca	accatccact	cccacgattg	gagccaatgg	cagaagagca	ggcacgccat	1920
gtcaaaaacg	gactggaatg	catccgggct	ctcaaggccg	agcccatcgg	ctcactggcc	1980
atcgaggaag	ctatggcagc	atggtcagaa	atatcagaca	accagggaca	ggagcgagcc	2040
acctgcaggg	aagagaaggc	aggcagttcg	ggtctcagca	aacctgcct	ctcagcaatt	2100
ggatcaactg	aaggcgggtg	acctcgcata	cgcggtcagg	gacctggaga	gagcgatgac	2160
gacgctgaaa	ctttgggaat	cccccaaga	aatctccagg	catcaagcac	tgggttacag	2220
tgttattacg	tttatgatca	cagcggtgaa	gcggttaagg	gaatccaaga	tgctgactct	2280
atcatggttc	aatcaggcct	tgatggtgat	agcaccctct	caggaggaga	caatgaatct	2340
gaaaacagcg	atgtggatat	tggcgaacct	gataccgagg	gatatgctat	cactgaccgg	2400
ggatctgctc	ccatctctat	ggggttcagg	gcttctgatg	ttgaaactgc	agaaggaggg	2460

gagatccacg agctcctgag actccaatcc agaggcaaca actttccgaa gcttgggaaa	2520
actctcaatg ttctctccgcc cccggacccc ggtagggcca gcacttccgg gacacccatt	2580
aaaaagggca cagacgcgag attagcctca tttggaacgg agatcgcgtc tttattgaca	2640
ggtggtgcaa cccaatgtgc tcgaaagtca ccctcggaac catcagggcc aggtgcacct	2700
gcggggaatg tccccgagtg tgtgagcaat gccgcactga tacaggagtg gacacccgaa	2760
tctggtacca caatctcccc gagatcccag aataatgaag aagggggaga ctattatgat	2820
gatgagctgt tctctgatgt ccaagatatt aaaacagcct tggccaaaat acacgaggat	2880
aatcagaaga taatctccaa gctagaatca ctgctgttat tgaagggaga agttgagtca	2940
attaagaagc agatcaacag gcaaaatatc agcatatcca ccctggaagg acacctctca	3000
agcatcatga tcgccattcc tggacttggg aaggatccca acgaccccac tgcagatgtc	3060
gaaatcaatc ccgacttgaa acccatcata ggcagagatt caggccgagc actggccgaa	3120
gttctcaaga aacccgttgc cagccgacaa ctccaaggaa tgacaaatgg acggaccagt	3180
tccagaggac agctgctgaa ggaatttcag ctaaagccga tcgggaaaaa gatgagctca	3240
gccgtcgggt ttgttctga caccggccct gcatcacgca gtgtaatccg ctccattata	3300
aaatccagcc ggctagagga ggatcggaag cgttacctga tgactctcct tgatgatatc	3360
aaaggagcca atgatcttgc caagttccac cagatgctga tgaagataat aatgaagtag	3420
ctacagctca acttacctgc caaccccatg ccagtcgacc caactagcct accctccatc	3480
attgttataa aaaacttagg aaccaggctc acacagccgc cagcccatca acgcgtacgg	3540
ccaccatggc acgcagagga gcggatacgt cagttggcat tgtgggcttg ctctcacca	3600
ccgctatggc cgcagaagtt acaagaagag ggtctgccta ctacatgtat ctggacagga	3660
acgatgctgg cgaagccatc tcctttccca caaccctggg gatgaacaag tgctacattc	3720
agatcatgga tcttggtcac atgtgcgatg ccacaatgtc ctatgagtgt cccatgctcg	3780
atgagggcgt cgagcctgac gacgttgatt gctggtgtaa caccaccagc acctgggtgg	3840
tctatggcac ttgccatcac aagaaggggtg aagcacggag gtcacgacgg gcagtgacat	3900
tgccaagtca tagcactagg aaactgcaga ctcgctccca gacctggctt gaatcccagag	3960
agtacacgaa acacctcatt cgtgtggaga actggatctt ccggaatccc gggtttgccc	4020
tggtgctgc cgctattgcc tggttgctcg gctctagcac atcacagaaa gtcattacc	4080
tggtgatgat cttgctcatt gctccagcct actctatcag atgcatcgga gtttccaatc	4140
gtgactttgt cgaagggatg tccggaggca cctgggttga cgtggtgctt gagcatggtg	4200

gctgcgtaac ggtaatggct caggacaaac ccacggttga catagaactg gtgaccacga	4260
ctgtcagtaa tatggccgaa gtgcgaagct actgctatga ggccctctatc tctgacatgg	4320
catcagacag ccggtgtcca actcaaggcg aagcttatct ggacaagcaa tccgatacac	4380
agtacgtgtg caagcggact ctctgtgata gaggttgggg caatgggtgt ggtctgtttg	4440
ggaaaggcag tctggtaaca tgcgcaaagt tcgcatgttc caagaaaatg acaggaaaga	4500
gcattcagcc ggaaaatctg gagtatagga ttatgctcag cgtgcatggg agccagcaca	4560
gtggcatgat tgtcaatgat acaggccacg aaaccgacga gaacagagcg aaggttgaga	4620
tcactcccaa ttcacctcgc gcagaggcca ctctgggagg gtttggaagt ctcggtctgg	4680
actgtgaacc tcgcactggc ctggacttca gcgatctgta ttacctgacg atgaacaaca	4740
agcattggct ggtccataag gagtggttcc atgatattcc gcttccttgg catgccggag	4800
ccgataccgg aacaccccac tggaacaaca aagaggcttt ggtggagttc aaagatgcac	4860
acgctaagcg ccaaaccgtc gtggctcctgg gtagccaaga aggagcgggt cacactgcgc	4920
ttgccggagc cctggaggcg gaaatggatg gggccaaagg gcgcctttcc agtggacacc	4980
tgaagtgtcg gctgaaaatg gacaagctga gactgaaagg tgtgtcttac agcctgtgca	5040
ccgcagcctt cactttcacc aaaatccctg ctgaaacctt gcacggaaca gtgacagtag	5100
aggtgcagta tgcaggcaca gatggcccat gtaagggtgcc agctcagatg gcagtggaca	5160
tgcagaccct gactccagtg ggaaggctca taactgcaa tccggtcac acagagtcta	5220
ccgagaactc aaagatgatg ctggagctgg accctccctt tggggactct tacatagtca	5280
taggggtagg cgagaagaaa atcaccatc actggcacag gagctaatga taagcgcgca	5340
gcgcttagac gtctcgcgat cgatactagt acaacctaaa tccattataa aaaacttagg	5400
agcaaagtga ttgcctccca aggtccacaa tgacagagac ctacgacttc gacaagtcgg	5460
catgggacat caaagggtcg atcgctccga tacaaccac cacctacagt gatggcaggc	5520
tggtgcccca ggtcagagtc atagatcctg gtctaggcga caggaaggat gaatgcttta	5580
tgtacatgtt tctgctgggg gttgttgagg acagcgattc cctagggcct ccaatcgggc	5640
gagcatttgg gttcctgccc ttaggtgttg gcagatccac agcaaagccc gaaaaactcc	5700
tcaaagaggc cactgagctt gacatagttg ttagacgtac agcagggtc aatgaaaaac	5760
tgggtgttcta caacaacacc ccactaactc tcctcacacc ttggagaaaag gtcctaacaa	5820
cagggagtgt cttcaacgca aaccaagtgt gcaatgcggt taatctgata ccgctcgata	5880
ccccgcagag gttccgtgtt gtttatatga gcatcaccg tctttcggat aacgggtatt	5940

acaccgttcc tagaagaatg ctggaattca gatcgggtcaa tgcagtggcc ttcaacctgc	6000
tggtgaccct taggattgac aaggcgatag gccctgggaa gatcatcgac aatacagagc	6060
aacttcctga ggcaacattt atgggtccaca tcgggaactt caggagaaag aagagtgaag	6120
tctactctgc cgattattgc aaaatgaaaa tcgaaaagat gggcctgggtt tttgcacttg	6180
gtgggatagg gggcaccagt cttcacatta gaagcacagg caaaatgagc aagactctcc	6240
atgcacaact cgggttcaag aagaccttat gttacccgct gatggatatc aatgaagacc	6300
ttaatcgatt actctggagg agcagatgca agatagtaag aatccaggca gttttgcagc	6360
catcagttcc tcaagaattc cgcatttacg acgacgtgat cataaatgat gaccaaggac	6420
tattcaaagt tctgtagacc gtagtgccca gcaatgcccg aaaacgaccc cctcacaaat	6480
gacagccaga aggcccgac aaaaaagccc cctccgaaag actccacgga ccaagcgaga	6540
ggccagccag cagccgacgg caagcgcgaa caccaggcgg cccagcaca gaacagccct	6600
gacacaaggc caccaccagc caccccaatc tgcatacctc tcgtgggacc cccgaggacc	6660
aacccccaaag gctgcccccg atccaaacca ccaaccgcat cccaccacc cccgggaaag	6720
aaacccccag caattggaag gccctcccc ctcttcctca acacaagaac tccacaaccg	6780
aaccgcacaa gcgaccgagg tgaccaaac gcaggcatcc gactccctag acagatcctc	6840
tctccccggc aaactaaaca aaacttaggg ccaaggaaca tacacacca acagaacca	6900
gacccccggc cagggcgccg cgccccaac ccccgacaac cagagggagc cccaaccaa	6960
tcccgccggc tcccccggtg cccacaggca gggacaccaa ccccgacaac gaccagcac	7020
ccaaccatcg acaatccaag acgggggggc cccccaaaa aaaggcccc aggggccgac	7080
agccagcacc gcgaggaagc ccaccaccc cacacacgac cacggcaacc aaaccagaac	7140
ccagaccacc ctggggccacc agtcccaga ctcggccatc acccgcaga aaggaaaggc	7200
cacaacccgc gcaccccagc cccgatccgg cggggagcca cccaaccga accagcacc	7260
aagagcgatc cccgaaggac cccgaaccg caaaggacat cagtatcca cagcctctcc	7320
aagtcccccg gtctcctcct cttctcgaag ggacaaaaag atcaatccac cacacccgac	7380
gacactcaac tccccacccc taaaggagac accgggaatc ccagaatcaa gactcatcca	7440
atgtccatca tgggtctcaa ggtgaacgtc tctgccatat tcatggcagt actgttaact	7500
ctccaaacac ccaccggtca aatccattgg ggcaatctct ctaagatagg ggtggtagga	7560
ataggaagtg caagctacaa agttatgact cgttcagcc atcaatcatt agtcataaaa	7620
ttaatgcca atataactct cctcaataac tgcacgagg tagagattgc agaatacagg	7680

agactactga	gaacagtttt	ggaaccaatt	agagatgcac	ttaatgcaat	gacccagaat	7740
ataagaccgg	ttcagagtgt	agcttcaagt	aggagacaca	agagatttgc	gggagtagtc	7800
ctggcaggtg	cggccctagg	cgttgccaca	gctgctcaga	taacagccgg	cattgcactt	7860
caccagtcca	tgctgaactc	tcaagccatc	gacaatctga	gagcgagcct	ggaaactact	7920
aatcaggcaa	ttgagacaat	cagacaagca	gggcaggaga	tgatattggc	tgttcagggt	7980
gtccaagact	acatcaataa	tgagctgata	ccgtctatga	accaactatc	ttgtgattta	8040
atcggccaga	agctcgggct	caaattgctc	agatactata	cagaaatcct	gtcattattt	8100
ggccccagtt	tacgggaccc	catatctgcy	gagatatcta	tccaggcttt	gagctatgcy	8160
cttgaggag	acatcaataa	ggtgttagaa	aagctcggat	acagtggagg	tgatttactg	8220
ggcatcttag	agagcggagg	aataaaggcc	cggataactc	acgtcgacac	agagtcctac	8280
ttcattgtcc	tcagtatagc	ctatccgacg	ctgtccgaga	ttaagggggg	gattgtccac	8340
cggctagagg	gggtctcgta	caacataggc	tctcaagagt	ggtataccac	tgtgcccaag	8400
tatgttgcaa	cccaagggta	ccttatctcg	aatthttgatg	agtcacgtg	tactttcatg	8460
ccagagggga	ctgtgtgcag	ccaaaatgcc	ttgtacccga	tgagtcctct	gctccaagaa	8520
tgccctccgg	ggtacaccaa	gtcctgtgct	cgtacactcg	tatccggggtc	ttttgggaac	8580
cggttcattt	tatcacaagg	gaacctaata	gccaatgtg	catcaatcct	ttgcaagtgt	8640
tacacaacag	gaacgatcat	taatcaagac	cctgacaaga	tcctaacata	cattgctgcc	8700
gatcactgcc	cggtagtcga	ggtgaacggc	gtgaccatcc	aagtcgggag	caggaggtat	8760
ccagacgctg	tgtacttgca	cagaattgac	ctcggtcctc	ccatatcatt	ggagaggttg	8820
gacgtaggga	caaatctggg	gaatgcaatt	gctaagttgg	aggatgccaa	ggaattgttg	8880
gagtcacg	accagatatt	gaggagtatg	aaaggthtat	cgagcactag	catagtctac	8940
atcctgattg	cagtgtgtct	tggagggttg	atagggatcc	ccgctthtaat	atgttgctgc	9000
agggggcg	gtaacaaaaa	gggagaacaa	gthggtatgt	caagaccagg	cctaaagcct	9060
gatcttacgg	gaacatcaaa	atcctatgta	aggtcgctct	gatcctctac	aactcttgaa	9120
acacaaatgt	cccacaagtc	tcctcttcgt	catcaagcaa	ccaccgcacc	cagcatcaag	9180
cccacctgaa	attatctccg	gcttcctctc	ggccgaacaa	tatcggtagt	taatcaaaac	9240
ttagggtgca	agatcatcca	caatgtcacc	acaacgagac	cggataaatg	ccttctacaa	9300
agataacccc	catcccaagg	gaagtaggat	agtcattaac	agagaacatc	ttatgattga	9360
tagaccttat	gtthttgctg	ctgttctgth	tgtcatgtht	ctgagcttga	tcgggttgct	9420

agccattgca ggcattagac ttcacgggc agccatctac accgcagaga tccataaaag	9480
cctcagcacc aatctagatg taactaactc aatcgagcat caggtcaagg acgtgctgac	9540
accactcttc aaaatcatcg gtgatgaagt gggcctgagg acacctcaga gattcactga	9600
cctagtgaag ttaatctctg acaagattaa attccttaac ccgcataggg agtacgactt	9660
cagagatctc acttggtgta tcaacccgcc agagagaatc aaattggatt atgatcaata	9720
ctgtgcagat gtggctgctg aagagctcat gaatgcattg gtgaactcaa ctctactgga	9780
gaccagaaca accaatcagt tcctagctgt ctcaaaggga aactgctcag ggcccactac	9840
aatcagaggt caattctcaa acatgtcgct gtccctgtta gacttgtatt taggtcgagg	9900
ttacaatgtg tcatctatag tcactatgac atcccaggga atgtatgggg gaacttacct	9960
agtggaaaag cctaactctga gcagcaaaag gtcagagttg tcacaactga gcatgtaccg	10020
agtgtttgaa gtaggtgtta tcagaaatcc ggggtttgggg gctccggtgt tccatatgac	10080
aaactatctt gagcaaccag tcagtaatga tctcagcaac tgtatggtgg ctttggggga	10140
gctcaaactc gcagcccttt gtcacgggga agattctatc acaattccct atcagggatc	10200
agggaaagg gtcagcttcc agctcgtcaa gctaggtgtc tggaaatccc caaccgacat	10260
gcaatcctgg gtccccttat caacggatga tccagtata gacaggcttt acctctcatc	10320
tcacagaggt gttatcgctg acaatcaagc aaaatgggct gtcccgacaa cacgaacaga	10380
tgacaagttg cgaatggaga catgcttcca acaggcgtgt aagggtaaaa tccaagcact	10440
ctgcgagaat cccgagtggg caccattgaa ggataacagg attccttcat acggggtctt	10500
gtctgttgat ctgagtctga cagttgagct taaaatcaaa attgcttcgg gattcggggc	10560
attgatcaca cacggttcag ggatggacct atacaaatcc aaccacaaca atgtgtattg	10620
gctgactatc ccgccaatga agaacctagc cttaggtgta atcaacacat tggagtggat	10680
accgagattc aaggtttagtc cctacctctt cactgtccca attaaaggaag caggcgaaga	10740
ctgccatgcc ccaacatacc tacctgcgga ggtggatggt gatgtcaaac tcagttccaa	10800
tctggtgatt ctacctggtc aagatctcca atatgttttg gcaacctacg atacttccag	10860
ggttgaacat gctgtggttt attacgttta cagcccaagc cgctcatttt cttactttta	10920
tccttttagg ttgcctataa agggggtccc catcgaatta caagtggaaat gcttcacatg	10980
ggacaaaaa ctctggtgcc gtcacttctg tgtgcttgcg gactcagaat ctggtggaca	11040
tatcactcac tctgggatgg tgggcatggg agtcagctgc acagtcaccc gggaagatgg	11100
aaccaatcgc agatagggt gctagtgaac caatcacatg atgtcaccca gacatcaggc	11160

atacccacta	gtgtgaaata	gacatcagaa	ttaagaaaaa	cgtaggggtcc	aagtgggttcc	11220
ccgttatgga	ctcgctatct	gtcaaccaga	tcttataccc	tgaagttcac	ctagatagcc	11280
cgatagttac	caataagata	gtagccatcc	tggagtatgc	tcgagtcacct	cacgcttaca	11340
gcctggagga	ccctacactg	tgtcagaaca	tcaagcaccg	cctaaaaaac	ggattttcca	11400
accaaagtat	tataaacaat	gtggaagttg	ggaatgtcat	caagtccaag	cttaggagtt	11460
atccggccca	ctctcatatt	ccatatccaa	attgtaatca	ggattttattt	aacatagaag	11520
acaaagagtc	aacgaggaag	atccgtgaac	tcctcaaaaa	ggggaattcg	ctgtactcca	11580
aagtcagtga	taagggttttc	caatgcttaa	gggacactaa	ctcacggctt	ggcctaggct	11640
ccgaattgag	ggaggacatc	aaggagaaag	ttattaactt	gggagtttac	atgcacagct	11700
cccagtgggt	tgagcccttt	ctgttttggt	ttacagtcaa	gactgagatg	aggtcagtga	11760
ttaaatcaca	aaccataact	tgccatagga	ggagacacac	acctgtattc	ttcactggta	11820
gttcagtga	gttgctaata	tctcgtgacc	ttgttgctat	aatcagtaaa	gagtctcaac	11880
atgtatatta	cctgacattt	gaactgggtt	tgatgtattg	tgatgtcata	gaggggaggt	11940
taatgacaga	gaccgctatg	actattgatg	ctaggtatac	agagcttcta	ggaagagtca	12000
gatacatgtg	gaaactgata	gatggtttct	tcctgcact	cggaatcca	acttatcaaa	12060
ttgtagccat	gctggagcct	ctttcacttg	cttacctgca	gctgagggat	ataacagtag	12120
aactcagagg	tgctttcctt	aaccactgct	ttactgaaat	acatgatgtt	cttgaccaa	12180
acgggttttc	tgatgaaggt	acttatcatg	agttaactga	agctctagat	tacattttca	12240
taactgatga	catacatctg	acaggggaga	ttttctcatt	tttcagaagt	ttcgccacc	12300
ccagacttga	agcagtaacg	gctgctgaaa	atgttaggaa	atacatgaat	cagcctaaag	12360
tcattgtgta	tgagactctg	atgaaaggtc	atgccatatt	ttgtggaatc	ataatcaacg	12420
gctatcgtga	caggcacgga	ggcagttggc	caccgctgac	cctccccctg	catgctgcag	12480
acacaatccg	gaatgctcaa	gcttcaggtg	aagggttaac	acatgagcag	tgcgttgata	12540
actggaaatc	ttttgctgga	gtgaaatttg	gctgctttat	gcctcttagc	ctggatagtg	12600
atctgacaat	gtacctaaag	gacaaggcac	ttgctgctct	ccaaagggaa	tgggattcag	12660
tttacccgaa	agagttcctg	cgttacgacc	ctccaagggt	aaccgggtca	cggaggcttg	12720
tagatgtttt	ccttaatgat	tcgagctttg	acccatatga	tgtgataatg	tatgttgtaa	12780
gtggagctta	cctccatgac	cctgagttca	acctgtctta	cagcctgaaa	gaaaaggaga	12840
tcaaggaaac	aggtagactt	tttgctaaaa	tgacttacaa	aatgagggca	tgccaagtga	12900

ttgctgaaaa	tctaattctca	aacgggattg	gcaaataat	taaggacaat	gggatggcca	12960
aggatgagca	cgatttgact	aaggcactcc	acactctagc	tgtctcagga	gtccccaag	13020
atctcaaaga	aagtcacagg	ggggggccag	tcttaaaaac	ctactcccga	agcccagtcc	13080
acacaagtac	caggaacgtg	agagcagcaa	aagggtttat	agggttcct	caagtaattc	13140
ggcaggacca	agacactgat	catccggaga	atatggaagc	ttacgagaca	gtcagtgc	13200
ttatcacgac	tgatctcaag	aagtactgcc	ttaattggag	atatgagacc	atcagcttgt	13260
ttgcacagag	gctaaatgag	atttacggat	tgccctcatt	tttcagtg	ctgcataaga	13320
ggcttgagac	ctctgtcctg	tatgtaagt	accctcattg	ccccccgac	cttgacgccc	13380
atatcccgtt	atataaagtc	ccaatgatc	aaatcttcat	taagtaccct	atgggaggta	13440
tagaagggt	ttgtcagaag	ctgtggacca	tcagcaccat	tccctatcta	tacctggctg	13500
cttatgagag	cggagtaagg	attgcttcgt	tagtgcaagg	ggacaatcag	accatagccg	13560
taacaaaaag	ggtaccagc	acatggccct	acaacctta	gaaacgggaa	gctgctagag	13620
taactagaga	ttactttgta	attcttaggc	aaaggctaca	tgatattggc	catcacctca	13680
aggcaaatga	gacaattggt	tcatcacatt	tttttgtcta	ttcaaaagga	atatattatg	13740
atgggctact	tgtgtcccaa	tcactcaaga	gcatcgcaag	atgtgtattc	tggtcagaga	13800
ctatagttga	tgaaacaagg	gcagcatgca	gtaatatgtc	tacaacaatg	gctaaaagca	13860
tcgagagagg	ttatgaccgt	taccttgc	attccctgaa	cgtcctaaaa	gtgatacagc	13920
aaattctgat	ctctcttggc	ttcacaatca	attcaaccat	gaccgggat	gtagtcatac	13980
ccctcctcac	aaacaacgac	ctcttaataa	ggatggcact	gttgcccgct	cctattgggg	14040
ggatgaatta	tctgaatatg	agcaggctgt	ttgtcagaaa	catcgggtgat	ccagtaacat	14100
catcaattgc	tgatctcaag	agaatgattc	tcgcctcact	aatgcctgaa	gagaccctcc	14160
atcaagtaat	gacacaacaa	ccgggggact	cttcattcct	agactgggct	agcgaccctt	14220
actcagcaaa	tcttgtatgt	gtccagagca	tcactagact	cctcaagaac	ataactgcaa	14280
ggtttgtcct	gatccatagt	ccaaacccaa	tgttaaaagg	attattccat	gatgacagta	14340
aagaagagga	cgagggactg	gcggcattcc	tcatggacag	gcatattata	gtacctaggg	14400
cagctcatga	aatcctggat	catagtgtca	caggggcaag	agagtctatt	gcaggcatgc	14460
tgataaccac	aaaaggcttg	attcgagcca	gcatgaggaa	gggggggtta	acctctcgag	14520
tgataaccag	attgtccaat	tatgactatg	aacaattcag	agcagggatg	gtgctattga	14580
caggaagaaa	gagaaatgtc	ctcattgaca	aagagtcatg	ttcagtgcag	ctggcgagag	14640

ctctaagaag	ccatatgtgg	gcgaggctag	ctcgaggacg	gcctatttac	ggccttgagg	14700
tccctgatgt	actagaatct	atgcgaggcc	accttattcg	gcgtcatgag	acatgtgtca	14760
tctgcgagt	tgatcagtc	aactacggat	ggttttttgt	cccctcgggt	tgccaactgg	14820
atgatattga	caaggaaaca	tcatccttga	gagtcccata	tattggttct	accactgatg	14880
agagaacaga	catgaagctt	gccttcgtaa	gagccccaag	tcgatccttg	cgatctgctg	14940
ttagaatagc	aacagtgtac	tcatgggctt	acggtgatga	tgatagctct	tggaacgaag	15000
cctggttggt	ggctaggcaa	agggccaatg	tgagcctgga	ggagctaagg	gtgatcactc	15060
ccatctcaac	ttcgactaat	ttagcgcata	ggttgaggga	tcgtagcact	caagtgaat	15120
actcaggtac	atcccttgtc	cgagtggcga	ggtataccac	aatctccaac	gacaatctct	15180
catttgtcat	atcagataag	aaggttgata	ctaactttat	ataccaacaa	ggaatgcttc	15240
tagggttggg	tgtttttagaa	acattgtttc	gactcgagaa	agataccgga	tcatctaaca	15300
cggtattaca	tcttcacgtc	gaaacagatt	gttgcgatga	cccgatgata	gatcatccca	15360
ggatacccag	ctcccgcaag	ctagagctga	gggcagagct	atgtaccaac	ccattgatat	15420
atgataatgc	acctttaatt	gacagagatg	caacaaggct	atacaccag	agccatagga	15480
ggcaccttgt	ggaatttgtt	acatgggtcca	caccccaact	atatcacatt	ttagctaagt	15540
ccacagcact	atctatgatt	gacctggtaa	caaaatttga	gaaggaccat	atgaatgaaa	15600
tttcagctct	cataggggat	gacgatatca	atagtttcat	aactgagttt	ctgctcatag	15660
agccaagatt	attcactatc	tacttggggc	agtgtgcggc	catcaattgg	gcatttgatg	15720
tacattatca	tagaccatca	gggaaatata	agatgggtga	gctgttgtca	tcgttccttt	15780
ctagaatgag	caaaggagt	tttaagggtgc	ttgtcaatgc	tctaagccac	caaagatct	15840
acaagaaatt	ctggcattgt	ggtattatag	agcctatcca	tggtccttca	cttgatgctc	15900
aaaacttgca	cacaactgtg	tgcaacatgg	tttacacatg	ctatatgacc	tacctcgacc	15960
tgttgttgaa	tgaagagtta	gaagagttca	catttctctt	gtgtgaaagc	gacgaggatg	16020
tagtaccgga	cagattcgac	aacatccagg	caaaacactt	atgtgttctg	gcagatttgt	16080
actgtcaacc	agggacctgc	ccaccaattc	gaggtctaag	accggtagag	aaatgtgcag	16140
ttctaaccga	ccatatcaag	gcagaggcta	tgttatctcc	agcaggatct	tcgtggaaca	16200
taaatccaat	tattgtagac	cattactcat	gctctctgac	ttatctccgg	cgaggatcga	16260
tcaaacagat	aagattgaga	gttgatccag	gattcatttt	cgacgccctc	gctgaggtaa	16320
atgtcagtca	gccaaagatc	ggcagcaaca	acatctcaaa	tatgagcatc	aaggctttca	16380

gacccccaca	cgatgatggt	gcaaaattgc	tcaaagatat	caacacaagc	aagcacaatc	16440
ttcccatttc	agggggcaat	ctcgccaatt	atgaaatcca	tgctttccgc	agaatcgggt	16500
tgaactcatc	tgcttgctac	aaagctgttg	agatatcaac	attaattagg	agatgccttg	16560
agccagggga	ggacggcctg	ttcttgggtg	agggatcggg	ttctatgttg	atcacttata	16620
aagagatact	taaactaaac	aagtgccttc	ataatagtgg	ggtttccgcc	aattctagat	16680
ctgggtcaaag	ggaattagca	ccctatccct	ccgaagttag	ccttgtcgaa	cacagaatgg	16740
gagtaggtaa	tattgtcaaa	gtgctcttta	acgggaggcc	cgaagtcacg	tgggtaggca	16800
gtgtagattg	cttcaatttc	atagttagta	atatccctac	ctctagtgtg	gggtttatcc	16860
attcagatat	agagaccttg	cctgacaaag	atactataga	gaagctagag	gaattggcag	16920
ccatcttata	gatggctctg	ctcctgggca	aaataggatc	aatactgggtg	attaagctta	16980
tgccctttcag	cggggatttt	gttcagggat	ttataagtta	tgtaggggtct	cattatagag	17040
aagtgaacct	tgtataccct	agatacagca	acttcatctc	tactgaatct	tatttggtta	17100
tgacagatct	caaggctaac	cggctaataa	atcctgaaaa	gattaagcag	cagataattg	17160
aatcatctgt	gaggacttca	cctggactta	taggtcacat	cctatccatt	aagcaactaa	17220
gctgcataca	agcaattgtg	ggagacgcag	ttagtagagg	tgatatcaat	cctactctga	17280
aaaaacttac	acctatagag	caggtgctga	tcaattgcgg	gttggcaatt	aacggacctt	17340
agctgtgcaa	agaattgatc	caccatgatg	ttgcctcagg	gcaagatgga	ttgcttaatt	17400
ctatactcat	cctctacagg	gagttggcaa	gattcaaaga	caaccaaaga	agtcaacaag	17460
ggatgttcca	cgcttaccct	gtattggtta	gtagcaggca	acgagaactt	atatctagga	17520
tcacccgcaa	attctggggg	cacattcttc	tttactccgg	gaacaaaaag	ttgataaata	17580
agtttatcca	gaatctcaag	tccggctatc	tgataactaga	cttacaccag	aatatcttcg	17640
ttaagaatct	atccaagtca	gagaaacaga	ttattatgac	gggggggttg	aaacgtgagt	17700
gggtttttta	ggtaacagtc	aaggagacca	aagaatggta	taagttagtc	ggatacagtg	17760
ccctgattaa	ggactaattg	gttgaactcc	ggaaccctaa	tcctgcccta	ggtggttagg	17820
cattatttgc	aatatattaa	agaaaacttt	gaaaatacga	agtttctatt	cccagctttg	17880
tctggtggcc	ggcatggtcc	cagcctcctc	gctggcgccg	gctgggcaac	attccgaggg	17940
gaccgtcccc	tcggtaatgg	cgaatgggac	gcggccgatc	cggctgctaa	caaagcccga	18000
aaggaagctg	agttggctgc	tgccaccgct	gagcaataac	tagcataacc	ccttggggcc	18060
tctaaacggg	tcttgagggg	ttttttgctg	aaaggaggaa	ctatatccgg	atgcggccgc	18120

gggccctatg	gtaccagct	tttgttcct	ttagttaggg	ttaattccga	gcttggcgta	18180
atcatgggtca	tagctgtttc	ctgtgtgaaa	ttgttatccg	ctcacaattc	cacacaacat	18240
aggagccgga	agcataaagt	gtaaagcctg	gggtgcctaa	tgagttaggt	aactcacatt	18300
aattgcggtg	cgctcactgc	ccgctttcca	gtcgggaaac	ctgtcgtgcc	agctgcatta	18360
atgaatcggc	caacgcgcgg	ggagaggcgg	tttgcgtatt	gggcgctctt	ccgcttcctc	18420
gctcactgac	tcgctgcgct	cggtcgttcg	gctgcggcga	gcggtatcag	ctcactcaaa	18480
ggcggtaata	cggttatcca	cagaatcagg	ggataacgca	ggaaagaaca	tgtgagcaaa	18540
aggccagcaa	aaggccagga	accgtaaaaa	ggccgcgttg	ctggcgtttt	tccataggct	18600
cggccccct	gacgagcatc	acaaaaatcg	acgctcaagt	cagaggtggc	gaaacccgac	18660
aggactataa	agataccagg	cgttcccccc	tggaagctcc	ctcgtgcgct	ctcctgttcc	18720
gaccctgccg	cttaccggat	acctgtccgc	ctttctccct	tcgggaagcg	tggcgctttc	18780
tcaatgctca	cgctgtaggt	atctcagttc	ggtgtaggtc	gttcgctcca	agctgggctg	18840
tgtgcacgaa	cccccgttc	agcccgaccg	ctgcgcctta	tccggtaaact	atcgtcttga	18900
gtccaacccg	gtaagacacg	acttatcgcc	actggcagca	gccactggta	acaggattag	18960
cagagcgagg	tatgtaggcg	gtgctacaga	gttcttgaag	tgggtggccta	actacggcta	19020
cactagaagg	acagtatttg	gtatctgcgc	tctgctgaag	ccagttacct	tcggaaaaag	19080
agttggtagc	tcttgatccg	gcaaacaaac	caccgctggg	agcgggtgggt	tttttgtttg	19140
caagcagcag	attacgcgca	gaaaaaaagg	atctcaagaa	gaccccttga	tcttttctac	19200
gggggtctgac	gctcagtggg	acgaaaactc	acgttaaggg	atcttggtca	tgagattatc	19260
aaaaaggatc	ttcacctaga	tcctttttaa	ttaaaaatga	agtttttaa	caatctaaag	19320
tatatatgag	taaacttggg	ctgacagtta	ccaatgctta	atcagttagg	cacctatctc	19380
agcgatctgt	ctatttcgtt	catccatagt	tgcctgactg	cccgtcgtgt	agataactac	19440
gatacgggag	ggcttaccat	ctggccccag	tgctgcaatg	ataccgcgag	accacgctc	19500
accggctcca	gatttatcag	caataaacca	gccagccgga	agggccgagc	gcagaagtgg	19560
tcctgcaact	ttatccgcct	ccatccagtc	tattaattgt	tgccgggaag	ctagagtaag	19620
tagttcgcca	gttaatagtt	tgcgcaacgt	tgttgccatt	gctacaggca	tcgtggtgtc	19680
acgctcgtcg	tttgggtatg	cttcattcag	ctccggttcc	caacgatcaa	ggcgagttac	19740
atgatcccc	atgttgtgaa	aaaaagcggg	tagctccttc	ggtcctccga	tcgttgtcag	19800
aagtaagttg	gccgcagtgt	tatcactcat	gcttatggca	gcactgcata	attctcttac	19860

tgtcatgcc	tccgtaagat	gcttttctgt	gactgggtgag	tactcaacca	agtcattctg	19920
agaatagtgt	atgcggcgac	cgagttgctc	ttgcccggcg	tcaatacggg	ataataccgc	19980
gccacatagc	agaactttta	aagtgtctcat	cattggaaaa	cgttcttcgg	ggcgaaaact	20040
ctcaaggatc	ttaccgctgt	tgagatccag	ttcgatgtaa	cccactcgtg	cacccaactg	20100
atcttcagca	tcttttactt	tcaccagcgt	ttctgggtga	gcaaaaacag	gaaggcaaaa	20160
tgccgcaaaa	aagggaataa	gggcgacacg	gaaatgttga	atactcatac	tcttcctttt	20220
tcaatattat	tgaagcattt	atcagggtta	ttgtctcatg	agcggataca	tatttgaatg	20280
tatttagaaa	aataaaca	taggggttcc	gcgcacattt	ccccgaaaag	tgccacctga	20340
aattgtaaac	gttaatat	tgtaaaaatt	cgcgttaaat	ttttgttaaa	tcagctcatt	20400
ttttaaccaa	taggccgaaa	tcggcaaaat	cccttataaa	tcaaaagaat	agaccgagat	20460
agggttgagt	gttggtccag	tttggaaaca	gagtccacta	ttaaagaacg	tggtactcaa	20520
cgtcaaagg	cgaaaaaccg	tctatcagg	cgatggccca	ctacgtgaac	catcaccta	20580
atcaagtttt	ttgggggtcg	ggtgccgtaa	agcactaaat	cggaacccta	aaggagagccc	20640
ccgatttaga	gcttgacggg	gaaagccggc	gaacgtggcg	agaaaggaag	ggaagaaagc	20700
gaaaggagcg	ggcgctaggg	cgctggcaag	tgtagcggtc	acgctgcgcg	taaccaccac	20760
acccgccgcg	cttaatgcgc	cgctacagg	cgcgtcccat	tcgccattca	ggctgcgcaa	20820
ctgttgggaa	gggcgatcgg	tgcgggcctc	ttcgctatta	cgccagccac	cgcggtgatc	20880
cttataaagc	tagatg					20896

<210> 58
 <211> 21196
 <212> DNA
 <213> Artificial sequence

<220>
 <223> MV Zika RSP codon optimization (human) L107D

<400> 58						
tcatgaacgc	ggccgcta	acgactcact	atagggccaa	ctttgtttgg	tctgatgagt	60
ccgtgaggac	gaaaccgga	gtcccgggtc	accaaaca	gttgggtaag	gatagttcaa	120
tcaatgatca	tcttctagt	cacttaggat	tcaagatcct	attatcagg	acaagagcag	180
gattagggat	atccgagat	gccacacttt	taaggagctt	agcattgttc	aaaagaaaca	240
aggacaaacc	accattaca	tcaggatccg	gtggagccat	cagaggaatc	aaacacatta	300
ttatagtacc	aatccctgga	gattcctcaa	ttaccactcg	atccagactt	ctggaccggt	360

tggtgaggtt aattggaaac ccgatgtga gcgggcccac actaacaggg gcactaatag	420
gtatattatc cttatttgtg gagtctccag gtcaattgat tcagaggatc accgatgacc	480
ctgacgttag cataaggctg ttagaggttg tccagagtga ccagtcacaa tctggcctta	540
ccttcgcac cagaggtacc aacatggagg atgaggcgga ccaatacttt tcacatgatg	600
atccaattag tagtgatcaa tccaggttcg gatggttcgg gaacaaggaa atctcagata	660
ttgaagtgca agaccctgag ggattcaaca tgattctggg taccatccta gcccaaattt	720
gggtcttgct cgcaaaggcg gttacggccc cagacacggc agctgattcg gagctaagaa	780
ggtggataaa gtacacccaa caaagaagg tagttggtga atttagattg gagagaaaat	840
ggttgatgt ggtgaggaa aggattgcc aggacctct cttacgccga ttcattggtc	900
ctctaatacct ggatatcaag agaacacccg gaaacaaacc caggattgct gaaatgatat	960
gtgacattga tacatatatc gtagaggcag gattagccag ttttatcctg actattaagt	1020
ttgggataga aactatgtat cctgctcttg gactgcatga atttgctggg gagttatcca	1080
cacttgagtc cttgatgaac cttaccagc aaatggggga aactgcaccc tacatggtaa	1140
tcctggagaa ctcaattcag aacaagttca gtgcaggatc ataccctctg ctctggagct	1200
atgccatggg agtaggagtg gaacttgaaa actccatggg aggtttgaac tttggccgat	1260
cttactttga tccagcatat ttagattag ggcaagagat ggtaaggagg tcagctggaa	1320
aggtcagttc cacattggca tctgaactcg gtatcactgc cgaggatgca aggcttgttt	1380
cagagattgc aatgcatact actgaggaca agatcagtag agcggttgga cccagacaag	1440
cccaagtatc atttctacac ggtgatcaaa gtgagaatga gctaccgaga ttgggggggca	1500
aggaagatag gaggggtcaaa cagagtcgag gagaagccag ggagagctac agagaaaccg	1560
ggcccagcag agcaagtgat gcgagagctg cccatcttcc aaccggcaca cccctagaca	1620
ttgacactgc aacggagtcc agccaagatc cgcaggacag tcgaagggtca gctgacgccc	1680
tgcttaggct gcaagccatg gcaggaatct cggaagaaca aggtcagac acggacaccc	1740
ctatagtgt caatgacaga aatcttctag actaggtgcg agaggccgag ggccagaaca	1800
acatccgcct accatccatc attgttataa aaaacttagg aaccagggtc acacagccgc	1860
cagcccatca accatccact cccacgattg gagccaatgg cagaagagca ggcacgcat	1920
gtcaaaaacg gactggaatg catccgggct ctcaaggccg agcccatcgg ctactggcc	1980
atcgaggaag ctatggcagc atggtcagaa atatcagaca acccaggaca ggagcgagcc	2040
acctgcaggg aagagaaggc aggcagttcg ggtctcagca aacctgcct ctgagcaatt	2100

ggatcaactg aaggcgggtgc acctcgcata cgcggtcagg gacctggaga gagcgatgac	2160
gacgctgaaa ctttgggaat ccccccaaga aatctccagg catcaagcac tgggttacag	2220
tgttattacg tttatgatca cagcggtgaa gcgggttaagg gaatccaaga tgctgactct	2280
atcatggttc aatcaggcct tgatgggtgat agcacctctt caggaggaga caatgaatct	2340
gaaaacagcg atgtggatat tggcgaacct gataccgagg gatatgctat cactgaccgg	2400
ggatctgctc ccatctctat ggggttcagg gcttctgatg ttgaaactgc agaaggaggg	2460
gagatccacg agctcctgag actccaatcc agaggcaaca actttccgaa gcttgggaaa	2520
actctcaatg ttctctcgcc cccggacccc ggtagggcca gcacttccgg gacacccatt	2580
aaaaagggca cagacgcgag attagcctca tttggaacgg agatcgcgctc tttattgaca	2640
ggtggtgcaa cccaatgtgc tcgaaagtca ccctcggaac catcagggcc aggtgcacct	2700
gcgggggaatg tccccgagtg tgtgagcaat gccgcactga tacaggagtg gacacccgaa	2760
tctggtacca caatctcccc gagatcccag aataatgaag aagggggaga ctattatgat	2820
gatgagctgt tctctgatgt ccaagatatt aaaacagcct tggccaaaat acacgaggat	2880
aatcagaaga taatctccaa gctagaatca ctgctgttat tgaagggaga agttgagtca	2940
attaagaagc agatcaacag gcaaaatata agcatatcca ccctggaagg acacctctca	3000
agcatcatga tcgccattcc tggacttggg aaggatccca acgaccccac tgcagatgtc	3060
gaaatcaatc ccgacttgaa acccatcata ggcagagatt caggccgagc actggccgaa	3120
gttctcaaga aacccgttgc cagccgacaa ctccaaggaa tgacaaatgg acggaccagt	3180
tccagaggac agctgctgaa ggaatttcag ctaaagccga tcgggaaaaa gatgagctca	3240
gccgtcgggt ttgttctga caccggccct gcatcacgca gtgtaatccg ctccattata	3300
aaatccagcc ggctagagga ggatcggaag cgttacctga tgactctcct tgatgatata	3360
aaaggagcca atgatcttgc caagttccac cagatgctga tgaagataat aatgaagtag	3420
ctacagctca acttacctgc caaccccatg ccagtcgacc caactagcct accctccatc	3480
attgttataa aaaacttagg aaccaggctc acacagccgc cagcccatca acgcgtacgg	3540
ccaccatggc acgcagaggc gctgatacct cagttggtat agtgggattg ctgttgacaa	3600
ccgccatggc cgcagaagtg acgagaaggg gttctgccta ctatatgtac cttgatcgga	3660
atgacgctgg agaggcaatc tcattcccga ccaccttggg catgaacaaa tgctacatcc	3720
agattatgga cctgggacat atgtgcgatg ccactatgag ctatgagtgc cccatgctgg	3780
atgagggagt agagcctgac gatgttgact gctggtgtaa caccactagt acatgggtgg	3840

tgtacggaac	gtgccaccac	aagaaaggag	aagctcgaag	atcccgtcgc	gcggttactc	3900
ttccctccca	ttccacaagg	aaactccaaa	cccgtagcca	gacatggctt	gaaagccgag	3960
aatacactaa	acacttgata	cgggtagaga	actggatttt	ccgcaatccc	gggtttgctc	4020
ttgcagctgc	ggcaattgct	tggctcctcg	ggtcaagcac	atcccagaag	gtgatctacc	4080
tggtgatgat	cctgctgatt	gcaccagcct	attcaatccg	gtgtatcggt	gtctcaaatc	4140
gtgacttcgt	cgaggggatg	agtggcggga	cctgggtgga	tgtcgttctg	gaacatggag	4200
gctgtgtaac	ggtgatggct	caagacaagc	caaccgttga	catcgaactg	gtaacgacga	4260
cagtcagcaa	tatggccgaa	gtccgctctt	actgctatga	agccagcatc	agcgatatgg	4320
ccagcgatag	tcgatgtccg	actcaaggcg	aagcctatct	cgacaaacag	tctgacaccc	4380
agtacgtgtg	caagaggact	ctcgtggata	gaggggtggg	caatggttgt	ggggatttcg	4440
gcaaggggtc	actggtaacc	tgtgcaaagt	tcgcctgctc	taagaagatg	actgggaaga	4500
gtatccagcc	cgagaatctg	gagtatagga	tcatgctgag	cgttcatgga	tcccagcata	4560
gcgggatgat	cgtgaatgat	acgggtcacg	aaacagacga	gaaccgcgca	aaggtcgaga	4620
ttactcccaa	ttcccctagg	gccgaagcca	cactcggagg	ctttggcagt	ctcggcctgg	4680
attgcgagcc	tcgcactgga	ctggatttct	ccgacctgta	ctacctgact	atgaacaaca	4740
aacattggct	ggtgcacaag	gaatggtttc	acgacattcc	cctgccttgg	cacgctgggg	4800
ctgacactgg	tacacctcat	tggaacaaca	aagaggctct	ggtggagttc	aaagatgcac	4860
atgccaagag	acaaaccgtg	gtggttctgg	gatcacagga	aggcgccgtg	cataccgcgc	4920
ttgccggagc	actggaagca	gagatggacg	gtgctaaagg	ccggttgagc	tctggccacc	4980
ttaagtgtcg	gctgaagatg	gacaagctga	gattgaaagg	agtctcctat	agtctgtgta	5040
cagccgcgtt	tacctttacg	aaaatccccg	ctgagacact	gcacggaaca	gtgaccgtgg	5100
aggtgcaata	tgcagggact	gatggcccat	gtaagggtgcc	agcacagatg	gctgttgaca	5160
tgcagactct	caccccagtc	ggcaggctta	ttactgccaa	tccggtcata	accgagagta	5220
cagagaatag	caagatgatg	ctggagcttg	accctccatt	cggagactcc	tacattgtca	5280
ttggcgtcgg	tgagaagaag	attaccacc	actggcacag	gtctggctcc	acaatcggtg	5340
aagccttcga	agcgacagtg	agaggagcca	aacggatggc	ggtactcgga	gacacagcct	5400
gggatttcgg	gagcgttggg	ggcgtctga	actctctcgg	gaaaggtatc	caccagatat	5460
ttggggcagc	ctttaaatca	ctctttggcg	gcatgagctg	gttttctcag	atcctgattg	5520
ggaccctcct	gatgtggctg	gggctgaaca	ccaagaacgg	ctctataagc	ctgatgtgct	5580

tggccctggg	cggggtggtg	attttctgt	ccaccgctgt	gagtgcctaa	tgagcgcgca	5640
gcgcttagac	gtctcgcgat	cgatactagt	acaacctaaa	tccattataa	aaaacttagg	5700
agcaaagtga	ttgcctccca	aggtccacaa	tgacagagac	ctacgacttc	gacaagtcgg	5760
catgggacat	caaagggtcg	atcgctccga	tacaaccac	cacctacagt	gatggcaggc	5820
tggtgcccc	ggtcagagtc	atagatcctg	gtctaggcga	caggaaggat	gaatgcttta	5880
tgtacatgtt	tctgctgggg	gttgttgagg	acagcgattc	cctagggcct	ccaatcgggc	5940
gagcatttgg	gttcctgccc	ttaggtggtg	gcagatccac	agcaaagccc	gaaaaactcc	6000
tcaaagaggc	cactgagctt	gacatagttg	ttagacgtac	agcagggctc	aatgaaaaac	6060
tggtgttcta	caacaacacc	ccactaactc	tcctcacacc	ttggagaaaag	gtcctaacaa	6120
cagggagtgt	cttcaacgca	aaccaagtgt	gcaatgcggt	taatctgata	ccgctcgata	6180
ccccgcagag	gttcctgtgt	gtttatatga	gcatcacccg	tctttcggat	aacgggtatt	6240
acaccgttcc	tagaagaatg	ctggaattca	gatcgggtcaa	tgcagtggcc	ttcaacctgc	6300
tggtgaccct	taggattgac	aaggcgatag	gccctgggaa	gatcatcgac	aatacagagc	6360
aacttcctga	ggcaacatth	atgggtccaca	tcgggaactt	caggagaaaag	aagagtgaag	6420
tctactctgc	cgattattgc	aaaatgaaaa	tcgaaaagat	gggcctgggt	tttgacttg	6480
gtgggatagg	gggcaccagt	cttcacatta	gaagcacagg	caaaatgagc	aagactctcc	6540
atgcacaact	cggtttcaag	aagaccttat	gttaccgcgt	gatggatatc	aatgaagacc	6600
ttaatcgatt	actctggagg	agcagatgca	agatagtaag	aatccaggca	gttttgagc	6660
catcagttcc	tcaagaattc	cgcatttacg	acgacgtgat	cataaatgat	gaccaaggac	6720
tattcaaagt	tctgtagacc	gtagtgccca	gcaatgcccg	aaaacgaccc	ccctcacaat	6780
gacagccaga	aggcccggac	aaaaaagccc	cctccgaaag	actccacgga	ccaagcgaga	6840
ggccagccag	cagccgacgg	caagcgcgaa	caccaggcgg	ccccagcaca	gaacagccct	6900
gacacaaggc	caccaccagc	cacccaatc	tgcatcctcc	tcgtggggacc	cccgaggacc	6960
aacccccaa	gctgcccccg	atccaaacca	ccaaccgcat	ccccaccacc	cccgggaaag	7020
aaacccccag	caattggaag	gccctcccc	ctcttcctca	acacaagaac	tccacaaccg	7080
aaccgcacaa	gcgaccgagg	tgaccaaac	gcaggcatcc	gactccctag	acagatcctc	7140
tctccccggc	aaactaaaca	aaacttaggg	ccaaggaaca	tacacacca	acagaacca	7200
gaccccgcc	cacggcgccg	cgcccccaac	ccccgacaac	cagaggggagc	ccccaaccaa	7260
tcccgccggc	tcccccggtg	cccacaggca	gggacaccaa	ccccgaaca	gaccagcac	7320

ccaaccatcg	acaatccaag	acggggggggc	ccccccaaaa	aaaggccccc	agggggccgac	7380
agccagcacc	gcgaggaagc	ccacccaccc	cacacacgac	cacggcaacc	aaaccagaac	7440
ccagaccacc	ctggggccacc	agctcccaga	ctcgggccatc	accccgcaga	aaggaaaggc	7500
cacaacccgc	gcaccccagc	cccgatccgg	cggggagcca	cccaacccga	accagcaccc	7560
aagagcgatc	cccgaaggac	ccccgaaccg	caaaggacat	cagtatccca	cagcctctcc	7620
aagtcccccg	gtctcctcct	cttctcgaag	ggaccaaaaag	atcaatccac	cacacccgac	7680
gacactcaac	tccccacccc	taaaggagac	accgggaatc	ccagaatcaa	gactcatcca	7740
atgtccatca	tgggtctcaa	ggtgaacgtc	tctgccatat	tcatggcagt	actgttaact	7800
ctccaaacac	ccaccggtca	aatccattgg	ggcaatctct	ctaagatagg	ggtggtagga	7860
ataggaagtg	caagctacaa	agttatgact	cgttccagcc	atcaatcatt	agtcataaaa	7920
ttaatgccca	atataactct	cctcaataac	tgcacgaggg	tagagattgc	agaatacagg	7980
agactactga	gaacagtttt	ggaaccaatt	agagatgcac	ttaatgcaat	gacccagaat	8040
ataagaccgg	ttcagagtgt	agcttcaagt	aggagacaca	agagatttgc	gggagtagtc	8100
ctggcaggtg	cggccctagg	cgttgccaca	gctgctcaga	taacagccgg	cattgcactt	8160
caccagtcca	tgctgaactc	tcaagccatc	gacaatctga	gagcgagcct	ggaaactact	8220
aatcaggcaa	ttgagacaat	cagacaagca	gggcaggaga	tgatattggc	tgttcagggc	8280
gtccaagact	acatcaataa	tgagctgata	cgtctatga	accaactatc	ttgtgattta	8340
atcggccaga	agctcgggct	caaattgctc	agatactata	cagaaatcct	gtcattattt	8400
ggccccagtt	tacgggaccc	catatctgcg	gagatatcta	tccaggcttt	gagctatgcg	8460
cttgaggagg	acatcaataa	ggtgttagaa	aagctcggat	acagtggagg	tgatttactg	8520
ggcatcttag	agagcggagg	aataaaggcc	cggataactc	acgtcgacac	agagtcctac	8580
ttcattgtcc	tcagtatagc	ctatccgacg	ctgtccgaga	ttaagggggc	gattgtccac	8640
cggctagagg	gggtctcgta	caacataggc	tctcaagagt	ggtataccac	tgtgcccaag	8700
tatgttgcaa	cccaagggta	ccttatctcg	aattttgatg	agtcatcgtg	tactttcatg	8760
ccagagggga	ctgtgtgcag	ccaaaatgcc	ttgtacccga	tgagtcctct	gctccaagaa	8820
tgctccggg	ggtacaccaa	gtcctgtgct	cgtacactcg	tatccgggct	ttttgggaac	8880
cggttcattt	tatcacaagg	gaacctaata	gccaatgtg	catcaatcct	ttgcaagtgt	8940
tacacaacag	gaacgatcat	taatcaagac	cctgacaaga	tcctaacata	cattgctgcc	9000
gatcactgcc	cggtagtcga	ggtgaacggc	gtgaccatcc	aagtcgggag	caggaggtat	9060

ccagacgctg	tgtacttgca	cagaattgac	ctcggtcctc	ccatatcatt	ggagagggttg	9120
gacgtaggga	caaactctggg	gaatgcaatt	gctaagttgg	aggatgccaa	ggaattgttg	9180
gagtcacg	accagatatt	gaggagtatg	aaagggtttat	cgagcactag	catagtctac	9240
atcctgattg	cagtgtgtct	tggaggggttg	atagggatcc	ccgctttaat	atgttgctgc	9300
agggggcg	gtaacaaaaa	gggagaacaa	gttggtatgt	caagaccagg	cctaaagcct	9360
gatcttacg	gaacatcaaa	atcctatgta	aggtcgctct	gatcctctac	aactcttgaa	9420
acacaaatgt	cccacaagtc	tcctcttcgt	catcaagcaa	ccaccgcacc	cagcatcaag	9480
cccacctgaa	attatctccg	gcttccctct	ggccgaacaa	tatcggtagt	taatcaaac	9540
ttagggtgca	agatcatcca	caatgtcacc	acaacgagac	cggataaatg	ccttctacaa	9600
agataacccc	catccaag	gaagtaggat	agtcattaac	agagaacatc	ttatgattga	9660
tagaccttat	gttttgctgg	ctgttctgtt	tgtcatgttt	ctgagcttga	tcgggttgct	9720
agccattgca	ggcattagac	ttcatcgggc	agccatctac	accgcagaga	tccataaaag	9780
cctcagcacc	aatctagatg	taactaactc	aatcgagcat	caggtcaagg	acgtgctgac	9840
accactcttc	aaaatcatcg	gtgatgaagt	gggcctgagg	acacctcaga	gattcactga	9900
cctagtghaa	ttaatctctg	acaagattaa	attccttaat	ccggataggg	agtacgactt	9960
cagagatctc	acttggtgta	tcaaccgcgc	agagagaatc	aaattggatt	atgatcaata	10020
ctgtgcagat	gtggctgctg	aagagctcat	gaatgcattg	gtgaactcaa	ctctactgga	10080
gaccagaaca	accaatcagt	tcctagctgt	ctcaaaggga	aactgctcag	ggcccactac	10140
aatcagaggt	caattctcaa	acatgtcgct	gtccctgtta	gacttgtatt	taggtcgagg	10200
ttacaatgtg	tcacttatag	tcactatgac	atcccaggga	atgtatgggg	gaacttacct	10260
agtggaaaag	cctaactctga	gcagcaaaag	gtcagagttg	tcacaactga	gcatgtaccg	10320
agtgtttgaa	gtaggtgtta	tcagaaatcc	gggtttgggg	gctccggtgt	tccatatgac	10380
aaactatctt	gagcaaccag	tcagtaatga	tctcagcaac	tgtatgggtg	ctttggggga	10440
gctcaaactc	gcagcccttt	gtcacgggga	agattctatc	acaattccct	atcagggatc	10500
agggaaaggt	gtcagcttcc	agctcgtcaa	gctaggtgtc	tggaaatccc	caaccgacat	10560
gcaatcctgg	gtccccttat	caacggatga	tccagtgata	gacaggcttt	acctctcatc	10620
tcacagaggt	gttatcgctg	acaatcaagc	aaaatgggct	gtcccgacaa	cacgaacaga	10680
tgacaagttg	cgaatggaga	catgcttcca	acaggcgtgt	aagggtaaaa	tccaagcact	10740
ctgcgagaat	cccaggtggg	caccattgaa	ggataacagg	attccttcat	acgggtctt	10800

gtctgttgat ctgagtctga cagttgagct taaaatcaaa attgcttcgg gattcggggcc	10860
attgatcaca cacggttcag ggatggacct atacaaatcc aaccacaaca atgtgtattg	10920
gctgactatc ccgccaatga agaacctagc cttagggtga atcaacacat tggagtggat	10980
accgagattc aaggtttagtc cctacctctt cactgtccca attaaggaag caggcgaaga	11040
ctgccatgcc ccaacatacc tacctgcgga ggtggatggt gatgtcaaac tcagttccaa	11100
tctggtgatt ctacctgggc aagatctcca atatgttttg gcaacctacg atacttccag	11160
ggttgaacat gctgtgggttt attacgttta cagcccaagc cgctcatttt cttactttta	11220
tccttttagg ttgcctataa aggggggtccc catcgaatta caagtggaat gcttcacatg	11280
ggaccaaaaa ctctggtgcc gtcacttctg tgtgcttgcg gactcagaat ctggtggaca	11340
tatcactcac tctgggatgg tgggcatggg agtcagctgc acagtcaccc gggaagatgg	11400
aaccaatcgc agataggggt gctagtgaac caatcacatg atgtcaccca gacatcaggc	11460
atacccacta gtgtgaaata gacatcagaa ttaagaaaaa cgtaggggtcc aagtggttcc	11520
ccgttatgga ctcgctatct gtcaaccaga tcttataccc tgaagttcac ctagatagcc	11580
cgatagttag caataagata gtagccatcc tggagtatgc tcgagtcocct cacgcttaca	11640
gcctggagga ccctacactg tgtcagaaca tcaagcacgc cctaaaaaac ggattttcca	11700
accaaagatg tataaacaat gtggaagttg ggaatgtcat caagtccaag cttaggagtt	11760
atccggccca ctctcatatt ccatatccaa attgtaatca ggattttattt aacatagaag	11820
acaaagagtc aacgaggaag atccgtgaac tcctcaaaaa ggggaattcg ctgtactcca	11880
aagtcagtga taaggttttc caatgcttaa gggacactaa ctcacggctt ggcttaggct	11940
ccgaattgag ggaggacatc aaggagaaag ttattaactt gggagtttac atgcacagct	12000
cccagtgggt tgagcccttt ctgttttgggt ttacagtcaa gactgagatg aggtcagtga	12060
ttaaatcaca aaccatact tgccatagga ggagacacac acctgtattc ttactggta	12120
gttcagttga gttgctaata tctcgtgacc ttgttgctat aatcagtaaa gagtctcaac	12180
atgtatatta cctgacattt gaactgggtt tgatgtattg tgatgtcata gaggggaggt	12240
taatgacaga gaccgctatg actattgatg ctaggtatac agagcttcta ggaagagtca	12300
gatacatgtg gaaactgata gatggtttct tcctgcact cggaatcca acttatcaaa	12360
ttgtagccat gctggagcct ctttcacttg cttacctgca gctgagggat ataacagtag	12420
aactcagagg tgctttcctt aaccactgct ttactgaaat acatgatgtt cttgaccaa	12480
acgggttttc tgatgaaggt acttatcatg agttaactga agctctagat tacattttca	12540

taactgatga	catacatctg	acaggggaga	ttttctcatt	tttcagaagt	ttcggccacc	12600
ccagacttga	agcagtaacg	gctgctgaaa	atgttaggaa	atacatgaat	cagcctaaag	12660
tcatttgtga	tgagactctg	atgaaaggtc	atgccatatt	ttgtggaatc	ataatcaacg	12720
gctatcgtga	caggcacgga	ggcagttggc	caccgctgac	cctccccctg	catgctgcag	12780
acacaatccg	gaatgctcaa	gcttcaggtg	aagggttaac	acatgagcag	tgcgttgata	12840
actggaaatc	ttttgctgga	gtgaaatttg	gctgctttat	gcctcttagc	ctggatagtg	12900
atctgacaat	gtacctaaag	gacaaggcac	ttgctgctct	ccaaagggaa	tgggattcag	12960
tttacccgaa	agagttcctg	cgttacgacc	ctcccaaggg	aaccgggtca	cggaggcttg	13020
tagatgtttt	ccttaatgat	tcgagctttg	acccatatga	tgtgataatg	tatgttgtaa	13080
gtggagctta	cctccatgac	cctgagttca	acctgtctta	cagcctgaaa	gaaaaggaga	13140
tcaaggaaac	aggtagactt	tttgctaaaa	tgacttacia	aatgagggca	tgccaagtga	13200
ttgctgaaaa	tctaactctca	aacgggattg	gcaaataattt	taaggacaat	gggatggcca	13260
aggatgagca	cgatttgact	aaggcactcc	acactctagc	tgtctcagga	gtccccaag	13320
atctcaaaga	aagtcacagg	ggggggccag	tcttaaaaaac	ctactcccga	agcccagtcc	13380
acacaagtac	caggaacgtg	agagcagcaa	aagggtttat	agggttccct	caagtaattc	13440
ggcaggacca	agacactgat	catccggaga	atatggaagc	ttacgagaca	gtcagtgcac	13500
ttatcacgac	tgatctcaag	aagtactgcc	ttaattggag	atatgagacc	atcagcttgt	13560
ttgcacagag	gctaaatgag	atttacggat	tgccctcatt	tttccagtgg	ctgcataaga	13620
ggcttgagac	ctctgtcctg	tatgtaagtg	accctcattg	cccccccgac	cttgacgccc	13680
atatcccgtt	atataaagtc	cccaatgac	aaatcttcat	taagtaccct	atgggaggta	13740
tagaagggtg	ttgtcagaag	ctgtggacca	tcagcaccat	tccctatcta	tacctggctg	13800
cttatgagag	cggagtaagg	attgcttcgt	tagtgcaagg	ggacaatcag	accatagccg	13860
taacaaaaag	ggtaccacgc	acatggccct	acaaccttaa	gaaacgggaa	gctgctagag	13920
taactagaga	ttactttgta	attcttaggc	aaaggctaca	tgatattggc	catcacctca	13980
aggcaaatga	gacaattgtt	tcacacatt	tttttgtcta	ttcaaaagga	atatattatg	14040
atgggctact	tgtgtcccaa	tcactcaaga	gcatcgcaag	atgtgtattc	tggtcagaga	14100
ctatagttga	tgaacaagag	gcagcatgca	gtaatatattg	tacaacaatg	gctaaaagca	14160
tcgagagagg	ttatgaccgt	taccttgcat	attccctgaa	cgctcctaaa	gtgatacagc	14220
aaattctgat	ctctcttggc	ttcacaatca	attcaaccat	gacccgggat	gtagtcatac	14280

ccctcctcac	aaacaacgac	ctcttaataa	ggatggcact	gttgcccgct	cctattgggg	14340
ggatgaatta	tctgaatatg	agcaggctgt	ttgtcagaaa	catcgggtgat	ccagtaacat	14400
catcaattgc	tgatctcaag	agaatgattc	tcgcctcact	aatgcctgaa	gagaccctcc	14460
atcaagtaat	gacacaacaa	ccgggggact	cttcattcct	agactgggct	agcgaccctt	14520
actcagcaaa	tcttgtatgt	gtccagagca	tcactagact	cctcaagaac	ataactgcaa	14580
ggtttgtcct	gatccatagt	ccaaacccaa	tgttaaaagg	attattccat	gatgacagta	14640
aagaagagga	cgaggggactg	gcggcattcc	tcatggacag	gcatattata	gtacctaggg	14700
cagctcatga	aatcctggat	catagtgtca	caggggcaag	agagtctatt	gcaggcatgc	14760
tggataccac	aaaaggcttg	attcgagcca	gcatgaggaa	gggggggtta	acctctcgag	14820
tgataaccag	attgtccaat	tatgactatg	aacaattcag	agcagggatg	gtgctattga	14880
caggaagaaa	gagaaatgtc	ctcattgaca	aagagtcatg	ttcagtgcag	ctggcgagag	14940
ctctaagaag	ccatatgtgg	gcgaggctag	ctcgaggacg	gcctatttac	ggccttgagg	15000
tccctgatgt	actagaatct	atgcgaggcc	accttattcg	gcgtcatgag	acatgtgtca	15060
tctgcgagtg	tggatcagtc	aactacggat	ggttttttgt	cccctcgggt	tgccaactgg	15120
atgatattga	caaggaaaca	tcatccttga	gagtcccata	tattggttct	accactgatg	15180
agagaacaga	catgaagctt	gccttcgtaa	gagccccaag	tcgatccttg	cgatctgctg	15240
ttagaatagc	aacagtgtac	tcatgggctt	acggtgatga	tgatagctct	tggaacgaag	15300
cctggttggt	ggctaggcaa	agggccaatg	tgagcctgga	ggagctaagg	gtgatcactc	15360
ccatctcaac	ttcgactaat	ttagcgcata	ggttgaggga	tcgtagcact	caagtgaat	15420
actcaggtac	atcccttgtc	cgagtggcga	ggtataccac	aatctccaac	gacaatctct	15480
catttgtcat	atcagataag	aaggttgata	ctaactttat	ataccaacaa	ggaatgcttc	15540
tagggttggg	tgtttttagaa	acattgtttc	gactcgagaa	agataccgga	tcatctaaca	15600
cggtattaca	tcttcacgtc	gaaacagatt	gttgcgatgat	cccgatgata	gatcatccca	15660
ggatacccag	ctcccgcaag	ctagagctga	gggcagagct	atgtaccaac	ccattgatat	15720
atgataatgc	acctttaatt	gacagagatg	caacaaggct	atacaccag	agccatagga	15780
ggcaccttgt	ggaatttggt	acatggtcca	caccccaact	atatcacatt	ttagctaagt	15840
ccacagcact	atctatgatt	gacctggtaa	caaaatttga	gaaggaccat	atgaatgaaa	15900
tttcagctct	cataggggat	gacgatatca	atagtttcat	aactgagttt	ctgctcatag	15960
agccaagatt	attcactatc	tacttgggcc	agtgtgcggc	catcaattgg	gcatttgatg	16020

tacattatca tagaccatca gggaaatata agatgggtga gctgttgtca tcgttccttt	16080
ctagaatgag caaaggagtg tttaagggtgc ttgtcaatgc tctaagccac ccaaagatct	16140
acaagaaatt ctggcattgt ggtattatag agcctatcca tggtccttca cttgatgctc	16200
aaaacttgca cacaactgtg tgcaacatgg ttacacatg ctatatgacc tacctcgacc	16260
tggtgttgaa tgaagagtta gaagagttca ctttctctt gtgtgaaagc gacgaggatg	16320
tagtaccgga cagattcgac aacatccagg caaaacactt atgtgttctg gcagatttgt	16380
actgtcaacc agggacctgc ccaccaattc gaggtctaag accggtagag aaatgtgcag	16440
ttctaaccga ccatatcaag gcagaggcta tggtatctcc agcaggatct tcgtggaaca	16500
taaatccaat tattgtagac cattactcat gctctctgac ttatctccgg cgaggatcga	16560
tcaaacagat aagattgaga gttgatccag gattcatttt cgacgccctc gctgaggtaa	16620
atgtcagtca gccaaagatc ggcagcaaca acatctcaaa tatgagcatc aaggctttca	16680
gacccccaca cgatgatgtt gcaaaattgc tcaaagatat caacacaagc aagcacaatc	16740
ttcccatttc agggggcaat ctgcgaatt atgaaatcca tgctttccgc agaatcgggt	16800
tgaactcatc tgcttgctac aaagctgttg agatatcaac attaattagg agatgccttg	16860
agccagggga ggacggcttg ttcttgggtg agggatcggg ttctatgttg atcacttata	16920
aagagatact taaactaaac aagtgccttct ataatagtgg ggtttccgcc aattctagat	16980
ctgggtcaaag ggaattagca ccctatccct ccgaagttagg ccttgtcgaa cacagaatgg	17040
gagtaggtaa tattgtcaaa gtgctcttta acgggaggcc cgaagtcacg tgggtaggca	17100
gtgtagattg cttcaatttc atagttagta atatccctac ctctagtgtg gggtttatcc	17160
attcagatat agagaccttg cctgacaaag atactataga gaagctagag gaattggcag	17220
ccatcttata gatggctctg ctctgggca aaataggatc aatactgggtg attaagctta	17280
tgcccttcag cggggatttt gttcagggat ttataagtta tgtagggtct cattatagag	17340
aagtgaacct tgtataccct agatacagca acttcatctc tactgaatct tatttggtta	17400
tgacagatct caaggctaac cggctaata atcctgaaaa gattaagcag cagataattg	17460
aatcatctgt gaggacttca cctggactta taggtcacat cctatccatt aagcaactaa	17520
gctgcataca agcaattgtg ggagacgcag ttagtagagg tgatatcaat cctactctga	17580
aaaaacttac acctatagag caggtgctga tcaattgcgg gttggcaatt aacggacct	17640
agctgtgcaa agaattgatc caccatgatg ttgcctcagg gcaagatgga ttgcttaatt	17700
ctatactcat cctctacagg gagttggcaa gattcaaaga caaccaaaga agtcaacaag	17760

ggatgttcca	cgcttacccc	gtattggtaa	gtagcaggca	acgagaactt	atatctagga	17820
tcacccgcaa	attctggggg	cacattcttc	tttactccgg	gaacaaaaag	ttgataaata	17880
agtttatcca	gaatctcaag	tccggctatc	tgataactaga	cttacaccag	aatatcttcg	17940
ttaagaatct	atccaagtca	gagaaacaga	ttattatgac	gggggggttg	aaacgtgagt	18000
gggtttttta	ggtaacagtc	aaggagacca	aagaatggta	taagttagtc	ggatacagtg	18060
ccctgattaa	ggactaattg	gttgaactcc	ggaaccctaa	tcctgcccta	ggtgggttagg	18120
cattatttgc	aatatattaa	agaaaacttt	gaaaatacga	agtttctatt	cccagctttg	18180
tctggtggcc	ggcatgggtc	cagcctcctc	gctggcgccg	gctgggcaac	attccgaggg	18240
gaccgtcccc	tcggtaatgg	cgaatgggac	gcggccgac	cggctgctaa	caaagcccga	18300
aaggaagctg	agttggctgc	tgccaccgct	gagcaataac	tagcataacc	ccttggggcc	18360
tctaaacggg	tcttgagggg	ttttttgctg	aaaggaggaa	ctatatccgg	atgcggccgc	18420
gggccctatg	gtaccagct	tttgttccct	ttagtgaggg	ttaattccga	gcttggcgta	18480
atcatggtca	tagctgtttc	ctgtgtgaaa	ttgttatccg	ctcacaattc	cacacaacat	18540
aggagccgga	agcataaagt	gtaaagcctg	gggtgcctaa	tgagtgaggt	aactcacatt	18600
aattgcgttg	cgctcactgc	ccgctttcca	gtcgggaaac	ctgtcgtgcc	agctgcatta	18660
atgaatcggc	caacgcgcgg	ggagaggcgg	tttgcgatt	gggcgctctt	ccgcttcctc	18720
gctcactgac	tcgctgcgct	cggtcgttcg	gctgcggcga	gcggtatcag	ctcactcaaa	18780
ggcggtaata	cggttatcca	cagaatcagg	ggataacgca	ggaaagaaca	tgtgagcaaa	18840
aggccagcaa	aaggccagga	accgtaaaaa	ggccgcgttg	ctggcgtttt	tccataggct	18900
cggccccct	gacgagcatc	acaaaaatcg	acgctcaagt	cagaggtggc	gaaacccgac	18960
aggactataa	agataccagg	cgttcccccc	tggaagctcc	ctcgtgcgct	ctcctgttcc	19020
gaccctgccg	cttaccggat	acctgtccgc	ctttctccct	tcgggaagcg	tggcgctttc	19080
tcaatgctca	cgctgtaggt	atctcagttc	ggtgtaggtc	gttcgctcca	agctgggctg	19140
tgtgcacgaa	cccccgttc	agcccagacc	ctgcgcctta	tccggtaact	atcgtcttga	19200
gtccaacccg	gtaagacacg	acttatcgcc	actggcagca	gccactggta	acaggattag	19260
cagagcgagg	tatgtaggcg	gtgctacaga	gttcttgaag	tgggtggccta	actacggcta	19320
cactagaagg	acagtatttg	gtatctgcgc	tctgctgaag	ccagttacct	tcggaaaaag	19380
agttggtagc	tcttgatccg	gcaaacaac	caccgctggt	agcgggtggt	tttttgtttg	19440
caagcagcag	attacgcgca	gaaaaaaagg	atctcaagaa	gatcctttga	tcttttctac	19500

ggggtctgac gctcagtgga acgaaaactc acgttaaggg attttgggtca tgagattatc	19560
aaaaaggatc ttcacctaga tcctttttaa ttaaaaatga agtttttaa caatctaaag	19620
tatatatgag taaacttggt ctgacagtta ccaatgctta atcagtgagg cacctatctc	19680
agcgatctgt ctatttcggt catccatagt tgcctgactg cccgtcgtgt agataactac	19740
gatacgggag ggcttaccat ctggccccag tgctgcaatg ataccgagag acccagctc	19800
accggctcca gatttatcag caataaacca gccagccgga agggccgagc gcagaagtgg	19860
tcctgcaact ttatccgcct ccatccagtc tattaattgt tgccgggaag ctagagtaag	19920
tagttcgcca gttaatagtt tgcgcaacgt tgttgccatt gctacaggca tcgtggtgtc	19980
acgctcgtcg tttgggtatgg cttcattcag ctccggttcc caacgatcaa ggcgagttac	20040
atgatcccc atgttgtgaa aaaaagcggg tagctccttc ggtcctccga tcgttgtcag	20100
aagtaagttg gccgcagtgt tatcactcat gcttatggca gcactgcata attctcttac	20160
tgatcatgcca tccgtaagat gcttttctgt gactggtgag tactcaacca agtcattctg	20220
agaatagtgt atgcggcgac cgagttgctc ttgcccggcg tcaatacggg ataataccgc	20280
gccacatagc agaactttaa aagtgctcat cattggaaaa cgttcttcgg ggcgaaaact	20340
ctcaaggatc ttaccgctgt tgagatccag ttcgatgtaa cccactcgtg cacccaactg	20400
atcttcagca tcttttactt tcaccagcgt ttctgggtga gcaaaaacag gaaggcaaaa	20460
tgccgcaaaa aagggaataa gggcgacacg gaaatgttga atactcatac tcttcctttt	20520
tcaatattat tgaagcattt atcagggtta ttgtctcatg agcggataca tatttgaatg	20580
tatttagaaa aataaacaaa taggggttcc gcgcacattt ccccgaaaag tgccacctga	20640
aattgtaaac gttaatatTT tgttaaaatt cgcgttaa at ttttgttaaa tcagctcatt	20700
ttttaaccaa taggccgaaa tcggcaaaat cccttataaa tcaaaagaat agaccgagat	20760
agggttgagt gttgttccag tttggaacaa gagtccacta ttaaagaacg tggactccaa	20820
cgtcaaaggg cgaaaaaccg tctatcaggg cgatggccca ctacgtgaac catcacccta	20880
atcaagtttt ttggggtcga ggtgccgtaa agcactaaat cggaacccta aaggagccc	20940
ccgatttaga gcttgacggg gaaagccggc gaacgtggcg agaaaggaag ggaagaaagc	21000
gaaaggagcg ggcgctaggg cgctggcaag tgtagcggtc acgctgcgcg taaccaccac	21060
accgcccgcg cttaatgcgc cgctacaggg cgcgtcccat tcgccattca ggctgcgcaa	21120
ctgttgggaa gggcgatcgg tgcgggcctc ttcgctatta cgccagccac cgcggtgatc	21180
cttataaagc tagatg	21196

<210> 59
 <211> 18994
 <212> DNA
 <213> Measles virus Schwarz strain pTM - pTM MV Schw

<400> 59
 tcatgaacgc ggccgctaatac gactcact atagggccaa cttgttttg tctgatgagt 60
 ccgtgaggac gaaacccgga gtcccgggtc accaaacaaa gttgggtaag gatagttcaa 120
 tcaatgatca tcttctagt cacttaggat tcaagatcct attatcaggg acaagagcag 180
 gattagggat atccgagatg gccacacttt taaggagctt agcattgttc aaaagaaaca 240
 aggacaaacc acccattaca tcaggatccg gtggagccat cagaggaatc aaacacatta 300
 ttatagtacc aatccctgga gattcctcaa ttaccactcg atccagactt ctggaccggt 360
 tggtgagggt aattggaaac ccgatgtga gcgggcccaa actaacaggg gcactaatag 420
 gtatatatc cttatttgtg gactctccag gtcaattgat tcagaggatc accgatgacc 480
 ctgacgttag cataaggctg ttagagggtt tccagagtga ccagtcacaa tctggcctta 540
 ccttcgcatac aagagggtacc aacatggagg atgaggcgga ccaatacttt tcacatgatg 600
 atccaattag tagtgatcaa tccagggttc gatgggttcg gaacaaggaa atctcagata 660
 ttgaagtgca agaccctgag ggattcaaca tgattctggg taccatccta gcccaaattt 720
 gggctcttgct cgcaaaggcg gttacggccc cagacacggc agctgattcg gagctaagaa 780
 ggtggataaa gtacacccaa caaagaaggg tagttggtga atttagattg gagagaaaat 840
 ggttggtatg ggtgaggaac aggattgccg aggacctctc cttacgccga ttcattggtc 900
 ctctaatacct ggatatcaag agaacacccg gaaacaaacc caggattgct gaaatgatat 960
 gtgacattga tacatatatc gtagaggcag gattagccag ttttatcctg actattaagt 1020
 ttgggataga aactatgtat cctgctcttg gactgcatga atttgctggg gagttatcca 1080
 cacttgagtc cttgatgaac cttaccagc aaatggggga aactgcaccc tacatggtaa 1140
 tcctggagaa ctcaattcag aacaagttca gtgcaggatc ataccctctg ctctggagct 1200
 atgccatggg agtaggagtg gaacttgaaa actccatggg aggtttgaac tttggccgat 1260
 cttactttga tccagcatat tttagattag ggcaagagat ggtaaggagg tcagctggaa 1320
 aggtcagttc cacattggca tctgaactcg gtatcactgc cgaggatgca aggcttgttt 1380
 cagagattgc aatgcatact actgaggaca agatcagtag agcggttgga ccagacaag 1440
 cccaagtatc atttctacac ggtgatcaaa gtgagaatga gctaccgaga ttggggggca 1500

aggaagatag gaggggtcaaa cagagtcgag gagaagccag ggagagctac agagaaaccg	1560
ggcccagcag agcaagtgat gcgagagctg cccatcttcc aaccggcaca cccctagaca	1620
ttgacactgc aacgggagtc agccaagatc cgcaggacag tcgaagggtca gctgacgccc	1680
tgcttaggct gcaagccatg gcaggaatct cggaagaaca aggctcagac acggacaccc	1740
ctatagtgtg caatgacaga aatcttctag actagggtgc agaggccgag ggccagaaca	1800
acatccgcct accatccatc attgttataa aaaacttagg aaccagggtcc acacagccgc	1860
cagcccatca accatccact cccacgattg gagccaatgg cagaagagca ggcacgccat	1920
gtcaaaaacg gactggaatg catccgggct ctcaaggccg agcccatcgg ctactggcc	1980
atcgaggaag ctatggcagc atggtcagaa atatcagaca acccaggaca ggagcgagcc	2040
acctgcaggg aagagaaggc aggcagttcg ggtctcagca aacctgcct ctgagcaatt	2100
ggatcaactg aaggcggtgc acctcgcac cgcggtcagg gacctggaga gagcgatgac	2160
gacgctgaaa ctttgggaat cccccaaga aatctccagg catcaagcac tgggttacag	2220
tggtattacg tttatgatca cagcggtgaa gcggttaagg gaatccaaga tgctgactct	2280
atcatggttc aatcaggcct tgatggtgat agcaccctct caggaggaga caatgaatct	2340
gaaaacagcg atgtggatat tggcgaacct gataccgagg gatatgctat cactgaccgg	2400
ggatctgctc ccatctctat ggggttcagg gcttctgatg ttgaaactgc agaaggaggg	2460
gagatccacg agctcctgag actccaatcc agaggcaaca actttccgaa gcttgggaaa	2520
actctcaatg ttctctcgcc cccggacccc ggtagggcca gcacttccgg gacaccatt	2580
aaaaagggca cagacgcgag attagcctca tttggaacgg agatcgcgtc tttattgaca	2640
ggtggtgcaa cccaatgtgc tcgaaagtca ccctcggaac catcagggcc aggtgcacct	2700
gcgggggaatg tccccgagtg tgtgagcaat gccgcactga tacaggagtg gacacccgaa	2760
tctggtacca caatctcccc gagatcccag aataatgaag aagggggaga ctattatgat	2820
gatgagctgt tctctgatgt ccaagatatt aaaacagcct tggccaaaat acacgaggat	2880
aatcagaaga taatctccaa gctagaatca ctgctgttat tgaagggaga agttgagtca	2940
attaagaagc agatcaacag gcaaaatatc agcatatcca ccctggaagg acacctctca	3000
agcatcatga tcgccattcc tggacttggg aaggatccca acgacccac tgcagatgtc	3060
gaaatcaatc ccgacttgaa acccatcata ggcagagatt caggccgagc actggccgaa	3120
gttctcaaga aaccggttgc cagccgacaa ctccaaggaa tgacaaatgg acggaccagt	3180
tccagaggac agctgctgaa ggaatttcag ctaaagccga tcgggaaaaa gatgagctca	3240

gccgtcgggt ttgttcctga caccggccct gcatcacgca gtgtaatccg ctccattata	3300
aaatccagcc ggctagagga ggatcggaag cgttacctga tgactctcct tgatgatatc	3360
aaaggagcca atgatcttgc caagttccac cagatgctga tgaagataat aatgaagtag	3420
ctacagctca acttacctgc caaccccatg ccagtcgacc caactagtag aacctaatac	3480
cattataaaa aacttaggag caaagtgatt gcctcccaag gtccacaatg acagagacct	3540
acgacttcga caagtcggca tgggacatca aagggtcgat cgctccgata caaccacca	3600
cctacagtga tggcaggctg gtgccccagg tcagagtcac agatcctggg ctaggcgaca	3660
ggaaggatga atgctttatg tacatgtttc tgctgggggt tgttgaggac agcgattccc	3720
tagggcctcc aatcgggcca gcatttgggt tcctgccctt aggtggtggc agatccacag	3780
caaagcccga aaaactcctc aaagaggcca ctgagcttga catagttggt agacgtacag	3840
cagggctcaa tgaaaaactg gtgttctaca acaacacccc actaactctc ctcacacctt	3900
ggagaaaggt cctaacaaca gggagtgtct tcaacgcaa ccaagtgtgc aatgcggtta	3960
atctgatacc gctcgatacc ccgcagaggt tccgtgttgt ttatatgagc atcacccgtc	4020
tttcggataa cgggtattac accgttccta gaagaatgct ggaattcaga tcggtcaatg	4080
cagtggcctt caacctgctg gtgaccctta ggattgacaa ggcgataggc cctgggaaga	4140
tcacgacaa tacagagcaa cttcctgagg caacatttat ggtccacatc gggaacttca	4200
ggagaaagaa gagtgaagtc tactctgccg attattgcaa aatgaaaatc gaaaagatgg	4260
gcctggtttt tgcacttggg gggatagggg gcaccagtct tcacattaga agcacaggca	4320
aaatgagcaa gactctccat gcacaactcg ggttcaagaa gaccttatgt taccgctga	4380
tggatatcaa tgaagacctt aatcgattac tctggaggag cagatgcaag atagtaagaa	4440
tccaggcagt ttgacagcca tcagttcctc aagaattccg catttacgac gacgtgatca	4500
taaatgatga ccaaggacta ttcaaagttc tgtagaccgt agtgcccagc aatgcccga	4560
aacgaccccc ctcacaatga cagccagaag gcccgacgca aaagaccccc tccgaaagac	4620
tccacggacc aagcgagagg ccagccagca gccgacggca agcgcgacaa ccaggcggcc	4680
ccagcacaga acagccctga cacaaggcca ccaccagcca cccaatctg catcctctc	4740
gtgggacccc cgaggaccaa ccccaaggc tgccccgat ccaaaccacc aaccgcatcc	4800
ccaccacccc cgggaaagaa acccccagca attggaaggc ccctccccct cttcctcaac	4860
acaagaactc cacaaccgaa ccgcacaagc gaccgaggtg acccaaccgc aggcattccga	4920
ctccctagac agatcctctc tccccgcaa actaaacaaa acttagggcc aaggaacata	4980

cacacccaac	agaacccaga	ccccggccca	cggcgccgcg	ccccaaccc	ccgacaacca	5040
gagggagccc	ccaaccaatc	ccgccggctc	ccccggtgcc	cacaggcagg	gacaccaacc	5100
cccgaacaga	cccagcacc	aaccatcgac	aatccaagac	ggggggggccc	ccccaaaaa	5160
aggccccag	gggccgacag	ccagcaccgc	gaggaagccc	accacccca	cacacgacca	5220
cggcaaccaa	accagaaccc	agaccaccct	gggccaccag	ctcccagact	cggccatcac	5280
cccgagaaa	ggaaaggcca	caaccgcgc	accagagccc	cgatccggcg	gggagccacc	5340
caaccgaac	cagcacccaa	gagcgatccc	cgaaggaccc	ccgaaccgca	aaggacatca	5400
gtatcccaca	gcctctccaa	gtcccccggt	ctcctcctct	tctcgaaggg	acaaaagat	5460
caatccacca	caccgcagca	cactcaactc	cccaccccta	aaggagacac	cgggaatccc	5520
agaatcaaga	ctcatccaat	gtccatcatg	ggtctcaagg	tgaacgtctc	tgccatattc	5580
atggcagtac	tgtaaactct	ccaaacaccc	accggtcaaa	tccattgggg	caatctctct	5640
aagatagggg	tggtaggaat	aggaagtgca	agctacaaag	ttatgactcg	ttccagccat	5700
caatcattag	tcataaaatt	aatgcccaat	ataactctcc	tcaataactg	cacgagggtg	5760
gagattgcag	aatacaggag	actactgaga	acagttttgg	aaccaattag	agatgcactt	5820
aatgcaatga	cccagaatat	aagaccggtt	cagagtgtag	cttcaagtag	gagacacaag	5880
agatttgcg	gagtagtcct	ggcaggtgcg	gccctaggcg	ttgccacagc	tgctcagata	5940
acagccggca	ttgcacttca	ccagtccatg	ctgaactctc	aagccatcga	caatctgaga	6000
gcgagcctgg	aaactactaa	tcaggcaatt	gagacaatca	gacaagcagg	gcaggagatg	6060
atattggctg	ttcaggggtg	ccaagactac	atcaataatg	agctgatacc	gtctatgaac	6120
caactatctt	gtgatttaat	cggccagaag	ctcgggctca	aattgctcag	atactataca	6180
gaaatcctgt	cattattttg	ccccagttta	cgggacccca	tatctgcgga	gatatctatc	6240
caggctttga	gctatgcgct	tggaggagac	atcaataagg	tgttagaaaa	gctcggatac	6300
agtggaggtg	atctactggg	catcttagag	agcggaggaa	taaaggcccg	gataactcac	6360
gtcgacacag	agtcctactt	cattgtcctc	agtatagcct	atccgacgct	gtccgagatt	6420
aagggggtga	ttgtccaccg	gctagagggg	gtctcgtaca	acataggctc	tcaagagtgg	6480
tataccactg	tgcccaagta	tggtgcaacc	caaggggtacc	ttatctcgaa	ttttgatgag	6540
tcatcgtgta	ctttcatgcc	agaggggact	gtgtgcagcc	aaaatgcctt	gtacccgatg	6600
agtcctctgc	tccaagaatg	cctccggggg	tacaccaagt	cctgtgctcg	tacactcgta	6660
tccgggtctt	ttgggaaccg	gttcatttta	tcacaaggga	acctaatagc	caattgtgca	6720

tcaatccttt gcaagtgtta cacaacagga acgatcatta atcaagaccc tgacaagatc	6780
ctaacataca ttgctgccga tctactgcccg gtagtcgagg tgaacggcgt gaccatccaa	6840
gtcgggagca ggaggtatcc agacgctgtg tacttgcaca gaattgacct cggtcctccc	6900
atatcattgg agaggttgga cgtagggaca aatctgggga atgcaattgc taagttggag	6960
gatgccaaagg aattgttgga gtcacgagac cagatattga ggagtatgaa aggtttatcg	7020
agcactagca tagtctacat cctgattgca gtgtgtcttg gagggttgat agggatcccc	7080
gctttaatat gttgctgcag ggggcgttgt aacaaaaagg gagaacaagt tggatatgtca	7140
agaccaggcc taaagcctga tcttacggga acatcaaaat cctatgtaag gtcgctctga	7200
tcctctacaa ctcttgaaac acaaatgtcc cacaagtctc ctcttcgtca tcaagcaacc	7260
accgcaccca gcatcaagcc cacctgaaat tatctccggc ttccctctgg ccgaacaata	7320
tcggtagtta atcaaaactt aggggtgcaag atcatccaca atgtcaccac aacgagaccg	7380
gataaatgcc ttctacaaag ataacccccca tcccaaggga agtaggatag tcattaacag	7440
agaacatctt atgattgata gaccttatgt tttgctggct gttctgtttg tcatgtttct	7500
gagcttgatc gggttgctag ccattgcagg cattagactt catcgggcag ccatctacac	7560
cgcagagatc cataaaagcc tcagcaccaa tctagatgta actaactcaa tcgagcatca	7620
ggatcaaggac gtgctgacac cactcttcaa aatcatcggc gatgaagtgg gcctgaggac	7680
acctcagaga ttcactgacc tagtgaaatt aatctctgac aagattaaat tccttaatcc	7740
ggatagggag tacgacttca gagatctcac ttgggtgtatc aaccgcccag agagaatcaa	7800
attggattat gatcaatact gtgcagatgt ggctgctgaa gagctcatga atgcattggc	7860
gaactcaact ctactggaga ccagaacaac caatcagttc ctagctgtct caaagggaaa	7920
ctgctcaggg ccactacaa tcagagggtca attctcaaac atgtcgtgtg ccctgttaga	7980
cttgatttta ggtcgagggt acaatgtgtc atctatagtc actatgacat ccaggggaat	8040
gtatggggga acttacctag tggaaaagcc taatctgagc agcaaaaggc cagagttgtc	8100
acaactgagc atgtaccgag tgtttgaagt aggtgttatc agaaatccgg gtttgggggc	8160
tccggtgttc catatgacaa actatcttga gcaaccagtc agtaatgatc tcagcaactg	8220
tatggtggct ttgggggagc tcaaactcgc agccctttgt cacggggaag attctatcac	8280
aattccctat cagggatcag ggaaagggtg cagcttccag ctcgtcaagc taggtgtctg	8340
gaaatcccca accgacatgc aatcctgggt ccccttatca acggatgatc cagtgataga	8400
caggctttac ctctcatctc acagaggtgt tatcgctgac aatcaagcaa aatgggctgt	8460

cccgacaaca	cgaacagatg	acaagttgcg	aatggagaca	tgcttccaac	aggcgtgtaa	8520
gggtaaaatc	caagcactct	gcgagaatcc	cgagtgggca	ccattgaagg	ataacaggat	8580
tccttcatac	ggggctcttg	ctgttgatct	gagtctgaca	gttgagctta	aaatcaaaat	8640
tgcttcggga	ttcggggccat	tgatcacaca	cggttcaggg	atggacctat	acaaatccaa	8700
ccacaacaat	gtgtattggc	tgactatccc	gccaatgaag	aacctagcct	taggtgtaat	8760
caacacattg	gagtggatac	cgagattcaa	ggttagtccc	tacctcttca	ctgtcccaat	8820
taaggaagca	ggcgaagact	gccatgcccc	aacataccta	cctgcggagg	tggatgggtga	8880
tgtcaaactc	agttccaatc	tggtgattct	acctgggtcaa	gatctccaat	atgttttggc	8940
aacctacgat	acttccaggg	ttgaacatgc	tgtggtttat	tacgtttaca	gccaagccg	9000
ctcattttct	tacttttatc	cttttaggtt	gcctataaag	ggggccccca	tcgaattaca	9060
agtggaatgc	ttcacatggg	acaaaaaact	ctggtgccgt	cacttctgtg	tgcttgcgga	9120
ctcagaatct	ggtggacata	tcactcactc	tgggatgggtg	ggcatgggag	tcagctgcac	9180
agtcacccgg	gaagatggaa	ccaatcgag	atagggctgc	tagtgaacca	atcacatgat	9240
gtcacccaga	catcaggcat	accactagt	gtgaaataga	catcagaatt	aagaaaaacg	9300
taggggccaa	gtgggtcccc	gttatggact	cgctatctgt	caaccagatc	ttataccctg	9360
aagttcacct	agatagcccc	atagttacca	ataagatagt	agccatcctg	gagtatgctc	9420
gagtccctca	cgcttacagc	ctggaggacc	ctacactgtg	tcagaacatc	aagcacccgc	9480
taaaaaacgg	attttccaac	caaatgatta	taaacaatgt	ggaagttggg	aatgtcatca	9540
agtccaagct	taggagttat	ccggcccact	ctcatattcc	atatccaaat	tgtaatcagg	9600
atttattta	catagaagac	aaagagtcaa	cgaggaagat	ccgtgaactc	ctcaaaaagg	9660
ggaattcgct	gtactccaaa	gtcagtgata	aggttttcca	atgcttaagg	gacactaact	9720
cacggcttgg	cctaggctcc	gaattgaggg	aggacatcaa	ggagaaagtt	attaacttgg	9780
gagtttacat	gcacagctcc	cagtggtttg	agccctttct	gttttggttt	acagtcaaga	9840
ctgagatgag	gtcagtgatt	aaatcacaaa	cccatacttg	ccataggagg	agacacacac	9900
ctgtattctt	cactggtagt	tcagttgagt	tgctaactct	tcgtgacctt	gttgctataa	9960
tcagtaaaga	gtctcaacat	gtatattacc	tgacatttga	actggttttg	atgtattgtg	10020
atgtcataga	ggggagggtta	atgacagaga	ccgctatgac	tattgatgct	aggtatacag	10080
agcttctagg	aagagtcaga	tacatgtgga	aactgataga	tggtttcttc	cctgcactcg	10140
ggaatccaac	ttatcaaatt	gtagccatgc	tggagcctct	ttcacttgct	tacctgcagc	10200

tgagggatat	aacagtagaa	ctcagaggtg	ctttccttaa	ccactgcttt	actgaaatac	10260
atgatgttct	tgacccaaaac	gggttttctg	atgaaggtac	ttatcatgag	ttaaactgaag	10320
ctctagatta	cattttcata	actgatgaca	tacatctgac	aggggagatt	ttctcatttt	10380
tcagaagttt	cggccacccc	agacttgaag	cagtaacggc	tgctgaaaat	gttaggaaat	10440
acatgaatca	gcctaaagtc	attgtgtatg	agactctgat	gaaagggtcat	gccatatttt	10500
gtggaatcat	aatcaacggc	tatcgtgaca	ggcacggagg	cagttggcca	ccgctgaccc	10560
tccccctgca	tgctgcagac	acaatccgga	atgctcaagc	ttcaggtgaa	gggttaacac	10620
atgagcagtg	cgttgataac	tggaatcctt	ttgctggagt	gaaatttggc	tgctttatgc	10680
ctcttagcct	ggatagtgat	ctgacaatgt	acctaaagga	caaggcactt	gctgctctcc	10740
aaagggaatg	ggattcagtt	tacccgaaag	agttcctgcg	ttacgaccct	ccaaggga	10800
ccgggtcacg	gaggcttgta	gatgttttcc	ttaatgattc	gagctttgac	ccatatgatg	10860
tgataatgta	tgttgtaagt	ggagcttacc	tccatgaccc	tgagttcaac	ctgtcttaca	10920
gcctgaaaga	aaaggagatc	aaggaaacag	gtagactttt	tgctaaaatg	acttacaaaa	10980
tgagggcatg	ccaagtgatt	gctgaaaatc	taatctcaaa	cgggattggc	aaatatttta	11040
aggacaatgg	gatggccaag	gatgagcacg	atttgactaa	ggcactccac	actctagctg	11100
tctcaggagt	ccccaaagat	ctcaaagaaa	gtcacagggg	ggggccagtc	ttaaaaacct	11160
actcccgaag	cccagtccac	acaagtacca	ggaacgtgag	agcagcaaaa	gggtttatag	11220
ggttccctca	agtaattcgg	caggaccaag	acactgatca	tccggagaat	atggaagctt	11280
acgagacagt	cagtgcattt	atcacgactg	atctcaagaa	gtactgcctt	aattggagat	11340
atgagaccat	cagcttgttt	gcacagaggc	taaatgagat	ttacggattg	ccctcatttt	11400
tccagtggct	gcataagagg	cttgagacct	ctgtcctgta	tgtaagtgac	cctcattgcc	11460
cccccgacct	tgacgcccac	atcccgttat	ataaagtccc	caatgatcaa	atcttcatta	11520
agtaccctat	gggagggtata	gaagggtatt	gtcagaagct	gtggaccatc	agcaccattc	11580
cctatctata	cctggctgct	tatgagagcg	gagtaaggat	tgcttcgtta	gtgcaagggg	11640
acaatcagac	catagccgta	acaaaaaggg	taccagcac	atggccctac	aaccttaaga	11700
aacgggaagc	tgctagagta	actagagatt	actttgtaat	tcttaggcaa	aggctacatg	11760
atattggcca	tcacctcaag	gcaaatgaga	caattgtttc	atcacatttt	tttgtctatt	11820
caaaaggaat	atattatgat	gggctacttg	tgtcccaatc	actcaagagc	atcgcaagat	11880
gtgtattctg	gtcagagact	atagttgatg	aaacaagggc	agcatgcagt	aatattgcta	11940

caacaatggc	taaaagcatc	gagagagggt	atgaccgtta	ccttgcatat	tccctgaacg	12000
tcctaaaagt	gatacagcaa	attctgatct	ctcttggctt	cacaatcaat	tcaacctatga	12060
cccgggatgt	agtcataccc	ctcctcacia	acaacgacct	cttaataagg	atggcactgt	12120
tgcccgtctc	tattgggggg	atgaattatc	tgaatatgag	caggctgttt	gtcagaaaca	12180
tcggtgatcc	agtaacatca	tcaattgctg	atctcaagag	aatgattctc	gcctcactaa	12240
tgctgaaga	gacctccat	caagtaatga	cacaacaacc	gggggactct	tcattcctag	12300
actgggctag	cgacccttac	tcagcaaata	ttgtatgtgt	ccagagcatc	actagactcc	12360
tcaagaacat	aactgcaagg	tttgtcctga	tccatagtcc	aaacccaatg	ttaaaggat	12420
tattccatga	tgacagtaaa	gaagaggacg	agggactggc	ggcattcctc	atggacaggc	12480
atattatagt	acctagggca	gctcatgaaa	tcctggatca	tagtgtcaca	ggggcaagag	12540
agtctattgc	aggcatgctg	gataccacia	aaggcttgat	tcgagccagc	atgaggaagg	12600
gggggttaac	ctctcgagtg	ataaccagat	tgtccaatta	tgactatgaa	caattcagag	12660
cagggatggg	gctattgaca	ggaagaaaga	gaaatgtcct	cattgacaaa	gagtcattgt	12720
cagtgcagct	ggcgagagct	ctaagaagcc	atatgtgggc	gaggctagct	cgaggacggc	12780
ctatttacgg	ccttgagggt	cctgatgtac	tagaatctat	gcgaggccac	cttattcggc	12840
gtcatgagac	atgtgtcatc	tgcgagtgtg	gatcagtcaa	ctacggatgg	ttttttgtcc	12900
cctcgggttg	ccaactggat	gatattgaca	aggaaacatc	atccttgaga	gtcccatata	12960
ttgggttctac	cactgatgag	agaacagaca	tgaagcttgc	cttcgtaaga	gccccaaagtc	13020
gatccttgcg	atctgctgtt	agaatagcaa	cagtgtactc	atgggcttac	ggtgatgatg	13080
atagctcttg	gaacgaagcc	tggttggttg	ctaggcaaag	ggccaatgtg	agcctggagg	13140
agctaagggt	gatcactccc	atctcaactt	cgactaattt	agcgcatagg	ttgagggatc	13200
gtagcactca	agtgaataac	tcaggtacat	cccttgctcg	agtggcgagg	tataccacia	13260
tctccaacga	caatctctca	tttgtcatat	cagataagaa	ggttgatact	aactttatat	13320
accaacaagg	aatgcttcta	gggttggttg	ttttagaaac	attgtttcga	ctcgagaaag	13380
ataccggatc	atctaacacg	gtattacatc	ttcacgtcga	aacagattgt	tgctgatcc	13440
cgatgataga	tcatcccagg	atacccagct	cccgcaagct	agagctgagg	gcagagctat	13500
gtaccaaccc	attgatatat	gataatgcac	ctttaattga	cagagatgca	acaaggctat	13560
acaccagag	ccataggagg	caccttggtg	aatttggtac	atgggccaca	ccccactat	13620
atcacatttt	agctaagtcc	acagcactat	ctatgattga	cctggtaaca	aaatttgaga	13680

aggaccatat	gaatgaaatt	tcagctctca	taggggatga	cgatatcaat	agtttcataa	13740
ctgagtttct	gctcatagag	ccaagattat	tcactatcta	cttggggccag	tgtgcggcca	13800
tcaattgggc	atttgatgta	cattatcata	gaccatcagg	gaaatatcag	atgggtgagc	13860
tgttgtcatc	gttcctttct	agaatgagca	aaggagtgtt	taagggtgctt	gtcaatgctc	13920
taagccaccc	aaagatctac	aagaaattct	ggcattgtgg	tattatagag	cctatccatg	13980
gtccttcact	tgatgctcaa	aacttgcaca	caactgtgtg	caacatgggtt	tacacatgct	14040
atatgaccta	cctcgacctg	ttgttgaatg	aagagttaga	agagttcaca	tttctcttgt	14100
gtgaaagcga	cgaggatgta	gtaccggaca	gattcgacaa	catccaggca	aaacacttat	14160
gtgttctggc	agatttgtac	tgtcaaccag	ggacctgccc	accaattcga	ggtctaagac	14220
cggtagagaa	atgtgcagtt	ctaaccgacc	atatcaaggc	agaggctatg	ttatctccag	14280
caggatcttc	gtggaacata	aatccaatta	ttgtagacca	ttactcatgc	tctctgactt	14340
atctccggcg	aggatcgatc	aaacagataa	gattgagagt	tgatccagga	ttcattttcg	14400
acgccctcgc	tgaggtaaata	gtcagtcagc	caaagatcgg	cagcaacaac	atctcaaata	14460
tgagcatcaa	ggctttcaga	ccccacacg	atgatgttgc	aaaattgctc	aaagatatca	14520
acacaagcaa	gcacaatctt	cccatttcag	ggggcaatct	cgccaattat	gaaatccatg	14580
ctttccgcag	aatcgggttg	aactcatctg	cttgctacaa	agctgttgag	atatcaacat	14640
taattaggag	atgccttgag	ccaggggagg	acggcttggt	cttgggtgag	ggatcgggtt	14700
ctatgttgat	cacttataaa	gagatactta	aactaaacaa	gtgcttctat	aatagtgggg	14760
tttccgcaa	ttctagatct	ggtcaaaggg	aattagcacc	ctatccctcc	gaagttggcc	14820
ttgtcgaaca	cagaatggga	gtaggtaata	ttgtcaaagt	gctctttaac	gggaggcccg	14880
aagtcacgtg	ggtaggcagt	gtagattgct	tcaatttcat	agttagtaat	atccctacct	14940
ctagtgtggg	gtttatccat	tcagatatag	agaccttgcc	tgacaaagat	actatagaga	15000
agctagagga	attggcagcc	atcttatcga	tggctctgct	cctgggcaaa	ataggatcaa	15060
tactggtgat	taagcttatg	cctttcagcg	gggattttgt	tcagggattt	ataagttatg	15120
tagggtctca	ttatagagaa	gtgaaccttg	tataccctag	atacagcaac	ttcatctcta	15180
ctgaatctta	tttggttatg	acagatctca	aggctaaccg	gctaataaat	cctgaaaaga	15240
ttaagcagca	gataattgaa	tcatctgtga	ggacttcacc	tggacttata	ggtcacatcc	15300
tatccattaa	gcaactaagc	tgcatacaag	caattgtggg	agacgcagtt	agtagaggtg	15360
atatcaatcc	tactctgaaa	aaacttacac	ctatagagca	ggtgctgatc	aattgcggggt	15420

tggcaattaa	cggacctaag	ctgtgcaaag	aattgatcca	ccatgatggt	gcctcagggc	15480
aagatggatt	gcttaattct	atactcatcc	tctacaggga	gttggcaaga	ttcaaagaca	15540
accaaagaag	tcaacaaggg	atgttccacg	cttaccctgt	attggtaagt	agcaggcaac	15600
gagaacttat	atctaggatc	acccgcaaat	tctgggggca	cattcttctt	tactccggga	15660
acaaaaagtt	gataaataag	tttatccaga	atctcaagtc	cggctatctg	atactagact	15720
tacaccagaa	tatcttcgtt	aagaatctat	ccaagtcaga	gaaacagatt	attatgacgg	15780
ggggtttgaa	acgtgagtgg	gtttttaagg	taacagtcaa	ggagaccaa	gaatggtata	15840
agttagtcgg	atacagtgcc	ctgattaagg	actaattggt	tgaactccgg	aaccctaata	15900
ctgccctagg	tggttaggca	ttatttgcaa	tatattaaag	aaaactttga	aaatacgaag	15960
tttctattcc	cagctttgtc	tggtggccgg	catggtccca	gcctcctcgc	tggcgccggc	16020
tgggcaacat	tccgagggga	ccgtcccctc	ggtaatggcg	aatgggacgc	ggccgatccg	16080
gctgctaaca	aagcccgaaa	ggaagctgag	ttggctgctg	ccaccgctga	gcaataacta	16140
gcataacccc	ttggggcctc	taaacgggtc	ttgagggggt	ttttgctgaa	aggaggaact	16200
atatccggat	gcggccgcgg	gccctatggt	accagctttt	tgttcccttt	agtgaggggt	16260
aattccgagc	ttggcgtaat	catggtcata	gctgtttcct	gtgtgaaatt	gttatccgct	16320
cacaattcca	cacaacatag	gagccggaag	cataaagtgt	aaagcctggg	gtgcctaata	16380
agtgaggtaa	ctcacattaa	ttgcgttgcg	ctcactgccc	gctttccagt	cgggaaacct	16440
gtcgtgccag	ctgcattaat	gaatcggcca	acgcgcgggg	agaggcggtt	tgcgtattgg	16500
gcgctcttcc	gcttccctgc	tactgactc	gctgcgctcg	gtcgttcggc	tgcggcgagc	16560
ggtatcagct	cactcaaagg	cggtaatacg	gttatccaca	gaatcagggg	ataacgcagg	16620
aaagaacatg	tgagcaaaaag	gccagcaaaa	ggccaggaac	cgtaaaaagg	ccgcgttgct	16680
ggcgtttttc	cataggctcg	gccccctga	cgagcatcac	aaaaatcgac	gctcaagtca	16740
gaggtggcga	aacccgacag	gactataaag	ataccaggcg	ttccccctg	gaagctccct	16800
cgtgcgctct	cctgttccga	ccctgccgct	taccggatac	ctgtccgcct	ttctcccttc	16860
gggaagcgtg	gcgctttctc	aatgctcacg	ctgtaggtat	ctcagttcgg	tgtaggtcgt	16920
tcgctccaag	ctgggctgtg	tgcacgaacc	ccccgttcag	cccgaccgct	gcgccttatc	16980
cggtaactat	cgtcttgagt	ccaaccgggt	aagacacgac	ttatcgccac	tggcagcagc	17040
cactggtaac	aggattagca	gagcgaggta	tgtaggcggt	gctacagagt	tcttgaagtg	17100
gtggcctaac	tacggctaca	ctagaaggac	agtatttggt	atctgcgctc	tgctgaagcc	17160

agttaccttc	ggaaaaagag	ttggtagctc	ttgatccggc	aaacaaacca	ccgctggtag	17220
cggtggtttt	tttgtttgca	agcagcagat	tacgcgcaga	aaaaaaggat	ctcaagaaga	17280
tcctttgatc	ttttctacgg	ggtctgacgc	tcagtggaac	gaaaactcac	gttaagggat	17340
tttggtcatg	agattatcaa	aaaggatctt	cacctagatc	cttttaaatt	aaaaatgaag	17400
ttttaaatca	atctaaagta	tatatgagta	aacttggtct	gacagttacc	aatgcttaat	17460
cagtgaggca	cctatctcag	cgatctgtct	atttcgttca	tccatagttg	cctgactgcc	17520
cgtcgtgtag	ataactacga	tacgggaggg	cttaccatct	ggccccagtg	ctgcaatgat	17580
accgcgagac	ccacgctcac	cggctccaga	tttatcagca	ataaaccagc	cagccggaag	17640
ggccgagcgc	agaagtggtc	ctgcaacttt	atccgcctcc	atccagtcta	ttaattgttg	17700
ccgggaagct	agagtaagta	gttcgccagt	taatagtttg	cgcaacgttg	ttgccattgc	17760
tacaggcatc	gtggtgtcac	gctcgtcgtt	tggtatggct	tcattcagct	ccggttccca	17820
acgatcaagg	cgagttacat	gatcccccat	gttgtgaaaa	aaagcggtta	gctccttcgg	17880
tcctccgatc	gttgtcagaa	gtaagttggc	cgcagtgtta	tcactcatgc	ttatggcagc	17940
actgcataat	tctcttactg	tcatgccatc	cgtaagatgc	ttttctgtga	ctggtgagta	18000
ctcaaccaag	tcattctgag	aatagtgtat	gcggcgaccg	agttgctctt	gccggcgctc	18060
aatacgggat	aataccgcgc	cacatagcag	aactttaaaa	gtgctcatca	ttggaaaacg	18120
ttcttcgggg	cgaaaactct	caaggatctt	accgctgttg	agatccagtt	cgatgtaacc	18180
cactcgtgca	cccaactgat	cttcagcatc	ttttactttc	accagcgttt	ctgggtgagc	18240
aaaaacagga	aggcaaaatg	ccgcaaaaaa	gggaataagg	gcgacacgga	aatgttgaat	18300
actcactatc	ttcctttttc	aatattattg	aagcatttat	cagggttatt	gtctcatgag	18360
cggatacata	tttgaatgta	tttagaaaaa	taaacaaata	ggggttccgc	gcacatttcc	18420
ccgaaaagtg	ccacctgaaa	ttgtaaacgt	taatatTTTT	ttaaaattcg	cgttaaattt	18480
ttgttaaadc	agctcatttt	ttaaccaata	ggccgaaatc	ggcaaaatcc	cttataaatc	18540
aaaagaatag	accgagatag	ggttgagtgt	tgttccagtt	tggaacaaga	gtccactatt	18600
aaagaacgtg	gactccaacg	tcaaagggcg	aaaaaccgtc	tatcagggcg	atggcccact	18660
acgtgaacca	tcaccctaata	caagtttttt	ggggtcgagg	tgccgtaaag	cactaaatcg	18720
gaaccctaaa	gggagccccc	gatttagagc	ttgacgggga	aagccggcga	acgtggcgag	18780
aaaggaaggg	aagaaagcga	aaggagcggg	cgctagggcg	ctggcaagtg	tagcggtcac	18840
gctgcgcgta	accaccacac	ccgccgcgct	taatgcgccg	ctacagggcg	cgtcccattc	18900

gccattcagg ctgcgcaact gttgggaagg gcgatcgggtg cgggcctctt cgctattacg 18960
ccagccaccg cgggtgatcct tataaagcta gatg 18994

<210> 60
<211> 19107
<212> DNA
<213> Artificial sequence

<220>
<223> pTM 2ATU MV Schw - Measles virus scaffold with ATU

<400> 60
tccaaccgcg cgcgcgggccg ctaatacgac tcactatagg gccaaactttg tttgggtctga 60
tgagtccgtg aggacgaaac ccggagtccc gggtcaccaa acaaagttgg gtaaggatag 120
ttcaatcaat gatcatcttc tagtgcactt aggattcaag atcctattat cagggacaag 180
agcaggatta gggatatccg agatggccac acttttaagg agcttagcat tgttcaaaag 240
aaacaaggac aaaccaccca ttacatcagg atccgggtgga gccatcagag gaatcaaaca 300
cattattata gtaccaatcc ctggagattc ctcaattacc actcgatcca gacttctgga 360
ccggttggtg aggttaattg gaaaccgga tgtgagcggg cccaaactaa caggggcact 420
aataggtata ttatccttat ttgtggagtc tccagggtcaa ttgattcaga ggatcaccga 480
tgaccctgac gttagcataa ggctgttaga ggttgtccag agtgaccagt cacaatctgg 540
ccttaccttc gcatcaagag gtaccaacat ggaggatgag gcggaccaat acttttcaca 600
tgatgatcca attagtagtg atcaatccag gttcggatgg ttcgggaaca aggaaatctc 660
agatattgaa gtgcaagacc ctgagggatt caacatgatt ctgggtacca tcctagccca 720
aatTTgggtc ttgctcgcaa aggcgggttac ggccccagac acggcagctg attcggagct 780
aagaaggtgg ataaagtaca cccaacaaag aagggtagtt ggtgaattta gattggagag 840
aaaatggttg gatgtggtga ggaacaggat tgccgaggac ctctccttac gccgattcat 900
ggtcgctcta atcctggata tcaagagaac acccggaac aaaccagga ttgctgaaat 960
gatatgtgac attgatacat atatcgtaga ggcaggatta gccagtttta tcctgactat 1020
taagtttggg atagaaacta tgtatcctgc tcttggtactg catgaatttg ctggtgagtt 1080
atccacactt gagtccctga tgaaccttta ccagcaaatg ggggaaactg caccctacat 1140
ggtaatcctg gagaactcaa ttcagaacaa gttcagtga ggatcatacc ctctgctctg 1200
gagctatgcc atgggagtag gagtggaact tgaaaactcc atgggagggt tgaactttgg 1260
ccgatcttac tttgatccag catatttttag attagggcaa gagatggtaa ggaggtcagc 1320

tggaaaggtc agttccacat tggcatctga actcggatc actgccgagg atgcaaggct	1380
tgtttcagag attgcaatgc atactactga ggacaagatc agtagagcgg ttggacccag	1440
acaagcccaa gtatcatttc tacacggtga tcaaagtgag aatgagctac cgagattggg	1500
gggcaaggaa gataggaggg tcaaacagag tcgaggagaa gccagggaga gctacagaga	1560
aaccggggccc agcagagcaa gtgatgagag agctgcccac cttccaaccg gcacaccct	1620
agacattgac actgcaacgg agtccagcca agatccgcag gacagtcgaa ggtcagctga	1680
cgccctgctt aggctgcaag ccatggcagg aatctcggaa gaacaaggct cagacacgga	1740
caccctata gtgtacaatg acagaaatct tctagactag gtgcgagagg ccgagggcca	1800
gaacaacatc cgcctaccat ccatcattgt tataaaaaac ttaggaacca ggtccacaca	1860
gccgccagcc catcaaccat ccactcccac gattggagcc aatggcagaa gagcaggcac	1920
gccatgtcaa aaacggactg gaatgcatcc gggctctcaa ggccgagccc atcggctcac	1980
tggccatcga ggaagctatg gcagcatggt cagaaatc agacaacca ggacaggagc	2040
gagccacctg cagggaagag aaggcaggca gttcgggtct cagcaaacca tgcctctcag	2100
caattggatc aactgaaggc ggtgcacctc gcatccgcgg tcagggacct ggagagagcg	2160
atgacgagcg tgaaactttg ggaatcccc caagaaatct ccaggcatca agcactgggt	2220
tacagtgtta ttacgtttat gatcacagcg gtgaagcggg taagggaatc caagatgctg	2280
actctatcat ggttcaatca ggccttgatg gtgatagcac cctctcagga ggagacaatg	2340
aatctgaaaa cagcgatgtg gatattggcg aacctgatac cgagggatat gctatcactg	2400
accggggatc tgctcccatc tctatggggg tcagggcttc tgatgttgaa actgcagaag	2460
gaggggagat ccacgagctc ctgagactcc aatccagagg caacaacttt ccgaagcttg	2520
ggaaaactct caatgttcct ccgccccggg accccggtag ggccagcact tccgggacac	2580
ccattaaaaa gggcacagac gcgagattag cctcatcttg aacggagatc gcgtctttat	2640
tgacaggtgg tgcaacccaa tgtgctcgaa agtcaccctc ggaaccatca gggccaggtg	2700
cacctgcggg gaatgtcccc gagtgtgtga gcaatgccgc actgatacag gagtggacac	2760
ccgaatctgg taccacaatc tccccgagat ccagaataa tgaagaaggg ggagactatt	2820
atgatgatga gctgttctct gatgtccaag atattaaaac agccttggcc aaaatacacg	2880
aggataatca gaagataatc tccaagctag aatcactgct gttattgaag ggagaagttg	2940
agtcaattaa gaagcagatc aacaggcaaa atatcagcat atccaccctg gaaggacacc	3000
tctcaagcat catgatcgcc attcctggac ttgggaagga tcccaacgac cccactgcag	3060

atgtcgaaat caatccccgac ttgaaaccca tcataggcag agattcaggc cgagcactgg	3120
ccgaagtctt caagaaaccc gttgccagcc gacaactcca aggaatgaca aatggacgga	3180
ccagttccag aggacagctg ctgaaggaat ttcagctaaa gccgatcggg aaaaagatga	3240
gctcagccgt cgggttttgtt cctgacaccg gccctgcatc acgcagtgta atccgctcca	3300
ttataaaatc cagccgggcta gaggaggatc ggaagcgta cctgatgact ctccttgatg	3360
atatcaaagg agccaatgat cttgccaaagt tccaccagat gctgatgaag ataataatga	3420
agtagctaca gctcaactta cctgccaaacc ccatgccagt cgacccaact agcctaccct	3480
ccatcattgt tataaaaaaac ttaggaacca ggtccacaca gccgccagcc catcaacgcg	3540
tacggcgcgc agcgcttaga cgtctcgcga tcgatactag tacaacctaa atccattata	3600
aaaaacttag gagcaaagtg attgcctccc aagggtccaca atgacagaga cctacgactt	3660
cgacaagtcg gcatgggaca tcaaagggtc gatcgctccg atacaacca ccacctacag	3720
tgatggcagg ctggtgcccc aggtcagagt catagatcct ggtctaggcg acaggaagga	3780
tgaatgcttt atgtacatgt ttctgctggg ggttggtgag gacagcgatt ccctagggcc	3840
tccaatcggg cgagcatttg ggttcctgcc cttagggtgtt ggcatatcca cagcaaagcc	3900
cgaaaaactc ctcaaagagg ccatgagct tgacatagtt gttagacgta cagcagggt	3960
caatgaaaaa ctggtgttct acaacaacac ccactaact ctcctcacac cttggagaaa	4020
ggtcctaaca acagggagtg tcttcaacgc aaaccaagtg tgcaatgcgg ttaatctgat	4080
accgctcgat acccgcgaga ggttcctgtg tgtttatatg agcatcacc gtctttcgga	4140
taacgggtat tacaccgttc ctagaagaat gctggaattc agatcgggtca atgcagtggc	4200
cttcaacctg ctggtgaccc ttaggattga caaggcgata ggccctggga agatcatcga	4260
caatacagag caacttcctg aggcaacatt tatgggtccac atcgggaaact tcaggagaaa	4320
gaagagtga gtctactctg ccgattattg caaaatgaaa atcgaaaaga tgggcctggt	4380
ttttgcactt ggtgggatat ggggcaccag tcttcacatt agaagcacag gcaaaatgag	4440
caagactctc catgcacaac tcgggttcaa gaagacctta tgttaccgcg tgatggatat	4500
caatgaagac cttaatcgat tactctggag gagcagatgc aagatagtaa gaatccaggc	4560
agttttgcag ccatcagttc ctcaagaatt ccgcatttac gacgacgtga tcataaatga	4620
tgaccaagga ctattcaaag ttctgtagac cgtagtgcc agcaatgcc gaaaacgacc	4680
cccctcacia tgacagccag aaggcccga caaaaaagcc ccctccgaaa gactccacgg	4740
accaagcgag aggccagcca gcagccgacg gcaagcgca acaccaggcg gcccagcac	4800

agaacagccc	tgacacaagg	ccaccaccag	ccaccccaat	ctgcatcctc	ctcgtggggac	4860
ccccgaggac	caacccccaa	ggctgcccc	gatccaaacc	accaaccgca	tccccaccac	4920
ccccgggaaa	gaaaccccc	gcaattggaa	ggcccctccc	cctcttctc	aacacaagaa	4980
ctccacaacc	gaaccgcaca	agcgaccgag	gtgacccaac	cgagggcatc	cgactcccta	5040
gacagatcct	ctctccccgg	caaaactaac	aaaacttagg	gccaaaggaac	atacacaccc	5100
aacagaaccc	agacccccgg	ccacggcgcc	gcgcccccaa	cccccgacaa	ccagaggggag	5160
cccccaacca	atcccggccg	ctcccccggt	gccacaggc	agggacacca	acccccgaac	5220
agaccagca	cccaaccatc	gacaatccaa	gacggggggg	cccccccaa	aaaaggcccc	5280
caggggccga	cagccagcac	cgcgaggaag	cccaccacc	ccacacacga	ccacggcaac	5340
caaaccagaa	cccagaccac	cctggggcac	cagctcccag	actcggccat	cacccccgag	5400
aaaggaaagg	ccacaacccg	cgcaccccag	ccccgatccg	gcgggggagcc	acccaacccg	5460
aaccagcacc	caagagcgat	ccccgaagga	ccccgaacc	gcaaaggaca	tcagtatccc	5520
acagcctctc	caagtcccc	ggtctcctcc	tcttctcgaa	gggacaaaa	gatcaatcca	5580
ccacacccga	cgacactcaa	ctccccaccc	ctaaaggaga	caccgggaat	cccagaatca	5640
agactcatcc	aatgtccatc	atgggtctca	aggtgaacgt	ctctgccata	ttcatggcag	5700
tactgttaac	tctccaaaca	cccaccggtc	aaatccattg	gggcaatctc	tctaagatag	5760
gggtggtagg	aataggaagt	gcaagctaca	aagttatgac	tcgttccagc	catcaatcat	5820
tagtcataaa	attaatgccc	aatataactc	tcctcaataa	ctgcacgagg	gtagagattg	5880
cagaatacag	gagactactg	agaacagttt	tggaaccaat	tagagatgca	cttaatgcaa	5940
tgaccagaa	tataagaccg	gttcagagt	tagcttcaag	taggagacac	aagagatttg	6000
cgggagtagt	cctggcagg	gcggccctag	gcgttgccac	agctgctcag	ataacagccg	6060
gcattgcact	tcaccagtcc	atgctgaact	ctcaagccat	cgacaatctg	agagcgagcc	6120
tggaaactac	taatcaggca	attgagacaa	tcagacaagc	agggcaggag	atgatattgg	6180
ctgttcagg	tgtccaagac	tacatcaata	atgagctgat	accgtctatg	aaccaactat	6240
cttgtgattt	aatcggccag	aagctcgggc	tcaaattgct	cagatactat	acagaaatcc	6300
tgtcattatt	tggccccagt	ttacgggacc	ccatatctgc	ggagatatct	atccaggctt	6360
tgagctatgc	gcttgaggga	gacatcaata	aggtgttaga	aaagctcgga	tacagtggag	6420
gtgatttact	gggcatctta	gagagcggag	gaataaaggc	ccggataact	cacgtcgaca	6480
cagagtccta	cttcattgtc	ctcagtatag	cctatccgac	gctgtccgag	attaaggggg	6540

tgattgtcca	ccggctagag	ggggtctcgt	acaacatagg	ctctcaagag	tggtatacca	6600
ctgtgcccaa	gtatgttgca	acccaagggg	accttatctc	gaattttgat	gagtcacgt	6660
gtactttcat	gccagagggg	actgtgtgca	gccaaaatgc	cttgtaccgc	atgagtcctc	6720
tgctccaaga	atgcctccgg	gggtacacca	agtcctgtgc	tcgtacactc	gtatccgggt	6780
cttttgggaa	ccggttcatt	ttatcacaag	ggaaccta	agccaattgt	gcatcaatcc	6840
tttgcaagtg	ttacacaaca	ggaacgatca	ttaatcaaga	ccctgacaag	atccta	6900
acattgctgc	cgatcactgc	ccggtagtcg	aggtgaacgg	cgtagaccatc	caagtcggga	6960
gcaggaggta	tccagacgct	gtgtacttgc	acagaattga	cctcggtcct	cccatatcat	7020
tggagagggt	ggacgtaggg	acaaatctgg	ggaatgcaat	tgctaagttg	gaggatgcca	7080
aggaattgtt	ggagtcacgc	gaccagatat	tgaggagtat	gaaaggttta	tcgagcacta	7140
gcatagtcta	catcctgatt	gcagtgtgtc	ttggaggggt	gatagggatc	cccgctttaa	7200
tatgttgctg	cagggggcgt	tgtaacaaaa	agggagaaca	agttggatatg	tcaagaccag	7260
gcctaaagcc	tgatcttacg	ggaacatcaa	aatcctatgt	aaggtcgctc	tgatcctcta	7320
caactcttga	aacacaaatg	tcccacaagt	ctcctcttcg	tcacaaagca	accaccgcac	7380
ccagcatcaa	gccacactga	aattatctcc	ggcttccctc	tggccgaaca	atatcggtag	7440
ttaatcaaaa	cttaggggtgc	aagatcatcc	acaatgtcac	cacaacgaga	ccggataaat	7500
gccttctaca	aagataaacc	ccatcccaag	ggaagtagga	tagtcattaa	cagagaacat	7560
cttatgattg	atagacctta	tgttttgctg	gctgttctgt	ttgtcatggt	tctgagcttg	7620
atcgggttgc	tagccattgc	aggcattaga	cttcatcggg	cagccatcta	caccgcagag	7680
atccataaaa	gcctcagcac	caatctagat	gtaactaact	caatcgagca	tcaggtcaag	7740
gacgtgctga	caccactctt	caaaatcatc	ggtgatgaag	tgggcctgag	gacacctcag	7800
agattcactg	acctagtga	attaatctct	gacaagatta	aattccttaa	tccggatagg	7860
gagtagcact	tcagagatct	cacttggtgt	atcaaccgcg	cagagagaat	caaattggat	7920
tatgatcaat	actgtgcaga	tgtggctgct	gaagagctca	tgaatgcatt	ggtgaactca	7980
actctactgg	agaccagaac	aaccaatcag	ttcctagctg	tctcaaaggg	aaactgctca	8040
gggcccaact	caatcagagg	tcaattctca	aacatgtcgc	tgtccctggt	agacttgat	8100
ttaggtcgag	gttacaatgt	gtcatctata	gtcactatga	catcccaggg	aatgtatggg	8160
ggaacttacc	tagtggaaaa	gcctaactctg	agcagcaaaa	ggtcagagtt	gtcacaactg	8220
agcatgtacc	gagtgtttga	agtaggtgtt	atcagaaatc	cgggtttggg	ggctccggtg	8280

ttccatatga	caaactatct	tgagcaacca	gtcagtaatg	atctcagcaa	ctgtatgggtg	8340
gctttggggg	agctcaaact	cgagccctt	tgtcacgggg	aagattctat	cacaattccc	8400
tatcagggat	cagggaaagg	tgtcagcttc	cagctcgtca	agctaggtgt	ctggaaatcc	8460
ccaaccgaca	tgcaatcctg	gtccccctta	tcaacggatg	atccagtgat	agacaggctt	8520
tacctctcat	ctcacagagg	tgttatcgct	gacaatcaag	caaaatgggc	tgtcccgaca	8580
acacgaacag	atgacaagtt	gcgaatggag	acatgcttcc	aacaggcgtg	taagggtaaa	8640
atccaagcac	tctgcgagaa	tcccgagtgg	gcaccattga	aggataacag	gattccttca	8700
tacggggtct	tgtctggtga	tctgagtctg	acagttgagc	ttaaaatcaa	aattgcttcg	8760
ggattcgggc	cattgatcac	acacggttca	gggatggacc	tatacaaatc	caaccacaac	8820
aatgtgtatt	ggctgactat	cccgccaatg	aagaacctag	ccttaggtgt	aatcaacaca	8880
ttggagtgga	taccgagatt	caaggttagt	ccctacctct	tcactgtccc	aattaaggaa	8940
gcaggcgaag	actgccatgc	ccaacatac	ctacctgcgg	aggtggatgg	tgatgtcaaa	9000
ctcagttcca	atctgggtgat	tctacctggt	caagatctcc	aatatgtttt	ggcaacctac	9060
gatacttcca	gggttgaaca	tgctgtgggt	tattacgttt	acagcccaag	ccgctcattt	9120
tcttactttt	atccttttag	gttgccctata	aagggggtcc	ccatcgaatt	acaagtggaa	9180
tgcttcacat	gggacaaaaa	actctggtgc	cgtcacttct	gtgtgcttgc	ggactcagaa	9240
tctggtggac	atatcactca	ctctgggatg	gtgggcatgg	gagtcagctg	cacagtcacc	9300
cgggaagatg	gaaccaatcg	cagatagggc	tgctagtga	ccaatcacat	gatgtcaccc	9360
agacatcagg	catacccact	agtgtgaaat	agacatcaga	attaagaaaa	acgtagggtc	9420
caagtggttc	cccgttatgg	actcgctatc	tgtcaaccag	atcttatacc	ctgaagttca	9480
cctagatagc	ccgatagtta	ccaataagat	agtagccatc	ctggagtatg	ctcgagtccc	9540
tcacgcttac	agcctggagg	accctacact	gtgtcagaac	atcaagcacc	gcctaaaaaa	9600
cggattttcc	aaccaaataga	ttataaacia	tgtggaagtt	gggaatgtca	tcaagtccaa	9660
gcttaggagt	tatccggccc	actctcatat	tccatatcca	aattgtaatc	aggatttatt	9720
taacatagaa	gacaaagagt	caacgaggaa	gatccgtgaa	ctcctcaaaa	aggggaattc	9780
gctgtactcc	aaagtcagtg	ataaggtttt	ccaatgctta	agggacacta	actcacggct	9840
tggcctaggc	tccgaattga	gggaggacat	caaggagaaa	gttattaact	tgggagttta	9900
catgcacagc	tcccagtggg	ttgagccctt	tctgttttgg	tttacagtca	agactgagat	9960
gaggtcagtg	attaaatcac	aaaccatac	ttgccatagg	aggagacaca	cacctgtatt	10020

cttcactggg	agttcagttg	agttgcta	ctctcgtgac	cttggttgcta	taatcagtaa	10080
agagtctcaa	catgtatatt	acctgacatt	tgaactgggt	ttgatgtatt	gtgatgtcat	10140
agaggggagg	ttaatgacag	agaccgctat	gactattgat	gctaggtata	cagagcttct	10200
aggaagagtc	agatacatgt	ggaaactgat	agatgggttc	ttccctgcac	tcgggaatcc	10260
aacttatcaa	attgtagcca	tgctggagcc	tctttcactt	gcttacctgc	agctgaggga	10320
tataacagta	gaactcagag	gtgctttcct	taaccactgc	tttactgaaa	tacatgatgt	10380
tcttgaccaa	aacggggttt	ctgatgaagg	tacttatcat	gagttaactg	aagctctaga	10440
ttacattttc	ataactgatg	acatacatct	gacaggggag	attttctcat	ttttcagaag	10500
tttcggccac	cccagacttg	aagcagtaac	ggctgctgaa	aatgttagga	aatacatgaa	10560
tcagcctaaa	gtcattgtgt	atgagactct	gatgaaaggt	catgccatat	tttgtggaat	10620
cataatcaac	ggctatcgtg	acaggcacgg	aggcagttgg	ccaccgctga	ccctccccct	10680
gcatgctgca	gacacaatcc	ggaatgctca	agcttcaggt	gaagggttaa	cacatgagca	10740
gtgcgttgat	aactggaaat	cttttgctgg	agtgaaattt	ggctgcttta	tgctcttag	10800
cctggatagt	gatctgacaa	tgtacctaaa	ggacaaggca	cttgctgctc	tccaaaggga	10860
atgggattca	gtttacccga	aagagttcct	gcgttacgac	cctcccaagg	gaaccgggtc	10920
acggaggctt	gtagatgttt	tccttaatga	ttcgagcttt	gacccatatg	atgtgataat	10980
gtatgttgta	agtgagctt	acctccatga	ccctgagttc	aacctgtctt	acagcctgaa	11040
agaaaaggag	atcaaggaaa	caggtagact	ttttgctaaa	atgacttaca	aatgaggggc	11100
atgccaagtg	attgctgaaa	atctaattct	aaacgggatt	ggcaaataat	ttaaggacaa	11160
tgggatggcc	aaggatgagc	acgatttgac	taaggcactc	cacactctag	ctgtctcagg	11220
agtccccaaa	gatctcaaag	aaagtcacag	gggggggcca	gtcttaaaaa	cctactcccg	11280
aagcccagtc	cacacaagta	ccaggaacgt	gagagcagca	aaagggttta	tagggttccc	11340
tcaagtaatt	cggcaggacc	aagacactga	tcatccggag	aatatggaag	cttacgagac	11400
agtcagtgca	tttatcacga	ctgatctcaa	gaagtactgc	cttaattgga	gatatgagac	11460
catcagcttg	tttgcacaga	ggctaaatga	gatttacgga	ttgccctcat	ttttccagtg	11520
gctgcataag	aggcttgaga	cctctgtcct	gtatgtaagt	gaccctcatt	gcccccccga	11580
ccttgacgcc	catatcccgt	tatataaagt	ccccaatgat	caaatcttca	ttaagtaccc	11640
tatgggaggt	atagaagggt	attgtcagaa	gctgtggacc	atcagcacca	ttccctatct	11700
atacctggct	gcttatgaga	gcggagtaag	gattgcttcg	ttagtgcaag	gggacaatca	11760

gaccatagcc gtaacaaaaa gggtagccag cacatggccc tacaacctta agaaacggga	11820
agctgctaga gtaactagag attactttgt aattccttagg caaaggctac atgatattgg	11880
ccatcacctc aaggcaaagt agacaattgt ttcatcacat ttttttgtct attcaaaagg	11940
aatatattat gatgggctac ttgtgtccca atcactcaag agcatcgcaa gatgtgtatt	12000
ctggtcagag actatagttg atgaaacaag ggcagcatgc agtaatattg ctacaacaat	12060
ggctaaaagc atcgagagag gttatgaccg ttaccttgca tattccctga acgtcctaaa	12120
agtgatacag caaattctga tctctcttgg cttcacaatc aattcaacca tgacccggga	12180
tgtagtcata cccctcctca caaacaacga cctcttaata aggatggcac tgttgcccgc	12240
tcctattggg gggatgaatt atctgaatat gagcaggctg tttgtcagaa acatcggtga	12300
tccagtaaca tcatcaattg ctgatctcaa gagaatgatt ctgcctcac taatgcctga	12360
agagaccctc catcaagtaa tgacacaaca accgggggac tcttcattcc tagactgggc	12420
tagcgaccct tactcagcaa atcttgtatg tgtccagagc atcactagac tcctcaagaa	12480
cataactgca aggtttgtcc tgatccatag tccaaacca atgttaaaag gattattcca	12540
tgatgacagt aaagaagagg acgagggact ggcggcattc ctcatggaca ggcatattat	12600
agtacctagg gcagctcatg aaatcctgga tcatagtgtc acaggggcaa gagagtctat	12660
tgcaggcatg ctggatacca caaaaggctt gattcgagcc agcatgagga aggggggggt	12720
aacctctcga gtgataacca gattgtccaa ttatgactat gaacaattca gagcagggat	12780
ggtgctattg acaggaagaa agagaaatgt cctcattgac aaagagtcac gttcagtgca	12840
gctggcgaga gctctaagaa gccatatgtg ggcgaggcta gctcgaggac ggctatttta	12900
cggccttgag gtccctgatg tactagaatc tatgagaggc caccttattc ggcgtcatga	12960
gacatgtgtc atctgcgagt gtggatcagt caactacgga tggttttttg tcccctcggg	13020
ttgccaactg gatgatattg acaaggaaac atcatccttg agagtcccat atattggttc	13080
taccactgat gagagaacag acatgaagct tgccttcgta agagcccaa gtcgatcctt	13140
gcgatctgct gttagaatag caacagtgtc ctcatgggct tacgggtgatg atgatagctc	13200
ttggaacgaa gcctggttgt tggctaggca aagggccaat gtgagcctgg aggagctaag	13260
ggtgatcact cccatctcaa cttcgactaa tttagcgcat aggttgaggg atcgtagcac	13320
tcaagtgaat tactcaggta catcccttgt ccgagtggcg aggtatacca caatctccaa	13380
cgacaatctc tcatttgtca tatcagataa gaaggttgat actaacttta tataccaaca	13440
aggaatgctt ctaggggttg gtgtttttaga aacattgttt cgactcgaga aagataccgg	13500

atcatctaac	acggtattac	atcttcacgt	cgaacacagat	tgttgcggtga	tcccgatgat	13560
agatcatccc	aggataccca	gctcccgcaa	gctagagctg	agggcagagc	tatgtaccaa	13620
cccattgata	tatgataatg	cacctttaat	tgacagagat	gcaacaaggc	tatacaccca	13680
gagccatagg	aggcaccttg	tggaatttgt	tacatgggtcc	acaccccaac	tatatcacat	13740
tttagctaag	tccacagcac	tatctatgat	tgacctggta	acaaaatttg	agaaggacca	13800
tatgaatgaa	atttcagctc	tcatagggga	tgacgatatc	aatagtttca	taactgagtt	13860
tctgctcata	gagccaagat	tattcactat	ctacttgggc	cagtgtgcgg	ccatcaattg	13920
ggcatttgat	gtacattatc	atagaccatc	agggaaatat	cagatgggtg	agctgttgtc	13980
atcgcttctt	tctagaatga	gcaaaggagt	gtttaagggtg	cttgtcaatg	ctctaagcca	14040
cccaaagatc	tacaagaaat	tctggcattg	tggtattata	gagcctatcc	atggtccttc	14100
acttgatgct	caaaacttgc	acacaactgt	gtgcaacatg	gtttacacat	gctatatgac	14160
ctacctcgac	ctgttggtga	atgaagagtt	agaagagttc	acatttctct	tgtgtgaaag	14220
cgacgaggat	gtagtaccgg	acagattcga	caacatccag	gcaaaacact	tatgtgttct	14280
ggcagatttg	tactgtcaac	cagggacctg	cccaccaatt	cgagggtctaa	gaccggtaga	14340
gaaatgtgca	gttctaaccg	accatatcaa	ggcagaggct	atgttatctc	cagcaggatc	14400
ttcgtggaac	ataaatccaa	ttattgtaga	ccattactca	tgctctctga	cttatctccg	14460
gcgaggatcg	atcaaacaga	taagattgag	agttgatcca	ggattcattt	tcgacgcctt	14520
cgctgaggta	aatgtcagtc	agccaaagat	cggcagcaac	aacatctcaa	atatgagcat	14580
caaggctttc	agacccccac	acgatgatgt	tgcaaaattg	ctcaaagata	tcaacacaag	14640
caagcacaat	cttcccattt	cagggggcaa	tctcgccaat	tatgaaatcc	atgctttccg	14700
cagaatcggg	ttgaactcat	ctgcttgcta	caaagctggt	gagatatcaa	cattaattag	14760
gagatgcctt	gagccagggg	aggacggctt	gttcttgggt	gagggatcgg	gttctatggt	14820
gatcacttat	aaagagatac	ttaaactaaa	caagtgcctc	tataatagtg	gggtttccgc	14880
caattctaga	tctggtcaaa	gggaattagc	accctatccc	tccgaagttg	gccttgtcga	14940
acacagaatg	ggagtaggta	atattgtcaa	agtgcctctt	aacgggaggc	ccgaagtcac	15000
gtgggtaggc	agtgtagatt	gcttcaattt	catagttagt	aatatcccta	cctctagtgt	15060
ggggtttatc	cattcagata	tagagacctt	gcctgacaaa	gatactatag	agaagctaga	15120
ggaattggca	gccatcttat	cgatggctct	gctcctgggc	aaaataggat	caatactggt	15180
gattaagctt	atgcctttca	gcggggattt	tgttcaggga	tttataagtt	atgtagggtc	15240

tcattataga	gaagtgaacc	ttgtataccc	tagatacagc	aacttcatct	ctactgaatc	15300
ttatttggtt	atgacagatc	tcaaggctaa	ccggctaagt	aatcctgaaa	agattaagca	15360
gcagataatt	gaatcatctg	tgaggacttc	acctggactt	ataggtcaca	tcctatccat	15420
taagcaacta	agctgcatac	aagcaattgt	gggagacgca	gttagtagag	gtgatatcaa	15480
tcctactctg	aaaaaactta	cacctataga	gcaggtgctg	atcaattgcg	ggttggcaat	15540
taacggacct	aagctgtgca	aagaattgat	ccaccatgat	gttgccctcag	ggcaagatgg	15600
attgcttaat	tctatactca	tcctctacag	ggagttggca	agattcaaag	acaaccaaag	15660
aagtcaacaa	gggatgttcc	acgcttacct	cgtattggta	agtagcaggc	aacgagaact	15720
tatatctagg	atcacccgca	aattctgggg	gcacattctt	ctttactccg	ggaacaaaaa	15780
gttgataaat	aagtttatcc	agaatctcaa	gtccggctat	ctgatactag	acttacacca	15840
gaatatcttc	gttaagaatc	tatccaagtc	agagaaacag	attattatga	cgggggggtt	15900
gaaacgtgag	tgggttttta	aggtaacagt	caaggagacc	aaagaatggt	ataagttagt	15960
cggatacagt	gccctgatta	aggactaatt	ggttgaactc	cggaacccta	atcctgccct	16020
aggtggttag	gcattatttg	caatatatta	aagaaaactt	tgaaaatacg	aagtttctat	16080
tcccagcttt	gtctggtggc	cggcatggtc	ccagcctcct	cgctggcgcc	ggctgggcaa	16140
cattccgagg	ggaccgtccc	ctcggtaatg	gcgaatggga	cgcgcccgat	ccggctgcta	16200
acaaagcccg	aaaggaagct	gagttggctg	ctgccaccgc	tgagcaataa	ctagcataac	16260
cccttggggc	ctctaaacgg	gtcttgaggg	gttttttgct	gaaaggagga	actatatccg	16320
gatgcggccg	cgggccctat	ggtaccacgc	ttttgttccc	tttagtgagg	gttaattccg	16380
agcttggcgt	aatcatggtc	atagctgttt	cctgtgtgaa	attgttatcc	gctcacaatt	16440
ccacacaaca	taggagccgg	aagcataaag	tgtaaagcct	ggggtgccta	atgagtgagg	16500
taactcacat	taattgcgtt	gcgctcactg	cccgccttcc	agtcgggaaa	cctgtcgtgc	16560
cagctgcatt	aatgaatcgg	ccaacgcgcg	gggagaggcg	gtttgcgtat	tgggcgctct	16620
tccgcttcct	cgctcactga	ctcgtgcgc	tcggtcgttc	ggctgcggcg	agcggtatca	16680
gctcactcaa	aggcggtaat	acggttatcc	acagaatcag	gggataacgc	aggaaagaac	16740
atgtgagcaa	aaggccagca	aaaggccagg	aaccgtaaaa	aggccgcggt	gctggcggtt	16800
ttccataggc	tcggcccccc	tgacgagcat	cacaaaaatc	gacgctcaag	tcagaggtgg	16860
cgaaacccga	caggactata	aagataccag	gcgttcccc	ctggaagctc	cctcgtgcgc	16920
tctcctgttc	cgaccctgcc	gcttaccgga	tacctgtccg	cctttctccc	ttcgggaagc	16980

gtggcgcttt	ctcaatgctc	acgctgtagg	tatctcagtt	cggtgtaggt	cgttcgctcc	17040
aagctgggct	gtgtgcacga	acccccggtt	cagcccgacc	gctgcgcctt	atccggtaac	17100
tatcgtcttg	agtccaaccc	ggtaagacac	gacttatcgc	cactggcagc	agccactggg	17160
aacaggatta	gcagagcgag	gtatgtaggc	gggtgctacag	agttcttgaa	gtggtggcct	17220
aactacggct	acactagaag	gacagtattt	ggatatctgcg	ctctgctgaa	gccagttacc	17280
ttcggaaaaa	gagttggtag	ctcttgatcc	ggcaaacaaa	ccaccgctgg	tagcggtggt	17340
ttttttgttt	gcaagcagca	gattacgcgc	agaaaaaaag	gatctcaaga	agatcctttg	17400
atctttttcta	cggggtctga	cgctcagtgg	aacgaaaact	cacgttaagg	gattttggtc	17460
atgagattat	caaaaaggat	cttcacctag	atccttttta	attaaaaatg	aagttttaaa	17520
tcaatctaaa	gtatatatga	gtaaaacttg	tctgacagtt	accaatgctt	aatcagtga	17580
gcacctatct	cagcgatctg	tctatttcgt	tcatccatag	ttgcctgact	gcccgctcgtg	17640
tagataacta	cgatacggga	gggcttacca	tctggcccca	gtgctgcaat	gataccgcga	17700
gaccacgct	caccggctcc	agatttatca	gcaataaacc	agccagccgg	aagggccgag	17760
cgcagaagtg	gtcctgcaac	tttatccgcc	tccatccagt	ctattaattg	ttgccgggaa	17820
gctagagtaa	gtagttcgcc	agttaatagt	ttgcgcaacg	ttgttgccat	tgctacaggc	17880
atcgtgggtg	cacgctcgtc	gtttgggatg	gcttcattca	gctccgggtc	ccaacgatca	17940
aggcgagtta	catgatcccc	catgttgatg	aaaaaagcgg	ttagctcctt	cggtcctccg	18000
atcgttgtca	gaagtaagtt	ggccgcagtg	ttatcactca	tgcttatggc	agcactgcat	18060
aattctctta	ctgtcatgcc	atccgtaaga	tgcttttctg	tgactgggtg	gtactcaacc	18120
aagtcatctt	gagaatagtg	tatgcggcga	ccgagttgct	cttgcccggc	gtcaatacgg	18180
gataataccg	cgccacatag	cagaacttta	aaagtgctca	tcattggaaa	acgttcttcg	18240
gggcgaaaaa	tctcaaggat	cttaccgctg	ttgagatcca	gttcgatgta	accactcgt	18300
gcacccaact	gatcttcagc	atcttttact	ttcaccagcg	tttctgggtg	agcaaaaaca	18360
ggaaggcaaa	atgccgcaaa	aaagggaata	agggcgacac	ggaaatgttg	aatactcata	18420
ctcttccttt	ttcaatatta	ttgaagcatt	tatcagggtt	attgtctcat	gagcggatac	18480
atatttgaat	gtatttagaa	aaataaacia	ataggggttc	cgcgcacatt	tccccgaaaa	18540
gtgccacctg	aaattgtaaa	cgtaaatatt	ttgttaaaat	tcgcgttaaa	tttttgtaa	18600
atcagctcat	tttttaacca	ataggccgaa	atcggcaaaa	tcccttataa	atcaaaaagaa	18660
tagaccgaga	tagggttgag	tgttgttcca	gtttggaaca	agagtccact	attaaagaac	18720

gtggactcca acgtcaaagg gcgaaaaacc gtctatcagg gcgatggccc actacgtgaa 18780
ccatcacct aatcaagttt tttggggtcg aggtgccgta aagcactaaa tcggaaccct 18840
aaagggagcc cccgatttag agcttgacgg ggaaagccgg cgaacgtggc gagaaaggaa 18900
gggaagaaag cgaaaggagc gggcgctagg gcgctggcaa gtgtagcggc cacgctgcgc 18960
gtaaccacca caccgcccgc gcttaatgcg ccgctacagg gcgctgcca ttcgccattc 19020
aggctgcgca actgttggga agggcgatcg gtgcgggcct cttcgctatt acgccagcca 19080
ccgcggtgat cttataaag ctagatg 19107

<210> 61
<211> 591
<212> PRT
<213> Artificial sequence

<220>
<223> Protein encoded by SEQ ID NO: 53

<400> 61

Arg Arg Gly Ala Asp Thr Ser Val Gly Ile Val Gly Leu Leu Leu Thr
1 5 10 15

Thr Ala Met Ala Ala Glu Val Thr Arg Arg Gly Ser Ala Tyr Tyr Met
20 25 30

Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser Phe Pro Thr Thr
35 40 45

Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp Leu Gly His Met
50 55 60

Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu Asp Glu Gly Val
65 70 75 80

Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr Ser Thr Trp Val
85 90 95

Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala Arg Arg Ser Arg
100 105 110

Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys Leu Gln Thr Arg
115 120 125

Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys His Leu Ile Arg

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

Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu
 370 375 380

Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu
 385 390 395 400

Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly
 405 410 415

Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu
 420 425 430

Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser
 435 440 445

Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu
 450 455 460

Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg
 465 470 475 480

Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys
 485 490 495

Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly
 500 505 510

Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys
 515 520 525

Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly
 530 535 540

Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser
 545 550 555 560

Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val
 565 570 575

Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser
 580 585 590

<210> 62

<211> 692
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Protein encoded by SEQ ID NOs: 54

<400> 62

Arg Arg Gly Ala Asp Thr Ser Val Gly Ile Val Gly Leu Leu Leu Thr
 1 5 10 15

Thr Ala Met Ala Ala Glu Val Thr Arg Arg Gly Ser Ala Tyr Tyr Met
 20 25 30

Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser Phe Pro Thr Thr
 35 40 45

Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp Leu Gly His Met
 50 55 60

Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu Asp Glu Gly Val
 65 70 75 80

Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr Ser Thr Trp Val
 85 90 95

Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala Arg Arg Ser Arg
 100 105 110

Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys Leu Gln Thr Arg
 115 120 125

Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys His Leu Ile Arg
 130 135 140

Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala Leu Ala Ala Ala
 145 150 155 160

Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln Lys Val Ile Tyr
 165 170 175

Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser Ile Arg Cys Ile
 180 185 190

Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp

195					200					205					
Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys	Val	Thr	Val	Met	Ala	Gln
	210					215					220				
Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val	Thr	Thr	Thr	Val	Ser	Asn
225					230					235					240
Met	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Glu	Ala	Ser	Ile	Ser	Asp	Met
				245					250					255	
Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Ala	Tyr	Leu	Asp	Lys
			260					265					270		
Gln	Ser	Asp	Thr	Gln	Tyr	Val	Cys	Lys	Arg	Thr	Leu	Val	Asp	Arg	Gly
		275					280					285			
Trp	Gly	Asn	Gly	Cys	Gly	Asp	Phe	Gly	Lys	Gly	Ser	Leu	Val	Thr	Cys
	290					295					300				
Ala	Lys	Phe	Ala	Cys	Ser	Lys	Lys	Met	Thr	Gly	Lys	Ser	Ile	Gln	Pro
305					310					315					320
Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu	Ser	Val	His	Gly	Ser	Gln	His
				325					330					335	
Ser	Gly	Met	Ile	Val	Asn	Asp	Thr	Gly	His	Glu	Thr	Asp	Glu	Asn	Arg
			340					345					350		
Ala	Lys	Val	Glu	Ile	Thr	Pro	Asn	Ser	Pro	Arg	Ala	Glu	Ala	Thr	Leu
		355					360					365			
Gly	Gly	Phe	Gly	Ser	Leu	Gly	Leu	Asp	Cys	Glu	Pro	Arg	Thr	Gly	Leu
	370					375					380				
Asp	Phe	Ser	Asp	Leu	Tyr	Tyr	Leu	Thr	Met	Asn	Asn	Lys	His	Trp	Leu
385					390					395					400
Val	His	Lys	Glu	Trp	Phe	His	Asp	Ile	Pro	Leu	Pro	Trp	His	Ala	Gly
				405					410					415	
Ala	Asp	Thr	Gly	Thr	Pro	His	Trp	Asn	Asn	Lys	Glu	Ala	Leu	Val	Glu
			420					425					430		

Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser
435 440 445

Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu
450 455 460

Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg
465 470 475 480

Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys
485 490 495

Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly
500 505 510

Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys
515 520 525

Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly
530 535 540

Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser
545 550 555 560

Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val
565 570 575

Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly
580 585 590

Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg
595 600 605

Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
610 615 620

Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala
625 630 635 640

Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile
645 650 655

Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile

660

665

670

Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile Phe Leu Ser Thr
 675 680 685

Ala Val Ser Ala
 690

<210> 63
 <211> 1209
 <212> DNA
 <213> Artificial sequence

<220>
 <223> sE antigen no codon optimization

<400> 63
 atcagggtgca taggagtcag caatagggac tttgtggaag gtatgtcagg tgggacctgg 60
 gttgatgttg tcttggaaca tggaggttgt gtcaccgtaa tggcacagga caaaccgact 120
 gtcgacatag agctgggttac aacaacagtc agcaacatgg cggaggtaag atcctactgc 180
 tatgaggcat caatatcaga catggcttcg gacagccgct gcccaacaca aggtgaagcc 240
 taccttgaca agcaatcaga cactcaatat gtctgcaaaa gaacgttagt ggacagaggc 300
 tggggaaatg gatgtggact ttttgcaaaa gggagcctgg tgacatgcgc taagtttgca 360
 tgctccaaga aaatgaccgg gaagagcatc cagccagaga atctggagta ccggataatg 420
 ctgtcagttc atgggtccca gcacagtggg atgattgtta atgacacagg acatgaaact 480
 gatgagaata gagcgaaagt tgagataacg cccaattcac caagagccga agccaccctg 540
 ggggggtttt gaagcctagg acttgattgt gaaccgagga caggccttga cttttcagat 600
 ttgtattact tgactatgaa taacaagcac tggttggttc acaaggagtg gttccacgac 660
 attccattac cttggcacgc tggggcagac accggaactc cacactggaa caacaaagaa 720
 gcactggtag agttcaagga cgcacatgcc aaaaggcaaa ctgtcgtggt tctagggagt 780
 caagaaggag cagttcacac ggcccttgct ggagctctgg aggctgagat ggatggtgca 840
 aagggaaggc tgtcctctgg ccacttgaaa tgtcgcctga aaatggataa acttagattg 900
 aagggcgtgt catactcctt gtgtactgca gcgttcacat tcaccaagat cccggctgaa 960
 aactgacagc ggacagtcac agtggaggta cagtacgcag ggacagatgg accttgcaag 1020
 gttccagctc agatggcggg ggacatgcaa actctgaccc cagttgggag gttgataacc 1080
 gctaaccctg taatcactga aagcactgag aactctaaga tgatgctgga acttgatcca 1140

ccattttgggg actctttacat tgtcatagga gtcgggggaga agaagatcac ccaccactgg 1200
cacaggagt 1209

<210> 64
<211> 1209
<212> DNA
<213> Artificial sequence

<220>
<223> sE antigen codon optimization (human)

<400> 64
atcagatgca tcggagtttc caatcgtgac tttgtcgaag ggatgtccgg aggcacctgg 60
gttgacgtgg tgcttgagca tgggtggctgc gtaacggtaa tggctcagga caaacccacg 120
gttgacatag aactgggtgac cacgactgtc agtaatatgg ccgaagtgcg aagctactgc 180
tatgaggcct ctatctctga catggcatca gacagccggt gtccaactca aggcgaagct 240
tatctggaca agcaatccga tacacagtac gtgtgcaagc ggactctcgt ggatagaggt 300
tggggcaatg ggtgtggtct gtttgggaaa ggcagtctgg taacatgcgc aaagttcgca 360
tgttccaaga aaatgacagg aaagagcatt cagccggaaa atctggagta taggattatg 420
ctcagcgtgc atgggagcca gcacagtggc atgattgtca atgatacagg ccacgaaacc 480
gacgagaaca gagcgaaggt tgagatcact cccaattcac ctgcgcgaga ggccactctg 540
ggagggtttg gaagtctcgg tctggactgt gaacctcgca ctggcctgga cttcagcgat 600
ctgtattacc tgacgatgaa caacaagcat tggctggtcc ataaggagtg gttccatgat 660
attccgcttc cttggcatgc cggagccgat accggaacac cccactggaa caacaaagag 720
gcttttgttg agttcaaaga tgcacacgct aagcgccaaa ccgtcgtggg cctgggtagc 780
caagaaggag cggttcacac tgcgcttgcc ggagccctgg aggcggaaat ggatggggcc 840
aaagggcgcc tttccagtgg acacctgaag tgtcggctga aaatggacaa gctgagactg 900
aaaggtgtgt cttacagcct gtgcaccgca gccttcactt tcacccaaaat ccctgctgaa 960
accttgcacg gaacagtgac agtagagggtg cagtatgcag gcacagatgg cccatgtaag 1020
gtgccagctc agatggcagt ggacatgcag accctgactc cagtgggaag gtcataact 1080
gccaatccgg tcatcacaga gtctaccgag aactcaaaga tgatgctgga gctggaccct 1140
ccctttgggg actctttacat agtcataggg gtaggcgaga agaaaatcac ccatcactgg 1200
cacaggagc 1209

<210> 65

<211> 403
 <212> PRT
 <213> Artificial sequence

<220>
 <223> sE antigen L107D

<400> 65

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Asp Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
 180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn

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

<210> 66
 <211> 504
 <212> PRT

<213> Artificial sequence

<220>

<223> E antigen L107D

<400> 66

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Asp Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
 210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
 225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
 245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile

435

440

445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
 450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
 465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
 485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
 500

<210> 67

<211> 10272

<212> DNA

<213> Zika virus isolate GD01 polyprotein gene, complete cds

<400> 67

```

atgaaaaacc caaaaaagaa atccggagga ttccggattg tcaatatgct aaaacgcgga      60
gtagcccgctg tgagcccctt tgggggcttg aagaggctgc cagccggact tctgctgggt      120
catgggccca tcaggatggg cttggcgatt ctagcctttt tgagattcac ggcaatcaag      180
ccatcactgg gtctcatcaa tagatggggg tcagtgggga aaaaagaggc tatggaaata      240
ataaagaagt tcaagaaaga tctggctgcc atgctgagaa taatcaatgc taggaaggag      300
aagaagagac gaggcgcaga aactagtgtc ggaattgttg gcctcctgct gaccacagct      360
atggcagcgg aggtcactag acgtgggagt gcatactata tgtacttgga cagaaacgat      420
gctggggagg ccatatcttt tccaaccaca ttggggatga ataagtgtta tatacagatc      480
atggatcttg gacacatgtg tgatgccacc atgagctatg aatgccctat gctggatgag      540
ggggtggaac cagatgacgt cgattgttgg tgcaacacga cgtcaacttg ggttgtgtac      600
ggaacctgcc atcacaaaaa aggtgaagca cggagatcta gaagagctgt gacgctccct      660
tcccattcca ctaggaagct gcaaacgcgg tcgcaaacct ggttggaatc aagagaatac      720
acaaagcact tgattagagt cgaaaattgg atattcagga accctggcct cgcgttagca      780
gcagctgcta tcgcttggct tttgggaagc tcaacgagcc aaaaagtcac atacttggtc      840
atgatactgc tgattgcccc ggcatacagc atcaggtgca taggagtcag caatagggac      900
tttgtggaag gtatgtcagg tgggacttgg gttgatgttg tcttggaaca tggaggttgt      960
gtcaccgtaa tggcacagga caaacgact gtcgacatag agctgggttac aacaacagtc     1020

```

agcaacatgg	cggaggtaag	atcctactgc	tatgaggcat	caatatcaga	catggcttcg	1080
gacagccgct	gccaacaca	aggtgaagcc	taccttgaca	agcaatcaga	cactcaatat	1140
gtctgcaaaa	gaacgttagt	ggacagaggg	tggggaaatg	gatgtggact	ttttggcaaa	1200
gggagcctgg	tgacatgcgc	taagtttgca	tgctccaaga	aatgaccgg	gaaaagcatc	1260
cagccagaga	atctggagta	ccggataatg	ctgtcagttc	atggctccca	gcacagtggg	1320
atgattgtta	atggcacagg	acatgaaact	gatgagaata	gagcgaaagt	tgagataacg	1380
ccaattcac	caagagccga	agccaccctg	gggggttttg	gaagcctagg	acttgattgt	1440
gaaccgagga	caggccttga	cttttcagat	ttgtattact	tgactatgaa	taacaagcac	1500
tggttggttc	acaaggagtg	gttccacgac	attccattac	cttggcacgc	tggggcagac	1560
accggaactc	cacactggaa	caacaaagaa	gcactggtag	agttcaagga	cgcacatgcc	1620
aaaaggcaaa	ctgtcgtggt	tctagggagt	caagaaggag	cagttcacac	ggcccttgct	1680
ggagctctgg	aggctgagat	ggatggagca	aagggaaggc	tgtcctctgg	ccacttgaaa	1740
tgctgcctga	aatggataa	acttagattg	aagggcgtgt	catactcctt	gtgtactgca	1800
gcgttcacat	tcaccaagat	ccgggctgaa	acactgcacg	ggacagtcac	agtggaggta	1860
cagtacgcag	ggacagatgg	accttgcaag	gttccagctc	agatggcggt	ggacatgcaa	1920
actctgaccc	cagttgggag	gttgataacc	gctaaccccg	taatcactga	aagcactgag	1980
aactctaaga	tgatgctgga	acttgatcca	ccatttgggg	actcttacat	tgtcatagga	2040
gtcggggaga	agaagatcac	ccaccactgg	cacaggagtg	gcagcaccat	tggaaaagca	2100
tttgaagcca	ctgtgagagg	tgccaagaga	atggcagtct	tgggagacac	agcctgggac	2160
tttggatcag	ttggaggcgc	tctcaactca	ttgggcaagg	gcatccatca	aatttttgga	2220
gcagctttca	aatcattggt	tggaggaatg	tcctggttct	cacaaattct	cattggaacg	2280
ttgctgatgt	ggttgggtct	gaacacaaag	aatggatcta	tttcccttat	gtgcttggcc	2340
ttagggggag	tgttgatctt	cttatccaca	gccgtctctg	ctgatgtggg	gtgctcggtg	2400
gacttctcaa	agaaggagac	gagatgcggg	acaggggtgt	ttgtctataa	cgacgttgaa	2460
gcctggaggg	acaggtacaa	gtaccatcct	gactcccccc	gtagattggc	agcagcagtc	2520
aagcaagcct	gggaagatgg	tatctgcggg	atctcctctg	tttcaagaat	ggaaaacatc	2580
atgtggagat	cagtagaagg	ggagctcaac	gcaatcctgg	aagagaatgg	agttcaactg	2640
acggtcgttg	tgggatctgt	aaaaaacccc	atgtggagag	gtccacagag	attgcccgtg	2700
cctgtgaacg	agctgcccc	cggctggaag	gcttggggga	aatcgtactt	cgtcagagca	2760

gcaaagacaa	ataacagctt	tgtcgtggat	ggtgacacac	tgaaggaatg	cccactcaaa	2820
catagagcat	ggaacagctt	tcttgtggag	gatcatgggt	tcgggggtatt	tcacactagt	2880
gtctgggtca	aggttagaga	agactattca	ttagagtgtg	atccagccgt	tattggaaca	2940
gctgttaagg	gaaaggaggc	tgtacacagt	gatctaggct	actggattga	gagtgagaag	3000
aatgacacat	ggaggctgaa	gagggcccat	ctgatcgaga	tgaaaacatg	tgaatggcca	3060
aagtcccaca	cattgtggac	agatggaata	gaagagagtg	atctgatcat	acccaagtct	3120
ttagctgggc	cactcagcca	tcacaatacc	agagagggct	acaggaccca	aatgaaaggg	3180
ccatggcaca	gtgaggagct	tgaaattcgg	tttgaggaat	gcccaggcac	taaggtccac	3240
gtggaggaaa	catgtggaac	aagaggacca	tctctgagat	caaccactgc	aagcggaagg	3300
gtgatcgagg	aatggtgctg	cagggagtgc	acaatgcccc	cactgtcgtt	ccgggctaaa	3360
gatggctgtt	ggtatggaat	ggagataagg	cccaggaaag	aaccagaaag	caacttagta	3420
aggtcaatgg	tgactgcagg	atcaactgat	cacatggacc	acttctccct	tggagtgcct	3480
gtgatcctgc	tcatggtgca	ggaagggctg	aagaagagaa	tgaccacaaa	gatcatcata	3540
agcacatcaa	tggcagtgct	ggtagctatg	atcctgggag	gatttttcaat	gagtgcctg	3600
gctaagcttg	caattttgat	gggtgccacc	ttcgcgaaa	tgaacactgg	aggagatgta	3660
gctcatctgg	cgctgatagc	ggcattcaaa	gtcagaccag	cgttgctggg	atctttcatc	3720
ttcagagcta	attggacacc	ccgtgaaagc	atgctgctgg	ccttggcctc	gtgtcttttg	3780
caaactgcga	tctccgcctt	ggaaggcgac	ctgatggttc	tcatcaatgg	ttttgctttg	3840
gcctggttgg	cagtacgagc	gatggttgtt	ccacgcactg	ataacatcac	ccttagcaatc	3900
ctggctgctc	tgacaccact	ggcccggggc	acactgcttg	tggcgtggag	agcaggcctt	3960
gctacttgcg	gggggtttat	gctcctctct	ctgaagggaa	aaggcagtgt	gaagaagaac	4020
ttaccatttg	tcatggccct	gggactaacc	gctgtgaggc	tggtcgacct	catcaacgtg	4080
gtgggactgc	tgttgctcac	aaggagtggg	aagcggagct	ggccccctag	cgaagtactc	4140
acagctgttg	gcctgatatg	cgcattggct	ggagggttcg	ccaaggcaga	tatagagatg	4200
gctgggcca	tggccgcggt	cggtctgcta	attgtcagtt	acgtggtctc	aggaaagagt	4260
gtggacatgt	acattgaaaag	agcaggtgac	atcacatggg	aaaaagatgc	ggaagtcact	4320
ggaaacagtc	cccggctcga	tgtggcgcta	gatgagagtg	gtgatttctc	cctggtggag	4380
gatgacggtc	cccccatgag	agagatcata	ctcaagggtg	tcctgatgac	catctgtggc	4440
atgaacccaa	tagccatacc	ctttgcagct	ggagcgtggg	acgtatacgt	gaagactgga	4500

aaaaggagtg	gtgctctatg	ggatgtgcct	gctcccaagg	aagtaaaaaa	gggggagacc	4560
acagatggag	tgtacagagt	aatgactcgc	agactgctag	gttcaacaca	agttggagtg	4620
ggagttatgc	aagagggggg	ctttcacact	atgtggcacg	tcacaaaagg	atccgcgctg	4680
agaagcggtg	aagggagact	tgatccatac	tggggagatg	tcaagcagga	tctggtgtca	4740
tactgtggtc	catggaagct	agatgccgcc	tgggacgggc	acagcgaggt	gcagctcttg	4800
gccgtgcccc	ccggagagag	agcgaggaac	atccagactc	tgcccggaat	atttaagaca	4860
aaggatgggg	acattggagc	ggttgcgctg	gattaccag	caggaacttc	aggatctcca	4920
atcctagaca	agtgtgggag	agtgatagga	ctttatggca	atggggtcgt	gatcaaaaat	4980
gggagttatg	ttagtgccat	cacccaaggg	aggagggagg	aagagactcc	tgttgagtgc	5040
ttcgagcctt	cgatgctgaa	gaagaagcag	ctaactgtct	tagacttgca	tcttgagct	5100
gggaaaacca	ggagagttct	tcttgaaata	gtccgtgaag	ccataaaaac	aagactccgt	5160
actgtgatct	tagctccaac	cagggttgtc	gctgctgaaa	tggaggaggc	ccttagaggg	5220
cttccagtgc	gttatatgac	aacagcagtc	aatgtcaccc	actctggaac	agaaatcgtc	5280
gacttaatgt	gccatgccac	cttcacttca	cgtctactac	agccaattag	agtccccaac	5340
tataatctgt	atattatgga	tgaggcccac	ttcacagatc	cctcaagtat	agcagcaaga	5400
ggatacattt	caacaagggg	tgagatgggc	gaggcggctg	ccatcttcat	gaccgccacg	5460
ccaccaggaa	cccgtgacgc	atttccggac	tccaactcac	caattatgga	caccgaagtg	5520
gaagtcccag	agagagcctg	gagctcaggc	tttgattggg	tgacggatca	ttctggaaaa	5580
acagtttggg	ttgttccaag	cgtgaggaac	ggcaatgaga	tcgcagcttg	tctgacaaag	5640
gctggaaaac	gggtcataca	gctcagcaga	aagacttttg	agacagagtt	ccagaaaaca	5700
aaacatcaag	agtgggactt	tgtcgtgaca	actgacattt	cagagatggg	cgccaacttt	5760
aaagctgacc	gtgtcataga	ttccaggaga	tgcctaaagc	cggtcatact	tgatggcgag	5820
agagtcattc	tggctggacc	catgcctgtc	acacatgcca	gcgctgcca	gaggaggggg	5880
cgcataggca	ggaatcccaa	caaacctgga	gatgagtatc	tgtatggagg	tgggtgcgca	5940
gagactgacg	aagaccatgc	acactggctt	gaagcaagaa	tgctccttga	caatatttac	6000
ctccaagatg	gcctcatagc	ctcgtcttat	cgacctgagg	ccgacaaagt	agcagccatt	6060
gagggagagt	tcaagcttag	gacggagcaa	aggaagacct	ttgtggaact	catgaaaaga	6120
ggagatcttc	ctgtttggct	ggcctatcag	gttgcatctg	ccggaataac	ctacacagat	6180
agaagatggt	gctttgatgg	cacgaccaac	aacaccataa	tggaagacag	tgtgccggca	6240

gaggtgtgga ccagacacgg agagaaaaga gtgctcaaac cgaggtggat ggacgccaga	6300
gtttgttcag atcatgcggc cctgaagtca ttcaaggagt ttgccgctgg gaaaagagga	6360
gcggcttttg gagtgatgga agccctggga aactgcccag gacacatgac agagagattc	6420
caggaagcca ttgacaacct cgctgtgctc atgcgggcag agactggaag caggccttac	6480
aaagccgagg cagcccaatt gccggagacc ctagagacca ttatgctttt ggggttgctg	6540
ggaacagtct cgctgggaat cttcttcgtc ttgatgagga acaagggcat agggagatg	6600
ggcttttgaa tggtgactct tggggccagc gcatggctca tgtggctctc ggaaattgag	6660
ccagccagaa ttgcatgtgt cctcattgtt gtgttcctat tgctgggtgg gctcatacct	6720
gagccagaaa agcaaagatc tcccaggac aaccaaattg caatcatcat catggtagca	6780
gtaggtcttc tgggcttgat taccgccaat gaactcggat ggttgagag acaaagagt	6840
gacctagcc atctaattgg aaggagagag gagggggcaa ccataggatt ctcaatggac	6900
attgacctgc ggccagcctc agcttgggcc atctatgctg ccttgacaac tttcattacc	6960
ccagccgtcc aacatgcagt gaccacctca tacaacaact actccttaat ggcgatggcc	7020
acgcaagctg gagtggtgtt tggatatggc aaagggatgc cattctacgc atgggacttt	7080
ggagtccgc tgctaattgat aggctgctac tcacaattaa caccctgac cctaattagt	7140
gccatcattt tgctcgtggc gcactacatg tacttgatcc cagggtgca ggcagcagct	7200
gcgcgtgctg ccagaaagag aacggcagct ggcacatga agaaccctgt tgtggatgga	7260
atagtggatga ctgacattga cacaatgaca attgaccccc aagtggagaa aaagatggga	7320
caggtgctac tcatagcagt agccgtctcc agcgccatac tgtcgaggac cgctggggg	7380
tggggggagg ctggggccct gatcacagcc gcaacttcca ctttgtggga aggtctccg	7440
aacaagtact ggaactcctc tacagccact tcaactgtga acatttttag gggaagttac	7500
ttggctggag cttctctaata ctacacagta acaagaaacg ctggcttggt caagagacgt	7560
gggggtggaa caggagagac cctgggagag aaatggaagg cccgcttgaa ccagatgtcg	7620
gccctggagt tctactccta caaaaagtca ggcacaccg aggtgtgcag agaagaggcc	7680
cgccgcgcc tcaaggacgg tgtggcaacg ggaggccatg ctgtgtcccg aggaagtgca	7740
aagctgagat ggttggatgga gcggggatc ctgcagccct atggaaagg cattgatctt	7800
ggatgtggca gagggggctg gagttactac gccgccacca tccgcaaagt tcaagaagt	7860
aaaggataca caaaaggagg ccctggatcat gaagaacccg tgttggtgca aagctatggg	7920
tggaacatag tccgtcttaa gagtgggggtg gacgtctttc atatggcggc tgagccgtgt	7980

gacacgttgc	tgtgtgacat	aggtgagtca	tcatctagtc	ctgaagtgga	agaagcacgg	8040
acgctcagag	tcctctccat	ggtgggggat	tggcttgaaa	aaagaccagg	agccttttgt	8100
ataaaggtgt	tgtgcccata	caccagcact	atgatggaaa	ccctggagcg	actgcagcgt	8160
aggtatgggg	gaggactggg	cagagtgcc	ctctcccga	actctacaca	tgagatgtac	8220
tgggtctctg	gagcgaaaag	caacatcata	aaaagtgtgt	ccaccacgag	ccagctcctc	8280
ttggggcgca	tggacggggc	taggaggcca	gtgaaatatg	aggaggatgt	gaatctcggc	8340
tctggcacgc	gggctgtggc	aagctgcgct	gaagctccca	acatgaagat	cattggtaac	8400
cgcattgaaa	ggatccgcag	tgagcacgcg	gaaacgtggg	tctttgacga	gaaccacca	8460
tataggacat	gggcttacca	tggaagctat	gaggcccca	cacaaggggc	agcgtcctct	8520
ctaataaacg	gggttgtcag	gctcctgtca	aaaccctggg	atgtgggtgac	tggagtcaca	8580
ggaatagcca	tgaccgacac	cacaccgtat	ggtcagcaaa	gagttttcaa	ggaaaaagtg	8640
gacactaggg	tgccagaccc	ccaagaaggc	actcgtcagg	ttatgagcat	ggtctcttcc	8700
tggttgtgga	aagagctagg	caaacacaaa	cggccacgag	tctgtaccaa	agaagagttc	8760
atcaacaagg	ttcgtagcaa	tgcagcatta	ggggcaatat	ttgaagagga	aaaagagtgg	8820
aagactgcag	tggaagctgt	gaacgatcca	aggttctggg	ctctagtggg	caaggaaaga	8880
gagcaccacc	tgagaggaga	gtgccagagt	tgtgtgtaca	acatgatggg	aaaaagagaa	8940
aagaaacaag	gggaatttgg	aaaggccaag	ggcagccgcg	ccatctggta	tatgtggcta	9000
ggggctagat	ttctagagtt	cgaagccctt	ggattcttga	acgaggatca	ctggatgggg	9060
agagagaact	caggaggtgg	tgttgaaggg	ctgggattac	aaagactcgg	atatgtccta	9120
gaagagatga	gtcgtatacc	aggaggaagg	atgtatgcag	atgacactgc	tggctgggac	9180
acccgcatta	gcaggtttga	tctggagaat	gaagctctaa	tcaccaacca	aatggagaaa	9240
gggcacaggg	ccttggcatt	ggccataatc	aagtacacat	acaaaaacaa	agtggtaaag	9300
gtccttagac	cagctgaaaa	agggaaaaca	gttatggaca	ttatttcgag	acaagaccaa	9360
agggggagcg	gacaagttgt	cacttacgct	cttaacacat	ttaccaacct	agtggtgcaa	9420
ctcattcgga	atatggaggc	tgaggaagtt	ctagagatgc	aagacttggt	gctgctgcgg	9480
aggtcagaga	aagtgaccaa	ctggttgag	agcaacggat	gggataggct	caaacgaatg	9540
gcagtcagt	gagatgattg	cggtgtgaag	ccaattgatg	ataggtttgc	acatgccctc	9600
aggttcttga	atgatatggg	aaaagttagg	aaggacacac	aagagtggaa	accctcaact	9660
ggatgggaca	actgggaaga	agttccgttt	tgctcccacc	atttcaacaa	gctccatctc	9720

aaggacggga ggtccattgt ggttcctgc cgccaccaag atgaactgat tggccggggc	9780
cgcgtctctc caggggcggg atggagcatc cgggagactg cttgcctagc aaaatcatat	9840
gcgcaaatgt ggcagctcct ttatttccac agaagggacc tccgactgat ggccaatgcc	9900
atttgttcat ctgtgccagt tgactgggtt ccaactggga gaactacctg gtcaatccat	9960
ggaaaggag aatggatgac cactgaagac atgcttgtgg tgtggaacag agtgtggatt	10020
gaggagaacg accacatgga agacaagacc ccagttacga aatggacaga cattccctat	10080
ttgggaaaaa gggaagactt gtggtgtgga tctctcatag ggcacagacc gcgcaccacc	10140
tgggctgaga acattaaaaa cacagtcaac atggtgcgca ggatcatagg tgatgaagaa	10200
aagtacatgg actacctatc cacccaagtt cgctacttgg gtgaagaagg gtctacacct	10260
ggagtgtgt aa	10272

<210> 68

<211> 10617

<212> DNA

<213> Zika virus strain MRS_OPY_Martinique_PaRi_2015 polyprotein gene, complete cds

<400> 68

agtatcaaca ggttttatatt tggatttgga aacgagagtt tctgggtcatg aaaaacccaa	60
aaaagaaatc cggaggattc cggattgtca atatgctaaa acgcggagta gcccggtgtga	120
gccccttttg gggcttgaag aggctgccag ccggacttct gctgggtcat gggcccatca	180
ggatggtctt ggcgattcta gcctttttga gattcacggc aatcaagcca tcaactgggtc	240
tcatcaatag atggggttca gtggggaaaa aagaggctat ggaaataata aagaagttca	300
agaaagatct ggctgccatg ctgagaataa tcaatgctag gaaggagaag aagagacgag	360
gcgcagaaac tagtgtcgga attgttggcc tcctgctgac cacagctatg gcagcggagg	420
tcaactagacg tgggagtgca tactatatgt acttgacag aaacgatgct ggggaggcca	480
tatcttttcc aaccacattg gggatgaata agtgttatat acagatcatg gatcttggac	540
acatgtgtga tgccaccatg agctatgaat gccctatgct ggatgagggg gtggaaccag	600
atgacgtcga ttgttggtgc aacacgacgt caacttgggt tgtgtacgga acctgccatc	660
acaaaaaagg tgaagcacgg agatctagaa gagccgtgac gctcccctcc cattccacta	720
ggaagctgca aacgcggtcg caaacctggt tggaatcaag agaatacaca aagcacttga	780
ttagagtcga aaattggata ttcaggaacc ctggtttcgc tttagcagca gctgccatcg	840
cgtggctttt gggaagctca acgagccaaa aagtcataata cttgggtcatg atactgctga	900

ttgccccggc	atacagcatc	aggtgcatag	gagtcagcaa	tagggacttt	gtggaaggta	960
tgtcaggtag	gacttgggtt	gatgttgtct	tggaacatgg	aggttgtgtc	accgtaatgg	1020
cacaggacaa	accgactgtc	gacatagagc	tggttacaac	aacagtcagc	aacatggcgg	1080
aggtaagatc	ctactgctat	gaggcatcaa	tatcagacat	ggcttcggac	agccgctgcc	1140
caacacaagg	tgaagcctac	cttgacaagc	aatcagacac	tcaatatgtc	tgcaaaagaa	1200
cgttagtgga	cagaggctgg	ggaaatggat	gtggactttt	tggcaaaggg	agcctgggtga	1260
catgcgctaa	gtttgcatgc	tccaagaaaa	tgaccgggaa	gagcatccag	ccagagaatc	1320
tggagtaccg	gataatgttg	tcagttcatg	gctcccagca	cagtgggatg	atcgттаатg	1380
acacaggaca	tgaaactgat	gagaatagag	cgaaggttga	gataacgccc	aattcaccaa	1440
gagccgaagc	caccctgggg	ggttttggaa	gcctaggact	tgattgtgaa	ccgaggacag	1500
gccttgactt	ttcagatttg	tattacttga	ctatgaataa	caagcactgg	ttggttcaca	1560
aggagtgggt	ccacgacatt	ccattacctt	ggcacgctgg	ggcagacacc	ggaactccac	1620
actggaacaa	caaagaagca	ctggtagagt	tcaaggacgc	acatgccaaa	aggcaaactg	1680
tcgtggttct	agggagtcaa	gaaggagcag	ttcacacggc	ccttgctgga	gctctggagg	1740
ctgagatgga	tggtgcaaag	ggaaggctgt	cctctggcca	cttgaaatgt	cgctgaaaa	1800
tggataaact	tagattgaag	ggcgtgtcat	actccttggt	taccgcagcg	ttcacattca	1860
ccaagatccc	ggctgaaaca	ctgcacggga	cagtcacagt	ggaggtacag	tacgcaggga	1920
cagatggacc	ttgcaagggt	ccagcccaga	tggcgggtga	catgcaaact	ctgaccccag	1980
ttgggaggtt	gataaccgct	aaccccgtaa	tactgaaag	cactgagaac	tctaagatga	2040
tgctggaact	tgatccacca	tttggggact	cttacattgt	cataggagtc	ggggagaaga	2100
agatcaccca	ccactggcac	aggagtggca	gcaccattgg	aaaagcattt	gaagccactg	2160
tgagaggtgc	caagagaatg	gcagtcttgg	gagacacagc	ctgggacttt	ggatcagttg	2220
gaggcgctct	caactcattg	ggcaagggca	tccatcaaat	ttttggagca	gctttcaaat	2280
cattgtttgg	aggaatgtcc	tggttctcac	aaattctcat	tggaacgttg	ctgatgtggt	2340
tgggtctgaa	cacaaagaat	ggatctattt	cccttatgtg	cttggcctta	gggggagtgt	2400
tgatcttctt	atccacagcc	gtctctgctg	atgtggggtg	ctcgggtggac	ttctcaaaga	2460
aggagacgag	atgtggtaca	ggggtgttcg	tctataacga	cgttgaagcc	tggagggaca	2520
ggtacaagta	ccatcctgac	tcccccgta	gattggcagc	agcagtcaag	caagcctggg	2580
aagatggtat	ctgcgggatc	tcctctgttt	caagaatgga	aaacatcatg	tggagatcag	2640

tagaagggga gctcaacgca atcctggaag agaatggagt tcaactgacg gtcgttgtgg	2700
gatctgtaaa aaaccccatg tggagaggtc cacagagatt gcccgtcct gtgaacgagc	2760
tgccccacgg ctggaaggct tgggggaaat cgtacttcgt cagagcagca aagacaaata	2820
acagctttgt cgtggatggt gacacactga aggaatgccc actcaaacat agagcatgga	2880
acagctttct tgtggaggat catgggttcg gggatatttca cactagtgtc tggctcaagg	2940
ttagagaaga ttattcatta gagtgtgac cagccgttat tggaacagct gttaagggaa	3000
aggaggctgt acacagtgat ctaggctact ggattgagag tgagaagaat gacacatgga	3060
ggctgaagag ggcccatctg atcgagatga aaacatgtga atggccaaaa tcccacacat	3120
tgtggacaga tggaatagaa gagagtgatc tgatcatacc caagtcttta gctggggcac	3180
tcagccatca caataccaga gagggctaca ggacccaaat gaaagggcca tggcacagtg	3240
aagagcttga aattcggttt gaggaatgcc caggcactaa ggtccacgtg gaggaaacat	3300
gtggaacaag aggaccatct ctgagatcaa ccactgcaag cggaaggggtg atcgaggaat	3360
ggctgctgcag ggagtgcaca atgccccac tgtcgttctg ggctaaagat ggctgttgg	3420
atggaatgga gataaggccc aggaaagaac cagaaagcaa cttagtaagg tcaatgggtga	3480
ctgcaggatc aactgatcac atggatcact tctcccttgg agtgcttgtg attctgctca	3540
tggtgcagga agggctgaag aagagaatga ccacaaagat catcataagc acatcaatgg	3600
cagtgctggg agctatgatc ctgggaggat tttcaatgag tgacctggct aagcttgcaa	3660
ttttgatggg tgccaccttc gcggaaatga aactggagg agatgtagct catctggcgc	3720
tgacagcggc attcaaagtc agaccagcgt tgctggtatc tttcatcttc agagctaatt	3780
ggacaccccg tgaaagcatg ctgctggcct tggcctcgtg tcttttgcaa actgcgatct	3840
ctgccttggg aggcgacctg atggttctca tcaatggttt tgctttggcc tggttggcaa	3900
tacgagcgat ggttgttcca cgcactgaca acatcacctt ggcaatcctg gctgctctga	3960
caccactggc ccggggcaca ctgcttgtgg cgtggagagc aggccttgct acttgcgggg	4020
ggtttatgct cctctctctg aagggaaaag gcagtgtgaa gaagaactta ccatttgtca	4080
tggccctggg actaaccgct gtgaggctgg tcgaccccat caacgtgggtg ggactgctgt	4140
tgctcacaag gagtgggaag cggagctggc cccctagcga agtactcaca gctgttggcc	4200
tgatatgtgc attggctgga gggttcgcca aggcagatat agagatggct gggcccatgg	4260
ccgcggtcgg tctgctaatt gtcagttacg tggctctcagg aaagagtgtg gacatgtaca	4320
ttgaaagagc aggtgacatc acatgggaaa aagatgcgga agtcactgga aacagtcccc	4380

ggctcgacgt ggcgctagat gagagtgggtg atttctccct ggtggaggat gacgggtcccc	4440
ccatgagaga gatcatactc aaggtgggtcc tgatgaccat ctgtggcatg aaccaatag	4500
ccataccctt tgcagctgga gcgtgggtacg tatacgtgaa gactggaaaa aggagtgggtg	4560
ctctatggga tgtgcctgct cccaaggaag taaaaaaggg ggagaccaca gatggagtgt	4620
acagagtaat gactcgtaga ctgctaggtt caacacaagt tggagtggga gttatgcaag	4680
agggggtctt tcacactatg tggcacgtca caaaaggatc cgcgctgaga agcgggtgaag	4740
ggagacttga tccatactgg ggagatgtca agcaggatct ggtgtcatac tgtgggtccat	4800
ggaagctaga tgccgcctgg gacgggcaca gcgaggtgca gctcttggcc gtgcccccg	4860
gagagagagc gaggaacatc cagactctgc ccggaatatt taagacaaag gatggggaca	4920
ttggagcggg tgcgctggat taccagcag gaacttcagg atctccaatc ctagacaagt	4980
gtgggagagt gataggactt tatggcaatg gggtcgtgat caaaaatggg agttatgtta	5040
gtgccatcac ccaagggagg agggaggaag agactcctgt tgagtgtctc gagccttcga	5100
tgctgaagaa gaagcagcta actgtcttag acttgcattc tggagctggg aaaaccagga	5160
gagttcttcc tgaaatagtc cgtgaagcca taaaaacaag actccgtact gtgatcttag	5220
ctccaaccag ggttgctcgt gctgaaatgg aggaagccct tagagggctt ccagtgcgtt	5280
atatgacaac agcagtcaat gtcaccact ctggaacaga aatcgtcgac ttaatgtgcc	5340
atgccacctt cacttcacgt ctactacagc caatcagagt cccaactat aatctgtata	5400
ttatggatga ggcccacttc acagatccct caagtatagc agcaagagga tacatttcaa	5460
caagggttga gatgggagag gcggctgcca tcttcatgac cgccacgcca ccaggaaccc	5520
gtgacgcatt tccggactcc aactaccaa ttatggacac cgaagtggaa gtcccagaga	5580
gagcctggag ctgaggcttt gattgggtga cggatcattc tggaaaaaca gtttggtttg	5640
ttccaagcgt gaggaacggc aatgagatcg cagcttgtct gacaaaggct ggaaaacggg	5700
tcatacagct cagcagaaaag acttttgaga cagagttcca gaaaacaaaa catcaagagt	5760
gggactttgt cgtgacaact gacatttcag agatgggcgc caactttaaa gctgaccgtg	5820
tcatagattc caggagatgc ctaaagccgg tcatacttga tggcgagaga gtcattctgg	5880
ctggacccat gcctgtcaca catgccagcg ctgccagag gagggggcgc ataggcagga	5940
atccaataa acctggagat gagtatctgt atggaggtgg gtgcgcagag actgacgaag	6000
accatgcaca ctggcttgaa gcaagaatgc tccttgacaa tatttacctc caagatggcc	6060
tcatagcctc gctctatcga cctgaggccg acaaagtagc agccattgag ggagagttca	6120

agcttaggac	ggagcaaagg	aagacctttg	tggaactcat	gaaaagagga	gatcttcctg	6180
tttggtgctg	ctatcaggtt	gcatctgccg	gaataaccta	cacagataga	agatggtgct	6240
ttgatggcac	gaccaacaac	accataatgg	aagacagtgt	gccggcagag	gtgtggacca	6300
gacacggaga	gaaaagagt	ctcaaaccga	ggtggatgga	cgccagagtt	tggttcagatc	6360
atgcggccct	gaagtcattc	aaggagtttg	ccgctgggaa	aagaggagcg	gcttttgag	6420
tgatggaagc	cctgggaaca	ctgccaggac	acatgacaga	gagattccag	gaagccattg	6480
acaacctcgc	tgtgctcatg	cgggcagaga	ctggaagcag	gccttacaaa	gccgcggcgg	6540
cccaattgcc	ggagacccta	gagaccatta	tgcttttggg	gttgctggga	acagtctcgc	6600
tggaatctt	tttcgtcttg	atgaggaaca	agggcatagg	gaagatgggc	tttggaatgg	6660
tgactcttgg	ggccagcgca	tggctcatgt	ggctctcgga	aattgagcca	gccagaattg	6720
catgtgtcct	cattgttgtg	ttcctattgc	tggtggtgct	catacctgag	ccagaaaagc	6780
aaagatctcc	ccaggacaac	caaatggcaa	tcatcatcat	ggtagcagta	ggtcttctgg	6840
gcttgattac	cgccaatgaa	ctcggatggt	tggagagaac	aaagagtgac	ctaagccatc	6900
taatgggaag	gagagaggag	ggggcaacca	taggattctc	aatggacatt	gacctgcggc	6960
cagcctcagc	ttggggccatc	tatgctgcct	tgacaacttt	cattacccca	gccgtccaac	7020
atgcagtgac	cacttcatac	aacaactact	ccttaatggc	gatggccacg	caagctggag	7080
tggtgtttgg	tatgggcaaa	gggatgccat	tctacgcatg	ggactttgga	gtcccactgc	7140
taatgatagg	ttgctactca	caattaacac	ccctgaccct	aatagtggcc	atcattttgc	7200
tcgtggcgca	ctacatgtac	ttgatcccag	ggctgcaggc	agcagctgcg	cgtgctgccc	7260
agaagagaac	ggcagctggc	atcatgaaga	accctgttgt	ggatggaata	gtggtgactg	7320
acattgacac	aatgacaatt	gacccccaa	tggagaaaaa	gatgggacag	gtgctactca	7380
tagcagtagc	cgtctccagc	gccatactgt	cgcggaccgc	ctgggggtgg	ggggaggctg	7440
gggccctgat	cacagccgca	acttcactt	tgtgggaagg	ctctccgaac	aagtactgga	7500
actcctctac	agccacttca	ctgtgtaaca	tttttagggg	aagttacttg	gctggagctt	7560
ctctaactta	cacagtaaca	agaaacgctg	gcttgggtcaa	gagacgtggg	ggtggaacag	7620
gagagaccct	gggagagaaa	tggaaggccc	gcttgaacca	gatgtcggcc	ctggagttct	7680
actcctacaa	aaagtcaggc	atcaccgagg	tgtgcagaga	agaggcccg	cgcgccctca	7740
aggacggtgt	ggcaacggga	ggccatgctg	tgtcccagg	aagtgcaaag	ctgagatggt	7800
tggtggagcg	gggatacctg	cagccctatg	gaaaggatcat	tgatcttgga	tgtggcagag	7860

ggggctggag	ttactacgcc	gccaccatcc	gcaaagttca	agaagtgaaa	ggatacacia	7920
aaggaggccc	tggatcatgaa	gaacccgtgt	tggatgcaaag	ctatgggtgg	aacatagtcc	7980
gtcttaagag	tgggggtggac	gtctttcata	tggcggctga	gccgtgtgac	acgttgctgt	8040
gtgacatagg	tgagtcata	tctagtcttg	aagtggaga	agcacggacg	ctcagagtcc	8100
tctccatgg	gggggattgg	cttgaaaaa	gaccaggagc	ctttgtata	aaagtgtgt	8160
gccatacac	cagcactatg	atggaaaccc	tggagcgact	gcagcgtagg	tatgggggag	8220
gactggtcag	agtgcactc	tcccgcaact	ctacacatga	gatgtactgg	gtctctggag	8280
cgaaaagcaa	caccataaaa	agtgtgtcca	ccacgagcca	gctcctcttg	gggcgcatgg	8340
acgggcctag	gaggccagtg	aaatatgagg	aggatgtgaa	tctcggctct	ggcacgcggg	8400
ctgtggtgag	ctgcgctgaa	gctccaaca	tgaagatcat	tggtaaccgc	attgaaagga	8460
tccgcagtga	gcacgcggaa	acgtggttct	ttgacgagaa	ccaccatat	aggacatggg	8520
cttaccatgg	aagctatgag	gccccacac	aagggtcagc	gtcctctcta	ataaacgggg	8580
ttgtcaggct	cctgtcaaaa	ccctgggatg	tggatgactgg	agtcacagga	atagccatga	8640
ccgacaccac	accgtatgg	cagcaaagag	ttttcaagga	aaaagtggac	actaggggtgc	8700
cagaccccc	agaaggcact	cgtcagggtta	tgagcatgg	ctcttcctgg	ttgtggaaag	8760
agctaggcaa	acacaaacgg	ccacgagtct	gtaccaaaga	agagttcatc	aacaagggttc	8820
gtagcaatgc	agcattagg	gcaatatttg	aagaggaaaa	agagtggag	actgcagtgg	8880
aagctgtgaa	cgatccaagg	ttctgggctc	tagtggacaa	ggaaagagag	caccacctga	8940
gaggagagt	ccagagttgt	gtgtacaaca	tgatgggaaa	aagagaaaag	aaacaagggg	9000
aatttgga	ggccaagggc	agccgcgcca	tctggtatat	gtggctagg	gctagatttc	9060
tagagttcga	agcccttgga	ttcttgaacg	aggatcactg	gatggggaga	gagaactcag	9120
gagggtgt	tgaagggtg	ggattacaaa	gactcggata	tgtcctagaa	gagatgagtc	9180
gcataccagg	aggaaggatg	tatgcagatg	acactgctgg	ctgggacacc	cgcacagca	9240
ggtttgatct	ggagaatgaa	gctctaata	ccaaccaa	ggagaaagg	cacagggcct	9300
tggcattggc	cataatcaag	tacacatacc	aaaacaaagt	ggtaaaggtc	cttagaccag	9360
ctgaaaaagg	gaaaacagtt	atggacatta	tttcgagaca	agaccaaagg	gggagcggac	9420
aagttgtcac	ttacgtctct	aacacattta	ccaacctagt	ggtgcaactc	attcggaata	9480
tggaggctga	ggaagttcta	gagatgcaag	acttggtgg	gctgcggagg	tcagagaaag	9540
tgaccaactg	gttgacagagc	aacggatggg	ataggctcaa	acgaatggca	gtcagtggag	9600

atgattgcgt	tgtgaagcca	attgatgata	ggtttgcaca	tgccctcagg	ttcttgaatg	9660
atatgggaaa	agttaggaag	gacacacaag	agtggaaacc	ctcaactgga	tgggacaact	9720
gggaagaagt	tccgttttgc	tcccaccact	tcaacaagct	ccatctcaag	gacgggaggt	9780
ccattgtggt	tccctgccgc	caccaagatg	aactgattgg	ccgggcccgc	gtctctccag	9840
gggcgggatg	gagcatccgg	gagactgctt	gcctagcaaa	atcatatgcg	caaatgtggc	9900
agctccttta	tttccacaga	agggacctcc	gactgatggc	caatgccatt	tggtcatctg	9960
tgccagtga	ctgggttcca	actgggagaa	ctacctggtc	aatccatgga	aagggagaat	10020
ggatgaccac	tgaagacatg	cttgtgggtg	ggaacagagt	gtggattgag	gagaacgacc	10080
acatggaaga	caagacccca	gttgcgaaat	ggacagacat	tccctatttg	ggaaaaaggg	10140
aagacttggtg	gtgtggatct	ctcatagggc	acagaccgcg	caccacctgg	gctgagaaca	10200
ttaaaaacac	agtcaacatg	gtgcgcagga	tcataggtga	tgaagaaaag	tacatggact	10260
acctatccac	ccaagttcgc	tacttgggtg	aagaagggtc	tacacctgga	gtgctgtaag	10320
caccaatctt	aatgttgtca	ggcctgctag	tcagccacag	cttggggaaa	gctgtgcagc	10380
ctgtgacccc	cccaggagaa	gctgggaaac	caagcctata	gtcaggccga	gaacgccatg	10440
gcacggaaga	agccatgctg	cctgtgagcc	cctcagagga	cactgagtca	aaaaacccca	10500
cgcgcttgga	ggcgcaggat	gggaaaagaa	ggtggcgacc	ttccccaccc	ttcaatctgg	10560
ggcctgaact	ggagatcagc	tgtggatctc	cagaagaggg	actagtgggt	agaggag	10617

<210> 69

<211> 10617

<212> DNA

<213> Zika virus strain H/PF/2013 polyprotein gene, complete cds

<400> 69

agtatcaaca	ggttttat	ttt	tggattt	gga	aacgagag	tt	tctgg	tc	atg	aaaaac	cccaa	60		
aaaagaaatc	cggaggat	tc	cggatt	gt	ca	atatg	ctaaa	acgcgg	ag	ta	gcccgt	gtga	120	
gcccctttg	gggctt	gaag	aggct	gccag	ccggact	ttct	gctggg	tc	at	gggccc	atca	180		
ggatggtctt	ggcgatt	cta	gccttt	ttt	ga	gattc	ac	ggc	aatca	agcca	t	actggg	tc	240
tcatcaatag	atgggg	ttca	gtgggg	aaaa	aagagg	ctat	ggaa	ata	ata	aaga	ag	ttca	300	
agaaagatct	ggctg	ccatg	ctgaga	ataa	tcaatg	ctag	gaagg	aga	ag	aag	ac	gag	360	
gcgcagatac	tagt	gtc	gga	attgt	tg	gcc	tcctg	ct	gac	cacag	ctatg	gcagc	gag	420
tactagacg	tggg	ag	t	gca	tactat	atgt	acttg	gac	ag	aaacg	acgct	ggggag	gcca	480

tatcttttcc aaccacattg gggatgaata agtgttatat acagatcatg gatcttggac	540
acatgtgtga tgccaccatg agctatgaat gccctatgct ggatgagggg gtggaaccag	600
atgacgtcga ttgttgggtgc aacacgacgt caacttgggt tgtgtacgga acctgccatc	660
acaaaaaagg tgaagcacgg agatctagaa gagctgtgac gctcccctcc cattccacta	720
ggaagctgca aacgcgggtcg caaacctgggt tggaatcaag agaatacaca aagcacttga	780
ttagagtcga aaattggata ttcaggaacc ctggcttcgc gttagcagca gctgccatcg	840
cttggctttt gggaagctca acgagccaaa aagtcatata cttgggtcatg atactgctga	900
ttgccccggc atacagcatc aggtgcatag gagtcagcaa tagggacttt gtggaaggta	960
tgtcagggtg gacttgggtt gatgttgtct tggaaacatgg aggttgtgtc accgtaatgg	1020
cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc aacatggcgg	1080
aggtaagatc ctactgctat gaggcacaa tatcggacat ggcttcggac agccgctgcc	1140
caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc tgcaaaagaa	1200
cgttagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg agcctgggtga	1260
catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag ccagagaatc	1320
tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg atcgttaatg	1380
acacaggaca tgaaactgat gagaatagag cgaaggttga gataacgccc aattcaccaa	1440
gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa ccgaggacag	1500
gccttgactt ttcagatttg tattacttga ctatgaataa caagcactgg ttggttcaca	1560
aggagtgggt ccacgacatt ccattacctt ggcacgctgg ggcagacacc ggaactccac	1620
actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa aggcaaactg	1680
tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga gctctggagg	1740
ctgagatgga tggtgcaaag ggaaggctgt cctctggcca cttgaaatgt cgcctgaaaa	1800
tggataaact tagattgaag ggcgtgtcat actccttgtg taccgcagcg ttcacattca	1860
ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag tacgcaggga	1920
cagatggacc ttgcaagggt ccagctcaga tggcggtgga catgcaaact ctgaccccag	1980
ttgggaggtt gataaccgct aaccccgtaa tcaactgaaag cactgagaac tctaagatga	2040
tgctggaact tgatccacca tttggggact cttacattgt cataggagtc ggggagaaga	2100
agatcaccca ccaactggcac aggagtggca gcaccattgg aaaagcattt gaagccactg	2160
tgagaggtgc caagagaatg gcagtcttgg gagacacagc ctgggacttt ggatcagttg	2220

gaggcgctct caactcattg ggcaagggca tccatcaaat ttttggagca gctttcaa	2280
cattgtttgg aggaatgtcc tggttctcac aaattctcat tggaacgttg ctgatgtggt	2340
tgggtctgaa cacaagaat ggatctattt cccttatgtg cttggcctta gggggagtgt	2400
tgatcttctt atccacagct gtctctgctg atgtggggtg ctcggtggac ttctcaaaga	2460
aggagacgag atgcggtaca ggggtgttcg tctataacga cgttgaagcc tggagggaca	2520
ggtacaagta ccatcctgac tcccccgta gattggcagc agcagtcaag caagcctggg	2580
aagatggtat ctgtgggatc tcctctgttt caagaatgga aaacatcatg tggagatcag	2640
tagaagggga gctcaacgca atcctggaag agaatggagt tcaactgacg gtcgttgttg	2700
gatctgtaaa aaaccccatg tggagaggtc cacagagatt gcccgtcct gtgaacgagc	2760
tgccccacgg ctggaaggct tgggggaaat cgtacttcgt cagagcagca aagacaaata	2820
acagctttgt cgtggatggt gacacactga aggaatgcc actcaa	2880
acagctttct tgtggaggat catgggttcg gggatatttca cactagtgtc tggctcaagg	2940
ttagagaaga ttattcatta gagtgtgac cagccgttat tggaacagct gttaagggaa	3000
aggaggctgt acacagtgat ctaggctact ggattgagag tgagaagaat gacacatgga	3060
ggctgaagag ggcccatctg atcgagatga aaacatgtga atggccaaag tcccacacat	3120
tgtggacaga tggaatagaa gagagtgatc tgatcatacc caagtcttta gctgggccac	3180
tcagccatca caataccaga gagggctaca ggacccaaat gaaagggcca tggcacagtg	3240
aagagcttga aattcggttt gaggaatgcc caggcactaa ggtccacgtg gaggaaacat	3300
gtggaacaag aggaccatct ctgagatcaa ccactgcaag cggaaggggtg atcgaggaat	3360
ggctgctgcag ggagtgcaca atgccccac tgtcgttccg ggctaaagat ggctgttggt	3420
atggaatgga gataaggccc aggaaagaac cagaaagtaa cttagtaagg tcaatggtga	3480
ctgcaggatc aactgatcac atggatcact tctcccttgg agtgcttggt attctgctca	3540
tgggtgcagga agggctgaag aagagaatga ccacaaagat catcataagc acatcgatgg	3600
cagtgctggt agctatgatc ctgggaggat tttcaatgag tgacctggct aagcttgcaa	3660
ttttgatggg tgccaccttc gcggaaatga aactggagg agatgtagct catctggcgc	3720
tgatagcggc attcaaagtc agaccagcgt tgctggtatc tttcatcttc agagctaatt	3780
ggacaccccg tgaaagcatg ctgctggcct tggcctcgtg tcttttgcaa actgcgatct	3840
ccgccttgga aggcgacctg atggttctca tcaatggttt tgctttggcc tggttggcaa	3900
tacgagcgat ggttgttcca cgcactgata acatcacctt ggcaatcctg gctgctctga	3960

caccactggc	ccggggcaca	ctgcttgtgg	cgtggagagc	aggccttgct	acttgcgggg	4020
ggtttatgct	cctctctctg	aagggaaaag	gcagtgtgaa	gaagaactta	ccatttgtca	4080
tggccctggg	actaaccgct	gtgaggctgg	tcgaccccat	caacgtgggtg	ggactgctgt	4140
tgctcacaag	gagtgggaag	cggagctggc	cccctagcga	agtactcaca	gctgttgggc	4200
tgatatgcgc	attggctgga	gggttcgcca	aggcagatat	agagatggct	gggcccattg	4260
ccgcggtcgg	tctgctaatt	gtcagttacg	tggtctcagg	aaagagtgtg	gacatgtaca	4320
ttgaaagagc	aggtgacatc	acatgggaaa	aagatgcgga	agtcactgga	aacagtcccc	4380
ggctcgatgt	ggcgctagat	gagagtgggtg	atttctccct	ggtggaggat	gacgggtcccc	4440
ccatgagaga	gatacactc	aaggtgggtc	tgatgaccat	ctgtggcatg	aaccaatag	4500
ccataccctt	tgacagctga	gcgtgggtacg	tatacgtgaa	gactggaaaa	aggagtgggtg	4560
ctctatggga	tgtgcctgct	ccaaggaag	taaaaaagg	ggagaccaca	gatggagtgt	4620
acagagtaat	gactcgtaga	ctgctagggt	caacacaagt	tggagtggga	gttatgcaag	4680
agggggtctt	tcacactatg	tggcacgtca	caaaaggatc	cgcgctgaga	agcgggtgaag	4740
ggagacttga	tccatactgg	ggagatgtca	agcaggatct	ggtgtcatac	tgtgggtccat	4800
ggaagctaga	tgccgcctgg	gacgggcaca	gcgaggtgca	gctcttgggc	gtgcccccg	4860
gagagagagc	gaggaacatc	cagactctgc	ccggaatatt	taagacaaaag	gatggggaca	4920
ttggagcggg	tgcgctggat	taccagcag	gaacttcagg	atctccaatc	ctagacaagt	4980
gtgggagagt	gataggactt	tatggcaatg	gggtcgtgat	caaaaatggg	agttatgtta	5040
gtgccatcac	ccaagggagg	agggaggaag	agactcctgt	tgagtgtctc	gagccttcga	5100
tgctgaagaa	gaagcagcta	actgtcttag	acttgcattc	tggagctggg	aaaaccagga	5160
gagttcttcc	tgaaatagtc	cgtgaagcca	taaaaacaag	actccgtact	gtgatcttag	5220
ctccaaccag	ggttgctcgt	gctgaaatgg	aggaagccct	tagagggtt	ccagtgcgtt	5280
atatgacaac	agcagtcaat	gtcaccact	ctggaacaga	aatcgctcgac	ttaatgtgcc	5340
atgccacctt	cacttcacgt	ctactacagc	caatcagagt	ccccaaactat	aatctgtata	5400
ttatggatga	ggcccacttc	acagatccct	caagtatagc	agcaagagga	tacatttcaa	5460
caaggggtga	gatgggagag	gcggctgcca	tcttcatgac	cgccacgcca	ccaggaaccc	5520
gtgacgcatt	tccggactcc	aactcaccaa	ttatggacac	cgaagtggaa	gtcccagaga	5580
gagcctggag	ctcaggcttt	gattgggtga	cggatcattc	tggaaaaaca	gtttggtttg	5640
ttccaagcgt	gaggaacggc	aatgagatcg	cagcttgtct	gacaaaggct	ggaaaacggg	5700

tcatacagct	cagcagaaaag	acttttgaga	cagagttcca	gaaaacaaaa	catcaagagt	5760
gggactttgt	cgtgacaact	gacatttcag	agatgggcgc	caactttaaa	gctgaccgtg	5820
tcatagattc	caggagatgc	ctaaagccgg	tcataactga	tggcgagaga	gtcattctgg	5880
ctggacccat	gcctgtcaca	catgccagcg	ctgcccagag	gagggggcgc	ataggcagga	5940
atcccaacaa	acctggagat	gagtatctgt	atggaggtgg	gtgcgcagag	actgacgaag	6000
accatgcaca	ctggcttgaa	gcaagaatgc	tccttgacaa	tatttacctc	caagatggcc	6060
tcatagcctc	gctctatcga	cctgaggccg	acaaagtagc	agccattgag	ggagagttca	6120
agcttaggac	ggagcaaagg	aagacctttg	tggaaactcat	gaaaagagga	gatcttcctg	6180
tttggtggc	ctatcagggt	gcatctgccg	gaataaccta	cacagataga	agatggtgct	6240
ttgatggcac	gaccaacaac	accataatgg	aagacagtgt	gccggcagag	gtgtggacca	6300
gacacggaga	gaaaagagtg	ctcaaaccga	ggtggatgga	cgccagagtt	tgttcagatc	6360
atgcggccct	gaagtcattc	aaggagtttg	ccgctgggaa	aagaggagcg	gcttttggag	6420
tgatggaagc	cctgggaaca	ctgccaggac	acatgacaga	gagattccag	gaagccattg	6480
acaacctcgc	tgtgctcatg	cgggcagaga	ctggaagcag	gccttacaaa	gccgcggcgg	6540
cccaattgcc	ggagacccta	gagaccatta	tgcttttggg	gttgctggga	acagtctcgc	6600
tgggaatctt	tttcgtcttg	atgaggaaca	agggcatagg	gaagatgggc	tttggaatgg	6660
tgactcttgg	ggccagcgca	tggctcatgt	ggctctcgga	aattgagcca	gccagaattg	6720
catgtgtcct	cattgttgtg	ttcctattgc	tggtggtgct	catacctgag	ccagaaaagc	6780
aaagatctcc	ccaggacaac	caaatggcaa	tcatcatcat	ggtagcagta	ggtcttctgg	6840
gcttgattac	cgccaatgaa	ctcggatggt	tggagagaac	aaagagtgac	ctaagccatc	6900
taatgggaag	gagagaggag	ggggcaacca	taggattctc	aatggacatt	gacctgcggc	6960
cagcctcagc	ttgggccatc	tatgctgcct	tgacaacttt	cattacccca	gccgtccaac	7020
atgcagtgac	cacttcatac	aacaactact	ccttaatggc	gatggccacg	caagctggag	7080
tgttgtttgg	tatgggcaaa	gggatgccat	tctacgcatg	ggactttgga	gtcccgtgc	7140
taatgatagg	ttgctactca	caattaacac	ccctgaccct	aatagtggcc	atcattttgc	7200
tcgtggcgca	ctacatgtac	ttgatcccag	ggctgcaggc	agcagctgcg	cgtgctgccc	7260
agaagagaac	ggcagctggc	atcatgaaga	accctgttgt	ggatggaata	gtggtgactg	7320
acattgacac	aatgacaatt	gacccccaa	tggagaaaaa	gatgggacag	gtgctactca	7380
tagcagtagc	cgtctccagc	gccatactgt	cgcggaccgc	ctgggggtgg	ggggaggctg	7440

gggccctgat	cacagcggca	acttcactt	tgtgggaagg	ctctccgaac	aagtactgga	7500
actcctctac	agccacttca	ctgtgtaaca	tttttagggg	aagttacttg	gctggagctt	7560
ctctaatacta	cacagtaaca	agaaacgctg	gcttggtcaa	gagacgtggg	ggtggaacag	7620
gagagaccct	gggagagaaa	tggaaggccc	gcttgaacca	gatgtcggcc	ctggagttct	7680
actcctacaa	aaagtcaggc	atcaccgagg	tgtgcagaga	agaggcccg	cgcgccctca	7740
aggacggtgt	ggcaacggga	ggccatgctg	tgtcccgagg	aagtgcaaag	ctgagatggt	7800
tggtggagcg	gggatacctg	cagccctatg	gaaagggtcat	tgatcttgga	tgtggcagag	7860
ggggctggag	ttactacgcc	gccaccatcc	gcaaagttca	agaagtgaaa	ggatacacia	7920
aaggaggccc	tggtcatgaa	gaacccatgt	tggtgcaaag	ctatgggtgg	aacatagtcc	7980
gtcttaagag	tgggggtggac	gtctttcata	tggcggctga	gccgtgtgac	acgttgctgt	8040
gtgacatagg	tgagtcatca	tctagtcctg	aagtggaaga	agcacggacg	ctcagagtcc	8100
tctccatggt	gggggattgg	cttgaaaaaa	gaccaggagc	cttttgtata	aaagtgttgt	8160
gcccatacac	cagcactatg	atggaaaccc	tggagcgact	gcagcgtagg	tatgggggag	8220
gactggtcag	agtgccactc	tcccgcaact	ctacacatga	gatgtactgg	gtctctggag	8280
cgaaaagcaa	caccataaaa	agtgtgtcca	ccacgagcca	gctcctcttg	gggcgcatgg	8340
acgggcccag	gaggccagtg	aaatatgagg	aggatgtgaa	tctcggctct	ggcacgcggg	8400
ctgtggtgaa	ctgcgctgaa	gctcccaaca	tgaagatcat	tggtaacccg	attgaaagga	8460
tccgcagtga	gcacgcggaa	acgtggttct	ttgacgagaa	ccaccatat	aggacatggg	8520
cttaccatgg	aagctatgag	gccccacac	aagggtcagc	gtcctctcta	ataaacgggg	8580
ttgtcaggct	cctgtcaaaa	ccctgggatg	tggtgactgg	agtcacagga	atagccatga	8640
ccgacaccac	accgtatggt	cagcaaagag	ttttcaagga	aaaagtggac	actaggggtgc	8700
cagaccccc	agaaggcact	cgtcagggtta	tgagcatggt	ctcttcctgg	ttgtggaaa	8760
agctaggcaa	acacaaacgg	ccacgagtct	gtaccaaaga	agagttcatc	aacaagggttc	8820
gtagcaatgc	agcattaggg	gcaatatttg	aagaggaaaa	agagtgggag	actgcagtgg	8880
aagctgtgaa	cgatccaagg	ttctgggctc	tagtggacaa	ggaaagagag	caccacctga	8940
gaggagagtg	ccagagttgt	gtgtacaaca	tgatgggaaa	aagagaaaag	aaacaagggg	9000
aatttgga	ggccaagggc	agccgcgcca	tctggtatat	gtggctaggg	gctagatttc	9060
tagagttcga	agcccttgga	ttcttgaacg	aggatcactg	gatggggaga	gagaactcag	9120
gagggtggtg	tgaagggctg	ggattacaaa	gactcggata	tgtcctagaa	gagatgagtc	9180

gcataccagg	aggaaggatg	tatgcagatg	acactgctgg	ctgggacacc	cgcatcagca	9240
ggtttgatct	ggagaatgaa	gctctaata	ccaaccaa	ggagaaaggg	cacagggcct	9300
tggcattggc	cataatcaag	tacacatacc	aaaacaaagt	ggtaaagggtc	cttagaccag	9360
ctgaaaaagg	gaagacagtt	atggacatta	tttcgagaca	agaccaaagg	gggagcggac	9420
aagttgtcac	ttacgctctt	aacacattta	ccaacctagt	ggtgcaactc	attcgggaata	9480
tggaggctga	ggaagttcta	gagatgcaag	acttggtggct	gctgcggagg	tcagagaaag	9540
tgaccaactg	gttgcagagc	aacggatggg	ataggctcaa	acgaatggca	gtcagtggag	9600
atgattgcgt	tgtgaagcca	attgatgata	ggtttgcaca	tgccctcagg	ttcttgaatg	9660
atatgggaaa	agttaggaag	gacacacaag	agtggaaacc	ctcaactgga	tgggacaact	9720
gggaagaagt	tccgttttgc	tcccaccact	tcaacaagct	ccatctcaag	gacgggaggt	9780
ccattgtggt	tccctgccgc	caccaagatg	aactgattgg	ccgggcccg	gtctctccag	9840
gggcgggatg	gagcatccgg	gagactgctt	gcctagcaaa	atcatatgcg	caaagtggc	9900
agctccttta	tttccacaga	agggacctcc	gactgatggc	caatgccatt	tgttcatctg	9960
tgccagtga	ctgggttcca	actgggagaa	ctacctggtc	aatccatgga	aaggggagaat	10020
ggatgaccac	tgaagacatg	cttgtggtgt	ggaacagagt	gtggattgag	gagaacgacc	10080
acatggaaga	caagacccca	gttacgaaat	ggacagacat	tccctatttg	ggaaaaaggg	10140
aagacttggtg	gtgtggatct	ctcatagggc	acagaccg	caccacctgg	gctgagaaca	10200
ttaaaaacac	agtcaacatg	gtgcgcagga	tcataggtga	tgaagaaaag	tacatggact	10260
acctatccac	ccaagttcgc	tacttgggtg	aagaagggtc	tacacctgga	gtgctgtaag	10320
caccaatctt	agtgttgtca	ggcctgctag	tcagccacag	cttggggaaa	gctgtgcagc	10380
ctgtgacccc	cccaggagaa	gctgggaaac	caagcctata	gtcaggccga	gaacgccatg	10440
gcacggaaga	agccatgctg	cctgtgagcc	cctcagagga	caactgagtc	aaaaacccca	10500
cgcgcttgga	ggcgcaggat	gggaaaagaa	ggtggcgacc	ttccccaccc	ttcaatctgg	10560
ggcctgaact	ggagatcagc	tgtggatctc	cagaagaggg	actagtgggt	agaggag	10617

<210> 70

<211> 10766

<212> DNA

<213> Zika virus strain MR 766 polyprotein gene, complete cds

<400> 70

gatctgtgtg	agtcagactg	cgacagttcg	agtctgaagc	gagagctaac	aacagtatca	60
------------	------------	------------	------------	------------	------------	----

acaggtttaa	tttggatttg	gaaacgagag	tttctggtca	tgaaaaaccc	aaagaagaaa	120
------------	------------	------------	------------	------------	------------	-----

tccggaggat tccggattgt caatatgcta aaacgcggag tagcccgtgt aaacccttg	180
ggaggtttga agaggttgcc agccggactt ctgctgggtc atggacccat cagaatggtt	240
ttggcgatac tagccttttt gagatttaca gcaatcaagc catcactggg cttatcaac	300
agatgggggtt ccgtggggaa aaaagaggct atggaaataa taaagaagtt caagaaagat	360
cttgctgcca tgttgagaat aatcaatgct aggaaagaga ggaagagacg tggcgagac	420
accagcatcg gaatcattgg ctcctgctg actacagcca tggcagcaga gatcactaga	480
cgcgggagtg catactacat gtacttgat aggagcgatg ccgggaaggc catttcgttt	540
gctaccacat tgggagtga caagtgccac gtacagatca tggacctcg gcacatgtgt	600
gacgccacca tgagttatga gtgccctatg ctggatgagg gagtggaacc agatgatgtc	660
gattgctggg gcaacacgac atcaacttgg gttgtgtacg gaacctgtca tcacaaaaa	720
ggtgaggcac ggcgatctag aagagccgtg acgctccctt ctactctac aaggaagttg	780
caaacgcggt cgcagacctg gttagaatca agagaataca cgaagcactt gatcaaggtt	840
gaaaactgga tattcaggaa ccccggttt gcgctagtgg ccgttgccat tgcttggtt	900
ttgggaagct cgacgagcca aaaagtcata tacttgggtca tgatactgct gattgccccg	960
gcatacagta tcaggtgcat tggagtcagc aatagagact tcgtggaggg catgtcaggt	1020
gggacctggg ttgatgttgt cttggaacat ggaggctgcg ttaccgtgat ggcacaggac	1080
aagccaacag ttgacataga gttggtcacg acgacggtta gtaacatggc cgaggtaaga	1140
tcctattgct acgaggcatc gatatcggac atggcttcgg acagtcgttg cccaacacaa	1200
ggtgaagcct accttgacaa gcaatcagac actcaatatg tctgcaaaag aacattagt	1260
gacagagggtt ggggaaacgg ttgtggactt tttggcaaag ggagcttggg gacatgtgcc	1320
aagtttacgt gttctaagaa gatgaccggg aagagcattc aaccggaaaa tctggagtat	1380
cggataatgc tatcagtgca tggctcccag catagcggga tgattgtcaa tgatacagga	1440
tatgaaactg acgaaaatag agcgaaagtc gaggttacgc ctaattcacc aagagcggaa	1500
gcaaccttgg gaggttttgg aagcttagga cttgactgtg aaccaaggac aggccttgac	1560
ttttcagatc tgtattacct gaccatgaac aataagcatt ggttggtgca caaagagtgg	1620
tttcatgaca tcccattgcc ttggcatgct ggggcagaca ccggaactcc aactggaac	1680
aacaaagagg cattggtaga attcaaggat gccacgcca agaggcaaac cgtcgtcgtt	1740
ctggggagcc aggaaggagc cgttcacacg gctctcgctg gagctctaga ggctgagatg	1800
gatggtgcaa agggaaagct gttctctggc catttgaaat gccgcctaaa aatggacaag	1860

cttagattga agggcgtgtc atattccttg tgcactgcgg cattcacatt caccaaggtc	1920
ccagctgaaa cactgcatgg aacagtcaca gtggaggtgc agtatgcagg gacagatgga	1980
ccctgcaaga tcccagtcca gatggcggtg gacatgcaga ccctgacccc agttggaagg	2040
ctgataaccg ccaaccccggt gattactgaa agcactgaga actcaaagat gatgttgagg	2100
cttgaccac catttgggga ttcttacatt gtcataggag ttggggacaa gaaaatcacc	2160
caccactggc ataggagtgg tagcaccatc ggaaaggcat ttgaggccac tgtgagaggc	2220
gccaagagaa tggcagtcct gggggataca gcctgggact tcggatcagt cgggggtgtg	2280
ttcaactcac tgggtaagggt cattcaccag attttttgag cagccttcaa atcactgttt	2340
ggaggaatgt cctggttctc acagatcctc ataggcacgc tgctagtgtg gttaggtttg	2400
aacacaaaga atggatctat ctccctcaca tgcttgccc tggggggagt gatgatcttc	2460
ctctccacgg ctgtttctgc tgacgtgggg tgctcagtgg acttctcaa aaaggaaacg	2520
agatgtggca cgggggtatt catctataat gatgttgaag cctggaggga ccgtacaag	2580
taccatcctg actcccccg cagattggca gcagcagtca agcaggcctg ggaagagggg	2640
atctgtggga tctcatccgt ttcaagaatg gaaaacatca tgtggaaatc agtagaaggg	2700
gagctcaatg ctatcctaga ggagaatgga gttcaactga cagttgttgt gggatctgta	2760
aaaaaccca tgtggagagg tccacaaaga ttgccagtgc ctgtgaatga gctgccccat	2820
ggctggaaag cctgggggaa atcgtatttt gttagggcgg caaagaccaa caacagtttt	2880
gttgtcgacg gtgacacact gaaggaatgt ccgcttgagc acagagcatg gaatagtttt	2940
cttgtggagg atcacgggtt tggagtcttc cacaccagtg tctggcttaa ggtcagagaa	3000
gattactcat tagaatgtga ccagccgtc ataggaacag ctgttaaggg aagggaggcc	3060
gcgcacagtg atctgggcta ttggattgaa agtgaaaaga atgacacatg gaggctgaag	3120
agggccacc tgattgagat gaaaacatgt gaatggccaa agtctcacac attgtggaca	3180
gatggagtag aagaaagtga tcttatcata cccaagtctt tagctgggtcc actcagccac	3240
cacaacacca gagaggggta cagaaccaa gtgaaagggc catggcacag tgaagagctt	3300
gaaatccggt ttgaggaatg tccaggcacc aaggtttacg tggaggagac atgcggaact	3360
agaggacat ctctgagatc aactactgca agtggaaggg tcattgagga atggtgctgt	3420
agggaatgca caatgcccc actatcgttt cgagcaaaag acggctgctg gtatggaatg	3480
gagataaggc ccaggaaaga accagagagc aacttagtga ggtcaatggt gacagcgggg	3540
tcaaccgatc atatggacca cttctctctt ggagtgcctg tgattctact catggtgcag	3600

gaggggttga	agaagagaat	gaccacaaag	atcatcatga	gcacatcaat	ggcagtgctg	3660
gtagtcatga	tcttgggagg	atthttcaatg	agtgcactgg	ccaagcttgt	gatcctgatg	3720
ggtgctactt	tcgcagaaat	gaacactgga	ggagatgtag	ctcacttggc	attggtagcg	3780
gcatttaaag	tcagaccagc	cttgctggtc	tccttcattt	tcagagccaa	ttggacaccc	3840
cgtgagagca	tgctgctagc	cctggcttcg	tgtcttctgc	aaactgcat	ctctgctctt	3900
gaaggtagct	tgatggctct	cattaatgga	tttgctttgg	cctgggttggc	aattcgagca	3960
atggccgtgc	cacgcactga	caacatcgct	ctaccaatct	tggctgctct	aacaccacta	4020
gctcgaggca	cactgctcgt	ggcatggaga	gcgggcctgg	ctacttgtgg	agggatcatg	4080
ctcctctccc	tgaaggggaa	aggtagtgtg	aagaagaacc	tgccatttgt	catggccctg	4140
ggattgacag	ctgtgagggg	agtagaccct	attaatgtgg	taggactact	gttactcaca	4200
aggagtggga	agcggagctg	gccccctagt	gaagttctca	cagccgttgg	cctgatatgt	4260
gcactggccg	gagggtttgc	caaggcagac	attgagatgg	ctggacccat	ggctgcagta	4320
ggcttgctaa	ttgtcagcta	tgtggtctcg	ggaaagagtg	tggacatgta	cattgaaaga	4380
gcaggtgaca	tcacatggga	aaaggacgcg	gaagtcactg	gaaacagtcc	tcggcttgac	4440
gtggcactgg	atgagagtgg	tgatttctcc	ttggtagagg	aagatgggtcc	acctatgaga	4500
gagatcatac	tcaaggtggg	cctgatggcc	atctgtggca	tgaaccaat	agctatacct	4560
tttgctgcag	gagcgtggta	tgtgtatgtg	aagactggga	aaaggagtgg	cgccctctgg	4620
gacgtgcctg	ctcccaaaga	agtgaagaaa	ggagagacca	cagatggagt	gtacagagtg	4680
atgactcgca	gactgctagg	ttcaacacag	gttggagtgg	gagtcatgca	agagggagtc	4740
ttccacacca	tgtggcacgt	tacaaaagga	gccgcactga	ggagcgggtga	gggaagactt	4800
gatccatact	gggggggatgt	caagcaggac	ttgggtgtcat	actgtggggc	ttggaagttg	4860
gatgcagctt	gggatggact	cagcgaggta	cagcttttgg	ccgtacctcc	cggagagagg	4920
gccagaaaca	ttcagaccct	gcctggaata	ttcaagacaa	aggacgggga	catcgagaca	4980
gttgctctgg	actaccctgc	agggacctca	ggatctccga	tcctagacaa	atgtggaaga	5040
gtgataggac	tctatggcaa	tggggttgtg	atcaagaatg	gaagctatgt	tagtgctata	5100
accaggggaa	agagggagga	ggagactccg	gttgaatgtt	tcgaaccctc	gatgctgaag	5160
aagaagcagc	taactgtctt	ggatctgcat	ccaggagccg	gaaaaaccag	gagagttctt	5220
cctgaaatag	tccgtgaagc	cataaaaaag	agactccgga	cagtgatctt	ggcaccaact	5280
agggttgtcg	ctgctgagat	ggaggaggcc	ttgagaggac	ttccggtgcg	ttacatgaca	5340

acagcagtca	acgtcaccca	ttctgggaca	gaaatcgttg	atttgatgtg	ccatgccact	5400
ttcacttcac	gcttactaca	acccatcaga	gtccctaatt	acaatctcta	catcatggat	5460
gaagcccact	tcacagaccc	ctcaagtata	gctgcaagag	gatacatatc	aacaaggggt	5520
gaaatgggcg	aggcggctgc	catttttatg	actgccacac	caccaggaac	ccgtgatgcg	5580
tttctgact	ctaactcacc	aatcatggac	acagaagtgg	aagtcccaga	gagagcctgg	5640
agctcaggct	ttgattgggt	gacagaccat	tctgggaaaa	cagtttggtt	cgttccaagc	5700
gtgagaaacg	gaaatgaaat	cgcagcctgt	ctgacaaagg	ctggaaagcg	ggtcatacag	5760
ctcagcagga	agacttttga	gacagaattt	cagaaaacaa	aaaatcaaga	gtgggacttt	5820
gtcataaaca	ctgacatctc	agagatgggc	gccaaacttca	aggctgaccg	ggtcatagac	5880
tctaggagat	gcctaaaacc	agtcatactt	gatggtgaga	gagtcatctt	ggctggggccc	5940
atgcctgtca	cgcatgctag	tgctgctcag	aggagaggac	gtataggcag	gaaccctaac	6000
aaacctggag	atgagtacat	gtatggaggt	gggtgtgcag	agactgatga	aggccatgca	6060
cactggcttg	aagcaagaat	gcttcttgac	aacatctacc	tccaggatgg	cctcatagcc	6120
tcgctctatc	ggcctgaggc	cgataaggta	gccgccattg	agggagagtt	taagctgagg	6180
acagagcaaa	ggaagacctt	cgtggaactc	atgaagagag	gagaccttcc	cgtctggcta	6240
gcctatcagg	ttgcatctgc	cggaataact	tacacagaca	gaagatgggtg	ctttgatggc	6300
acaaccaaca	acaccataat	ggaagacagc	gtaccagcag	agggtgtggac	aaagtatgga	6360
gagaagagag	tgctcaaacc	gagatggatg	gatgctaggg	tctgttcaga	ccatgcggcc	6420
ctgaagtcgt	tcaaagaatt	cgccgctgga	aaaagaggag	cggctttggg	agtaatggag	6480
gccctgggaa	cactgccagg	acacatgaca	gagaggtttc	aggaagccat	tgacaacctc	6540
gccgtgctca	tgcgagcaga	gactggaagc	aggccttata	aggcagcggc	agcccaactg	6600
ccggagaccc	tagagaccat	tatgctctta	ggtttgctgg	gaacagtttc	actggggatc	6660
ttcttcgtct	tgatgcggaa	taagggcatc	gggaagatgg	gctttggaat	ggtaaccctt	6720
ggggccagtg	catggctcat	gtggctttcg	gaaattgaac	cagccagaat	tgcatgtgtc	6780
ctcattgttg	tgtttttatt	actggtgggtg	ctcatacccg	agccagagaa	gcaaagatct	6840
ccccaagata	accagatggc	aattatcatc	atggtggcag	tgggccttct	aggtttgata	6900
actgcaaacg	aacttggatg	gctggaaaga	acaaaaaatg	acatagctca	tctaattgga	6960
aggagagaag	aaggagcaac	catgggattc	tcaatggaca	ttgatctgcg	gccagcctcc	7020
gcctgggcta	tctatgccgc	attgacaact	ctcatcaccc	cagctgtcca	acatgcggta	7080

accacttcat	acaacaacta	ctccttaatg	gcgatggcca	cacaagctgg	agtgctgttt	7140
ggcatgggca	aagggatgcc	attttatgca	tgggaccttg	gagtcccgct	gctaattgatg	7200
ggttgctatt	cacaattaac	acccttgact	ctgatagtag	ctatcattct	gcttggtggcg	7260
cactacatgt	acttgatccc	aggcctacaa	gcggcagcag	cgcgtgctgc	ccagaaaagg	7320
acagcagctg	gcattcatgaa	gaatcccgtt	gtggatggaa	tagtggtaac	tgacattgac	7380
acaatgacaa	tagaccccca	ggtggagaag	aagatgggac	aagtgttact	catagcagta	7440
gccatctcca	gtgctgtgct	gctgcggaac	gcctggggat	ggggggaggc	tggagctctg	7500
atcacagcag	cgacctccac	cttgtgggaa	ggctctccaa	aaaataactg	gaactcctct	7560
acagccacct	cactgtgcaa	catcttcaga	ggaagctatc	tggcaggagc	ttcccttadc	7620
tatacagtga	cgagaaacgc	tggcctgggt	aagagacgtg	gaggtgggac	gggagagact	7680
ctgggagaga	agtggaagc	tcgtctgaat	cagatgtcgg	ccctggagtt	ctactcttat	7740
aaaaagtcag	gtatcactga	agtggttaga	gaggaggctc	gccgtgccct	caaggatgga	7800
gtggccacag	gaggacatgc	cgtatcccg	ggaagtgcaa	agctcagatg	gttggtggag	7860
agaggatadc	tgcagcccta	tgggaagggt	gttgacctcg	gatgtggcag	agggggctgg	7920
agctattatg	ccgccaccat	ccgcaaagt	caggaggtga	gaggatacac	aaaggagggt	7980
cccgtcatg	aagaacccat	gctggtgcaa	agctatgggt	ggaacatagt	tcgtctcaag	8040
agtgagtggt	acgtcttcca	catggcggt	gagccgtgtg	acactctgct	gtgtgacata	8100
ggtgagtcat	catctagtcc	tgaagtggaa	gagacacgaa	cactcagagt	gctctctatg	8160
gtgggggact	ggcttgaaaa	aagaccagg	gccttctgta	taaagggtgct	gtgccatac	8220
accagcacta	tgatggaaac	catggagcga	ctgcaacgta	ggcatggggg	aggattagtc	8280
agagtgccat	tgtctcgcaa	ctccacacat	gagatgtact	gggtctctgg	ggcaaagagc	8340
aacatcataa	aaagtgtgtc	caccacaagt	cagctcctcc	tgggacgcac	ggatggcccc	8400
aggaggccag	tgaaatatga	ggaggatgtg	aacctcggct	cgggtacacg	agctgtggca	8460
agctgtgctg	aggctcctaa	catgaaaatc	atcggcaggc	gcattgagag	aatccgcaat	8520
gaacatgcag	aaacatgggt	tcttgatgaa	aaccacccat	acaggacatg	ggcctaccat	8580
gggagctacg	aagccccac	gcaaggatca	gcgtcttccc	tcgtgaacgg	ggttggttaga	8640
ctcctgtcaa	agccttggga	cgtggtgact	ggagttacag	gaatagccat	gactgacacc	8700
acaccatacg	gccaacaaag	agtcttcaaa	gaaaaagtgg	acaccagggt	gccagatccc	8760
caagaaggca	ctcgccagg	aatgaacata	gtctcttcct	ggctgtggaa	ggagctgggg	8820

aaacgcaagc	ggccacgcgt	ctgcaccaaa	gaagagttta	tcaacaaggt	gcgagcaat	8880
gcagcactgg	gagcaatatt	tgaagaggaa	aaagaatgga	agacggctgt	ggaagctgtg	8940
aatgatccaa	ggttttgggc	cctagtggat	agggagagag	aacaccacct	gagaggagag	9000
tgtcacagct	gtgtgtacaa	catgatggga	aaaagagaaa	agaagcaagg	agagtctggg	9060
aaagcaaaaag	gtagccgcgc	catctggtac	atgtggttgg	gagccagatt	cttgagttt	9120
gaagcccttg	gattcttgaa	cgaggaccat	tggatgggaa	gagaaaactc	aggaggtgga	9180
gtcgaagggt	taggattgca	aagacttgga	tacattctag	aagaaatgaa	tcgggcacca	9240
ggaggaaaga	tgtacgcaga	tgacactgct	ggctgggaca	cccgcattag	taagtttgat	9300
ctggagaatg	aagctctgat	taccaaccaa	atggaggaag	ggcacagaac	tctggcgttg	9360
gccgtgatta	aatacacata	ccaaaacaaa	gtggtgaagg	ttctcagacc	agctgaagga	9420
ggaaaaacag	ttatggacat	catttcaaga	caagaccaga	gagggagtgg	acaagttgtc	9480
acttatgctc	tcaacacatt	caccaacttg	gtggtgcagc	ttatccggaa	catggaagct	9540
gaggaagtgt	tagagatgca	agacttatgg	ttgttgagga	agccagagaa	agtgaccaga	9600
tggttgacga	gcaatggatg	ggatagactc	aaacgaatgg	cggtcagtgg	agatgactgc	9660
gttgtgaagc	caatcgatga	taggtttgca	catgccctca	ggttcttgaa	tgacatggga	9720
aaagttagga	aagacacaca	ggagtggaaa	ccctcgactg	gatggagcaa	ttgggaagaa	9780
gtcccgttct	gctcccacca	cttcaacaag	ctgtacctca	aggatgggag	atccattgtg	9840
gtcccttgcc	gccaccaaga	tgaactgatt	ggccgagctc	gcgtctcacc	aggggcagga	9900
tggagcatcc	gggagactgc	ctgtcttgca	aaatcatatg	cgcagatgtg	gcagctcctt	9960
tatttccaca	gaagagacct	tcgactgatg	gctaattgcca	tttgctcggc	tgtgccagtt	10020
gactgggtac	caactgggag	aaccacctgg	tcaatccatg	gaaagggaga	atggatgacc	10080
actgaggaca	tgctcatggt	gtggaataga	gtgtggattg	aggagaacga	ccatatggag	10140
gacaagactc	ctgtaacaaa	atggacagac	attccctatc	taggaaaaag	ggaggactta	10200
tggtgtggat	cccttatagg	gcacagaccc	cgcaccactt	gggctgaaaa	catcaaagac	10260
acagtcaaca	tggtgcgcag	gatcataggt	gatgaagaaa	agtacatgga	ctatctatcc	10320
acccaagtcc	gctacttggg	tgaggaaggg	tccacacccg	gagtgttgta	agcaccaatt	10380
ttagtggtgt	caggcctgct	agtcagccac	agtttgggga	aagctgtgca	gcctgtaacc	10440
cccccaggag	aagctgggaa	accaagctca	tagtcaggcc	gagaacgcca	tggcacggaa	10500
gaagccatgc	tgctgtgag	cccctcagag	gacactgagt	caaaaaaccc	cacgcgcttg	10560

gaagcgcagg atgggaaaag aaggtggcga ccttccccac cttcaatct ggggcctgaa	10620
ctggagacta gctgtgaatc tccagcagag ggactagtgg ttagaggaga ccccccgaa	10680
aacgcacaac agcatattga cgctgggaaa gaccagagac tccatgagtt tccaccacgc	10740
tggccgccag gcacagatcg ccgaac	10766

<210> 71

<211> 10272

<212> DNA

<213> Zika virus strain 8375 polyprotein gene, complete cds

<400> 71

atgaaaaacc caaaaaagaa atccggagga ttccggattg tcaatatgct aaaacgcgga	60
gtagcccgctg tgagcccctt tgggggcttg aagaggctgc cagccggact tctgctgggt	120
catgggcca tcaggatggt cttggcgatt ctgaccttt tgagattcac ggcaatcaag	180
ccatcactgg gtctcatcaa tagatggggg tcaagtggga aaaaagaggc tatggaaata	240
ataaagaagt tcaagaaaga tctggctgcc atgctgagaa taatcaatgc taggaaggag	300
aagaagagac gaggcgcaga tactagtgtc ggaattgttg gcctcctgct gaccacagct	360
atggcagcgg aggtcactag acgtgggagt gcatactata tgtacttgga cagaaacgat	420
gctggggagg ccatatcttt tccaaccaca ttggggatga ataagtgtta tatacagatc	480
atggatcttg gacacatgtg tgatgccacc atgagctatg aatgccctat gctggatgag	540
ggggtggaac cagatgacgt cgattgttgg tgcaacacga cgtcaacttg ggttgtgtac	600
ggaacctgcc atcacaaaaa aggtgaagca cggagatcta gaagagctgt gacgctcccc	660
tcccattcca ctaggaagct gcaaacgcgg tcgcaaacct ggttggaatc aagagaatac	720
acaaagcact tgattagagt cgaaaattgg atattcagga accctggctt cgcgttagca	780
gcagctgcca tcgcttggtt tttgggaagc tcaacgagcc aaaaagtc atacttggtc	840
atgatactgc tgattgcccc ggcatacagc atcaggtgca taggagtcag caatagggac	900
tttgtggaag gtatgtcagg tgggacttgg gttgatgttg tcttggaaca tggaggttgt	960
gtcaccgtaa tggcacagga caaacgact gtcgacatag agctggttac aacaacagtc	1020
agcaacatgg cggagataag atcctactgc tatgaggcat caatatcaga catggcttcg	1080
gacagccgct gcccaacaca aggtgaagcc taccttgaca agcaatcaga cactcaatat	1140
gtctgcaaaa gaacgttagt ggacagaggc tggggaaatg gatgtggact ttttggcaaa	1200
gggagcctgg tgacatgcgc taagtttgca tgctccaaga aatgaccgg gaagagcatc	1260

cagccagaga atctggagta ccggataatg ctgtcagttc atggctccca gcacagtggg	1320
atgatcgтта atgacacagg acatgaaact gatgagaata gagcgaaggt tgagataacg	1380
ccaattcac caagagccga agccaccctg ggggggttttg gaagcctagg acttgattgt	1440
gaaccgagga caggccttga cttttcagat ttgtattact tgactatgaa taacaagcac	1500
tggttggttc acaaggagtг gttccacgac attccattac cttggcacgc tggggcagac	1560
accggaactc cacactggaa caacaaagaa gcactgggtg agttcaagga cgcacatgcc	1620
aaaaggcaaa ctgtcgtggт tctagggagt caagaaggag cagttcacac ggccttgct	1680
ggagctctgg aggctgagat ggatggтgca aagggaaggc tgtcctctgg ccacttgaaa	1740
tgtcgctga aaatggataa acttagattg aagggcgtgt catactcctt gtgtaccgca	1800
gcgttcacat tcaccaagat cccggctgaa acactgcacg ggacagtcac agtgгaggta	1860
cagtacgcag ggacagatgg accttgcaag gttccagctc agatggcggt ggacatgcaa	1920
actctgaccc cagttgggag gttgataacc gctaaccccг таатсactga aagcactgag	1980
aactctaaga tgatgctgga acttgatcca ccatttgggg actcttacat tgtcatagga	2040
gtcggggaga agaagatcac ccaccactgg cacaggagtг gcagcaccat tggaaaagca	2100
tttgaagcca ctgtgagagg tgccaagaga atggcagtct tgggagacac agcctgggac	2160
tttggatcag ttggaggcgc tctcaactca ttgggcaagg gcatccatca aatttttgga	2220
gctgctttca aatcattgtt tggaggaatg tcctggttct cacaaattct cattggaacg	2280
ttgctgatgt ggttgggtct gaacacaaag aatggatcta tttcccttat gtgcttgгcc	2340
ttagggggag tgttgatctt cttatccaca gccgtctctг ctgatgtggg gtgctcggtг	2400
gacttctcaa agaaggagac gagatgcggt acaggggtgt tcgtctataa cgacgttgaa	2460
gcctggaggг acaggtacaa gtaccatcct gactcccccc gtagattggc agcagcagtc	2520
aagcaagcct gggagatgg tatctgcggg atctcctctг tttcaagaat ggaaaacatc	2580
atgtggagat cagtagaagg ggagctcaac gcaatcctgg aagagaatgg agttcaactг	2640
acggtcgttg tgggatctgt aaaaaacccc atgtggagag ctccacagag attgcccgtг	2700
cctgtgaacг agctgccccа cggtggaag gcttggggga aatcgtactt cgtcagagca	2760
gcaaagacaa атаacagctt tgtcgtggat ggtgacacac tgaaggaatг ccactcaaa	2820
catagagcat ggaacagctt tcttgтggag gatcatgggt tcggggтatt tcacactagt	2880
gtctggctca aggttagaga agattattca ttagagtgtг atccagccgt tattggaaca	2940
gctgttaagg gaaaggaggc tgtacacagt gatctaggct actggattga gagtгagaag	3000

aatgacacat ggaggctgaa gagggcccat ctgatcgaga tgaaaacatg tgaatggcca	3060
aagtcacaca cattgtggac agatggaata gaagagagt atctgatcat acccaagtct	3120
ttagctgggc cactcagcca tcacaatacc agagagggct acaggaccca aatgaaaggg	3180
ccatggcaca gtgaagagct tgaaattcgg tttgaggaat gcccaggcac taaggtccac	3240
gtggaggaaa catgtggaac aagaggacca tctctgagat caaccactgc aagcggaagg	3300
gtgatcgagg aatgggtgctg cagggagtgc acaatgcccc cactgtcggt ccgggctaaa	3360
gatggctgtt ggtatggaat ggagataagg cccaggaaag aaccagaaag caacttagta	3420
aggtcaatgg tgactgcagg atcaactgat cacatggatc acttctccct tggagtgtt	3480
gtgattctgc tcatgggtgca ggaagggcta aagaagagaa tgaccacaaa gatcatcata	3540
agcacatcaa tggcagtgtt ggtagctatg atcctgggag gatcttcaat gagtgacctg	3600
gctaagcttg caatcttgat ggggtgccacc ttcgcggaaa tgaacactgg aggagatgta	3660
gctcatctgg cgctgatagc ggcatcaca gtcagaccag cgttgctgggt atctttcatc	3720
ttcagagcta attggacacc ccgtgaaagc atgctactgg ccttggcctc gtgtcttttg	3780
caaactgcga tctccgcctt ggaaggcgac ctgatggttc tcatcaatgg ttttgctttg	3840
gcctggttgg caatacgagc gatggttgtt ccacgcactg ataacatcac cttggcaatc	3900
ctggctgctc tgacaccact ggcccggggc aactgcttg tggcgtggag agcaggcctt	3960
gctacttgcg gggggtttat gtcctctct ctgaagggaa aaggcagtgt gaagaagaac	4020
ttaccatttg tcatggccct gggactaacc gctgtgaggc tggctgaccc catcaacgtg	4080
gtgggactgc tgttgctcac aaggagtggg aagcggagct ggccccctag cgaagtactc	4140
acagctgttg gcctgatatg cgcattggct ggaggggttcg ccaaggcaga tatagagatg	4200
gctgggcca tggccgcggt cggctctgcta attgtcagtt acgtggcttc aggaaagagt	4260
gtggacatgt acattgaaag agcaggtgac atcacatggg aaaaagatgc ggaagtcact	4320
ggaaacagtc cccggctcga tgtggcgcta gatgagagt gtgatttctc cctggtggag	4380
gatgacggtc ccccatgag agagatcata ctcaagggtg tcctgatgac catctgtggc	4440
atgaacccaa tagccatacc ctttgcagct ggagcgtggt acgtatacgt gaagactgga	4500
aaaaggagt gtgctctatg ggatgtgcct gctccaagg aagtaaaaaa gggggagacc	4560
acagatggag tgtacagagt aatgactcgt agactgctag gttcaacaca agttggagt	4620
ggagttatgc aagaggggggt ctttcacact atgtggcacg tcacaaaagg atccgcactg	4680
agaagcgtg aaggagagact tgatccatac tggggagatg tcaagcagga tctggtgtca	4740

tactgtggtc	catggaagct	agatgccgcc	tgggacgggc	acagcgaggt	gcagctcttg	4800
gccgtgcccc	ccggagagag	agcgaggaac	atccagactc	tgcccggaat	atttaagaca	4860
aaggatgggg	acattggagc	ggttgcgctg	gattaccag	caggaacttc	aggatctcca	4920
atcctagaca	agtgtgggag	agtgatagga	ctttatggca	atggggtcgt	gatcaaaaat	4980
gggagttatg	ttagtgccat	cacccaaggg	aggagggagg	aagagactcc	tgttgagtgc	5040
ttcgagcctt	cgatgctgaa	gaagaagcag	ctaactgtct	tagacttaca	tcctggagct	5100
gggaaaacca	ggagagttct	tcctgaaata	gtccgtgaag	ccataaaaac	aagactccgt	5160
actgtgatct	tagctccaac	cagggttgct	gctgctgaaa	tggaggaggc	ccttagaggg	5220
cttcagtg	gttatatgac	aacagcagtc	aatgtcacc	actctggaac	agaaatcgtc	5280
gacttaatgt	gcatgccac	cttcacttca	cgtctactac	agccaatcag	agtccccaac	5340
tataatctgt	atattatgga	tgaggccac	ttcacagatc	cctcaagtat	agcagcaaga	5400
ggatacattt	caacaaggg	tgagatggg	gaggcggctg	ccatcttcat	gaccgccacg	5460
ccaccaggaa	cccgtgacgc	atttccggac	tccaactcac	caattatgga	caccgaagtg	5520
gaagtcccag	agagagcctg	gagctcaggc	tttgattggg	tgacggatca	ttctggaaaa	5580
acagtttggt	ttgttccaag	cgtgaggaac	ggcaatgaga	tcgcagcttg	tctgacaaag	5640
gctggaaaac	gggtcataca	gctcagcaga	aagacttttg	agacagagtt	ccagaaaaca	5700
aaacatcaag	agtgggactt	tgtcgtgaca	actgacattt	cagagatggg	cgccaacttt	5760
aaagctgacc	gtgtcataga	ttccaggaga	tgcctaaagc	cggtcatact	tgatggcgag	5820
agagtcattc	tggctggacc	catgcctgtc	acacatgcc	gcgctgcca	gaggagggg	5880
cgcataggca	ggaatcccaa	caaactgga	gatgagtatc	tgtatggagg	tgggtgcgca	5940
gagactgacg	aagaccatgc	acactggctt	gaagcaagaa	tgctccttga	caatatttac	6000
ctccaagatg	gcctcatagc	ctcgtcttat	cgacctgagg	ccgacaaagt	agcagccatt	6060
gaggagagat	tcaagcttag	gacggagcaa	aggaagacct	ttgtggaact	catgaaaaga	6120
ggagatcttc	ctgtttggct	ggcctatcag	gttgcattct	ccggaataac	ctacacagat	6180
agaagatggt	gctttgatgg	cacgaccaac	aacaccatac	tggaagacag	tgtgccggca	6240
gaggtgtgga	ccagacacgg	agagaaaaga	gtgctcaaac	cgaggtggat	ggacgccaga	6300
gtttgttcag	atcatgcggc	cctgaagtca	ttcaaggagt	ttgccgctgg	gaaaagagga	6360
gcggcttttg	gagtgatgga	agccttggga	acactgccag	gacacatgac	agagagattc	6420
caggaagcca	ttgacaacct	cgctgtgctc	atgcgggcag	agactggaag	caggccttac	6480

aaagccgcgg	cggcccaatt	gccggagacc	ctagagacca	ttatgctttt	ggggttgctg	6540
ggaacagtct	cgctgggaat	ctttttcgtc	ttgatgagga	acaagggcat	agggaagatg	6600
ggcttttgaa	tggtgaccct	tggggccagt	gcatggctca	tgtggctctc	ggaaattgag	6660
ccagccagaa	ttgcatgtgt	cctcattggt	gtgttcctat	tgctgggtgg	gctcatacct	6720
gagccagaaa	agcaaagatc	tccccaggac	aaccaaattg	caatcatcat	catggtagca	6780
gtaggtcttc	tgggcttgat	taccgccaat	gaactcggat	ggttggagag	aacaaagagt	6840
gacctaagcc	atctaattgg	aaggagagag	gagggagcaa	ccataggatt	ctcaatggac	6900
attgacctgc	ggccagcctc	agcttggggc	atctatgctg	ccttgacaac	tttcattacc	6960
ccagccgtcc	aacatgcagt	gaccacttca	tacaacaact	actccttaat	ggcgatggcc	7020
acgcaagctg	gagtgttggt	tggtatgggc	aaagggatgc	cattctacgc	atgggacttt	7080
ggagtccgcg	tgctaattgat	aggttgctac	tcacaattaa	caccctgac	cctaattagt	7140
gccatcattt	tgctcgtggc	gcactacatg	tacttgatcc	cagggctgca	ggcagcagct	7200
gcgcgtgctg	cccagaagag	aacggcagct	ggcatcatga	agaaccctgt	tgtggatgga	7260
atagtgggtg	ctgacattga	cacaatgaca	attgaccccc	aagtggagaa	aaagatggga	7320
caggtgctac	tcatagcagt	agccgtctcc	agcgccatac	tgtcgcggac	cgctggggg	7380
tggggggagg	ctggggccct	gatcacagcc	gcaacttcca	ctttgtggga	aggctctccg	7440
aacaagtact	ggaactcctc	tacagccact	tcactgtgta	acatttttag	gggaagttac	7500
ttggctggag	cttctctaat	ctacacagta	acaagaaacg	ctggcttggt	caagagacgt	7560
gggggtggaa	caggagagac	cctgggagag	aatggaagg	ccgccttgaa	ccagatgtcg	7620
gccctggagt	tctactccta	caaaaagtca	ggcatcactg	aggtgtgcag	agaagaggcc	7680
cgccgcgccc	tcaaggacgg	tgtggcaacg	ggaggccatg	ctgtgtcccg	aggaagtgca	7740
aagctgagat	ggttgggtgga	gcggggatac	ctgcagccct	atggaaagg	cattgatctt	7800
ggatgtggca	gagggggctg	gagttactac	gccgccacca	tccgcaaagt	tcaagaagtg	7860
aaaggataca	caaaaggagg	ccctggtcac	gaagaacccg	tgttgggtgca	aagctatggg	7920
tggaacatag	tccgtcttaa	gagtgggggtg	gacgtctttc	atatggcggc	tgagccgtgt	7980
gacacgttgc	tgtgtgacat	aggcgagtca	tcacttagtc	ctgaagtgga	agaagcacgg	8040
acgctcagag	tcctctccat	ggtgggggat	tggcttgaaa	gaagaccagg	agccttttgt	8100
ataaaagtgt	tgtgcccata	caccagcact	atgatggaaa	ccctggagcg	actgcagcgt	8160
aggtatgggg	gaggactggg	cagagtgcc	ctctcccgca	actctacaca	tgagatgtac	8220

tgggtctctg	gagcgaaaag	caacaccata	aaaagtgtgt	ccaccacgag	ccagctcctc	8280
ttggggcgca	tggacggggc	taggaggcca	gtgaaatatg	aggaggatgt	gaatctcggc	8340
tctggcacgc	gggctgtggt	aagctgcgct	gaagctccca	acatgaagat	cattggtaac	8400
cgcattgaaa	ggatccgcag	tgagcacgcg	gaaacgtggt	tctttgacga	gaaccacca	8460
tataggacat	gggcttacca	tggaagctat	gaggcccca	cacaagggtc	agcgtcctct	8520
ctaataaacg	gggttgtcag	gctcctgtca	aaaccctggg	atgtggtgac	tggagtcaca	8580
ggaatagcca	tgaccgacac	cacaccgtat	ggtcagcaaa	gagttttcaa	ggaaaaagtg	8640
gacactaggg	tgccagaccc	ccaagaaggc	actcgtcagg	ttatgagcat	ggtctcttcc	8700
tggttgtgga	aagagctagg	caaacacaaa	cggccacgag	tctgtacca	agaagagttc	8760
atcaacaagg	ttcgtagcaa	tgcagcatta	ggggcaatat	ttgaagagga	aaaagagtgg	8820
aagactgcag	tggaagctgt	gaacgatcca	aggttctggg	ctctagtgga	caaggaaaga	8880
gagcaccacc	tgagaggaga	gtgccagagt	tgtgtgtaca	acatgatggg	aaaaagagaa	8940
aagaaacaag	gggaatttgg	aaaggccaag	ggcagccgcg	ccatctggta	tatgtggcta	9000
ggggctagat	ttctagagtt	cgaagccctt	ggattcttga	acgaggatca	ctggatgggg	9060
agagagaact	caggaggtgg	tgttgaaggg	ctgggattac	aaagactcgg	atatgtccta	9120
gaagagatga	gttgcatacc	aggaggaagg	atgtatgcag	atgacactgc	tggctgggac	9180
acccgcatca	gcaggtttga	tctggagaat	gaagctctaa	tcaccaacca	aatggagaaa	9240
gggcacaggg	ccttggcatt	ggccataatc	aagtacacat	acaaaaacaa	agtggtaaag	9300
gtccttagac	cagctgaaaa	agggaaaaca	gttatggaca	ttatttcaag	acaagaccaa	9360
agggggagcg	gacaagttgt	cacttacgct	cttaacacat	ttaccaacct	agtggtgcaa	9420
ctcattcggg	atatggaggc	tgaggaagtt	ctagagatgc	aagacttggt	gctgctgcgg	9480
aggtcagaga	aagtgaccaa	ctggttgcag	agcaacggat	gggataggct	caaacgaatg	9540
gcagtcaagt	gagatgattg	cgttgtgaag	ccaattgatg	ataggtttgc	acatgccctc	9600
aggttcttga	atgatatggg	aaaagttagg	aaggacacac	aagagtggaa	accctcaact	9660
ggatgggaca	actgggaaga	agttccgttt	tgctcccacc	acttcaacaa	gctccatctc	9720
aaggacggga	ggtccattgt	ggttccttgc	cgccaccaag	atgaactgat	tggccggggc	9780
cgcgtctctc	caggggcggg	atggagcatc	cgggagactg	cttgccctagc	aaaatcatat	9840
gcgcaaatgt	ggcagctcct	ttatttccac	agaagggacc	tccgactgat	ggccaatgcc	9900
atttgttcat	ctgtgccagt	tgactggggt	ccaactggga	gaactacctg	gtcaatccat	9960

ggaaagggag aatggatgac cactgaagac atgcttgtgg tgtggaacag agtgtggatt	10020
gaggagaacg accacatgga agacaagacc ccagttacga aatggacaga cattccctat	10080
ttgggaaaaa gggaagactt gtggtgtgga tctctcatag ggcacagacc gcgaccacc	10140
tgggctgaga acattaaaaa cacagtcaac atggtgcgca ggatcatagg tgatgaagaa	10200
aagtacatgg actacctatc cacccaagtt cgctacttgg gtgaagaagg gtctacacct	10260
ggagtgtctgt aa	10272

<210> 72

<211> 10272

<212> DNA

<213> Zika virus strain 103344 polyprotein gene, complete cds

<400> 72

atgaaaaacc caaaaaagaa atccggagga ttccggattg tcaatatgct aaaacgcgga	60
gtagcccgctg tgagcccctt tgggggcttg aagaggctgc cagccggact tctgctgggt	120
catgggcca tcaggatggc cttggcgatt ctagcctttt tgagattcac ggcaatcaag	180
ccatcactgg gtctcatcaa tagatggggc tcagtgggga aaaaagaggc tatggaaata	240
ataaagaagt tcaagaaaga tctggctgcc atgctgagaa taatcaatgc taggaaggag	300
aagaagagac gaggcgcaga tactagtgtc ggaattgttg gcctcctgct gaccacagct	360
atggcagcgg aggtcactag acgtgggagt gcatactata tgtacttgga cagaaacgat	420
gctggggagg ccatatcttt tccaaccaca ttggggatga ataagtgtta tatacagatc	480
atggatcttg gacacatgtg tgatgccacc atgagctatg aatgccctat gctggatgag	540
ggggtggaac cagatgacgt cgattgttgg tgcaacacga cgtcaacttg ggttgtgtac	600
ggaacctgcc atcacaaaaa aggtgaagca cggagatcta gaagagctgt gacgctcccc	660
tcccattcca ctaggaagct gcaaacgcgg tcgcaaacct ggttggaatc aagagaatac	720
acaaagcact tgattagagt cgaaaattgg atattcagga accctggctt cgcgttagca	780
gcagctgcca tcgcttggtt tttgggaagc tcaacgagcc aaaaagtcac atacttggtc	840
atgatactgc tgattgcccc ggcatacagc atcaggtgca taggagtcag caatagggac	900
tttgtggaag gtatgtcagg tgggacttgg gttgatgttg tcttggaaca tggaggttgt	960
gtcaccgtaa tggcacagga caaacgact gtcgacatag agctgggttac aacaacagtc	1020
agcaacatgg cggagataag atcctactgc tatgaggcat caatatcaga catggcttcg	1080
gacagccgct gcccaacaca aggtgaagcc taccttgaca agcaatcaga cactcaatat	1140
gtctgcaaaa gaacgttagt ggacagaggc tggggaaatg gatgtggact ttttggcaaa	1200

gggagcctgg	tgacatgcg	taagtttgca	tgctccaaga	aatgaccgg	gaagagcatc	1260
cagccagaga	atctggagta	ccggataatg	ctgtcagttc	atggctccca	gcacagtggg	1320
atgatcgтта	atgacacagg	acatgaaact	gatgagaata	gagcgaaggt	tgagataacg	1380
cccaattcac	caagagccga	agccaccctg	gggggttttg	gaagcctagg	acttgattgt	1440
gaaccgagga	caggccttga	cttttcagat	ttgtattact	tgactatgaa	taacaagcac	1500
tggttggttc	acaaggagtg	gttccacgac	attccattac	cttggcacgc	tggggcagac	1560
accggaactc	cacactggaa	caacaaagaa	gcactggtgg	agttcaagga	cgcacatgcc	1620
aaaaggcaaa	ctgtcgtggт	tctagggagt	caagaaggag	cagttcacac	ggcccttgct	1680
ggagctctgg	aggctgagat	ggatggtgca	aagggaaggc	tgtcctctgg	ccacttgaaa	1740
tgtcgctga	aatggataa	acttagattg	aagggcgtgt	catactcctt	gtgtaccgca	1800
gcgttcacat	tcaccaagat	ccgggctgaa	acactgcacg	ggacagtcac	agtggaggta	1860
cagtacgcag	ggacagatgg	accttgcaag	gttccagctc	agatggcggt	ggacatgcaa	1920
actctgaccc	cagttgggag	gttgataacc	gctaaccccg	taatcactga	aagcactgag	1980
aactctaaga	tgatgctgga	acttgatcca	ccatttgggg	actcttacat	tgtcatagga	2040
gtcggggaga	agaagatcac	ccaccactgg	cacaggagtg	gcagcaccat	tggaaaagca	2100
tttgaagcca	ctgtgagagg	tgccaagaga	atggcagtct	tgggagacac	agcctgggac	2160
tttggatcag	ttggaggcgc	tctcaactca	ttgggcaagg	gcatccatca	aatttttgga	2220
gctgctttca	aatcattggt	tggaggaatg	tcctggttct	cacaaattct	cattggaacg	2280
ttgctgatgt	ggttgggtct	gaacacaaag	aatggatcta	tttcccttat	gtgcttggcc	2340
ttagggggag	tgttgatctt	cttatccaca	gccgtctctg	ctgatgtggg	gtgctcggtg	2400
gacttctcaa	agaaggagac	gagatgcggт	acaggggtgt	tcgtctataa	cgacgttgaa	2460
gcctggaggg	acaggtacaa	gtaccatcct	gactcccccc	gtagattggc	agcagcagtc	2520
aagcaagcct	gggaagatgg	tatctgcggg	atctcctctg	tttcaagaat	ggaaaacatc	2580
atgtggagat	cagtagaagg	ggagctcaac	gcaatcctgg	aagagaatgg	agttcaactg	2640
acggtcgttg	tgggatctgt	aaaaaacccc	atgtggagag	ctccacagag	attgcccgtg	2700
cctgtgaacg	agctgccccа	cggctggaag	gcttggggga	aatcgtactt	cgtcagagca	2760
gcaaagacaa	ataacagctt	tgtcgtggat	ggtgacacac	tgaaggaatg	cccactcaaa	2820
catagagcat	ggaacagctt	tcttgtggag	gatcatgggt	tcgggggtatt	tcacactagt	2880
gtctggctca	aggтtagaga	agattattca	ttagagtgtg	atccagccgt	tattggaaca	2940

gctgttaagg gaaaggaggc tgtacacagt gatctaggct actggattga gagtgagaag	3000
aatgacacat ggaggctgaa gagggcccat ctgatcgaga tgaaaacatg tgaatggcca	3060
aagtcccaca cattgtggac agatggaata gaagagagtg atctgatcat acccaagtct	3120
ttagctgggc cactcagcca tcacaatacc agagagggct acaggaccca aatgaaaggg	3180
ccatggcaca gtgaagagct tgaaattcgg tttgaggaat gcccaggcac taaggtccac	3240
gtggaggaaa catgtggaac aagaggacca tctctgagat caaccactgc aagcggaagg	3300
gtgatcgagg aatgggtgctg cagggagtgc acaatgcccc cactgtcgtt ccgggctaaa	3360
gatggctgtt ggtatggaat ggagataagg cccaggaaaag aaccagaaaag caacttagta	3420
aggtcaatgg tgactgcagg atcaactgat cacatggatc acttctccct tggagtgcct	3480
gtgattctgc tcatgggtgca ggaagggcta aagaagagaa tgaccacaaa gatcatcata	3540
agcacatcaa tggcagtgct ggtagctatg atcctgggag gatthttcaat gagtgcctg	3600
gctaagcttg caatthttgat gggtgccacc ttcgcggaaa tgaacactgg aggagatgta	3660
gctcatctgg cgctgatagc ggcattcaaa gtcagaccag cgttgctgggt atctthtcac	3720
ttcagagcta attggacacc ccgtgaaagc atgctactgg ccttggcctc gtgtctthttg	3780
caaactgcga tctccgcctt ggaaggcgac ctgatggttc tcatcaatgg thttgcttht	3840
gcctggthtg caatacgagc gatggtthgt ccacgcactg ataacatcac cthggcaatc	3900
ctggctgctc tgacaccact ggcccggggc aactgcttg tggcgtggag agcaggcctt	3960
gctacttgcg gggggttht gtcctctct ctgaagggaa aaggcagtgt gaagaagaac	4020
ttaccattht tcatggccct gggactaacc gctgtgaggc tggctgaccc catcaacgtg	4080
gtgggactgc tgttgctcac aaggagtggg aagcggagct ggccccctag cgaagtactc	4140
acagctgtht gcctgatatg cgcattggct ggagggthtc ccaaggcaga tatagagatg	4200
gctgggcca tggccgcgt cggtctgcta attgtcagtt acgtggtctc aggaaagagt	4260
gtggacatgt acattgaaag agcaggtgac atcacatggg aaaaagatgc ggaagtcact	4320
ggaaacagtc cccggctcga tgtggcgcta gatgagagtg gtgattthtc cctggtggag	4380
gatgacggtc ccccatgag agagatcata ctcaaggtht tcctgatgac catctgtggc	4440
atgaacccaa tagccatacc cthtgagct ggagcgtggt acgtatacgt gaagactgga	4500
aaaaggagtg gtgctctatg ggatgtgcct gctccaagg aagtaaaaaa gggggagacc	4560
acagatggag tgtacagagt aatgactcgt agactgctag gthcaacaca agthggagt	4620
ggagthtatgc aagagggggt cthtcacact atgtggcacg tcacaaaagg atccgcactg	4680

agaagcgggtg aagggagact tgatccatac tggggagatg tcaagcagga tctggtgtca	4740
tactgtggtc catggaagct agatgccgcc tgggacgggc acagcgaggt gcagctcttg	4800
gccgtgcccc ccggagagag agcgaggaac atccagactc tgcccggaat atttaagaca	4860
aaggatgggg acattggagc ggttgcgctg gattaccag caggaacttc aggatctcca	4920
atcctagaca agtgtgggag agtgatagga ctttatggca atggggtcgt gatcaaaaat	4980
gggagttatg ttagtgccat cacccaaggg aggagggagg aagagactcc tgttgagtgc	5040
ttcgagcctt cgatgctgaa gaagaagcag ctaactgtct tagacttaca tcctggagct	5100
gggaaaacca ggagagttct tcctgaaata gtccgtgaag ccataaaaac aagactccgt	5160
actgtgatct tagctccaac cagggttgtc gctgctgaaa tggaggaggc ccttagaggg	5220
cttcagtg cgttatatgac aacagcagtc aatgtcacc actctggaac agaaatcgtc	5280
gacttaatgt gccatgccac cttcacttca cgtctactac agccaatcag agtccccaac	5340
tataatctgt atattatgga tgaggccac ttcacagatc cctcaagtat agcagcaaga	5400
ggatacattt caacaagggg tgagatgggc gaggcggctg ccatcttcat gaccgccacg	5460
ccaccaggaa cccgtgacgc atttccggac tccaactcac caattatgga caccgaagtg	5520
gaagtcccag agagagcctg gagctcaggc tttgattggg tgacggatca ttctggaaaa	5580
acagtttggg ttgttccaag cgtgaggaac ggcaatgaga tcgcagcttg tctgacaaag	5640
gctggaaaac gggtcataca gctcagcaga aagacttttg agacagagtt ccagaaaaca	5700
aaacatcaag agtgggactt tgtcgtgaca actgacattt cagagatggg cgccaacttt	5760
aaagctgacc gtgtcataga ttccaggaga tgcctaaagc cggtcatact tgatggcgag	5820
agagtcattc tggctggacc catgcctgtc acacatgcca gcgctgcca gaggaggggg	5880
cgcataggca ggaatcccaa caaacctgga gatgagtatc tgtatggagg tgggtgcgca	5940
gagactgacg aagaccatgc aactggctt gaagcaagaa tgctccttga caatatttac	6000
ctccaagatg gcctcatagc ctcgctctat cgacctgagg ccgacaaagt agcagccatt	6060
gagggagagt tcaagcttag gacggagcaa aggaagacct ttgtggaact catgaaaaga	6120
ggagatcttc ctgtttggct ggcctatcag gttgcatctg ccggaataac ctacacagat	6180
agaagatggg gctttgatgg cacgaccaac aacaccatac tggaagacag tgtgccggca	6240
gaggtgtgga ccagacacgg agagaaaaga gtgctcaaac cgaggtggat ggacgccaga	6300
gtttgttcag atcatgcggc cctgaagtca ttcaaggagt ttgccgctgg gaaaagagga	6360
gcggcttttg gagtgatgga agccttggga aactgccag gacacatgac agagagattc	6420

caggaagcca	ttgacaacct	cgctgtgctc	atgcgggcag	agactggaag	caggccttac	6480
aaagccgcgg	cggcccaatt	gccggagacc	ctagagacca	ttatgctttt	ggggttgctg	6540
ggaacagtct	cgctgggaat	ctttttcgctc	ttgatgagga	acaagggcat	agggaagatg	6600
ggctttggaa	tggtgaccct	tggggccagt	gcatggctca	tgtggctctc	ggaaattgag	6660
ccagccagaa	ttgcatgtgt	cctcattggt	gtgttcctat	tgctgggtgg	gctcatacct	6720
gagccagaaa	agcaaagatc	tccccaggac	aaccaaattg	caatcatcat	catggtagca	6780
gtaggtcttc	tgggcttgat	taccgccaat	gaactcggat	ggttgagag	aacaaagagt	6840
gacctaaagg	atctaattgg	aaggagagag	gagggagcaa	ccataggatt	ctcaatggac	6900
attgacctgc	ggccagcctc	agcttggggc	atctatgctg	ccttgacaac	tttcattacc	6960
ccagccgtcc	aacatgcagt	gaccacttca	tacaacaact	actccttaat	ggcgatggcc	7020
acgcaagctg	gagtgttggt	tggtatgggc	aaagggatgc	cattctacgc	atgggacttt	7080
ggagtcccgc	tgctaattgat	aggttgctac	tcacaattaa	caccctgac	cctaatagtg	7140
gccatcattt	tgctcgtggc	gcactacatg	tacttgatcc	cagggctgca	ggcagcagct	7200
gcgcgtgctg	cccagaagag	aacggcagct	ggcatcatga	agaaccctgt	tgtggatgga	7260
atagtgggtg	ctgacattga	cacaatgaca	attgaccccc	aagtggagaa	aaagatggga	7320
caggtgctac	tcatagcagt	agccgtctcc	agcgccatac	tgtcgcggac	cgctggggg	7380
tggggggagg	ctggggccct	gatcacagcc	gcaacttcca	ctttgtggga	aggctctccg	7440
aacaagtact	ggaactcctc	tacagccact	tcactgtgta	acatttttag	gggaagttat	7500
ttggctggag	cttctctaat	ctacacagta	acaagaaacg	ctggcttggt	caagagacgt	7560
gggggtggaa	caggagagac	cctgggagag	aatggaagg	ccgccttgaa	ccagatgtcg	7620
gccctggagt	tctactccta	caaaaagtca	ggcatcactg	aggtgtgcag	agaagaggcc	7680
cgccgcgccc	tcaaggacgg	tgtggcaacg	ggaggccatg	ctgtgtcccg	aggaagtgca	7740
aagctgagat	ggttggtgga	gcggggatac	ctgcagccct	atggaaagg	cattgatctt	7800
ggatgtggca	gagggggctg	gagttactac	gccgccacca	tccgcaaagt	tcaagaagtg	7860
aaaggataca	caaaaggagg	ccctgggtcat	gaagaacccg	tgttggtgca	aagctatggg	7920
tggaacatag	tccgtcttaa	gagtgggggtg	gacgtctttc	atatggcggc	tgagccgtgt	7980
gacacgttgc	tgtgtgacat	aggcgagtca	tcacttagtc	ctgaagtgga	agaagcacgg	8040
acgctcagag	tcctctccat	ggtgggggat	tggcttgaaa	gaagaccagg	agccttttgt	8100
ataaaagtgt	tgtgcccata	caccagcact	atgatggaaa	ccctggagcg	actgcagcgt	8160

aggtatgggg	gaggactggt	cagagtgcc	ctctcccgca	actctacaca	tgagatgtac	8220
tgggtctctg	gagcgaaaag	caacaccata	aaaagtgtgt	ccaccacgag	ccagctcctc	8280
ttggggcgca	tggacggggc	taggaggcca	gtgaaatatg	aggaggatgt	gaatctcggc	8340
tctggcacgc	gggctgtggt	aagctgcgct	gaagctccca	acatgaagat	cattggtaac	8400
cgcattgaaa	ggatccgcag	tgagcacgcg	gaaacgtggt	tctttgacga	gaaccacca	8460
tataggacat	gggcttacca	tggaagctat	gaggcccca	cacaagggtc	agcgtcctct	8520
ctaataaacg	gggttgtcag	gctcctgtca	aaaccctggg	atgtggtgac	tggagtcaca	8580
ggaatagcca	tgaccgacac	cacaccgtat	ggtcagcaaa	gagttttcaa	ggaaaaagtg	8640
gacactaggg	tgccagaccc	ccaagaaggc	actcgtcagg	ttatgagcat	ggtctcttcc	8700
tggttgtgga	aagagctagg	caaacacaaa	cggccacgag	tctgtaccaa	agaagagttc	8760
atcaacaagg	ttcgtagcaa	tgcagcatta	ggggcaatat	ttgaagagga	aaaagagtgg	8820
aagactgcag	tggaagctgt	gaacgatcca	aggttctggg	ctctagtgga	caaggaaaga	8880
gagcaccacc	tgagaggaga	gtgccagagt	tgtgtgtaca	acatgatggg	aaaaagagaa	8940
aagaaacaag	gggaatttgg	aaaggccaag	ggcagccgcg	ccatctggta	tatgtggcta	9000
ggggctagat	ttctagagtt	cgaagccctt	ggattcttga	acgaggatca	ctggatgggg	9060
agagagaact	caggaggtgg	tgttgaaggg	ctgggattac	aaagactcgg	atatgtccta	9120
gaagagatga	gttgcatacc	aggaggaagg	atgtatgcag	atgacactgc	tggctgggac	9180
acccgcatca	gcaggtttga	tctggagaat	gaagctctaa	tcaccaacca	aatggagaaa	9240
gggcacaggg	ccttggcatt	ggccataatc	aagtacacat	acaaaaaca	agtggtaaag	9300
gtccttagac	cagctgaaaa	agggaaaaca	gttatggaca	ttattttcaag	acaagaccaa	9360
agggggagcg	gacaagttgt	cacttacgct	cttaacacat	ttaccaacct	agtggtgcaa	9420
ctcattcgga	atatggaggc	tgaggaagtt	ctagagatgc	aagacttgtg	gctgctgcgg	9480
aggtcagaga	aagtgaccaa	ctggttgcag	agcaacggat	gggataggct	caaacgaatg	9540
gcagtcagtg	gagatgattg	cgttgtgaag	ccaattgatg	ataggtttgc	acatgccctc	9600
aggttcttga	atgatatggg	aaaagttagg	aaggacacac	aagagtggaa	accctcaact	9660
ggatgggaca	actgggaaga	agttccgttt	tgctcccacc	acttcaaca	gctccatctc	9720
aaggacggga	ggtccattgt	ggttccttgc	cggcaccaag	atgaactgat	tggccggggc	9780
cgcgtctctc	caggggcggg	atggagcatc	cgggagactg	cttgccctagc	aaaatcatat	9840
gcgcaaatgt	ggcagctcct	ttatttccac	agaagggacc	tccgactgat	ggccaatgcc	9900

at ttgt tcat	ctgtgccagt	tgactggggt	ccaactggga	gaactacctg	gtcaatccat	9960
ggaaagggag	aatggatgac	ca ctgaagac	atgcttgtgg	tgtggaacag	agtgtggatt	10020
gaggagaacg	accacatgga	agacaagacc	ccagttacga	aatggacaga	cattccctat	10080
ttgggaaaaa	gggaagactt	gtggtgtgga	tctctcatag	ggcacagacc	gcgccacc	10140
tgggctgaga	acattaaaaa	cacagtcaac	atggtgcgca	ggatcatagg	tgatgaagaa	10200
aagtacatgg	actacctatc	cacccaagtt	cgctacttgg	gtgaagaagg	gtctacacct	10260
ggagtgtctgt	aa					10272

<210> 73

<211> 10272

<212> DNA

<213> Zika virus strain ArD158084 polyprotein gene, complete cds

<400> 73

atgaaaaacc	caaagaagaa	atccggagga	ttccggattg	tcaatatgct	aaaacgcgga	60
gtagcccggtg	taaaccctt	gggaggtttg	aagagggtgc	cagccggact	tctgctgggt	120
catggacca	tcagaatggt	tttggcgata	ctagcctttt	tgagatttac	agcaatcaag	180
ccatcactgg	gccttatcaa	cagatgggggt	tccgtgggga	aaaaagaggc	tatggaaata	240
ataaagaagt	tcaagaaaga	tcttgctgcc	atggtgagaa	taatcaatgc	taggaaagag	300
aggaagagac	gtggcgcaga	caccagcatc	ggaatcattg	gcctcctgct	gactacagcc	360
atggcagcag	agatcactag	acgcgggagt	gcatactaca	tgtacttgga	taggagcgat	420
gccgggaagg	ccatttcgtt	tgctaccaca	ttgggagtga	acaagtgcc	cgtacagatc	480
atggacctcg	ggcacatgtg	tgacgccacc	atgagttatg	agtgccttat	gctggatgag	540
ggagtggaac	cagatgatgt	cgattgctgg	tgcaacacga	catcaacttg	ggttgtgtac	600
ggaacctgtc	atcacaaaaa	aggtgaggca	cggcgatcta	gaagagccgt	gacgctccct	660
tctcactcta	caaggaagtt	gcaaacgcgg	tcgcagacct	ggttagaatc	aagagaatac	720
acgaagcact	tgatcaaggt	tgaaaactgg	atattcagga	accccggtt	tgcgctagtg	780
gccgttgcca	ttgcctggct	tttgggaagc	tcgacgagcc	aaaaagtc	atatttggtc	840
atgatactgc	tgattgcccc	ggcatacagt	atcagggtgca	ttggagtcag	caatagagac	900
ttcgtggagg	gcatgtcagg	tgggacctgg	gttgatgttg	tcttggaaca	tggaggctgc	960
gttaccgtga	tggcacagga	caagccaaca	gttgacatag	agttggtcac	gacgacggtt	1020
agtaacatgg	ccgaggtaag	atcctattgc	tacgaggcat	cgatatcgga	catggcttcg	1080

gacagtcgtt	gccaacaca	aggtgaagcc	taccttgaca	agcaatcaga	cactcaatat	1140
gtctgcaaaa	gaacattagt	ggacagaggt	tggggaaatg	gttgtggact	ttttggcaaa	1200
gggagcttgg	tgacatgtgc	caagttcacg	tgttctaaga	agatgaccgg	gaagagcatt	1260
caaccgaaa	atctggagta	tcggataatg	ctatcagtgc	atggctccca	gcatagcggg	1320
atgattgtca	atgatatagg	acatgaaact	gacgaaaaca	gagcgaaagt	cgaggttacg	1380
cctaattcac	caagagcgga	agcaaccttg	ggaggctttg	gaagcttagg	acttgactgt	1440
gaaccaagga	caggccttga	cttttcagat	ctgtattacc	tgaccatgaa	caataagcat	1500
tggttggtgc	acaagagtg	gtttcatgac	atcccattgc	cttggcattgc	tggggcagac	1560
accggaactc	cacactggaa	caacaaagag	gcattggtag	aattcaagga	tgcccacgcc	1620
aagaggcaaa	ccgtcgtcgt	tctggggagc	caggaaggag	ccgttcacac	ggctctcgct	1680
ggagctctag	aggctgagat	ggatggtgca	aagggaaggc	tgttctctgg	ccatttgaia	1740
tgccgcctaa	aatggacaa	gcttagattg	aagggcgtgt	catattcctt	gtgcactgcg	1800
gcattcacat	tcaccaaggt	cccagctgaa	acactgcatg	gaacagtcac	agtggagggtg	1860
cagtatgcag	ggacagatgg	accctgcaag	gtcccagccc	agatggcggt	ggacatgcag	1920
accctgaccc	cagttggaag	gctgataacc	gccaaccccg	tgattactga	aagcactgag	1980
aactcaaaga	tgatgttgga	gcttgaccca	ccatttgggg	attcttacat	tgtcatagga	2040
gttggggaca	agaaaatcac	ccaccactgg	cataggagtg	gtagcaccat	cggaaaggca	2100
tttgaagcca	ctgtgagagg	cgccaagaga	atggcagtcc	tgggggatac	agcctgggac	2160
ttcggatcag	tcgggggtgt	gttcaactca	ctgggtaagg	gcattcacca	gatttttgga	2220
gcagccttca	aatcactgtt	tggaggaatg	tcctggttct	cacagatcct	cataggcacg	2280
ctgctagtgt	ggttaggttt	gaacacaaag	aatggatcta	tctccctcac	atgcttggcc	2340
ctggggggag	tgatgatctt	cctctccacg	gctgtttctg	ctgacgtggg	gtgctcagtg	2400
gacttctcaa	aaagagaaac	gagatgtggc	acgggggtat	tcattctataa	tgatgttgaa	2460
gcctggaggg	accggtacaa	gtaccatcct	gactcccccc	gcagattggc	agcagcagtc	2520
aagcaggcct	gggaagaggg	gatctgtggg	atctcatccg	tttcaagaat	ggaaaacatc	2580
atgtggaaat	cagtagaagg	ggagctcaat	gctatcctag	aggagaatgg	agttcaactg	2640
acagttgttg	tgggatctgt	aaaaaacccc	atgtggagag	gtccacaaaag	attgccagtg	2700
cctgtgaatg	ggctgccccca	tggctggaaa	gcctggggga	aatcgtattt	tgttagggcg	2760
gcaaagacca	acaacagttt	tgttgtcgac	ggtgacacac	tgaaggaatg	tccgcttaag	2820

cacagagcat ggaatagttt tcttgtggag gatcacgggt ttggagtctt ccacaccagt	2880
gtttggctta aggtcagaga agattactca ttagaatgtg acccagccgt cataggaaca	2940
gctgttaagg gaagggaggc cgcgcacagt gatctgggct attggattga aagtgaaaag	3000
aatgacacat ggaggctgaa gagggccac ctgattgaga tgaaaacatg tgaatggcca	3060
aagtctcaca cattgtggac agatggagta gaagaaagtg atcttatcat acccaagtct	3120
ttagctggtc cactcagcca ccacaacacc agagaggggt acagaacca agtgaaagg	3180
ccatggcaca gtgaagagct tgaaatccgg tttgaggaat gtccaggcac caaggttcac	3240
gtggaggaga catgcggaac tagaggacca tctctgagat caactactgc aagtggaagg	3300
gtcattgagg aatggtgctg tagggaatgc acaatgcccc cactatcggt tcgagcaaaa	3360
gacggctgct ggtatggaat ggagataagg cccaggaaag aaccagagag caacttagtg	3420
aggtcaatgg tgacagcggg gtcaaccgat catatggacc acttctctct tggagtgctt	3480
gtgattctac tcatggtgca ggaggggttg aagaagagaa tgaccacaaa gatcatcatg	3540
agcacatcaa tggcagtgct ggtagtcatg atcttgggag gatthttcaat gagtgcctg	3600
gccaagcttg tgatcctgat gggtgctact ttgcgagaaa tgaacactgg aggagatgta	3660
gctcacttg cattggtagc ggcatttaaa gtcagaccag ccttgctggt ctcttcatt	3720
ctcagagcca attggacacc ccgtgagagc atgctgctag ccctggcttc gtgtcttctg	3780
caaactgca tctctgctct tgaagggtgac ttgatggtcc tcgttaatgg atttgctttg	3840
gcctggttg caattcgagc aatggccgtg ccacgcactg acaacatcgc tctagcaatc	3900
ttggctgctc taacaccact agctcgagge acactgctcg tggcatggag agcgggcctg	3960
gctacttggt gagggttcat gtcctctctc ctgaaaggga aaggtagtgt gaagaagaac	4020
ctgccatttg tcatggccct gggattgaca gctgtgaggg tagtagacc tattaatgtg	4080
gtaggactac tgttactcac aaggagtggg aagcggagct ggccccctag tgaagttctc	4140
acagccgttg gcctgatatg tgcactggcc ggagggtttg ccaaggcaga cattgagatg	4200
gctggacca tggctgcagt aggcttgcta attgtcagct atgtggtctc gggaaagagt	4260
gtggacatgt acattgaaag agcaggtgac atcacatggg aaaaggacgc ggaagtcact	4320
ggaaacagtc ctgggcttga cgtggcactg gatgagagtg gtgatttctc cttggtagag	4380
gaagatggtc caccatgag agagatcata ctcaagggtg tcctgatggc catctgtggc	4440
atgaacccaa tagctatacc ttttgctgca ggagcgtggt atgtgtatgt gaagactggg	4500
aaaaggagtg gcgccctctg ggacgtgcct gctcccaaag aagtgaagaa aggagagacc	4560

acagatggag	tgtacagagt	gatgactcgc	agactgctag	gttcaacaca	ggttggagtg	4620
ggagtcatgc	aagagggagt	cttccacacc	atgtggcacg	ttacaaaagg	agccgcactg	4680
aggagcggtg	agggaagact	tgatccatac	tgggggggatg	tcaagcagga	cttgggtgtca	4740
tactgtgggc	cttggaaagt	ggatgcagct	tgggatggac	ttagcgaggt	acagcttttg	4800
gccgtacctc	ccggagagag	ggccagaaac	attcagaccc	tgcttggaat	attcaagaca	4860
aaggacgggg	acatcggagc	agttgctctg	gactaccctg	cagggacctc	aggatctccg	4920
atcctagaca	aatgtggaag	agtgatagga	ctctatggca	atggggttgt	gatcaagaat	4980
ggaagctatg	ttagtgtctat	aaccagggga	aagagggagg	aggagactcc	ggttgaatgt	5040
ttcgaaccct	cgatgctgaa	gaagaagcag	ctaactgtcc	tggatctgca	tccaggagcc	5100
ggaaaaacca	ggagagttct	tcctgaaata	gtccgtgaag	ccataaaaaa	gagactccgg	5160
acagtgatct	tggcaccaac	tagggttgtc	gctgctgaga	tggaggaagc	cttgagagga	5220
cttccggtgc	gttacatgac	aacagcagtc	aacgtcaccc	attctgggac	agaaatcggt	5280
gatttgatgt	gccatgccac	tttcaattca	cgcttactac	aaccatcag	agtccctaatt	5340
tacaatctca	acatcatgga	tgaagccac	ttcacagacc	cctcaagtat	agctgcaaga	5400
ggatacatat	caacaagggg	tgaaatgggc	gaggcggctg	ccatttttat	gactgccaca	5460
ccaccaggaa	cccgtgatgc	gtttcctgac	tctaactcac	caatcatgga	cacagaagtg	5520
gaagtcccag	agagagcctg	gagctcaggc	tttgattggg	tgacagacca	ttctgggaaa	5580
acagtttggt	tcgttccaag	cgtagaaaac	ggaaatgaaa	tcgcagcctg	tctgacaaag	5640
gctggaaaagc	gggtcataca	gctcagcagg	aagacttttg	agacagaatt	tcagaaaaca	5700
aaaaatcaag	agtgggactt	tgtcataaca	actgacatct	cagagatggg	cgccaacttc	5760
aaggctgacc	gggtcataga	ctctaggaga	tgccataaac	cagtcatact	tgatggtgag	5820
agagtcatct	tggctggggc	catgcctgtc	acgcatgcta	gtgctgctca	gaggagagga	5880
cgtataggca	ggaaccctaa	caaacctgga	gatgagtaca	tgtatggagg	tgggtgtgca	5940
gagactgatg	aaggccatgc	acactggctt	gaagcaagaa	tgcttcttga	caacatctac	6000
ctccaggatg	gcctcatagc	ctcgtcttat	cggcctgagg	ccgataaggt	agccgccatt	6060
gagggagagt	ttaagctgag	gacagagcaa	aggaagacct	tcgtggaact	catgaagaga	6120
ggagaccttc	ccgtctggct	agcctatcag	gttgcatctg	ccggaataac	ttacacagac	6180
agaagatggt	gctttgatgg	cacaaccaac	aacaccataa	tggaagacag	tgtaccagca	6240
gaggtttgga	caaagtatgg	agagaagaga	gtgctcaaac	cgagatggat	ggatgctagg	6300

gtctgttcag accatgcggc cctgaagtcg ttcaaagaat tcgccgctgg aaaaagagga	6360
gcggcctttgg gagtaatgga ggccctggga aactgccag gacacatgac agagaggttt	6420
caggaagcca ttgacaacct cgccgtgctc atgcgagcag agactggaag caggccttat	6480
aaggcagcgg cagcccaact gccggagacc ctagagacca ttatgctctt aggtttgctg	6540
ggaacagttt cactggggat cttctttgtc ttgatgcgga ataagggcat cggaagatg	6600
ggctttggaa tggtaacctt tggggccagt gcatggctca tgtggctttc ggaaattgaa	6660
ccagccagaa ttgcatgtgt cctcattgtt gtgtttttat tactggtggt gctcataccc	6720
gagccagaga agcaaagatc tccccaagat aaccagatgg caattatcat catggtggca	6780
gtgggccttc taggtttgat aactgcaaac gaacttggat ggctggaaag aacaaaaaat	6840
gacatagctc atctaattggg aaggagagaa gaaggagcaa ccatgggatt ctcaatggac	6900
attgatctgc ggccagcctc cgccctgggt atctatgccg cattgacaac tctcatcacc	6960
ccagctgtcc aacatgcggt aaccacttca tacaacaact actccttaat ggcgatggcc	7020
acacaagctg gagtgtctgtt tggcatgggc aaagggatgc cattttatgc atgggacttt	7080
ggagtccgc tgctaattgat gggttgctat tcacaattaa caccctgac tctgatagta	7140
gctatcattc tgcttgtggc gcactacatg tacttgatcc caggcctaca agcggcagca	7200
gcgcgtgctg ccagaaaaag gacagcagct ggcacatga agaatcccg tgtggatgga	7260
atagtggtaa ctgacattga cacaatgaca atagaccccc aggtggagaa gaagatggga	7320
caagtgttac tcatagcagt agccatctcc agtgctgtgc tgctgcggac cgccctggga	7380
tggggggagg ctggagctct gatcacagca gcgacctca ccttgtggga aggctctcca	7440
aacaaatact ggaactcctc tacagccacc tcaactgtgca acatcttcag aggaagctat	7500
ctggcaggag cttcccttat ctatacagtg acgagaaacg ctggcctggt taagagacgt	7560
ggaggtggga cgggagagac tctgggagag aagtggaaag ctgctctgaa tcagatgtcg	7620
gccctggagt tctactctta taaaaagtca ggtatcactg aagtgtgtag agaggaggct	7680
cgccgtgcc tcaaggatgg agtggccaca ggaggacatg ccgtatccc gggaagtgca	7740
aagctcagat ggttgggtgga gagaggatat ctgcagcccc atgggaagg tgttgacctc	7800
ggatgtggca gagggggctg gagctattat gccgccacca tccgcaaagt gcaggaggtg	7860
agaggataca caaagggagg tcccgtcat gaagaacca tgctggtgca aagctatggg	7920
tggaacatag ttcgtctcaa gagtggagtg gacgtcttcc acatggcggc tgagccgtgt	7980
gacactctgc tgtgtgacat aggtgagtca tcatctagtc ctgaagtgga agagacacga	8040

acactcagag	tgctctctat	ggtggggggac	tggcttgaaa	aaagaccagg	ggccttctgt	8100
ataaaggtgc	tgtgcccata	caccagcact	atgatggaaa	ccatggagcg	actgcaacgt	8160
aggcatgggg	gaggattagt	cagagtgcc	ttgtctcgca	actccacaca	tgagatgtac	8220
tgggtctctg	gggcaaaaag	caacatcata	aaaagtgtgt	ccaccacaag	tcagctcctc	8280
ctgggacgca	tggatggccc	caggaggcca	gtgaaatatg	aggaggatgt	gaacctcggc	8340
tcgggtacac	gagctgtggc	aagctgtgct	gaggctccta	acatgaaaat	catcggcagg	8400
cgcattgaga	gaatccgcaa	tgaacatgca	gaaacatggt	ttcttgatga	aaaccacca	8460
tacaggacat	gggcctacca	tgggagctac	gaagccccc	cgcaaggatc	agcgtcttcc	8520
ctcgtgaacg	gggttggttag	actcctgtca	aagccttggg	acgtggtgac	tggagttaca	8580
ggaatagcca	tgactgacac	cacaccatac	ggccaacaaa	gagtcttcaa	agaaaaagtg	8640
gacaccaggg	tgccagatcc	ccaagaaggc	actcgccagg	taatgaacat	ggtctcttcc	8700
tggctgtgga	aggagctggg	gaaacgcaag	cggccacgcg	tctgcaccaa	agaagagttt	8760
atcaacaagg	tgcgagcaaa	tgcagcactg	ggagcaatat	ttgaagagga	aaaagaatgg	8820
aagacggctg	tggaagctgt	gaatgatcca	aggttttggg	ccctagtgga	tagggagaga	8880
gaacaccacc	tgagaggaga	gtgtcacagc	tgtgtgtaca	acatgatggg	aaaaagagaa	8940
aagaagcaag	gagagttcgg	gaaagcaaaa	ggtagccgcg	ccatctggta	catgtggttg	9000
ggagccagat	tcttgaggtt	tgaagccctt	ggattcttga	acgaggacca	ttggatggga	9060
agagagaact	ctggaggcgg	agttgaagga	ctgggactgc	agagactggg	ctatgtcctt	9120
gaggagatga	gccaggcacc	aggagggaag	atgtacgcag	atgacactgc	tggctgggac	9180
acccgcatta	gtaagtttga	tctggagaat	gaagctttga	ttaccaacca	aatggaggaa	9240
gggcacagaa	ctctggcggt	ggccgtgatt	aaatacacat	acaaaaacaa	agtgggtgaag	9300
gtcctcagac	cagctgaagg	aggaaaaaca	gttatggaca	tcatttcaag	acaagaccag	9360
agagggagtg	gacaagttgt	cacttatgct	ctcaacacat	tcaccaactt	ggtggtgcag	9420
cttatccgga	acatggaagc	tgaggaagtg	ttagagatgc	aagacttatg	gctgttgagg	9480
aagccagaga	aagtgaccag	atggttgcag	agcaatggat	gggatggact	caaacgaatg	9540
gcggtcagtg	gagatgactg	cgttgtgaag	ccaatcgatg	ataggtttgc	acatgccctc	9600
aggttcttga	atgacatggg	aaaagttagg	aaagacacac	aggagtggaa	accctcgact	9660
ggatggagca	attgggaaga	agtcccgttc	tgctcccacc	acttcaacaa	gctgtacctc	9720
aaggatggga	gatccattgt	gtcccttgc	cgccaccaag	atgaactgat	tggccgagct	9780

cgcgtttcac caggggacagg atggagcatc cgggagactg cctgtcttgc aaaatcatat	9840
gcgcagatgt ggcagctcct ttatttccac agaagagacc ttcgactgat ggctaatagcc	9900
atttgctcgg ctgtaccagt tgactgggta ccaactggga gaaccacctg gtcaatccat	9960
ggaaagggag aatggatgac cactgaggac atgctcatgg tgtggaatag agtgtggatt	10020
gaggagaacg accatatgga ggacaagact cctgtaacaa aatggacaga cattccctat	10080
ctaggaaaaa gggaggactt atgggtgtgga tcccttatag ggcacagacc ccgcaccact	10140
tgggctgaaa acatcaaaga cacagtcaac atgggtgcga ggatcatagg tgatgaagaa	10200
aagtacatgg actatctatc cacccaagtc cgctacttgg gtgaggaagg gtccacaccc	10260
ggagtgttgt aa	10272

<210> 74
 <211> 10272
 <212> DNA
 <213> Zika virus strain ArD157995 polyprotein gene, complete cds

<220>
 <221> misc_feature
 <222> (2711)..(2711)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (8487)..(8487)
 <223> n is a, c, g, or t

<400> 74	
atgaaaaacc caaagaagaa atccggaaga ttccggattg tcaatatgct aaaacgcgga	60
gtagcccgtag taaaccctt gggaggtttg aagaggttgc cagccggact tctgctgggt	120
catggacca tcagaatggt tttggcgata ctagcctttt tgagatttac agcaatcaag	180
ccatcactgg gccttatcaa cagatggggg tccgtgggga aaaaagaggc tatggaaata	240
ataaagaagt tcaagaaaga tcttgctgcc atgttgagaa taatcaatgc taggaaagag	300
aggaagagac gtggcgcaga caccagcatc ggaatcattg gcctcctgct gactacagcc	360
atggcagcag agatcactag acgcgggagt gcatactaca tgtacttgga taggagcgat	420
gccgggaagg ccatttcgtt tgctaccaca ttgggagtga acaagtgcc cgtacagatc	480
atggacctcg ggcacatgtg tgacgccacc atgagttatg agtgccttat gctggatgag	540
ggagtggaac cagatgatgt cgattgctgg tgcaacacga catcaacttg ggttgtgtac	600
ggaacctgtc atcacaaaaa aggtgagaca cggcgatcta gaagatctgt gtcgctccgt	660

tatcactata caaggaagtt gcaaacgcgg tcgcagacat ggtagaatac aagagaatac	720
aagaagcact tgatcatggt cgaaaactgg atattcagga accccggggt tgccatagtg	780
tccgttgcca ttacctggct gatgggaagc ttgacgagcc aaaaagtc atacttggtc	840
atgatagtgt tgattgtccc ggcatacagt atcagctgca ttggagtcag caatagagac	900
ttagtggagg gcatgtcagg tgggacctgg gttgatgttg tcttggaaca tggagggtgc	960
gttaccgaga tggcacagga caagccaaca gttgacatag agttgggtcac gatgacgggt	1020
agtaacatgg ccgaggtaag atcctattgc tacgaggcat cgttatccga catggcttcg	1080
gccagtcgtt gccaacaca aggcgaaccc tccctcgaca agcaatcaga cactcaatct	1140
gtatgcaaaa gaacattagg agacagaggt tggggaaatg gttgtgggat ttttggcaaa	1200
gggagcttgg tgacatgttc caagttcacg tgttgtaaga agatgcccg gaagagcatt	1260
caaccgaaa atctggagta tcggataatg ctcccagtc atggctccca gcatagcggg	1320
atgattgtga atgacatagg acatgaaact gacgaaaaca gagcgaaagt cgaggtcaca	1380
ccaattcac caagagcaga agcaaccttg ggagggtttg gaagcttggg acttgactgt	1440
gaaccaagga caggccttga cttctcagat ctgtattatc tgaccatgaa caacaagcat	1500
tggttggtgc acaaggagtg gtttcatgac atcccattac cttggcatgc tgggtgcagac	1560
actggaactc cacactggaa caacaaagag gcattggtgg agttcaagga cgcccacgcc	1620
aagaggcaaa ctgttggtgt tctggggagc caagaggag ctgttcacac ggcctcgt	1680
ggagctctgg aggctgagat ggatggtgca aagggaaggc tattctcttg ccatttgaaa	1740
tgccgcctaa aaatggacaa gcttaggttg aagggtgtgt catattccct gtgtactgca	1800
gcgttcacat ttaccaaggt ccagctgaa acattgcatg gaacagttac agtggagggtg	1860
cagtctgcag ggacagatgg accctgcaag gtcccagccc agatggcggg ggacatgcag	1920
accctgacct cagttggaag gctgataacc gccaaacccg tgattactga aagcactgag	1980
aactcaaaga tgatgttgga gcttgacca ccatctgggg attcttacat tgtcatagga	2040
gttggggaca agaaaatcac ccaccactgg cataggagtg gtagcaccat cggaaggca	2100
tttgaagcca ctgtgagagg cgccaagaga atggcagtc tgggggatac agcctgggac	2160
ttcggatcag tcgggggtgt gttcaactca ctgggtaagg gcattcacca gatttttgga	2220
gcagccttca aatcactgtt tggaggaatg tcctggttct cacagatcct cataggcacg	2280
ctgctagtgt ggtaggttt gaacacaaag aatggatcta tctccctcac atgcttggcc	2340
ctggggggag tgatgatctt cctctccacg gctgtttctg ctgacgtggg gtgctcagt	2400

gacttctcaa	aaaaggaac	gagatgtggc	acgggggtat	tcattctataa	tgatgttgaa	2460
gcctggaggg	accggtacaa	gtaccatcct	gactcccccc	gcagattggc	agcagcagtc	2520
aagcaggcct	gggaagaggg	gatctgtggg	atctcatccg	tttcaagaat	ggaaaacatc	2580
atgtggaaat	cagtagaagg	ggagctcaat	gctatcctag	aggagaaatg	agttcaactg	2640
acagttgttg	tgggatctgt	aaaaaacccc	atgtggagag	gtccacaaa	attgccagtg	2700
cctgtgaatg	ngctgcccc	tggctggaaa	gcctggggga	aatcgtattt	tgtagggcg	2760
gcaaagacca	acaacagttt	tggtgtcgac	ggtgacacac	tgaaggaatg	tccgcttaag	2820
cacagagcat	ggaatagttt	tcttgtggag	gatcacgggt	ttggagtctt	ccacaccagt	2880
gtttggctta	aggtcagaga	agattactca	ttagaatgtg	accagccgt	cataggaaca	2940
gctgttaagg	gaagggaggg	cgcgcacagt	gatctgggct	attggattga	aagtgaaaag	3000
aatgacacat	ggaggctgaa	gagggccac	ctgattgaga	tgaaaacatg	tgaatggcca	3060
aagtctcaca	cattgtggac	agatggagta	gaagaaagtg	atcttatcat	accaagtct	3120
ttagctggtc	cactcagcca	ccacaacacc	agagaggggt	acagaacca	agtgaagg	3180
ccatggcaca	gtgaagagct	tgaaatccgg	tttgaggaat	gtccaggcac	caaggttcac	3240
gtggaggaga	catgcggaac	tagaggacca	tctctgagat	caactactgc	aagtggaagg	3300
gtcattgagg	aatggtgctg	tagggaatgc	acaatgcccc	cactatcggt	tcgagcaaaa	3360
gacggctgct	ggtatggaat	ggagataagg	cccaggaaa	aaccagagag	caacttagtg	3420
aggtcaatgg	tgacagcggg	gtcaaccgat	catatggacc	acttctctct	tggagtgtt	3480
gtgattctac	tcattggtgca	ggaggggttg	aagaagagaa	tgaccacaaa	gatcatcatg	3540
agcacatcaa	tggcagtgt	ggtagtcatg	atcttgggag	gattttcaat	gagtgcctg	3600
gccaagcttg	tgatcctgat	gggtgctact	tctgcagaaa	tgaacactgg	aggagatgta	3660
gctcacttgg	cattggtagc	ggcatttaaa	gtcagaccag	ccttgctggt	ctccttcatt	3720
ctcagagcca	attggacacc	ccgtgagagc	atgctgctag	ccctggcttc	gtgtcttctg	3780
caaactgcga	tctctgctct	tgaaggtgac	ttgatggtcc	tcgttaatgg	atttgctttg	3840
gcctggttgg	caattcgagc	aatggccgtg	ccacgcactg	acaacatcgc	tctagcaatc	3900
ttggctgctc	taacaccact	agctcgaggc	acactgctcg	tggcatggag	agcgggcctg	3960
gctacttgtg	gagggttcat	gctcctctcc	ctgaaaggga	aaggtagtgt	gaagaagaac	4020
ctgccatttg	tcattggccct	gggattgaca	gctgtgaggg	tagtagaccc	tattaatgtg	4080
gtaggactac	tgttactcac	aaggagtggg	aagcggagct	ggccccctag	tgaagttctc	4140

acagccgttg gcttgatatg tgcactggcc ggaggggttg ccaaggcaga cattgagatg	4200
gctggacca tggctgcagt aggcttgcta attgtcagct atgtggtctc gggaaagagt	4260
gtggacatgt acattgaaag agcaggtgac atcacatggg aaaaggacgc ggaagtcact	4320
ggaaacagtc ctcggttga cgtggcactg gatgagagt gtgatttctc cttggtagag	4380
gaagatggtc caccatgag agagatcata ctcaagggtg tcctgatggc catctgtggc	4440
atgaaccaa tagctatacc ttttgctgca ggagcgtggt atgtgtatgt gaagactggg	4500
aaaaggagt ggcgcctctg ggacgtgcct gctcccaaag aagtgaagaa aggagagacc	4560
acagatggag tgtacagagt gatgactcgc agactgctag gttcaacaca ggttggagt	4620
ggagtcatgc aagagggagt cttccacacc atgtggcacg ttacaaaagg agccgcactg	4680
aggagcggtg aggggaagact tgatccatac tggggggatg tcaagcagga cttggtgtca	4740
tactgtgggc cttggaagtt ggatgcagct tgggatggac ttagcgaggt acagcttttg	4800
gccgtacctc ccggagagag gcccagaaac attcagacc tgccctggaat attcaagaca	4860
aaggacgggg acatcggagc agttgctctg gactaccctg cagggacctc aggatctccg	4920
atcctagaca aatgtggaag agtgatagga ctctatggca atggggttgt gatcaagaat	4980
ggaagctatg ttagtgctat aaccaggga aagagggagg aggagactcc ggttgaatgt	5040
ttcgaaccct cgatgctgaa gaagaagcag ctaactgtcc tggatctgca tccaggagcc	5100
ggaaaaacca ggagagttct tcctgaaata gtccgtgaag ccataaaaaa gagactccgg	5160
acagtgatct tggcaccaac tccagttgag agatcatact caagggtggc cttgtggcca	5220
tctgtggcac gtaccagac aacagcagtc aacgtcacc attctgggac agaaatcggt	5280
gatttgatgt gccatgccac tttcacttca cgcttactac aaccatcag agtcctaata	5340
tacaatctca acatcatgga tgaagccac ttcacagacc cctcaagtat agctgcaaga	5400
ggatacatat caacaaggt tgaatgggc gaggcggctg ccatttttat gactgccaca	5460
ccaccaggaa ccggtgatgc gtttcctgac tctaactcac caatcatgga cacagaagt	5520
gaagtcccag agagagcctg gagctcaggc tttgattggg tgacagacca ttctgggaaa	5580
acagtttggt tcgttccaag cgtgagatct ggagaagaaa gcgcagcctg tctgacaaag	5640
gctggaaagc gggcataca gctcagcagg aagacttttg agacagaatt tcagaaaaca	5700
aaaaatcaag agtgggactt tgtcataaca actgacatct cagagatggg cgccaacttc	5760
aaggctgacc gggcataga ctctaggaga tgcctaaagc cagtcatact tgatggtgag	5820
agagtcatct tggctgggcc catgcctgtc acgcatgcta gtgctgctca gaggagagga	5880

cgtataggca ggaaccctaa caaacctgga gatgagtaca tgtatggagg tgggtgtgca	5940
gagactgatg aagaccatgc aactgggctt gaagcaagaa tgcttcttga caacatctac	6000
ctccaggatg gcctcatagc ctcgctctat cggcctgagg ccgataaggt agccgccatt	6060
gagggagagt ttaagctgag gacagagcaa aggaagacct tcgtggaact catgaagaga	6120
ggagaccttc ccgtctggct agcctatcag gttgcatctg ccggaataac ttacacagac	6180
agaagatggg gctttgatgg cacaaccaac aacaccataa tggaagacag cgtaccagca	6240
gaggtgtgga caaagtatgg agagaagaga gtgctcaaac cgagatggat ggatgctagg	6300
gtctgttcag accatgcggc cctgaagtcg ttcaaagaat tcgccgctgg aaaaagagga	6360
gcggcttttg gagtaatgga ggccctggga aactgccag gacacatgac agagaggttt	6420
caggaagcca ttgacaacct cgccgtgctc atgcgagcag agactggaag caggccttat	6480
aaggcagcgg cagcccaact gccggagacc ctagagacca ttatgctctt aggtttgctg	6540
ggaacagttt cactggggat cttcttcgtc ttgatgcgga ataagggcat cgggaagatg	6600
ggcttttgaa tggtaaccct tggggccagt gcatggctca tgtggctttc ggaaattgaa	6660
ccagccagaa ttgcatgtgt cctcattgtt gtgtttttat tactggtggt gtcataccc	6720
gagccagaga agcaaagatc tcccaagat aaccagatgg caattatcat catggtggca	6780
gtgggccttc taggtttgat aactgcaaac gaacttggat ggctggaaaag aacaaaaaat	6840
gacatagctc atctaattggg aaggagagaa gaaggagcaa ccatgggatt ctcaatggac	6900
attgatctgc ggccagcctc cgctgggct atctatgccg cattgacaac tctcatcacc	6960
ccagctgtcc aacatgcggg aaccacttca tacaacaact actccttaat ggcgatggcc	7020
acacaagctg gagtgtgtgt tggcatgggc aaagggatgc catttatgca tggggacctt	7080
ggagtcccg tgctaattgat gggttgctat tcacaattaa caccctgac tctgatagta	7140
gctatcattc tgcttgtggc gcactacatg tacttgatcc caggcctaca agcggcagca	7200
gcgcgtgctg ccagaaaaag gacagcagct ggcacatga agaattccgt tgtggatgga	7260
atagtggtaa ctgacattga cacaatgaca atagaccccc aggtggagaa gaagatggga	7320
caagtgttac tcatagcagt agccatctcc agtgctgtgc tgctgcggac cgctgggga	7380
tggggggagg ctggagctct gatcacagca gcgacctca ccttgtggga aggctctcca	7440
aacaaatact ggaactcctc tacagccacc tcaactgtga acatcttcag aggaagctat	7500
ctggcaggag cttcccttat ctatacagt acgagaaacg ctggcctggg taagagacgt	7560
ggaggtggga cgggagagac tctgggagag aagtggaaa ctcgtctgaa tcagatgtcg	7620

gccctggagt	tctactctta	taaaaagtca	ggtatcactg	aagtgtgtag	agaggaggct	7680
cgccgtgccc	tcaaggatgg	agtggccaca	ggaggacatg	ccgtatcccg	gggaagtgca	7740
aagctcagat	ggttgggtgga	gagaggatat	ctgcagcccc	atgggaaggt	tgttgacctc	7800
ggatgtggca	gagggggctg	gagctattat	gccgccacca	tccgcaaagt	gcaggaggtg	7860
agaggataca	caaagggagg	tcccgggtcat	gaagaaccca	tgctggtgca	aagctatggg	7920
tggaacatag	ttcgtctcaa	gagtggagtg	gacgtcttcc	acatggcggc	tgagccgtgt	7980
gacactctgc	tgtgtgacat	aggtgagtca	tcatctagtc	ctgaagtgga	agagacacga	8040
acactcagag	tgctctctat	ggtgggggac	tggcttgaaa	aaagaccagg	ggccttctgt	8100
ataaaggtgc	tgtgcccata	caccagcact	atgatggaaa	ccatggagcg	actgcaacgt	8160
aggcatgggg	gaggattagt	cagagtgccca	ttgtctcgca	actccacaca	tgagatgtac	8220
tgggtctctg	gggcaaaaag	caacatcata	aaaagtgtgt	ccaccacaag	tcagctcctc	8280
ctgggacgca	tggatggccc	caggaggcca	gtgaaatatg	aggaggatgt	gaacctcggc	8340
tcgggtacac	gagctgtggc	aagctgtgct	gaggctccta	acatgaaaat	catcggcagg	8400
cgcattgaga	gaatccgcaa	tgaacatgca	gaaacatggt	ttcttgatga	aaaccaccca	8460
tacaggacat	gggcctacca	tgggagntac	gaagccccc	cgcaaggatc	agcgtcttcc	8520
ctcgtgaacg	gggttggttag	actcctgtca	aagccttggg	acgtggtgac	tggagttaca	8580
ggaatagcca	tgactgacac	cacaccatac	ggccaacaaa	gagtcttcaa	agaaaaagtg	8640
gacaccaggg	tgccagatcc	ccaagaaggc	actcgccagg	taatgaacat	ggtctcttcc	8700
tggctgtgga	aggagctggg	gaaacgcaag	cggccacgcg	tctgcaccaa	agaagagttt	8760
atcaacaagg	tgcgagcaaa	tgcagcactg	ggagcaatat	ttgaagagga	aaaagaatgg	8820
aagacggctg	tggaagctgt	gaatgatcca	aggttttggg	ccctagtgga	tagggagaga	8880
gaacaccacc	tgagaggaga	gtgtcacagc	tgtgtgtaca	acatgatggg	aaaaagagaa	8940
aagaagcaag	gagagttcgg	gaaagcaaaa	ggtagccgcg	ccatctggta	catgtggttg	9000
ggagccaggt	ttctggagtt	tgaatcactg	gggtttctga	atgaagatca	ctggatggga	9060
agagagaact	ctggaggcgg	agttgaagga	ctgggactgc	agagactggg	ctatgtcctt	9120
gaggagatga	gccaggcacc	aggagggaag	atgtacgcag	atgacactgc	tggctgggac	9180
acccgcatta	gtaagtttga	tctggagaat	gaagctttga	ttaccaacca	aatggaggaa	9240
gggcacagaa	ctctggcggt	ggccgtgatt	aaatacacat	acaaaaacaa	agtgggtgaag	9300
gtcctcagac	cagctgaagg	aggaaaaaca	gttatggaca	tcatttcaag	acaagaccag	9360

agaggggagtg gacaagttgt cacttatgct ctcaacacat tcaccaactt ggtggtgcag	9420
cttatccgga acatggaagc tgaggaagtg ttagagatgc aagacttatg gctgttgagg	9480
aagccagaga aagtgaccag atggttgcag agcaatggat gggatagact caaacgaatg	9540
gcggtcagtg gagatgactg cgttgtgaag ccaatcgatg ataggtttgc acatgccttc	9600
aggttcttga atgacatggg aaaagttagg aaagacacac aggagtggaa accctcgact	9660
ggatggagca attgggaaga agtcccgttc tgctcccacc acttcaacaa gctgtacctc	9720
aaggatggga gatccattgt ggtcccttgc cgccaccaag atgaactgat tggccgagct	9780
cgcgtttcac caggggcagg atggagcatc cgggagactg cctgtcttgc aaaatcatat	9840
gcgcagatgt ggcagctcct ttatttccac agaagagacc ttcgactgat ggctaatagcc	9900
atttgctcgg ctgtaccagt tgactgggta ccaactggga gaaccacctg gtcaatccat	9960
ggaaagggag aatggatgac cactgaggac atgctcatgg tgtggaatag agtgtggatt	10020
gaggagaacg accatatgga ggacaagact cctgtaacaa aatggacaga cattccctat	10080
ctaggaaaaa gggaggactt atgggtgtgga tcccttatag ggcacagacc ccgcaccact	10140
tgggctgaaa acatcaaaga cacagtcaac atgggtgcgca ggatcatagg tgatgaagaa	10200
aagtacatgg actatctatc cacccaagtc cgctacttgg gtgaggaagg gtccacaccc	10260
ggagtgttgt aa	10272

<210> 75
 <211> 10272
 <212> DNA
 <213> Zika virus strain ArD128000 polyprotein gene, complete cds

<220>
 <221> misc_feature
 <222> (1324)..(1338)
 <223> n is a, c, g, or t

<400> 75	
atgaaaaacc caaagaggaa atccggagga ttccggattg tcaatatgct aaaacgcgga	60
gtagcccgctg taaaccctt ggggggtttg aagaggctgc cagccggact tctgctgggt	120
catggacca ttagaatggt tttggcgata ctagcctttt tgagatttac agcaatcaag	180
ccatcactgg gcctcatcaa tagatggggt tcagtgggga aaaaagaggc tatggagata	240
ataaagaagt ttaagaaaga tcttgctgcc atgttgagaa taatcaatgc taggaaggag	300
aggaagagac gtggtgcaga caccagtatc ggaatcattg gcctcctgct gactacagcc	360
atggcagcag agattactag acgaggaagt gcatactaca tgtacttgga caggagcgat	420

gctgggaagg ccatttcctt tgctaccaca ttgggagtga acaaatgcc a tgtacagatc	480
atggatctcg ggcacatgtg tgacgccacc atgagttatg agtgcctat gctagacgaa	540
ggagtgaac cagatgatgt cgattgctgg tgcaacacga catcaacttg ggttgtgtac	600
ggaacctgtc atcacaaaaa aggtgaagca cggcgatcta gaagagctgt gacgtccct	660
tctcactcca caaggaagtt gcaaacgcgg tcgcagacct ggtagaatc aagagaatac	720
acgaagcact tgatcaaggt tgaaaactgg atattcagga accccgggtt tgcgctagcg	780
gctgttgcca ttgcttggct tctgggaagc tcgacgagcc aaaaagtc atacttggtc	840
atgatattgt tgattgcccc ggcatacagc atcaggtgca taggagttag caatagagat	900
ttcgtagagg gcatgtcagg tgggacctgg gttgatgtcg tcttggaaca tgggggttgc	960
gtcaccgtga tggcacagga caagccaaca gttgacatcg agttggtcac gacaacggtt	1020
agcaacatgg ccgaggtaag atcctactgc tatgaggcat caatatcgga catggcctcg	1080
gacagccgct gtccaacaca aggtgaagcc taccttgaca agcaatcaga cactcaatat	1140
gtctgcaaaa gaacattagt ggacagaggt tggggaaacg gttgtggact ttttggcaaa	1200
gggagcttgg tgacatgtgc caagtttacg tgttctaaga agatgaccgg gaagagcatt	1260
cagccggaga acttgagta ccggataatg ctatcagtgc atggatccca gcacagtggg	1320
atgnnnnnnn nnnnnnnngg acatgaaact gacgaaaaca gagcaaaggt cgaggtcaca	1380
cccaattcac caagagcaga agcaaccttg ggaggttttg gaagcttggg acttgactgt	1440
gaaccaagga caggccttga cttctcagat ctgtattatc tgaccatgaa caacaagcat	1500
cggttggtgc gcaaggagtg gtttcatgac atcccattac cttggcatgc tgggtgcagac	1560
actggaactc cacactggaa caacaaagag gcattggtgg agttcaagga cgctcacgcc	1620
aagaggcaaa ctgttgttgt tctggggagc caagagggag ctgttcacac ggcctcgcct	1680
ggagctctgg aggctgagat ggatggtgca aagggaaggc tattctcttg ccatttgaaa	1740
tgccgcctaa aaatggacaa gcttaggttg aagggtgtgt catattccct gtgtactgca	1800
gcgttcacat ttaccaaggt ccagctgaa acattgcatg gaacagttac agtggaggtg	1860
cagtatgcag ggacagatgg accttgcaag gtcccagccc agatggcggg ggacatgcag	1920
actctgacct cagttggaag gctgataacc gccaacctg tgatcactga aagtactgag	1980
aattcaaaga tgatgttgga acttgacca ccatttgggg attcttacat tgtcatagga	2040
gtcggggaca agaaaatcac ccatcactgg ctcaagaaag ggagctccat cggaaaggca	2100
tttgaagcca ctgtgagagg tgccaagaga atggcagtct tgggggacac agcctgggac	2160

tttgatcag ttggaggtgt gtttaattca ttgggtaagg gtgttcatca gatctttgga	2220
gcagctttca aatcactgtt tggaggaatg tcctggttct cacagatcct cataggcaca	2280
ctgttggtgt ggttgggtct gaacacaaag aatggatcta tctccctcac atgcttagcc	2340
ctggggggag tgatgatttt ctttccacg gctgtttctg ctgatgttgg gtgctcgggtg	2400
gacttctcaa aaaaggaaac gagatgtggc acgggggtgt tcgtctacaa tgacgttgaa	2460
gcctggaggg accgttacaa gtatcatcct gactcccccc gcagattggc agcagctgtt	2520
aagcaggctt gggaagaggg gatttgtggg atctcctccg tttcgagaat ggaaaacatc	2580
atgtggaaat cagtgggaagg ggagcttaat gcaatcctag aggagaatgg agtccaactg	2640
acagttgtag tggggtctgt aaaaaacccc atgtggagag gtccacaaag attgccagtg	2700
cccgtgaatg agctgcccc a tggctggaaa gcctggggga aatcgtactt tgtcagagcg	2760
gcaaagacca acaacagttt tggtgtcgac ggagacacac tgaaggagtg tccgctcaaa	2820
catagagcat ggaatagctt cttgtggag gatcacgggt ttgggatttt ccacaccagt	2880
gtttggctga aggtcagaga ggactactca ttagagtgtg acccagccgt cataggaaca	2940
gctgtcaagg gaaaggaagc tgcacacagt gatctatgct attggattga gagtgaaaag	3000
aatgacacat ggaggctgag gagggccac ctgattgaga tgaaaacatg tgaatggcca	3060
aagtctcaca cattgtggac agatggagta gaagaaagt atcttatcat acccaagtct	3120
ttagctggtc cactcagcca ccacaacacc agagaggggt acagaacca agtgaaagg	3180
ccatggcaca gtgaagagct tgaaatccgg tttgaggaat gtccaggcac caaggtttac	3240
gtggaggaga catgcggaac tagaggacca tctctgagat caactactgc aagtggaagg	3300
gtcattgagg aatggtgctg tagggaatgc acaatgcccc cactatcggt tcgagcaaaa	3360
gacggctgct ggtatggaat ggagataagg ccaggaag aaccagagag caacttagtg	3420
aggtcaatgg tgacagcggg gtcaaccgat catatggacc acttctctct tggagtgtt	3480
gtgattctac tcatggtgca ggaggggttg aagaagagaa tgaccacaaa gatcatcatg	3540
agcacatcaa tggcagtgtt ggtagccatg gtcttgggag gattctcaat gagtgatctg	3600
gctaagcttg tgatcctgat gggtgccact ttcgcagaaa tgaacactgg aggagatgtg	3660
gctcacttgg cattgggttg gcatttaaa gtcagaccag cttgttggt ttcctttatc	3720
ttcagagcca actggacacc ccgtgagagc atgctgctag ccctggcttc gtgtctctg	3780
cagactgcga tctccgctct tgaaggcgag ctgatgtcc tcgttaatgg atttgctttg	3840
gcctggttgg caatacgagc aatggccgtg ccacgcactg acaatatcgc tctagcaact	3900

ctggccgctt taacaccatt ggccagaggc acactgctcg tggcatggag agcgggcctc	3960
gccacttggtg gagggttcat gcttctttcc ctgaaaggga aaggtagtgt gaagaagaac	4020
ctgccttttg tcatggcctt ggggttggcc gctgtgagga tagtggaccc catcaatgtg	4080
gtaggactac tgttactcac aaggagtgga aaacggagct ggccccccag tgaagtgcctt	4140
acagctgttg gcctgatatg tgcactggcc ggaggggttg ccaaggcaga catagagatg	4200
gctgggcca tggctgcagt aggctgcta attgtcagtt atgtggtctc gggaaagagt	4260
gtggacatgt acatcgaaag agcaggtgat atcacatggg aaaaagacgc ggaagtcact	4320
ggaaacagtc cccggcttga cgtggcactg gatgagagtg gtgatttctc cttggtagag	4380
gaggatggcc caccatgag agagatcata ctcaagggtg tcctgatggc catctgtggc	4440
atgaaccaa tagccatacc cttcgctgca ggagcgtggt atgtgtatgt aaagactggg	4500
aaaaggagtg gtgccctctg ggacgtgcct gctcccaaag aagtgaaaaa aggagagact	4560
acagatggag tgtacagagt gatgactcgc agactgctgg gttcaacaca ggttgagtg	4620
ggggtcatgc aagagggagt cttccacacc atgtggcacg tcacaaaagg agctgcattg	4680
aggagcggtg aaggaagact tgatccatat tggggggacg tcaagcagga cttggtgtca	4740
tattgtgggc cgtggaagtt ggacgcaacc tgggatggac taagtgaagt gcagcttttg	4800
gccgtacccc ccggagagag ggctagaaac attcagactc tgccctggaat attcaagaca	4860
aaggatgggg acatcggagc ggttgctcta gactaccccg caggaacctc aggatctcca	4920
atcctagaca aatgcggaag agtgatagga ctttatggca atggggttgt gatcaagaat	4980
ggaagctatg tcagtgcaat aaccagggga aaaagggagg aggaggcccc agttgagtgc	5040
tttgaaccct cgatgctgag gaagaagcag ctaacagtct tggatctgca tccaggagcc	5100
ggaaaaacca ggagggttct tcctgaaata gtccgtgaag ccataaaaaa gagactccgg	5160
acagtgatct tggcaccaac tagggttgtc gctgctgaga tggaggaggc cttgagagga	5220
cttccggtgc gttacatgac aacagcagtc aacgtcaccc attctgggac agaaatcggt	5280
gatttgatgt gccatgccac tttcacttca cgcttactac aaccatcag agtcctaata	5340
tacaatctca acatcatgga tgaagccac ttcacagacc cctcaagtat agctgcaaga	5400
ggatacatat caacaagggg tgaaatgggc gaggcggctg ccatttttat gactgccaca	5460
ccaccaggaa ccggtgatgc gtttcctgac tctaactcac caatcatgga cacagaagtg	5520
gaagtcccag agagagcctg gagctcaggc tttgattggg tgacagacca ttctgggaaa	5580
acaatttggt ttgttccaag tgtgagaaac ggaaatgaaa tcgcagcctg tctgacaaag	5640

gctggaaagc	gggttatata	gctcagcagg	aagacttttg	agacagagtt	tcagaagaca	5700
aaaaatcaag	agtgggactt	tgtcataaca	actgacattt	cagagatggg	tgccaatttc	5760
aaggctgacc	gggtcatcga	ttccaggaga	tgcctaaagc	cagtcatact	tgatggtgag	5820
agagtcatcc	tggctggggc	catgcctgtc	acgcatgcc	gtgctgctca	gaggagagga	5880
cgtataggca	ggaaccccaa	caaaccggga	gatgagtaca	tgtatggagg	tgggtgtgca	5940
gagactgatg	aagaccatgc	acactggctt	gaagcaagaa	tgcttcttga	caacatttac	6000
ctccaagatg	gcctcatagc	ctcgctctat	cggcctgagg	ccgacaaggt	agccgccatt	6060
gagggagagt	tcaagctgag	gacagagcaa	aggaagacct	ttgtggaact	catgaagaga	6120
ggagaccttc	ccgtttggct	ggcctatcaa	gtagcatctg	ccggaataac	ttacacagac	6180
agaagatggg	gctttgatgg	cactaccaac	aacaccataa	tggaagacag	tgtaccagca	6240
gaggtgtgga	ccaagtatgg	agagaagaga	gtgcttaaac	cgaggtggat	ggatgctagg	6300
gtctgttcag	atcatgcggc	tctgaagtcg	ttcaaagaat	ttgccgctgg	gaagagagga	6360
gcggctttgg	gagtaatgga	tgccctggga	acattgccag	gacacatgac	agagaggttt	6420
caggaagcca	ttgacaatct	tgctgtgctc	atgcgagcag	agactggaag	taggccctac	6480
aaagcagcgg	cagctcaact	gccggagacc	ctagagacca	tcatgctttt	gggcttattg	6540
ggaacagttt	cgctaggaat	cttctttgtc	ttgatgcgga	acaagggcat	cgggaagatg	6600
ggcttcggaa	tggtaaccct	tggggccagc	gcatggctca	tgtggctctc	ggaaattgaa	6660
ccagccagaa	tcgcatgtgt	cctcattgtc	gtgtttttgt	tactggtggg	gctcataccc	6720
gagccagaga	agcaaagatc	tccccaggat	aatcaaatgg	caatcatcat	catggtggca	6780
gttggccttt	tgggtttgat	aactgcaaat	gaactcggat	ggctggaaaag	gacaaaaagt	6840
gatatagctt	atctgatggg	aaggaaagaa	gaggggacaa	ccataggatt	ctcaatggat	6900
attgatctgc	ggccagcctc	tgcttgggct	atztatgccg	cattgacaac	tctcatcacc	6960
ccagccgtcc	aacatgcggt	aaccacctca	tacaacaact	actccctgat	ggcgatggcc	7020
acacaagctg	gagtgtctgt	tggcatgggc	aaagggatgc	catttttatgc	atgggacttt	7080
ggagtcccg	tgctaatgat	aggttgctac	tcacagttaa	caccctgac	cctgatagta	7140
gccatcattc	tgcttgtagc	acactacatg	tacttgatcc	caggtttgca	ggcagcagca	7200
gcacgtgctg	cccagaagag	gacagcagct	ggcatcatga	aaaatcccgt	tgtggatgga	7260
atagtgggtg	ctgacattga	cacaatgaca	attgaccccc	aagtggagaa	gaagatggga	7320
caagtgttac	tcatagcagt	agctgtctcc	agtgtgtgtc	tgctgcggac	cgctggggga	7380

tggggggagg	ctggggctct	gatcacagca	gctacctcca	ccttatggga	aggctctcca	7440
aacaaatact	ggaactcctc	tacagccacc	tcactatgca	acatcttttag	aggaagttat	7500
ttggcagggg	cttcccttat	ttacacagtg	acaagaaatg	ccggtctggg	taagagacgt	7560
ggaggtggaa	cgggagagac	cctgggagag	aagtggaaag	ccgcctgaa	ccagatgtcg	7620
gccctggagt	tttactctta	caaaaagtca	ggcatcaccg	aagtgtgtag	ggaggaggcg	7680
cgccgcgctc	tcaaggatgg	agtggccaca	ggagggcatg	ctgtatcccc	gggaagcgca	7740
aagcttagat	ggttggtaga	gagaggatac	ctgcagcccc	atggaaaggt	tgttgacctt	7800
ggatgtggca	gaggaggctg	gagttattac	gctgccacta	tccgtaaagt	gcaggaggtc	7860
agaggataca	caaagggagg	tcttggtcat	gaagaacca	tgctggtgca	aagctatggg	7920
tggaacatag	ttcgctcaa	gagtggagtg	gacgtcttcc	acatggcggc	tgagccgtgt	7980
gacactctgc	tgtgtgacat	aggcgagtca	tcatctagtc	ctgaagtgga	agagacgcga	8040
acactcagag	tgctctccat	ggtagaagac	tggcttgaga	aaagaccagg	ggccttctgc	8100
ataaagggtc	tgtgcccata	caccagcaca	atgatggaga	ccatggagcg	actgcaacgt	8160
aggcatgggg	gaggattggg	cagagtgcc	ttgtcccgca	actccacaca	tgagatgtat	8220
tgggtctctg	gagccaaaag	taacatcata	aagagtgtgt	ccaccacaag	tcagtcctc	8280
ttgggacgca	tggatggggc	taggaggcca	gtgaaatatg	aggaggatgt	gaacctcggc	8340
tcaggcacac	gagctgtggc	aagctgcgct	gaggctccca	acatgaagat	cattggtagg	8400
cgcattgaga	gaatccgcaa	tgaacatgca	gagacatggt	tctttgatga	aaaccacca	8460
tacaggacat	gggcctacca	tgggagctac	gaagcccca	cgcaggggtc	agcgtcatcc	8520
ctcgtgaatg	gggttggttag	actcttgta	aagccctggg	atgtggtgac	tggagttaca	8580
ggaatagcta	tgactgacac	cacgccatac	ggccaacaaa	gagtcttcaa	ggaaaaagtg	8640
gacacaaggg	tgccagatcc	ccaagaaggc	actcgccaag	taatgaacat	agtttcgtct	8700
tggctatgga	aggagctagg	aaaacgcaag	cgaccacgtg	tctgcacca	agaagagttc	8760
atcaataagg	tgcgcagcaa	tgcagcactg	ggagcaatat	ttgaagagga	aaaagaatgg	8820
aagacagctg	tagaagctgt	gaatgatcca	agattttggg	ctctagtgga	caaggaaaga	8880
gaacaccacc	tgagaggaga	gtgtcacagc	tgtgtgtaca	acatgatggg	taaaagagaa	8940
aagaagcaag	gagaattcgg	gaaagcaaaa	ggcagccgcg	caatctggta	catgtggttg	9000
ggagccagat	ttttggagtt	tgaagctctt	ggattcttga	acgaggatca	ctggatggga	9060
agagaaaact	caggaggtgg	tgttgaaggg	ctaggactgc	aaaggcttgg	atatatccta	9120

gaagaaatga accggggcacc aggaggaaag atgtatgcag atgacaccgc tggctgggac	9180
acccgtatta gtaagtttga tctagagaat gaagccctga tcactaacca gatggaagaa	9240
gggcacagag ctctggcgtt ggccgtgatt aaatacacat accaaaacaa agtgggtgaag	9300
gttctcagac cagctgaagg agggaaaaca gtcattggaca tcattctcaag acaagaccag	9360
agagggagtg gacaagttgt tacttatgcc ctcaacacat tcaccaacct ggtgggtgcag	9420
cttatccgga acatggaggc tgaggaagtg ctagagatgc atgatctgtg gttgttgagg	9480
aaaccagaga aagtgaccag atgggtgcag agtaatggat gggacagact caaacggatg	9540
gcagttagtg gagatgactg cgttgtaaag ccaattgatg ataggtttgc acatgccctc	9600
aggttcttga atgacatggg aaaggttagg aaagacacac aggaatggaa gccctcgact	9660
ggatggagca attgggagga ggtcccgttc tgttctcacc acttcaacaa gctgcacctc	9720
aaggacggga gatccattgt ggtcccctgc cgccaccaag atgaactgat tggccgagcc	9780
cgtgtctcac cagggggcagg atggagcatc cgtgagactg cttgccttgc aaaatcatat	9840
gcacagatgt ggcagcttct ttatttccac agaagagatc tccgactgat ggccaatgcc	9900
atttgttcgg ctgtgccagt tgattgggta ccaactggga gaaccacctg gtcaatccat	9960
ggaaagggag aatggatgac tactgaggac atgctcatgg tgtggaatag agtgtggatt	10020
gaggagaacg accacatgga ggacaagacc cctgttccaa aatggacaga aattccctac	10080
ttggggaaaaa gggagtccct atgggtgtgga tacattatag ggcacagacc tcgcaccact	10140
tgggctgaga acatcaaaga cacagtcaac atgggtgctta ggctcatagg tgatgaagaa	10200
aagtacatgg actacctatc cacccaagta cgctacttgg gtgaggaagg gtccacacct	10260
ggagtgctgt aa	10272

<210> 76
 <211> 10272
 <212> DNA
 <213> Zika virus strain ArD7117 polyprotein gene, complete cds

<220>
 <221> misc_feature
 <222> (4309)..(4309)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (5225)..(5226)
 <223> n is a, c, g, or t

<400> 76

atgaaaaacc	caaagaagag	atccggagga	ttccggattg	tcaatatgct	aaaacgcgga	60
gtagcccgtg	taaaccctt	ggggggttt	aagaggctgc	cggccggact	tctgctgggc	120
catggacca	tcagaatggt	tttggcgata	ctagcctttt	tgagattcac	agcaatcaag	180
ccatcactgg	gcctcatcaa	tagatgggg	tccgtgggga	agaaggaggc	tatggaaata	240
ataaaaaagt	tcaagaaaga	ccttgctgcc	atgttgagaa	ttatcaatgc	taggaaggag	300
aggaagagac	gtggcgctga	caccagcatc	ggaatcgtcg	gcctcctgct	gaccacagcc	360
atggcagccg	agatcaccag	acgtgggagt	gcatactaca	tgtacttgga	caggagcgat	420
gctggtaagg	ccatttcttt	tgctaccaca	ttgggggtga	acaaatgcca	tgtacagatc	480
atggacctcg	ggcacatgtg	tgacgccacc	atgagttatg	agtgccccat	gctggacgag	540
ggagtggagc	cagatgacgt	cgattgctgg	tgcaacacga	catcaacttg	ggttgtgtac	600
ggaacctgtc	aacataaaaa	aggtgaagca	cgacgatcca	gaagagccgt	gacgcttcct	660
tctcactcca	caaggaagct	gcaaacgcga	tcacagactt	ggctagaatc	aagagaatac	720
acaaagcacc	tgatcaaggt	tgagaattgg	atattcagga	accccggtt	tgcgctagt	780
gctgtagcta	ttgcctggct	cctgggaagc	tcgacgagcc	aaaaagtc	at	840
atgatattgt	tgattgcccc	ggcatacagc	atcagggtgca	taggagttag	caatagagac	900
ttcgtggagg	gcatgtcagg	tgggacctgg	gttgatgttg	tcttggaaca	tgggggttgc	960
gtcaccgtga	tggcacagga	caagccaaca	gttgacatcg	agttggtcac	gacaacggtt	1020
agcaacatgg	ccgaggtaag	atcctactgc	tatgaggcat	caatatcgga	catggcttcg	1080
gacagccgct	gtccaacaca	aggtgaagcc	taccttgaca	agcagtcaga	cactcaatat	1140
gtctgcaaga	gaacattggt	ggatagaggt	tggggaaatg	ggtgtggact	ttttggcaaa	1200
gggagcttgg	tgacatgtgc	caagtttacg	tgctccaaga	aatgacagg	caagagcatc	1260
cagccggaga	acttgagta	ccgataatg	ctatcagtgc	atggatcca	gcacagtggg	1320
atgattgtga	atgacatagg	acatgaaact	gacgaaaaca	gagcaaaagt	cgaggtcaca	1380
cccaattcac	caagagcaga	agcaaccttg	ggaggttttg	gaagcttggg	acttgactgt	1440
gaaccaagga	caggccttga	cttctcagat	ctgtattacc	tgaccatgaa	caataagcat	1500
tggttggtgc	acaaggagt	gtttcatgac	atcccattac	cttggcatgc	tggtgcagac	1560
actggaactc	cacactggaa	caacaaagag	gcattggtgg	agtttaagga	cggccacgcc	1620
aagaggcaaa	ctgttgtggt	tctggggagc	caagagggag	ctgttcacac	ggccctcgct	1680
ggagctttgg	aggctgagat	ggatggtgca	aagggaaggc	tattctctgg	ccatttgaaa	1740

tgccgcctaa	aaatggacaa	gcttaggttg	aaggggtgtg	catattccct	gtgtaccgca	1800
gtgtgtaccg	cagcgaaggt	cccagctgaa	acattgcatg	gaacagtcac	agtggaggtg	1860
cagtatgcag	ggacagatgg	accctgcaag	gtcccagccc	agatggcggt	agacatgcag	1920
accctgaccc	cagttggaag	gctgataacc	gccaaccttg	tgatcactga	aagtactgag	1980
aattcaaaga	tgatgttgga	gctcgaccca	ccatttgggg	attcttacat	tgtcatagga	2040
gtcggggaca	agaaaatcac	ccatcactgg	catcggagtg	gtagcaccat	cggaaaggca	2100
tttgaagcca	ctgtgagagg	tgccaagaga	atggcagtct	tgggggacac	agcctgggac	2160
tttgatcag	ttgggggtgt	gtttaattca	ttgggtaagg	gtattcacca	gatctttgga	2220
gcagctttta	aatcactggt	tggaggaatg	tcctggttct	cacagatcct	cataggcaca	2280
ctgttggtgt	ggttaggtct	gaacacaaag	aatggatcta	tctccctcac	atgcttagcc	2340
ctggggggag	tgatgatctt	cctttccacg	gctgtttctg	ctgatgttgg	gtgctcgggtg	2400
gacttctcaa	aaaaggaaac	gagatgtggc	acgggggtgt	tcgtctacaa	tgacgttgaa	2460
gcctggaggg	accggtacaa	gtaccatcct	gactcccccc	gcagattggc	agcagctgtc	2520
aagcaggctt	gggaagaggg	gatttgtggg	atctcctccg	tttcgagaat	ggaaaacatc	2580
atgtggaaat	cagtggaagg	ggagcttaat	gcaatcctag	aggagaatgg	agtccaactg	2640
acagttgtag	tggggctctgt	aaaaaacctt	atgtggagag	gtccacaaag	attgccagtg	2700
cccgtgaatg	agctgccccca	tggctggaaa	gcctggggga	aatcgtactt	tgtcagagcg	2760
gcaaagacca	acaacagttt	tgttgtcgac	ggtgacacac	tgaaggagtg	tccgctcaaa	2820
catagagcat	ggaatagctt	ccttgtggag	gatcacgggt	ttgggatctt	ccacaccagt	2880
gtttggctga	aggtcagaga	ggactactca	ttagagtgtg	accagccgt	cataggaaca	2940
gctgtcaagg	gaaaggaagc	tgcacacagt	gatctaggct	attggattga	gagtgaaaag	3000
aatgacacat	ggaggctgag	gagggctcat	ctgattgaga	tgaaaacatg	tgagtggcca	3060
aagtctcaca	cactgtggac	agatggagtg	gaagaaagtg	atctgatcat	acccaagtcc	3120
ttagctggtc	cactcagcca	ccacaacacc	agagaggggt	acagaactca	agtgaaaggg	3180
ccatggcata	gtgaagagct	cgaaatccgg	tttgaggagt	gcccaggaac	caaggttcac	3240
gtggaggaga	catgcggaac	tagaggacca	tctctgagat	caactactgc	aagtggaagg	3300
gtcatagagg	aatggtgctg	tagggaatgc	acaatgcctc	cactatcggt	ccgggcgaaa	3360
gacggctgct	ggtatggaat	ggagataagg	cccagaaagg	aaccagagag	caacttagta	3420
aggtctatgg	tgacagcagg	atcaaccgat	catatggatc	acttctctct	tggagtgcct	3480

gtgattctac	tcatgggtgca	ggaagggtttg	aagaagagaa	tgaccacaaa	gatcataatg	3540
agcacatcaa	tggcagtgct	ggtagccatg	gtcttgggag	gattctcaat	gagtgacctg	3600
gctaagcttg	tgatcctgat	gggtgccact	ttcgcagaaa	tgaacactgg	aggagatgtg	3660
gctcacttgg	cattgggttgc	ggcatttaaa	gtcagaccag	ccttgttggg	ttccttcac	3720
ttcagagcca	actggacacc	ccgtgagagc	atgctgctag	ccctggcttc	gtgtctcctg	3780
cagactgcga	tctccgctct	tgaaggcgag	ctgatgggtc	tcgttaatgg	atttgctttg	3840
gcctgggttg	caatacgagc	aatggccgtg	ccacgcactg	acaatatcgc	tctagcaatt	3900
ctggctgctc	taacaccatt	agccagaggc	acactgctcg	tggcatggag	agcgggcctc	3960
gccacttgtg	gagggttcat	gctcctttcc	ctgaaaggga	aaggtagtgt	gaagaagaac	4020
ctgccttttg	tcatggcctt	ggggttgacc	gctgtgagga	tagtggaccc	catcaatgtg	4080
gtaggactac	tgttactcac	acggagtgga	aaacggagct	ggccccctag	tgaagtgctt	4140
acagctgttg	gcctgatatg	tgcactggcc	ggaggggttg	ccaaggcaga	tatagagatg	4200
gctgggcca	tggctgcagt	aggcctgcta	attgtcagtt	atgtgggtctc	gggaaagagt	4260
gtggacatgt	acatcgaaaag	agcaggtgat	atcacatggg	aaaaagacnc	ggaagtcact	4320
ggaaacagtc	ctcggcttga	cgtggcacta	gatgagagtg	gtgatttctc	cttggtagag	4380
gaggatggcc	cacccatgag	agagatcata	ctcaagggtg	tcctgatggc	catctgtggc	4440
atgaacccaa	tagccatacc	cttcgctgca	ggagcgtggg	atgtgtatgt	aaagactgga	4500
aaaaggagtg	gtgccctctg	ggacgtgcct	gctcccaaag	aagtgaaaaa	aggagagact	4560
acagatggag	tgtacagagt	gatgactcgc	agactgctgg	gttcaacaca	ggttggagtg	4620
ggagtcatgc	aagagggagt	cttccacacc	atgtggcacg	tcacaaaagg	agccgcattg	4680
aggagcggtg	aaggaagact	tgatccatat	tggggggacg	tcaagcagga	cttggtgtca	4740
tattgtgggc	cgtggaagtt	ggatgcagcc	tgggatggac	taagtgaagt	gcagcttttg	4800
gccgtacccc	ccggagagag	ggctagaaac	attcagactc	tgcttggaat	attcaagaca	4860
aaggatgggg	acatcggagc	agtcgctcta	gactaccccg	caggaacctc	aggatctcca	4920
atcctagaca	aatgcggaag	agtgatagga	ctttatggca	atgggggttg	gatcaagaat	4980
ggaagctatg	ttagtgccat	aaccagggga	aaaagggagg	aggaggctcc	agttgagtgc	5040
tttgaaccct	cgatgctgag	gaagaagcag	ctaacagtct	tggatctgca	tccaggagcc	5100
gggaaaacca	ggaggggttct	tcctgaaata	gtccgtgaag	ccataaagaa	gagacttcgc	5160
acattgatcc	tagcaccaac	cagggtcgtt	gctgctgaga	tggaggaagc	cctaagagga	5220

cttcnngtgc gttacatgac aacagcagtc aacgtcaccc attctgggac agaaatcgtt	5280
gatttgatgt gccatgccac tttcacttca cgcttactac aacccatcag agtcacctaat	5340
tacaatctca acatcatgga tgaagccac ttcacagacc cctcaagtat agctgcaaga	5400
ggatacatat caacaagggg tgaaatgggc gaggcggctg ccatttttat gactgccaca	5460
ccaccaggaa cccgtgatgc gtttcctgac tctaactcac caatcatgga cacagaagtg	5520
gaagtcccag agagagcctg gagctcaggc ttgactggg tgacggacca ttctgggaaa	5580
acaatttggt ttgttccaag tgtgagatct ggagaagaaa gcgcagcctg tctgacaaag	5640
gctggaaagc gggttataca gctcagcagg aagacttttg agacagagtt tcagaagaca	5700
aaaaatcaag agtgggactt tgtcataaca actgacattt cagagatggg tgccaatttc	5760
aaggctgacc gggcataga ttccaggaga tgcctaaagc cagtcatact cgatggtgag	5820
agagtcatcc tggctgggcc catgcctgtc acgcatgcc gtgctgctca gaggagagga	5880
cgtataggca ggaaccccaa caaacctgga gatgagtaca tgtatggagg tgggtgtgca	5940
gagactgatg aagaccatgc aactggctt gaagcaagaa tgcttcttga caacatttac	6000
ctccaggatg gcctcatagc ctcgctctat cggcctgagg ccgacaaggt agccgccatt	6060
gagggagagt tcaagctgag gacagagcaa aggaagacct ttgtggaact catgaagaga	6120
ggagaccttc ccgtttggct ggcctatcaa gtagcatctg ccggaataac ttacacagac	6180
agaagatggg gctttgatgg cactaccaac aacaccataa tggaagacag tgtaccagca	6240
gaggtgtgga ccaagtatgg agagaagaga gtgcttaaac cgaggtggat ggatgctagg	6300
gtctgttcag atcatgcggc tttgaagtgc ttcaaagaat ttgccgctgg gaagagagga	6360
gcggctttgg gagtgatgga tgccctggga acattgccag gacacatgac agagaggttt	6420
caggaagcca ttgacaatct cgctgtgctc atgcgagcag agactggaag taggccctac	6480
aaagcagcgg cagctcaact gccggagacc ctagagacca tcatgctttt gggcttattg	6540
ggaacagttt cgctaggaat cttctttgtc ttgatgcgga acaagggcat cgggaagatg	6600
ggcttcggaa tggtaaccct tggggccagc gcatggctca tgtggctttc ggaaattgaa	6660
ccagccagaa tcgcatgtgt cctcattgtc gtgtttttgt tactggtggg gctcataccc	6720
gagccagaga agcaaagatc tcccaggat aatcaaattg caatcatcat catggtggca	6780
gttggccttc tgggtttgat aacagcaaat gaactcggat ggctggaaag gacaaaaagt	6840
gatatagctc atctaattgg aaggaaagaa gaggggacaa ccataggatt ctcaatggat	6900
attgatctgc ggccagcctc cgctgggct atttatgccg cattgacaac tctcatcacc	6960

ccagccgtcc	aacatgcggt	aaccacctca	tacaacaact	actccctgat	ggcgatggcc	7020
acacaagctg	gagtgcctgtt	tggcatgggc	aaagggatgc	catttttatgc	atgggacttt	7080
ggagtcccg	tgctaattgat	gggttgctac	tcacaattaa	cacccttgac	cctgatagtg	7140
gccatcattc	tgcttggtggc	acactacatg	tacttgatcc	caggtttgca	ggcagcagca	7200
gcacgtgctg	cccagaagag	gacagcagct	ggcatcatga	agaatcccgt	tgtggatgga	7260
atagtgggtga	ctgacattga	cacaatgaca	attgaccccc	aagtggagaa	gaagatggga	7320
caagtgttac	tcatagcagt	agctgtctcc	agtgcctgtgc	tgctgcggac	cgcttgggga	7380
tggggggagg	ctggggctct	gatcacagca	gcaacctcca	ccttatggga	aggctctcca	7440
aacaaatact	ggaactcctc	cacagccacc	tcactgtgca	acatctttag	aggaagttat	7500
ttggcagggg	cttcccttat	ttacacagtg	acaagaaatg	ccggtctggt	taagagacgt	7560
ggaggtggaa	cgggagagac	cctgggagag	aagtggaaag	ccgcctgaa	ccagatgtcg	7620
gccttgaggt	tttactctta	caaaaagtca	ggcatcacccg	aagtgtgtag	ggaggaggcg	7680
cgccgcgccc	tcaaggatgg	agtggccaca	ggaggacatg	ctgtatccccg	gggaagcgca	7740
aagcttagat	ggttggtaga	gagaggatac	ctgcagcccc	atggaaagggt	tgttgacctt	7800
ggatgtggca	gaggaggctg	gagttattac	gctgccacca	tccgtaaagt	gcaggaggtc	7860
agaggataca	caaagggagg	tcttggtcat	gaagaacca	tgctggtgca	aagctatggg	7920
tggaacatag	ttcgccctcaa	gagtggagtg	gacgtcttcc	acatggcggc	tgagccgtgt	7980
gacactctgc	tgtgtgacat	cggcgagtca	tcatctagtc	ctgaagtgga	agagacgca	8040
acactcagag	tgctctccat	ggtgggagac	tggcttgaga	aaagaccagg	ggccttctgc	8100
ataaagggtgc	tgtgcccata	caccagcaca	atgatggaga	ccatggagcg	actgcaacgt	8160
aggcatgggg	gaggattggt	cagagtgcc	ttgtcccga	actccacaca	tgagatgtat	8220
tgggtctctg	gagccaaaag	taacatcata	aagagtgtgt	ccaccacaag	tcagctcctc	8280
ttgggacgca	tggatggggc	taggaggcca	gtgaaatatg	aggaggatgt	gaacctcggc	8340
tcaggcacac	gagctgtggc	aagctgcgct	gaggctccca	acatgaagat	cattggtagg	8400
cgcattgaga	gaatccgcaa	tgaacatgca	gagacatggt	tctttgatga	aaaccacca	8460
tacaggacat	gggcctacca	tgggagctac	gaagcccca	cgcaggggtc	agcgtcatcc	8520
ctcgtgaacg	gggttggttag	actcttgctca	aaaccctggg	atgtggtgac	tggagttaca	8580
ggaatagcta	tgactgacac	cacgccatac	ggccaacaaa	gagtcttcaa	ggaaaaagtg	8640
gacactaggg	tgccagatcc	ccaagaaggc	actcgccaag	taatgaacat	ggtctcgtct	8700

tggctatgga	aggagctggg	aaaacgcaag	cggccacgtg	tctgcacca	agaagagttc	8760
attaataagg	tgcgagcaa	tgagcactg	ggagcaatat	ttgaagagga	aaaagaatgg	8820
aagacagctg	tagaagctgt	gaatgatcca	agatttttggg	ctctagtgga	caaggaaaga	8880
gaacaccacc	tgagaggaga	gtgtcacagc	tgtgtgtaca	acatgatggg	taaaagagaa	8940
aagaagcaag	gagaattcgg	gaaagcaaaa	ggcagccgcg	caatctggta	catgtggttg	9000
ggagccagat	ttttggagtt	tgaagctctt	ggattcttga	acgaggacca	ctggatggga	9060
agagaaaact	caggaggttg	cgttgaaggg	ctaggactgc	aaaggcttgg	atatatccta	9120
gaagaaatga	accgggcacc	aggaggaaag	atgtatgcag	atgacaccgc	tggctgggac	9180
acccgcatta	gcaagtttga	tctagagaat	gaagccctga	tcactaacca	gatggaagaa	9240
gggcacagag	ctctggcggt	ggccgtgatt	aaatacacat	acaaaacaa	agtgggtgaag	9300
gttctcagac	cagctgaagg	agggaaaaca	gtcatggaca	tcattctcaag	acaagaccag	9360
agagggagcg	gacaagttgt	tacttatgct	ctcaacacat	tcaccaacct	ggtggtgcag	9420
cttatccgga	acatggaggc	tgaggaagtg	ctagagatgc	atgatctatg	gttggttgagg	9480
aagccagaga	aagtgaccag	atggttgcag	agcaatggat	gggacagact	caaacggatg	9540
gcagttagtg	gagatgactg	cgttgtaaag	ccaattgatg	ataggtttgc	acatgccttc	9600
aggttcttga	atgacatggg	aaaggttagg	aaagacacac	aggaatggaa	accctcgact	9660
ggatggagca	attgggaaga	gtcccgttc	tgttctcacc	acttcaacaa	gctgcacctc	9720
aaggacggga	gatccattgt	gtcccctgc	cgccaccaag	atgaactgat	tggccgagcc	9780
cgtgtctcac	caggggcagg	atggagcatc	cgggagactg	cttgtcttgc	aaaatcatat	9840
gcacagatgt	ggcagcttct	ttatttccac	aaaagagacc	tccgactgat	ggccaatgcc	9900
atttgttcgg	ctgtgccagt	tgactgggta	ccaactggga	gaaccacctg	gtcaatccat	9960
ggaaagggag	aatggatgac	tactgaggac	atgctcatgg	tgtggaatag	agtgtggatt	10020
gaggagaacg	accacatgga	ggacaagacc	cctgtaacaa	aatggacaga	cattccctat	10080
ttggggaaaa	gggaggactt	atggtgtgga	tcccttatag	ggcacagacc	tcgcaccact	10140
tgggctgaga	acatcaaaga	cacagtcaac	atggtgcgta	ggatcatagg	tgatgaagaa	10200
aagtacatgg	actacctatc	cacccaagta	cgctacttgg	gtgaggaagg	gtccacacct	10260
ggagtgctgt	aa					10272

<210> 77

<211> 10272

<212> DNA
 <213> Zika virus strain ArB1362 polyprotein gene, complete cds

<220>
 <221> misc_feature
 <222> (1336)..(1356)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (5225)..(5226)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (5229)..(5229)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (8947)..(8947)
 <223> n is a, c, g, or t

<400> 77
 atgaaaaacc caaagaagaa atccggagga ttccggattg tcaatatgct aaaacgcgga 60
 gtagcccgctg taaaccacctt gggagggttg aagaggctgc cagccggact tctgctgggt 120
 catggacca ttagaatggt tttggcgata ctagcctttt tgagatttac agcaatcaag 180
 ccatcactgg gcctcatcaa tagatggggg tcaagtggga aaaaagaggc tatggagata 240
 ataaagaagt ttaagaaaga tcttgctgcc atgttgagaa taatcaatgc taggaaggag 300
 aggaagagac gtggtgcaga caccagtatc ggaatcattg gcctcctgct gactacagcc 360
 atggcagcag agattactag acgaggaagt gcatactaca tgtacttgga caggagcgat 420
 gctgggaagg ccatttcctt tgctaccaca ttgggagtga acaaatgcca tgtacagatc 480
 atggatctcg ggcacatgtg tgacgccacc atgagttatg agtgccttat gctagacgaa 540
 ggagtggaac cagatgatgt cgattgctgg tgcaacacga catcaacttg ggttgtgtac 600
 ggaacctgtc atcacaaaaa aggtgaagca cggcgatcta gaagagctgt gacgctccct 660
 tctcactcca caaggaagtt gcaaacgcgg tcgcagacct ggtagaatc aagagaatac 720
 acgaagcact tgatcaaggt tgaaaactgg atattcagga accccggggt tgcgctagcg 780
 gctgttgcca ttgcttggt tctgggaagt tcgacgagcc aaaaagtcac atacttgatc 840
 atgatactgc tgattgcccc ggcatacagc atcaggtgca ttggagtcag caacagagac 900
 ttcgtggaag gcatgtcagg tgggacctgg gttgatgtcg tcttggaaca tggaggttgc 960
 gtcaccgtaa tggcacagga caagccaaca gttgacatag agttgggtcac gacaacggtt 1020

agcaacatgg ctgaggtaag atcctactgc tacgaggcat caatatcgga catggcttcg	1080
gatagtcgct gccaacaca aggtgaagcc taccttgaca agcaatcaga cactcaatat	1140
gtttgcaaaa gaacattggg ggacagaggt tggggaaatg ggtgtggact ttttggcaaa	1200
gggagcctgg tgacatgtgc caagttcacg tgttccaaga agatgaccgg gaagagcatc	1260
cagccggaga atctggagta tcgaataatg ctatcggcgc atggctccca gcacagcggg	1320
atgattgtta atgacnnnnn nnnnnnnnnn nnnnnnaaca gagcggaagt cgaggtcacg	1380
cctaattcac caagagcaga agcaaccttg ggaggctttg gaagttagg acttgattgt	1440
gaaccaagga caggccttga cttttcagat ttgtattacc tgaccatgaa caataagcac	1500
tggtagtcc acaaagagtg gtttcatgac atcccattgc cttggcatgc tggggcagac	1560
accggaactc cacactggaa caacaagag gcattggtag agttcaagga tgcccacgcc	1620
aagaggcaaa ccgtcgtcgt tctggggagc caggaaggag ctgttcacac ggctcttgct	1680
ggagctttgg aggctgagat ggatggcgca aaaggaaggc tgttctctgg ccatttga	1740
tgccgcctaa aaatggacaa gcttagattg aaggcggtgt catattcctt gtgcaccgca	1800
gcgttcacat tcaccaaggt ccagctgaa aactgcatg gaacagtcac agtggaggtg	1860
cagtatgcag ggacagatgg accctgcaag gtcccagccc agatggcggg ggacatgcag	1920
actttgaccc cagtcggaag gctgataact gccaaacccg tgattactga aagcactgaa	1980
aattcaaaga tgatgttgga gctcgacca ccatttgggg attcttacat tgtcatagga	2040
gttgagagata agaaaatcac ccaccactgg cataggagtg gtagcaccat cggaaaagca	2100
tttgaggcca ctgtgagagg tgccaagaga atggcagttt tgggggacac agcttgggac	2160
tttggatccg tcgggggtgt gttcaactca ttgggcaagg gcatccacca gatctttgga	2220
gcagccttca aatcactgtt tggaggaatg tcttggttct cacagatcct cataggcacg	2280
ctgctagtgt ggttgggctt gaacacaaag aatggatcca tctccctcac atgcttggcc	2340
ctggggggag tgatgatctt cctctccacg gctgtttctg ctgatgtggg gtgctcggtg	2400
gacttctcaa aaagagaaac gagatgtggc acgggggtgt tcgtctacaa tgacgttgaa	2460
gcctggaggg ataggtacaa gtaccatcct gactcccccc gcagattggc agcagcagtc	2520
aagcaggctt gggaagaggg gatttgtggg atctcctccg tttcaagaat ggaaaacatc	2580
atgtggaaat cagtggaagg ggagctcaat gctatcttag aggagaatgg agttcaactg	2640
acagttgttg tgggatctgt aaaaaacccc atgtggagag gtccacaaag attgccagtg	2700
cctgtaaatg agctgccccca tggctggaaa gcctggggga aatcatatct tgtcagagcg	2760

gcaaagacca	acaacagttt	tgttgtcgac	ggtgacacac	tgaaggaatg	tccgctcaaa	2820
cacagagcat	ggaacagttt	ccttgtggag	gatcacgggt	ttgggggtctt	ccacactagt	2880
gtttggctta	aggttagaga	agattactca	ctagagtgtg	accagaccgt	cataggaaca	2940
gctgttaagg	gaaaggaggc	cgcgcacagt	gatctaggct	actggattga	aagtgaaaag	3000
aatgacacat	ggaggttgaa	gagggcccac	ctgattgaga	tgaaaacatg	tgagtggcca	3060
aagtctcaca	cactgtggac	agatggagta	gaagaaagtg	atctgatcat	acccaagtct	3120
ttagctggtc	cactcagcca	ccacaacacc	agagaggggt	acagaactca	ggcaaaaggg	3180
ccatggcata	gtgaagagct	tgaaatccgg	tttgaggaat	gtccaggcac	caaggttcac	3240
gtggaggaga	catgcggaac	tagaggacca	tctctgagat	caaccactgc	aagtggaagg	3300
gtcattgagg	aatggtgctg	tagagaatgc	acaatgcccc	cactatcatt	tcgagcgaaa	3360
gacggctgct	ggtatggaat	ggagataagg	cccaggaaaag	aaccagagag	caatttagtg	3420
aggtcaatgg	tgacagcggg	atcaaccgat	cacatggacc	acttctctct	tggagtgcct	3480
gtgattctac	tcatggtgca	ggaagggctg	aagaagagaa	tgaccacgaa	gatcattgtg	3540
agcacatcaa	tggcagtgct	ggtagccatg	atcttgggag	gattctcaat	gagtgcctg	3600
gctaagcttg	tgatcctgat	gggtgctact	ttcgcagaaa	tgaatactgg	aggagatgtg	3660
gctcacttgg	cattggctcg	ggcattcaaa	gtcagaccag	ccttgctggg	ctccttcatt	3720
ttcagagcca	attggacacc	ccgtgagagc	atgctgctag	ccctggcttc	gtgtcttttg	3780
caaactgcaa	tttcagctct	tgaaggtgac	ttgatgggcc	tcgttaatgg	atttgctttg	3840
gcctggttgg	caatacgagc	aatggccgtg	ccacgcactg	acaacattgc	tctagcaatc	3900
ctggctgctc	tgacaccact	agcccagagg	acactgctcg	tggcatggag	agcgggcctc	3960
gccacttgtg	gagggttcat	gctcctctcc	ttgaaaggaa	aaggtagtgt	gaagaagaac	4020
ctgccatttg	tcatggcctt	gggaatgacc	gctgtgagga	tagtggaccc	cattaacgtg	4080
gtgggactac	tactactcac	aaggagtggg	aagcggagct	ggccccccag	tgaagtgcct	4140
acagctgttg	gcctgatatg	tgactgggcc	ggagggtttg	ccaaggcaga	cattgagatg	4200
gctgggcca	tggctgcagt	aggcttgcta	attgtcagtt	atgtggtctc	aggaaagagt	4260
gtggatatgt	acattgaaaag	agcaggtgac	atcacatggg	aaaaagacgc	ggaagttact	4320
ggaaatagtc	ctcggcttga	cgtggcacta	gatgagagtg	gtgatttctc	tctggtagag	4380
gaagatggtc	cacccatgag	agagatcata	ctcaagggtg	tcctgatggc	catctgtggc	4440
atgaacccaa	tagccatacc	ttttgctgca	ggagcgtggg	atgtgtatgt	gaagactggg	4500

aaaaggagtg	gtgccctctg	ggatgtgcca	gctcctaaag	aagtgaaaaa	aggagagacc	4560
acagatggag	tatacagagt	gatgacccgc	agattgctgg	gttcaacaca	ggttgagagt	4620
ggagtcatgc	aggagggagt	cttccacacc	atgtggcacg	tcacaaaagg	agccgcactg	4680
aggagcggtg	aagggagact	tgatccatac	tggggtgatg	tcaagcagga	cttggtgtca	4740
tactgtgggc	cttggaagct	ggatgcagct	tgggatggac	ttagtgaggt	gcagctcttg	4800
gcagtacctc	ccggagagag	ggccagaaac	atccagactc	tgcttgggaat	attcaagaca	4860
aaggatgggg	acatcggagc	agttgctctg	gactaccccg	caggaacctc	aggatctccg	4920
atcctagaca	aatgcggaag	agtgatagga	ctttatggca	atggggttgt	gatcaagaat	4980
ggaagctatg	ttagtgccat	aaccaggga	aagagggagg	aggagactcc	ggttgaatgt	5040
ttcgaaccct	cgatgctgaa	gaagaagcag	ctaactgtcc	tggacctgca	tccaggagcc	5100
ggaaagacta	ggagagttct	tcttgaaata	gtccgtgaag	ccataaaaaa	gagactccgc	5160
acagtgatct	tggctccaac	cagggttgtc	gctgctgaga	tggaggaagc	cttgagagga	5220
cttcnngtnc	gttacatgac	aacagcagtc	aacgtcaccc	attctggggac	agaaatcggt	5280
gatttgatgt	gccatgccac	tttcacttca	cgcttactac	aacccatcag	agtcctaat	5340
tacaatctca	acatcatgga	tgaagccac	ttcacagacc	cctcaagtat	agctgcaaga	5400
ggatacatat	caacaagggg	tgaaatgggc	gaggcggctg	ccatttttat	gactgccaca	5460
ccaccaggaa	cccgtgatgc	gtttcctgac	tctaactcac	caatcatgga	cacagaagtg	5520
gaagtcccag	agagagcctg	gagctcaggc	tttgattggg	tgacagacca	ttctgggaaa	5580
acagtttggt	tcgttccaag	tgtgagaaat	ggaaatgaaa	tcacagcctg	cctgacaaaag	5640
gctggaaagc	gggtcataca	gctcagcagg	aagacttttg	agacagagtt	ccagaaaaca	5700
aaaaaccaag	agtgggactt	tgtcataaca	actgacatct	cagagatggg	cgccaatttc	5760
aaggctgacc	gggtcataga	ctctaggaga	tgccataaagc	cagtcatact	tgatggtgag	5820
agagtcatct	tggctggggc	catgcctgtc	acgcatgcta	gtgctgctca	gaggagagga	5880
cgtataggca	ggaaccctaa	caaacctgga	gatgagtaca	tgtatggagg	tgggtgtgca	5940
gagactgatg	aagaccacgc	acactggctt	gaagcaagaa	tgcttcttga	caacatctac	6000
ctccaggatg	gcctcatagc	ctcgtcttat	cggcctgagg	ccgataaggt	ggccgccatt	6060
gagggagagt	ttaagctgag	gacagagcaa	aggaagacct	ttgtggaact	tatgaagaga	6120
ggagaccttc	ccgtttggct	agcctatcag	gttgcatctg	ccggaataac	ttacacagac	6180
agaagatggt	gctttgatgg	cacaactaac	aacaccataa	tggaagacag	tgtaccagca	6240

gaggtgtgga	caaaatatgg	agagaagaga	gtgctcaaac	caagatggat	ggatgctaga	6300
gtctgttcag	atcatgccgc	cctgaagtcg	ttcaaagagt	ttgctgcccg	gaaaagagga	6360
gcggcttttg	gagtaatgga	ggccctggga	acattgccag	gacacatgac	agagaggttt	6420
caggaagcca	ttgacaatct	cgctgtgctt	atgcgagcag	aaactggaag	caggccttac	6480
aaggcagcgg	cagccccact	gccggagacc	ctagagacca	tcatgctctt	aggtttgctg	6540
ggaacagttt	cgttggggat	attctttgtc	ttgatgcgga	acaagggcat	cggaagatg	6600
gggttttgaa	tggtaactct	tggggccagt	gcatggctca	tgtggctttc	ggaaattgaa	6660
ccagccagaa	ttgcatgtgt	cctcattgtt	gtgtttttgt	tactggtggt	actcatacct	6720
gagccagaga	agcaaagatc	tccccaggat	aaccagatgg	caatcatcat	catggtggca	6780
gtgggccttc	tggggttgat	aactgcaaat	gaacttggat	ggctggaaag	aacaaaaaat	6840
gacatagctc	atctaattgg	aaggagagaa	gaaggagtaa	ctatgggatt	ctcaatggac	6900
atcgatttga	ggccggcctc	cgctggggct	atctatgctg	cattgacaac	tctcatcacc	6960
ccagccgtcc	aacatgcggt	aaccacttca	tataacaact	actccttaat	ggcgatggcc	7020
acacaagctg	gagtgcctgt	tggcatgggc	aaagggatgc	catttttatgc	atgggacttt	7080
ggagtcccg	tgctaattgat	gggttgctac	tcacaattaa	caccctgac	cctgatagtg	7140
gctatcattc	tgcttggtgg	acactacatg	tacttgatcc	caggcctaca	ggcagcagca	7200
gcgcgtgctg	cccagaagag	aacagcagct	ggcatcatga	agaatcccg	tgtggatgga	7260
atagtggtaa	ctgacattga	cacaatgaca	attgaccccc	aagtggagaa	gaagatggga	7320
caagtgttac	tcatagcagt	agccatctcc	agtgcctgtc	tgctgcccgc	tgcttgggga	7380
tggggggaag	ctggagctct	gatcacagca	gcaacctcca	ctttgtggga	aggttctcca	7440
aacaaatact	ggaactcctc	tacagccacc	tcactgtgca	acatcttttag	aggaagttac	7500
ctggcaggcg	cttctcttat	ttacacagtg	acaagaaatg	ctggcctggt	caagagacgt	7560
ggaggtggaa	cgggagagac	tctaggagag	aagtggaaag	ctgcctgaa	tcagatgtcg	7620
gccctggagt	tctactctta	caaaaagtcg	ggcatcactg	aagtgtgtag	agaggaggct	7680
cgccgcgccc	tcaaggatgg	agtggccaca	ggaggacatg	ctgtatcccc	gggaagcgca	7740
aagctcagat	ggctgggtgga	gagaggatac	ctgcagcccc	atggaaaggt	tgttgacctc	7800
ggatgtggca	gagggggttg	gagctattat	gccgctacca	tccggaaagt	gcaggaggtg	7860
aaaggataca	caaagggagg	tcccggtcac	gaagaacca	tgctggtgca	aagctatgga	7920
tggaacatag	ttcgtctcaa	gagtggagtg	gacgtcttcc	acatggcggc	tgagccgtgt	7980

gatactctgc	tgtgtgacat	aggtgagtca	tcattccagtc	ctgaagtaga	agagacgcga	8040
acactcagag	tgctctctat	ggtggggggac	tggcttgaaa	aaagaccagg	ggccttctgc	8100
ataaaggtgc	tgtgcccata	caccagcact	atgatggaga	ccatggagcg	actgcaacgt	8160
aggtatgggg	gaggattagt	cagagtgcc	ttgtctcgca	actccacaca	tgagatgtat	8220
tgggtctctg	gagcaaaaag	caacatcata	aaaagtgtgt	ccaccacaag	ccagctcctc	8280
ctgggacgca	tggatggggc	caggaggcca	gtgaaatatg	aggaggatgt	gaacctcggc	8340
tcgggcacac	gagctgtggc	aagctgtgct	gaggctccca	acatgaagat	cattggtaag	8400
cgcattgaga	gaatccgcag	tgaacatgca	gaaacatggt	tctttgatga	aaaccacca	8460
tacaggacat	gggcttacca	tgggagctac	gaagcccca	cgcaagggtc	agcgtcttcc	8520
ctcgtgaatg	gggttggttag	gctcctgtca	aagccctggg	atgtagtgc	tgagattaca	8580
ggaatagcta	tgactgacac	cacaccatat	ggccaacaaa	gagtcttcaa	agaaaaagtg	8640
gacaccagg	tgccagatcc	ccaagaaggc	actcgccaga	caatgaacat	ggtctcgctc	8700
tggctgtgga	aggagctggg	aaaacgcaag	cggccacgcg	tctgcaccaa	agaagagttc	8760
atcaacaagg	tgcgagcaa	tgcagcgctg	ggagcaatat	ttgaagagga	aaaagaatgg	8820
aagacggccg	tggaagctgt	gaatgatcca	aggttttggg	ccctagtggg	taaggagaga	8880
gagcatcacc	taagaggaga	gtgtcatagc	tgtgtgtaca	acatgatggg	aaaaagagag	8940
aagaagnaag	gagaattcgg	gaaagcaaaa	ggcagccgcg	ccatctggta	catgtggttg	9000
ggagccagg	ttctggagtt	tgaatcactg	gggtttctga	atgaagatca	ctggatggga	9060
agagagaact	caggaggtgg	tgtcgaagg	ctaggactgc	aaagacttgg	atatattcta	9120
gaagaaatga	atcgggcacc	aggaggaaag	atgtatgcag	atgacaccgc	tggttgggat	9180
accgcatta	gtaagtttga	tctggagaat	gaagccttga	ttaccaacca	aatggaggaa	9240
gggcacagag	ctctggcggt	ggctgtgatt	aaatacacat	acaaaacaa	agtgggtgaag	9300
gtccttagac	cagctgaagg	aggaaaaaca	gttatggaca	tcatttcaag	acaagaccag	9360
agagggagt	ggcaagttgt	cacttatgct	ctcaacacgt	ttaccaactt	agtgggtgcag	9420
cttattcgga	acatggaggc	tgaggaagt	ttagagatgc	aagacttatg	gctgttgagg	9480
aagccagaga	aagtgactag	atggttgcag	agtaatggat	gggacagact	caaacgaatg	9540
gcagtcaagt	gagatgactg	tggtgtgaag	ccaattgatg	ataggtttgc	atgctgcctc	9600
aggttcctaa	acgacatggg	gaaagttagg	aaagacacac	aggaatggaa	accctcgact	9660
ggatggagca	attgggaaga	agtccttttc	tgctcccacc	acttcaacaa	gctgcacctc	9720

aaggatggta gatccattgt ggtcccttgc cgccaccaag atgaactgat tggccgagcc	9780
cgtgtatcac caggggcagg atggagcatc cgggagactg cctgtcttgc aaaatcatat	9840
gcacagatgt ggcagcttct ttacttccac agaagagacc ttcgactgat ggccaacgcc	9900
atttgttcgg ctgtgccagt cgactgggta ccaaccggga gaaccacctg gtcaatccac	9960
gggaagggag aatggatgac cactgaggac atgctcatgg tgtggaatag agtgtggatt	10020
gaggagaacg accatatgga ggacaagact cctgtaacaa agtggactga cattccctac	10080
ctgggaaaaa gggaggactt atgggtgtgga tcccttatag ggcacagacc ccgcaccact	10140
tgggctgaga acatcaaaga cacagtcaac atgggtgcga ggatcatagg tgatgaagaa	10200
aaatacatgg actacctatc cacccaagtc cgctacttgg gtgaggaagg gtccacacct	10260
ggagtgttgt aa	10272

<210> 78

<211> 10272

<212> DNA

<213> Zika virus polyprotein gene, complete cds GenBank: EU545988.1

<400> 78

atgaaaaacc ccaaagaaga aatccggagg atccggattg tcaatatgct aaaacgcgga	60
gtagcccgctg tgagcccctt tgggggcttg aagaggctgc cagccggact tctgctgggt	120
catgggcca tcaggatggc cttggcgata ctagcctttt tgagattcac ggcaatcaag	180
ccatcactgg gtctcatcaa tagatggggg tcaagtggga aaaaagaggc tatggaaata	240
ataaagaagt tcaagaaaga tctggctgcc atgctgagaa taatcaatgc taggaaggag	300
aagaagagac gaggcacaga tactagtgtc ggaattgttg gcctcctgct gaccacagcc	360
atggcagtgg aggtcactag acgtgggagt gcatactata tgtacttgga cagaagcgat	420
gctggggagg ccatatcttt tccaaccaca ctggggatga acaagtgtta catacagatc	480
atggatcttg gacacatgtg tgatgccacc atgagctatg aatgccctat gttggatgag	540
ggggtagaac cagatgacgt cgattgttgg tgcaacacga catcaacttg ggttgtgtac	600
ggaacctgcc accacaaaaa aggtgaagca cggagatcta gaagagctgt gacgctcccc	660
tcccattcca ctaggaagct gcaaacgcgg tcgcagacct ggttggaatc aagagaatat	720
acaaagcacc tgattagagt cgaatttgg atattcagga accctggctt cgcgttagca	780
gcagctgcca tcgcctggct tttgggaagt tcaacgagcc aaaaagtc atacttggtc	840
atgatactgc tgattgcccc ggcatcacgc atcaggtgca taggagtcag caatagggac	900

tttgtggaag gtatgtcagg tgggacttgg gttgatgttg tcttggaaca tggaggttgt	960
gttaccgtaa tggcacagga caaaccggct gtcgacatag agctggttac aacaacagtc	1020
agcaacatgg cggaggtaag atcctattgc tatgaggcat caatatcgga catggcttcg	1080
gacagccgct gccaacaca aggtgaagcc taccttgaca agcagtcaga cactcaatat	1140
gtctgcaaaa gaacgttagt ggacagaggc tggggaaatg gatgtggact ttttggcaaa	1200
gggagcctgg tgacatgcmc taagtttgca tgctccaaga aaatgaccgg gaagagcatc	1260
cagccagaga atctggagta ccggataatg ctgtcagttc atggctccca gcacagtggg	1320
atgatcgta atgacacagg acatgaaact gatgagaata gagcgaaggt tgagataacg	1380
cccaattcac caagagctga agccaccctg ggggggtttt gaagcctagg acttgattgt	1440
gaaccgagga caggccttga cttttcagat ttgtattact tgactatgaa taacaagcac	1500
tggttggttc acaaggagtg gttccacgac attccattac cttggcatgc tggggcagac	1560
accggaactc cacattggaa caacaaagaa gcattggtag agttcaagga cgcacatgcc	1620
aaaaggcaaa ctgtcgtggt tctagggagt caagaaggag cagttcacac ggccttgct	1680
ggagctctgg aggctgagat ggatggtgca aagggaaggc tgtcctctgg ccacttgaaa	1740
tgctgcctga aaatggataa acttagattg aagggcgtgt catactcctt gtgtaccgca	1800
gcgttcacat tcaccaagat cccggctgaa aactgcacg ggacagtcac agtggaggta	1860
cagtacgcag ggacagatgg accctgcaag gttccagctc agatggcggg ggacatgcaa	1920
actctgacct cagttgggag gctgataacc gctaaccctg taatcactga aagcactgag	1980
aactctaaga tgatgctgga acttgatcca ccatttgggg actcttacat tgtcatagga	2040
gtcggggaga agaagatcac ccatcactgg cacaggagtg gcagcaccat tggaaaagca	2100
tttgaagcca ctgtgagagg tgccaagaga atggcagtct tgggagacac agcctgggat	2160
tttggatcag ttggaggtgc tctcaactca ttgggcaagg gcatccatca aatttttggg	2220
gcagctttca aatcattgtt tggaggaatg tcctggttct cacaaattct cattggaacg	2280
ttgctggtgt ggttgggtct gaatacaaag aatggatcta tttcccttac gtgcttgcc	2340
ttagggggag tgttgatctt tttatccaca gccgtctctg ctgatgtggg gtgctcggtg	2400
gacttctcaa agaaggaaac gagatgcggg acgggggtgt tcgtctataa cgacgttgat	2460
gcctggaggg acaggtacaa gtaccatcct gactcccctc gtagattagc agcagcagtc	2520
aagcaagcct gggragatgg gatctgtggg atctcctctg tttcaagaat ggaaaacatc	2580
atgtggagat cagtagaagg ggagctcaac gcaatcctgg aagagaatgg agttcaactg	2640

acggtcgttg	tgggatctgt	aaaaaacccc	atgtggagag	gtccacagag	attgcccggtg	2700
cctgtgaacg	agctgcccc	cggtctggaag	gcttggggga	aatcgtactt	cgtcagagca	2760
gcaaagacaa	ataacagctt	tgtcgtggat	ggtgacacac	tgaaggaatg	cccactcaaa	2820
catagagcat	ggaacagctt	tcttgtggag	gatcatgggt	tcgggggtatt	tcacactagt	2880
gtctgggtca	aggttagaga	agattattca	ttagagtgtg	atccagccgt	tattggaaca	2940
gctgctaagg	gaaaggaggc	tgtgcacagt	gatctaggct	actggattga	gagtgagaag	3000
aatgacacat	ggaggctgaa	gagggcccac	ctgatcgaga	tgaaaacatg	tgaatggcca	3060
aagtcccaca	cattgtggac	agatggaata	gaagaaagtg	atctgatcat	acccaagtct	3120
ttagctgggc	cactcagcca	tcacaacacc	agagagggt	acaggactca	aatgaaaggg	3180
ccatggcaca	gtgaagagct	tgaaattcgg	tttgaggaat	gcccaggcac	taagggtccac	3240
gtggaggaaa	catgtggaac	aagaggacca	tctctgagat	caaccactgc	aagcggaagg	3300
gtgatcgagg	aatggtgctg	cagggaatgc	acaatgcccc	cactgtcggt	ccgggctaaa	3360
gatggctgtt	ggtatggaat	ggagataagg	cccaggaaa	aaccagaaa	taacttagta	3420
aggtcaatgg	tgactgcagg	atcaactgat	cacatggatc	acttctccct	tggagtgtt	3480
gtgattctgc	tcatggtgca	ggaagggctg	aagaagagaa	tgaccacaaa	gatcatcata	3540
agcacatcaa	tggcagtgt	ggtagctatg	atcctgggag	gattttcaat	gagtgcctg	3600
gccaagcttg	caattttgat	gggtgccacc	tttgcgaaa	tgaacactgg	aggagatgta	3660
gctcatctgg	cgctgatagc	ggcattcaaa	gtcagacctg	cgttgctgg	atctttcatc	3720
ttcagagcta	attggacacc	ccgtgagagc	atgctgctgg	ccctggcttc	gtgtcttctg	3780
caaactgcga	tctccgcctt	ggaaggcgac	ctgatggttc	tcatcaatgg	ttttgctttg	3840
gcctggttgg	caatacgagc	gatggttgtt	ccacgcactg	acaacatcac	cttggcaatc	3900
ctgactgcgc	tgacaccact	ggcccggggc	acgtgcttg	tggcgtggag	agcaggcctt	3960
gctacttgcg	gggggttcat	gcttctctct	ctgaagggga	agggcagtgt	gaagaagaac	4020
ctaccatttg	tcatggcctt	gggactcacc	gctgtgaggc	tggtcgacct	catcaacgtg	4080
gtgggactgc	tgttgctcac	aaggagtggg	aagcggagct	ggccccctag	tgaagtactc	4140
acagctgttg	gtctgatatg	cgcgttggcc	ggagggttcg	ccaaggcgga	tatagagatg	4200
gctgggcca	tggccgcggt	cggtctgcta	attgtcagtt	acgtggtctc	aggaaagagt	4260
gtggacatgt	acattgaaag	agcaggtgac	atcacatggg	aaaaagatgc	ggaagtcact	4320
ggaaacagtc	cccggctcga	tgtggcactg	gatgagagt	gtgatttctc	cctagtggag	4380

gatgatggtc	cccccatgag	agagatcata	ctcaaagtgg	tcctgatgac	catctgtggc	4440
atgaacccaa	tagccatacc	ctttgcagct	ggagcgtggt	acgtgtatgt	gaagactgga	4500
aaaaggagtg	gtgctctatg	ggatgtgcct	gctcccaagg	aagtaaaaaa	gggggagacc	4560
acagatggag	tgtacagagt	aatgactcgt	agactgcttg	gttcaacaca	agttggagtg	4620
ggagtcatgc	aagagggggg	cttccacact	atgtggcacg	tcacaaaagg	atccgcgctg	4680
agaagcggtg	aaggggagact	tgatccatac	tggggagatg	tcaagcagga	tctggtgtca	4740
tattgtggtc	cgtggaagct	agacgccgcc	tgggacgggc	acagcgaggt	gcagctcttg	4800
gccgtgcccc	ccggagagag	agcgaggaa	atccagactc	cgcccggaat	atttaagaca	4860
aaggatgggg	acattggagc	agttgcgttg	gactaccag	caggaacttc	aggatctcca	4920
atcctagaca	agtgtgggag	agtgatagga	ctctatggta	atggggtcgt	gataaaaaat	4980
gggagttatg	ttagtgccat	caccaagggt	aggagggagg	aagagactcc	tgttgagtgc	5040
ttcgagcctt	cgatgttgaa	gaagaagcag	ctaactgtct	tagacctgca	tcctggagct	5100
gggaaaacca	ggagagttct	tcctgaaata	gtccgtgaag	ccataaaaac	aagactccgt	5160
actgtgatct	tagctccaac	cagggttgtc	gctgctgaaa	tggaggaagc	ccttagaggg	5220
cttccagtgc	gttatatgac	aacagcagtc	aatgtcacc	attctgggac	agaaattggt	5280
gacttaatgt	gccatgccac	cttcacttca	cgtctactac	aaccaatcag	agtccccaac	5340
tataatctgt	atattatgga	cgaggccac	ttcacagatc	cctcaagtat	agcagcaaga	5400
ggatacattt	caacaagggt	tgagatgggc	gaggcggccg	ccatcttcat	gaccgccacc	5460
ccaccaggaa	cccgtgacgc	attcccggac	tccaactcac	caattatgga	caccgaagtg	5520
gaagtcccag	agagagcctg	gagctcaggc	tttgattggg	tgacggatca	ttctggaaaa	5580
acagtttggg	ttgttccaag	cgtgaggaac	ggcaatgaga	tcgcagcttg	tctgacaaag	5640
gctggaaaac	gggtcataca	gctcagcaga	aagacttttg	agacagagtt	cctgaaaaca	5700
aaaaatcaag	agtgggactt	cgtcgtgaca	actgacattt	cagagatggg	cgccaacttt	5760
aaagctgacc	gtgtcataga	ttccaggaga	tgcctaaagc	cggtcatact	tgatggcgag	5820
agagtcattc	tggctggacc	catgcctgtc	acacatgcca	gcgctgcca	gaggaggggg	5880
cgcataggca	ggaatcccaa	caaacctgga	gatgagtatc	tgtatggagg	tgggtgcgca	5940
gagactgatg	aagaccatgc	acactggctt	gaagcaagaa	tgcttcttga	caacatttac	6000
ctccaagatg	gcctcatagc	ctcgtcttat	cgacctgagg	ccgacaaagt	agcagctatt	6060
gagggagagt	tcaagcttag	gacggagcaa	aggaagacct	ttgtggaact	catgaaaaga	6120

ggagatcttc ctgtttggct ggcctatcag gttgcatctg ccggaataac ctacacagat	6180
agaaaatggt gctttgatgg caccaccaac aacaccataa tggaagacag tgtgccggca	6240
gaggtgtgga ccagatacgg agagaaaaga gtgctcaaac caaggtggat ggacgccaga	6300
gtttgttcag atcatgcggc cctgaagtca ttcaaagagt ttgccgctgg gaaaagagga	6360
gyggcctttg gagtgatgga agccctggga acattgccgg gacacatgac agagagattc	6420
caggaagcca ttgacaacct cgctgtgctc atgcgggcag agactggaag caggccttac	6480
gaagccgcgg cggcccaatt gccggagacc ttagagacca tcatgctttt ggggttgctg	6540
ggaacagtct cgctgggaat ctttttcgtc ttgatgcgga ataagggcat cgggaagatg	6600
ggcttttgaa tggtgactct tggggccagc gcatggctta tgtggctctc ggaaattgag	6660
ccagccagaa ttgcatgtgt cctcattgtt gtgttcctat tgctggtggt gctcacacct	6720
gagccagaaa agcaaagatc tccccaggac aaccaaatgg caatcatcat catgatagca	6780
gtgggtcttc tgggtttgat taccgccaat gaacttggat ggttggaag aacaaagagt	6840
gacctaaagg atctaattgg aaggagagag gagggggcaa ccataggatt ctcaatggac	6900
attgacctgc ggccagcctc agcttgggct atctatgctg ctctgacaac tttcatcacc	6960
ccagccgtcc aacatgcggg gaccacttca tacaacaact actccttaat ggcgatggcc	7020
acgcaagctg gagtgttggt tggatatggg aaagggatgc cattctacgc atgggacttt	7080
ggagtccgc tgctaattgat gggttgctac tcacaattaa caccctgac cctaatagtg	7140
gccatcattt tgctcgtggc gcactacatg tacttgatcc cagggtgca ggcagcagct	7200
gcgcgtgctg ccagaagag aacggcagct ggcacatga agaaccctgt tgtggatgga	7260
atagtggatga ctgacattga cacaatgaca attgaccacc gagtggagaa aaagatggga	7320
caggtgctac tcatagcagt agccgtctcc agcgccatac tgtcgcggac cgctggggg	7380
tggggggagg ctggggccct gatcacagct gcaacttcca ctttgtggga aggctctccg	7440
aacaagtact ggaactcctc cacagccact tcaactgtga acatttttag gggaagttac	7500
ttggctggag cttctctaata ctacacagta acaagaaacg ctggcttggt caagagacgt	7560
gggggtggaa cgggagagac cctgggagag aaatggaagg cccgcctgaa ccagatgtcg	7620
gccctagagt tctactccta caaaaagtca ggcacaccg aggtgtgcag agaagaggcc	7680
cgccgcgcc tcaaggacgg tgtggcaaca ggaggccatg ctgtgtcccc aggaagtgca	7740
aagcttagat ggttggtgga gagaggatac ctgcagccct atggaaaggc cattgatctt	7800
ggatgtggca gagggggctg gagttactac gccgccacca tccgcaaagt tcaagaagtg	7860

aaaggataca	caaaaggagg	ccctgggtcat	gaagaaccca	tgttggtgca	aagctatggg	7920
tggaacatag	tccgtcttaa	gagtgggggtg	gacgtctttc	atatggcggc	tgagccgtgt	7980
gacactttgc	tgtgtgatat	aggtgagtca	tcattctagtc	ctgaagtgga	agaagcacgg	8040
acgctcagag	tcctttccat	ggtgggggat	tggcttgaaa	aaagaccagg	agccttttgt	8100
ataaaagtgt	tgtgcccata	caccagcact	atgatggaaa	ccctggagcg	actgcagcgt	8160
aggtatgggg	gaggactggg	cagagtgcc	ctctcccgca	actctacaca	tgagatgtac	8220
tgggtctctg	gagcgaaaag	caacaccata	aaaagtgtgt	ccaccacgag	ccagctcctc	8280
ttggggcgca	tggacggggc	caggaggcca	gtgaaatatg	aggaggatgt	gaatctcggc	8340
tccggcacgc	gggctgtggg	aagctgcgct	gaagctccca	acatgaagat	cattggtaac	8400
cgcattgaga	ggatccgcag	tgagcacgcg	gaaacgtggg	tctttgacga	gaaccacca	8460
tataggacat	gggcttacca	tggaagctat	gaggccccta	cacaagggtc	agcgtcctct	8520
ctaataaacg	gggttggtcag	gctcctgtca	aaaccctggg	atgtggtgac	tggagtcaca	8580
ggaatagcca	tgaccgacac	cacaccgtat	ggtcagcaaa	gagttttcaa	ggaaaaagtg	8640
gacactaggg	tgccagaccc	ccaagaaggc	actcgtcagg	ttatgagcat	ggtctcttcc	8700
tggttatgga	aagagctagg	caaacacaaa	cggccacgag	tctgtaccaa	agaagagttc	8760
atcaacaagg	ttcgtagcaa	tgcagcatta	ggggcaatat	ttgaagagga	aaaagagtgg	8820
aagactgcag	tggaagctgt	gaacgatcca	aggttctggg	ctctagtggg	caaggaaaga	8880
gagcaccacc	tgagaggaga	gtgtcagagc	tgtgtgtaca	acatgatggg	aaaaagagaa	8940
aagaaacaag	gggaatttgg	aaaggccaag	ggcagccgcg	ccatctggta	tatgtggcta	9000
ggggctagat	tcctggagtt	cgaagccctt	ggattcttga	acgaggatca	ctggatgggg	9060
agagagaatt	caggaggtgg	tgttgaaggg	ctgggattac	aaagactcgg	atatgtccta	9120
gaagagatga	gtcgcatacc	aggaggaagg	atgtatgctg	atgacacagc	tggctgggac	9180
acccgcatca	gcaggtttga	tctggagaat	gaagctctaa	tcaccaacca	aatggagaaa	9240
gggcacaggg	ccttggcatt	ggccataatc	aagtacacat	accaaaca	agtggtaaag	9300
gtcctcagac	cagctgaaaa	agggaagaca	gttatggaca	ttatttcaag	acaagaccaa	9360
agggggagcg	gacaagttgt	cacttacgct	cttaatacat	tcaccaacct	ggtggtgcag	9420
ctcattcgga	atatggaggc	tgaggaagtt	ctagagatgc	aagacttggtg	gctgctgcgg	9480
aggtcagaga	aagtgaccaa	ctggttgag	agcaacggat	gggataggct	caaacgaatg	9540
gcagtcagtg	gagatgattg	cgttgtgaaa	ccaattgatg	ataggtttgc	acatgcctc	9600

aggttcttga atgatatggg aaaagtcagg aaggacacac aagagtggaa accctcaact	9660
ggatgggaca attgggaaga agttccgttt tgctcccacc acttcaacaa gctccatctc	9720
aaggacggga ggtccattgt ggttccttgc cgccaccaag atgaactgat tggccgagcc	9780
cgcgctctcac caggggcggg atggagcatc cgggagactg cttgcctagc aaaatcatat	9840
gcgcaaatgt ggcagctcct ttatttccac agaagggacc tccgactgat ggccaatgcc	9900
atttgttcat ctgtgccagt tgactgggtt ccaactggga gaactacctg gtcaatccat	9960
ggaaagggag aatggatgac cactgaagac atgcttgtgg tgtggaacag agtgtggatt	10020
gaggagaacg accacatgga agacaagacc ccagttacga aatggacaga cattccctat	10080
ttgggaaaaa gggaagactt gtggtgtgga tctctcatag ggcacagacc gcgcactacc	10140
tgggctgaga acatcaaaaa cacagtcaac atgatgcgca ggatcatagg tgatgaagaa	10200
aagtacatgg actacctatc cacccaagtt cgctacttgg gtgaagaagg gtccacaccc	10260
ggagtgttgt aa	10272

<210> 79

<211> 10807

<212> DNA

<213> Zika virus isolate Zika virus/H.sapiens-tc/PHL/2012/CPC-0740, complete genome

<400> 79

agttgttgat ctgtgtgaat cagactgcga cagttcgagt ttgaagcgaa agctagcaac	60
agtatcaaca ggttttatatt tggatttgga aacgagagtt tctgggtcatg aaaaacccaa	120
aaaagaaatc cggaggattc cggattgtca atatgctaaa acgcgagta gcccggtgtga	180
gccccttttg gggcttgaag aggctgccag ccggacttct gctggggccat gggcccatca	240
ggatggtctt ggcgatacta gcctttttga gattcacggc aatcaagcca tcaactgggtc	300
tcatcaatag atgggggttca gtggggaaaa aagaggctat ggaaataata aagaagttca	360
agaaagatct ggctgccatg ctgagaataa tcaatgctag gaaggagaag aagagacgag	420
gcgcagatac tagcgtcgga attggtggcc tcctcctgac cacagccatg gcagtagagg	480
tcaactagacg tgggagtgca tactatatgt acttggacag aagcgatgct ggggaggcca	540
tatcttttcc aaccacactg gggatgaata agtgttacat acaaatcatg gatcttggac	600
acatgtgtga tgccaccatg agctatgaat gccctatggt ggatgagggg gtagaaccag	660
atgacgtcga ttgctggtgc aacacgacat caacttgggt tgtgtatgga acctgccacc	720
acaaaaaagg tgaagcacgg agatctagaa gagctgtgac gctcccctcc cattccacta	780

ggaagctgca aacgcgggtcg cagacctggt tggaatcaag agaatacaca aagcacctga	840
ttagagttga aaattggata ttcaggaacc ctggcttcgc gttagcagca gctgtcatcg	900
cttggctttt gggaagttca acgagccaaa aagtcataata tctgggtcatg atactgctga	960
ttgccccggc atacagcatc aggtgcatag gagtcagcaa tagggacttt gtggaaggta	1020
tgtcagggtg gacttgggtt gatgttgtct tggaaacatgg aggttgtgtt accgtaatgg	1080
cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc aacatggcgg	1140
aggtaagatc ctactgctat gaggcataca tatcggatat ggcttcggac agccgctgcc	1200
caacacaagg tgaggcctac cttgacaagc agtcagacac tcaatatgtc tgcaaaagaa	1260
cgttagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg agcctgggtga	1320
catgcgctaa gtttgcatgc tccaagaaaa tgaccgggaa gagcatccag ccagagaatc	1380
tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg atcgттаатг	1440
acacaggaca tgaaactgat gagaatagag cgaaggttga gataacgccc aattcaccaa	1500
gagccgaagc caccctgggg ggttttggga gcctaggact tgattgtgaa ccgaggacag	1560
gccttgactt ttcagatttg tattacctga ctatgaataa caagcactgg ttggttcaca	1620
aggagtgggt ccacgacatt ccattacctt ggcattgctgg ggcagacact ggaactccac	1680
attggaacaa caaagaagca ctggtagagt tcaaggacgc acatgcaaaa aggcaaactg	1740
tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga gctctggagg	1800
ctgagatgga tggagccaag ggaaggctgt cctctggcca cttgaaatgt cgctgaaaa	1860
tggataaact tagattgaag ggcgtgtcat actccttgtg cactgcagcg ttcacattca	1920
ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag tacgcaggga	1980
cagatggacc ttgcaagggt ccagctcaga tggcggtgga tatgcaaact ctgaccccag	2040
ttgggaggtt gataaccgct aaccctgtaa tcaactgaaag caccgagaac tctaagatga	2100
tgctggaact tgatccacca tttggggact cttacattgt cataggagtc ggggagaaga	2160
agatcaccca tcaactggcac aggagtggca gcaccattgg aaaagcattt gaagccactg	2220
tgagaggtgc caagagaatg gcagtcttgg gagacacagc ctgggacttt ggatcagttg	2280
ggggtgctct caactcattg ggcaagggca tccatcaaat ttttgagca gctttcaaat	2340
cattgttcgg aggaatgtcc tggttctcac aaattctcat tggaacgttg ctggtgtggt	2400
tgggtctgaa taaaaagaat ggatctatct cccttacgtg cttggcctta gggggagtgt	2460
tgatcttctt atccacagcc gtttctgctg atgtggggtg ctcggtggac ttctcaaaga	2520

aggaaacgag atgcggtaca ggggtgttcg tctataacga cgttgaagcc tggagggaca	2580
ggtacaagta ccatcctgac tcccctcgta gattggcagc agcagtcaag caagcctggg	2640
aagatgggat ctgtgggatc tcctctgtct caagaatgga aaacatcatg tggagatcag	2700
tagaagggga gctcaacgca atcctggaag agaatggagt tcaactgacg gtcgttgtgg	2760
gatctgtaaa aaaccccatg tggagaggtc cacagagatt gcccgtcct gtgaacgagc	2820
tgccccacgg ctggaaggct tgggggaaat cgtacttcgt cagagcagca aagacaaata	2880
acagctttgt cgtggatggg gacacactga aggaatgccc actcaaacat agagcatgga	2940
acagctttct tgtggaggat catgggtttg gggatatttca cactagtgtc tggctcaagg	3000
ttagagaaga ttattcatta gagtgtgac cagccgtcat tggaacagct gctaagggaa	3060
aggaggctgt gcacagcgat ctaggctact ggattgagag tgagaagaac gacacatgga	3120
ggctgaagag ggcccacctg atcgagatga aaacatgtga atggccaaag tcccacacat	3180
tgtggacaga tggagtagaa gaaagtgatc tgatcatacc caagtcttta gctgggccac	3240
tcagccatca caacaccaga gagggctaca ggactcaaat gaaagggcca tggcacagtg	3300
aagagcttga aattcggttt gaggaatgcc caggcactaa ggtccacgtg gaggaaacat	3360
gtgggacaag aggaccatcc ctgagatcaa ccaactgcaag cggaaggggtg atcgaggaat	3420
ggctgctgcag ggaatgcaca atgccccac tgtcgttcg agctaaagat ggctgttggg	3480
atggaatgga gataaggccc aggaaagaac cagaaagtaa cttagtaagg tcaatgggtga	3540
ctgcaggatc aactgatcac atggatcact tctctcttgg agtgcttgtg attttgctca	3600
tgggtgcagga agggctgaag aagagaatga ccacaaagat catcataagc acatcaatgg	3660
cagtgctggg agccatgatc ctgggaggat tttcaatgag tgacctggct aagcttgcaa	3720
ttttgatggg tgccaccttc gcggaaatga aactggagg agatgtagct catttggcgc	3780
tgatagcggc attcaaagtc agacctgcgt tgctggtatc tttcatcttc agagctaatt	3840
ggacaccccg tgagagcatg ctgctggcct tggcctcgtg tcttctgcaa actgcgatct	3900
ccgccttgga aggcgacctg atggttctca tcaatggttt tgctttggcc tggttggcaa	3960
tacgagcgat ggttgttcca cgcactgaca acatcacctt ggcaatcctg gctgctctga	4020
caccactggc ccggggcaca ctgcttgtgg cgtggagagc aggccttgct acttgcgggg	4080
ggttcatgct cctctctctg aaggggaaag gcagtgtgaa gaagaaccta ccatttgtca	4140
tggccttggg actaactgct gtgaggctgg tcgaccccat caacgtgggtg ggactgctgt	4200
tgctcacaag gagtgggaag cggagctggc cccctagtga agtactcaca gctgttggcc	4260

tgatatgcmc attggctgga gggttcgcca aggcggatat agagatggct gggcccatgg	4320
ccgcggtcgg tctgctaatt gtcagttacg tggctctcagg aaagagtgtg gacatgtaca	4380
ttgaaagagc aggtgacatc acatgggaaa aagatgcgga aatcactgga aacagtcccc	4440
ggctcgatgt ggcactagat gagagtgggtg atttctccct agtggaggat gatgggtccac	4500
ccatgagaga gatacactc aaagtgggtcc tgatgaccat ctgcggcatg aaccaatag	4560
ccataccctt tgcagctgga gcgtgggtacg tgtatgtgaa gactggaaaa aggagtgggtg	4620
ctctatggga tgtgcctgct cccaaggaag taaaaaaggg ggagaccaca gatggagtgt	4680
acagagtaat gactcgtaga ctgcttggtt caacacaagt tggagtggga gtcatgcaag	4740
agggggtctt ccacactatg tggcacgtca caaaaggatc cgcgctgaga agcgggtgaag	4800
ggagacttga tccatactgg ggagatgtca agcaggatct ggtgtcatac tgtgggtccgt	4860
ggaagctaga cgccgcctgg gacgggcaca gcgaggtgca gctcttggcc gtgccccccg	4920
gagagagagc gaggaacatc cagactctgc ccggaacatt taagacaaag gatggggaca	4980
ttggagcagt tgcgctggac taccagcag gaacttcagg atctccaatc ctagacaagt	5040
gtgggagagt gataggactc tatggtaatg gggctcgtgat aaaaaatggg agttatgtta	5100
gtgccatcac ccaaggagg agggaggaag agactcctgt tgagtgtctc gagccttcga	5160
tgctgaagaa gaagcagcta actgtcttag acctgcatcc tggagccggg aaaaccagga	5220
gagttcttcc tgaaatagtc cgtgaagcca taaaaacaag actccgtact gtgatcttag	5280
ctccaaccag ggtcgtcgct gctgaaatgg aggaagccct tagagggctt ccagttcggt	5340
atatgacaac agcagtcaat gtcaccatt ctgggacaga aatcgttgac ttaatgtgcc	5400
atgctacctt cacttcacgc ctactacaac caatcagagt cccaactat aatttgtata	5460
ttatggatga ggcccacttc acagatccct caagtatagc agcaagagga tacatttcaa	5520
caagggttga gatgggagc gcggctgcca tcttcatgac cgccacgcca ccaggaaccc	5580
gtgacgcatt cccggactcc aactaccaa ttatggacac cgaggtggaa gtcccagaga	5640
gagcctggag cacaggcttt gattgggtga cggatcattc tgggaaaaca gtctggtttg	5700
ttccaagcgt gaggaacggc aatgagatcg cagcttgtct gacaaaggct ggaaaacggg	5760
tcatacagct cagcagaaaag acttttgaga cagagttcca gaaaacgaaa aatcaagagt	5820
gggacttcgt cgtgacaacc gacatttcag agatgggcgc caactttaaa gctgaccgtg	5880
tcatagattc caggagatgc ttaaagccgg tcatacttga tggcgagaga gtcattttgg	5940
ctggacccat gcctgtcaca catgccagcg ctgctcagag gagggggcgc ataggcagga	6000

atcccaacaa	acctggagat	gagtatctgt	atggaggtgg	gtgcgcagag	actgatgaag	6060
atcacgcaca	ctggcttgaa	gcaagaatgc	ttcttgacaa	catttacctc	caagatggcc	6120
tcatagcttc	gctctatcga	cctgaggccg	acaaagtagc	agctattgag	ggagagttca	6180
agcttaggac	ggagcaaagg	aagacctttg	tggaactcat	gaaaagagga	gatcttccgg	6240
tttggttggc	ctatcagggt	gcatctgccg	gaataaccta	cacagataga	agatggtgct	6300
ttgatggcat	gaccaacaac	accataatgg	aagacagtgt	gccggcagag	gtgtggacca	6360
gatacggaga	gaaaagagtg	ctcaaaccga	ggtggatgga	cgccagagtt	tgttcagatc	6420
atgcggccct	gaagtcattc	aaagagtttg	ccgctgggaa	aagaggagcg	gcctttggag	6480
tgatagaagc	cctgggaaca	ctgccaggac	acatgacaga	gagattccag	gaagccattg	6540
acaacctcgc	tgtgctcatg	cgggcagaga	ctggaagcag	gccttacaaa	gccgcggcgg	6600
cccaattgcc	ggagacccta	gagaccatta	tgcttttggg	gttgctggga	acagtctcgc	6660
tgggaatctt	tttcgtcttg	atgcggaaca	agggcatggg	gaagatgggc	tttggaatgg	6720
tgactcttgg	ggccagcgca	tggcttatgt	ggctctcgga	aattgagcca	gccagaattg	6780
catgtgtcct	cattgtcgtg	ttcctattgc	tgggtggtgct	catacctgag	ccagaaaagc	6840
aaagatctcc	tcaggacaac	caaatggcaa	tcatcatcat	ggtagcagtg	ggtcttctgg	6900
gcttgattac	cgccaatgaa	ctcggatggt	tggagagaa	aaaaagtgac	ctaagccatc	6960
taatgggaag	gagagaggag	ggggcaacca	caggattctc	aatggacatt	gacctgcggc	7020
cagcctcagc	ttgggctatc	tatgctgctc	tgacaacttt	catcacccca	gccgtccaac	7080
atgcggtgac	cacttcatac	aacaactact	ccttaatggc	gatggccacg	caagctgggg	7140
tgttgtttgg	tatgggcaaa	gggatgccat	tctacgcatg	ggactttgga	gtcccgtgc	7200
taatgatggg	ttgctactca	caattaacac	ctctgaccct	aatagtggcc	atcattttgc	7260
tcgtggcgca	ctacatgtac	ttgatcccag	ggctgcaggc	agcagctgcg	cgggctgccc	7320
agaagagaa	ggcagctggc	atcatgaaga	accctgttgt	ggatggaata	gtggtgactg	7380
acattgacac	aatgacaatt	gacccccaa	tggaaaaaaa	gatggggcag	gtgctactca	7440
tagcagtagc	cgtctccagc	gccatactgt	cgcggaccgc	ctgggggtgg	ggggaggctg	7500
gggccctgat	cacagctgca	acttccacct	tgtgggaagg	ctctccgaac	aagtactgga	7560
actcctccac	agccacttca	ctgtgtaaca	tttttagggg	aagttacttg	gctggagctt	7620
ctctaatacta	cacagtaaca	agaaacgctg	gcttggtcaa	gagacgtggg	ggtggaacgg	7680
gagagaccct	gggagagaaa	tggaaggccc	gcctgaacca	gatgtcggcc	ctggagttct	7740

actcctacaa aaagtcaggc atcaccgagg tgtgcagaga agaggcccg cgtgccctca	7800
aggacggtgt ggcaacagga ggccatgctg tgtcccgagg aagtgc aaag cttagatggc	7860
tggtggagag aggatacctg cagccctatg gaaagggtcat tgatcttgga tgtggcagag	7920
ggggctggag ttactatgcc gccaccatcc gcaaagttca ggaagtgaaa ggatacacia	7980
aaggaggccc tggatcatgaa gaacccatgt tggtgcaaag ctatgggtgg aacatagtcc	8040
gtcttaagag tgggggtggac gtctttcaca tggcggctga gccgtgtgac actttgctgt	8100
gtgatatagg tgagtcacat tctagtcctg aagtgggaaga agcacggacg ctcagagtcc	8160
tctccatggt ggggggattgg cttgaaaaaa gaccaggagc cttttgtata aaagtgttgt	8220
gcccatacac cagcactatg atggaaaccc tggagcgcact gcagcgtagg tatgggggag	8280
gactggtcag ggtgccactc tcccgcaact ctacacatga gatgtactgg gtctctggag	8340
cgaaaagcaa caccataaaa agtgtgtcca ccacgagcca gctcctcttg gggcgcatgg	8400
acgggcccag gaggccagtg aaatatgagg aggatgtgaa tctcggctct ggcacgcggg	8460
ctgtggtaag ctgcgctgaa gctcccaaca tgaagatcat tggtaaccgc attgagagga	8520
tccgcagtga gcacgcggaa acgtggttct ttgacgagaa ccaccatat aggacatggg	8580
cttaccatgg aagctatgag gccctacac aagggtcagc gtcctctcta ataaacgggg	8640
ttgtcaggct cctgtcaaaa ccctgggatg tggtgactgg agtcacagga atagccatga	8700
ctgacaccac accgtatggt cagcaaagag ttttcaagga aaaagtggac actaggggtgc	8760
cagaccccca agaaggcact cgtcagggtta tgagcatggt ctcttcctgg ttatggaagg	8820
agctaggcaa acacaaacgg ccacgagtct gtaccaaaga agagtccatc aacaagggtc	8880
gtagcaatgc agcattaggg gcaatatttg aagaggaaaa agagtgggaag actgcagtgg	8940
aagctgtgaa tgatccaagg ttctgggctc tagtggacaa ggaaagagag catcacctga	9000
gaggagagtg tcagagctgt gtgtacaaca tgatgggaaa aagagaaaag aaacaagggg	9060
aatttggaag ggccaagggc agccgcgcca tctgggtatat gtggctaggg gctagattcc	9120
tagagttcga agcccttgga ttcttgaatg aggatcattg gatggggaga gagaattcag	9180
gaggtggtgt tgaaggactg ggattacaaa gactcggata tgtcctagaa gagatgagtc	9240
gcataccagg aggaaggatg tatgcagatg atactgctgg ctgggacacc cgcacagca	9300
ggtttgatct ggagaatgaa gctctaata ccaaccaaag ggagaaaagg cacagggcct	9360
tggcattggc cataatcaag tacacatacc aaaacaaagt ggtaaagggt cttagaccag	9420
ctgaaaaagg gaagacagtt atggacatta tttcaagaca agaccaaagg gggagcggac	9480

aagttgtcac ttacgctctt aatacattca ccaacctggt ggtgcagctc attcggaata	9540
tggaggctga ggaagttcta gagatgcaag acttgtggct gctgcggagg ccagagaaag	9600
tgaccaactg gttgcaaagc aacggatggg ataggctcaa aagaatggca gtcagtggag	9660
atgattgcgt tgtgaaacca attgatgata ggtttgcaca tgccttcagg ttcttgaatg	9720
atatgggaaa agttaggaag gacacacaag agtggaaacc ctcaactgga tgggacaact	9780
gggaagaagt tccgttttgc tcccaccact tcaacaaact ccatcttaag gacgggaggt	9840
ccattgtggt tccctgccgc caccaagatg aactgattgg ccgagccgc gtatcaccag	9900
gggcgggatg gagcatccgg gagactgctt gcctagcaaa atcatatgcg caaatgtggc	9960
agctccttta tttccacaga aggacctcc gactgatggc caatgccatt tgttcatctg	10020
tgccagttga ttgggttcca actgggagaa ctacctggc aatccatgga aagggagaat	10080
ggatgaccac tgaagacatg cttgtggtat ggaacagagt gtggattgag gaaaacgacc	10140
acatggaaga caagacccca gttacaaaat ggacagacat tccctatttg ggaaaaagag	10200
aagacttgtg gtgtggatct ctcatagggc acagaccgc tactacctgg gctgagaaca	10260
tcaaaaatac agtcaacatg atgcgagga tcataggtga tgaagaaaag tacatggact	10320
acctatccac ccaggttcgc tacttgggtg aagaagggtc cacacctgga gtgctgtaag	10380
caccaatctt agtgttgtca ggctgctag tcagccacag cttggggaaa gctgtgcagc	10440
ctgtgacccc cccaggagaa gctgggaaac caagcctata gtcaggccga gaacgccatg	10500
gcacggaaga agccatgctg cctgtgagcc cctcagagga cactgagtca aaaaacccca	10560
cgcgcttga ggcgaggat gggaaaagaa ggtggcgacc ttccccaccc ttcaatctgg	10620
ggcctgaact ggagatcagc tgtggatctc cagaagaggg actagtgggt agaggagacc	10680
ccccggaaaa cgcaaacag catattgacg ctgggaaaga ccagagactc catgagtttc	10740
caccacgctg gccgccaggc acagatcgcc gaatagcggc ggccggtgtg gggaaatcca	10800
tgggtct	10807

<210> 80

<211> 10807

<212> DNA

<213> Zika virus isolate Zika virus/H.sapiens-tc/THA/2014/SV0127- 14, complete genome

<400> 80

agttgttgat ctgtgtgaat cagactgcga cagttcgagt ttgaagcgaa agctagcaac	60
---	----

agtatcaaca ggttttatatt tggatttga aacgagagtt tctgggtcatg aaaaacccaa	120
--	-----

aaaagaaatc cggaggattc cggattgtca atatgctaaa acgcgaggta gcccgtgtga	180
gccccttttg gggcttgaag aggctgccag ccggacttct gctgggtcat gggcccatca	240
ggatggtctt ggcgattcta gcctttttga gattcacggc aatcaagcca tctactgggtc	300
tcatcaatag atgggggttca gtgggaaaaa aagaggctat ggaaataata aagaagttca	360
agaaagatct ggctgccatg ctgagaataa tcaatgctag gaaggagaag aagagacgag	420
gcacagatac tagtgtcgga attgttggcc tcctgctgac cacagctatg gcagcggagg	480
tactagacg tgggagtgc tactatatgt acttgacag aagcgatgct ggggaggcca	540
tatcttttcc aaccacactg gggatgaata agtggtatat acagatcatg gatcttggac	600
acatgtgtga tgccaccatg agctatgaat gccctatgct ggatgagggg gtagaaccag	660
atgacgtcga ttgttgggtc aacacgacgt caacttgggt tgtgtacgga acctgccatc	720
acaaaaaagg tgaagcacgg agatccagaa gagctgtgac gctcccctcc cattccacta	780
ggaagctgca aacgcgggtc cagacctggt tggaatcaag agaatacaca aagcacttga	840
ttagagtcca aaattggata ttcaggaacc ctggcttcgc gttagcagca gctgccatcg	900
cttggttttt gggaagctca acgagccaaa aagtcataata cttggtcatg atactgctga	960
ttgccccggc atacagcatc aggtgcatag gagtcagtaa tagggacttt gtggaaggta	1020
tgtcagggtg gacttgggtt gatgttgtct tggaacatgg aggttgtgtc accgtaatgg	1080
cacaggacaa accgactgtc gacatagagc tggttacaac aacagtcagc aacatggcgg	1140
aggtaagatc ctactgctat gaggcacaa tatcggacat ggcttcggac agccgctgcc	1200
caacacaagg tgaagcctac cttgacaagc aatcagacac tcaatatgtc tgcaaaagaa	1260
cgtagtgga cagaggctgg ggaaatggat gtggactttt tggcaaaggg agcctggtga	1320
catgcgctaa gtttgcacgc tccaagaaaa tgaccgggaa gagcatccag ccagagaatc	1380
tggagtaccg gataatgctg tcagttcatg gctcccagca cagtgggatg atcgttaatg	1440
acacaggaca tgaaactgat gagaatagag cgaagggtga gataacgccc aattcaccaa	1500
gagccgaagc caccctgggg ggttttggaa gcctaggact tgattgtgaa ccgaggacag	1560
gccttgactt ttcagatttg tattacttga ctatgaacaa caagcactgg ttggttcaca	1620
aggagtgggt ccacgacatt ccattacctt ggcacactgg ggcagacacc ggaactccac	1680
actggaacaa caaagaagca ctggtagagt tcaaggacgc acatgccaaa aggcaaactg	1740
tcgtggttct agggagtcaa gaaggagcag ttcacacggc ccttgctgga gctctggagg	1800
ctgagatgga tgggtgcaaag ggaaggctgt cctctggcca cttgaaatgt cgctgaaaa	1860

tggataaaact tagattgaag ggcgtgtcat actccttgtg taccgcagcg ttcacattca	1920
ccaagatccc ggctgaaaca ctgcacggga cagtcacagt ggaggtacag tacgcaggga	1980
cagatggacc ttgcaagggt ccagctcaga tggcgggtga catgcaaact ctgaccccag	2040
ttgggaggtt gataaccgct aaccccgtaa tctactgaagg cactgagaac tctaagatga	2100
tgctggaact tgatccacca tttggggact cttacattgt cataggagtc ggggagaaga	2160
agatcaccca ccactggcac aggagtggca gcaccattgg aaaagcattt gaagccactg	2220
tgagaggtgc caagagaatg gcagtcttgg gagacacagc ctgggacttt ggatcagttg	2280
gaggcgttct taactcattg ggcaagggca tccatcaaata ttttgagca gctttcaaat	2340
cattgttttg aggaatgtcc tggttctcac aaattctcat tggaacgttg ctgatgtggt	2400
tgggtctgaa tacaagaat ggatctattt cccttatgtg cttggcctta gggggagtgt	2460
tgatcttctt atccacagcc gtctccgctg atgtggggtg ctcggtggac ttctcaaaga	2520
aggaaacgag atgcggtaca ggggtgttcg tctataacga cgttgaagcc tggagggaca	2580
ggtacaagta ccatcctgac tcccctcgta gattggcagc agtagtcaag caagcctggg	2640
aagatggtat ctgtgggatc tcctctgttt caagaatgga aaacatcatg tggagatcag	2700
tagaagggga gctcaacgca atcctggaag agaatggagt tcaactgacg gtcgttgttg	2760
gatctgtaaa aaaccccatg tggagaggtc cacagagatt gcccgtcct gtgaacgagc	2820
tgccccacgg ctggaaggct tgggggaaat cgtacttcgt cagagcagca aagacaaata	2880
acagctttgt cgtggatggt gacacactga aggaatgccc actcaaakat agagcatgga	2940
acagctttct tgtggaggat catgggttcg gggatatttca cactagtgtc tggctcaagg	3000
ttagagaaga ttattcacta gagtgtgatc cagccgtcat tggaacagct gttaagggaa	3060
aggaggctgt acacagtgat ctaggctact ggattgagag tgagaagaac gacacatgga	3120
ggctgaggag ggcccacctg atcgagatga aaacatgtga atggccaaag tcccacacat	3180
tgtggacaga tggaatagaa gagagtgatc tgatcatacc caagtcttta gctgggccac	3240
tcagccatca caacaccaga gagggctaca ggacccaaat gaaagggcca tggcacagtg	3300
aagagcttga aattcggttt gaggaatgcc caggcactaa ggtccacgtg gaggaaacat	3360
gtggaacaag aggaccatct ctgagatcaa ccactgcaag cggaaggggtg atcgaggaat	3420
ggtgctgcag ggagtgcaca atgccccac tgtcgttccg ggctaaagat ggctgttggt	3480
atggaatgga gataaggccc aggaaagaac cagaaagtaa cttagtaagg tcaatggtga	3540
ctgcaggatc aactgatcac atggatcact tttcccttgg agtgcttgtg attctgctca	3600

tggtgcagga	agggctgaag	aagagaatga	ccacaaagat	catcataagc	acatcaatgg	3660
cagtgcctgg	agctatgatc	ctgggaggat	tttcaatgag	tgatctggct	aagcttgcaa	3720
ttttgatggg	tgccaccttt	gcggaatga	acactggagg	agatgtagct	catctggcgc	3780
tggtagcggc	attcaaagtc	agaccagcgt	tgctggatc	tttcatcttc	agagctaatt	3840
ggacaccccg	tgaaagcatg	ctgctggcct	tggcctcgtg	tcttttgcaa	actgcgatct	3900
ccgccttgga	aggcgacctg	atggttctca	tcaatggttt	tgctttggcc	tggttggtgaa	3960
tacgagcgat	ggttgttcca	cgcactgaca	atatcacctt	ggcaatcctg	gctgctctga	4020
caccactggc	ccggggcaca	ctgcttgtgg	cgtggagagc	aggccttgct	acttgccggg	4080
ggttcatgct	cctctctctg	aaggggaaag	gcagtgtgaa	gaagaactta	ccatttgtca	4140
tgccctggg	actaaccgct	gtgaggctgg	tcgaccccat	caacgtgggtg	ggactgctgt	4200
tgctcacaag	gagtgggaag	cggagctggc	cccctagcga	agtactcaca	gctgttggcc	4260
tgatatgcgc	attggctgga	gggttcgcca	aggcagatat	agagatggct	gggcccatgg	4320
ccgcggtcgg	tctgctaatt	gtcagttacg	tggtctcagg	aaagagtgtg	gacatgtaca	4380
ttgaaagagc	aggtgacatc	acatgggaaa	aagatgcgga	agttactgga	aacagtcccc	4440
ggctcgatgt	ggcactagat	gagagtgggtg	atctctccct	ggtggaggat	gacgggtcccc	4500
ccatgagaga	gatcatactc	aaagtgggtc	tgatgaccat	ctgtggcatg	aaccaatag	4560
ccataccctt	tgacagctgga	gcgtgggtacg	tatacgtgaa	aactggaaaa	aggagtgggtg	4620
ctctatggga	tgtgcctgct	ccaaggaag	taaaaaagg	ggagaccaca	gatggagtgt	4680
acagagtaat	gactcgtaga	ctgctagggtt	caacacaagt	tggagtggga	gttatgcaag	4740
aggggggtctt	tcacactatg	tggcatgtca	caaaaggatc	cgcgctgaga	agcgggtgaag	4800
ggagacttga	tccatactgg	ggagatgtca	agcaggatct	ggtgtcatac	tgtgggtccat	4860
ggaagctaga	tgccgcctgg	gacgggcaca	gcgaggtgca	gctcttggcc	gtgccccccg	4920
gagagagagc	gaggaacatc	cagactctgc	ccggaatatt	taagacaaaag	gatggggaca	4980
ttggagcggg	tgcgctggac	tatccagcag	gaacttcagg	atctccaatc	ctagacaagt	5040
gtgggagagt	gataggactc	tatggcaatg	gggtcgtgat	caagaatggg	agttatgtca	5100
gtgccatcac	ccaagggagg	agggaggaag	agactcctgt	tgagtgcctc	gagccttcga	5160
tgctgaagaa	gaagcagcta	actgtcttag	acttgcatcc	tggagctggg	aaaaccagga	5220
gagttcttcc	tgaaatagtc	cgtgaagcca	taaaaacgag	actccgtact	gtgatcttag	5280
ctccaaccag	ggttgtcgct	gctgaaatgg	aggaagccct	tagagggctt	ccagtgcgtt	5340

atatgacaac	agcagtcaat	gtcacccatt	ctgggacaga	aatcgttgac	ttaatgtgcc	5400
atgccacctt	cacttcacgt	ctactacagc	caatcagagt	ccccaaactat	aatctgtata	5460
ttatggatga	ggcccacttc	acagatccct	caagtatagc	agcaagagga	tacatttcaa	5520
caagggttga	gatgggagag	gcagctgcca	tcttcatgac	cgccacgcca	ccaggaaccc	5580
gtgacgcatt	cccggactcc	aactcaccaa	ttatggacac	cgaagtggaa	gtcccagaga	5640
gagcctggag	ctcaggcttt	gattgggtga	cggatcattc	tggaaaaaca	gtttggtttg	5700
tccaagcgt	gaggaacggc	aatgagatcg	cagcttgtct	gacaaaggct	ggaaaacggg	5760
tcatacagct	cagcagaaaag	acttttgaga	cagagttcca	gaaaacaaaa	catcaagagt	5820
gggacttcgt	cgtgacaact	gacatttcag	agatgggagc	caactttaaa	gctgaccgtg	5880
tcatagattc	caggagatgc	ctaaagccgg	tcatacttga	tggcgagaga	gtcattctgg	5940
ctggacccat	gcctgtcaca	catgccagcg	ctgcccagag	gaggggggagc	ataggcagga	6000
atcccaacaa	acctggagat	gagtatctgt	atggaggtgg	gtgagcagag	actgatgaag	6060
accatgcaca	ctggcttgaa	gcaagaatgc	tccttgacaa	tatttacctc	caagatggcc	6120
tcatagcctc	gctctatcga	cctgaggccg	acaaagtagc	agccattgag	ggagagttca	6180
agcttaggac	ggagcaaagg	aagacctttg	tggaaactcat	gaaaagagga	gatcttcctg	6240
tttggtggc	ctatcagggt	gcctctgccg	gaataaccta	cacagataga	agatggtgct	6300
ttgatggcat	gaccaacaac	accataatgg	aagacagtgt	gccggcagag	gtgtggacca	6360
gacacggaga	gaaaagagtg	ctcaaaccga	ggtggatgga	cgccagagtt	tgttcagatc	6420
atgcggccct	gaagtcattc	aaggagtttg	ccgctgggaa	aagaggagcg	gcttttgag	6480
tgatggaagc	cctgggaaca	ctgccaggac	acatgacgga	gagattccag	gaagccattg	6540
acaacctcgc	tgtgctcatg	cgggcagaga	ctggaagcag	gccttacaaa	gccgcggcgg	6600
cccaattgcc	ggagacccta	gagaccatta	tgcttttggg	gttgctggga	acagtctcgc	6660
tgggaatctt	tttcgtcttg	atgcggaaca	agggcatagg	gaagatgggc	tttggaatgg	6720
tgactcttgg	ggccagcgca	tggctcatgt	ggctctcgga	aattgagcca	gccagaattg	6780
catgcgtcct	cattgttgtg	ttcctattgc	tggtggtgct	catacctgag	ccagaaaagc	6840
aaagatcccc	ccaggacaac	caaattggcaa	tcatcatcat	ggtagcagta	ggtcttctgg	6900
gcttgattac	cgccaatgaa	ctcggatggt	tggagagaac	aaagagtgac	ctaagccatc	6960
taatgggaag	gagagaggag	ggggcaacca	taggattctc	aatggacatt	gacctgcggc	7020
cagcctcggc	ctggggccatc	tatgctgccc	tgacaacttt	cattacccca	gccgtccaac	7080

atgcagtgac cacttcatac aacaactact ccttaatggc gatggccacg caagctggag	7140
tgttgttttg tatgggcaaa gggatgccat tctacgcatg ggacttttga gtccccgtgc	7200
taatgatagg ttgctactca caattaacac ccctgaccct aatagtggct atcattttgc	7260
tcgtggcgca ctacatgtac ttgatcccag ggctgcaggc agcagctgcg cgtgctgccc	7320
agaagagaac ggcagctggc atcatgaaga accctgttgt ggatggaata gtggtgactg	7380
acattgacac aatgactatt gacccccaaag tggagaaaaa gatgggacag gtgctactca	7440
tagcagtagc cgtctccagc gccatactgt cgcggaccgc ctgggggttg ggggaagctg	7500
gggccctgat cacagctgca acttccactt tgtgggaagg ctctccgaac aagtactgga	7560
actcctctac agccacttca ctgtgcaaca tttttagggg aagttacttg gctggagctt	7620
ctctaactca cacagtaaca agaaacgctg gcttggtcaa gagacgtggg ggtggaacag	7680
gagagaccct gggagagaaa tggaaggccc gcttgaacca gatgtcggcc ctggagttct	7740
actcctacaa aaagtcaggc atcaccgagg tgtgcagaga agaggcccg cgcgccctca	7800
aggacggtgt ggcaacggga ggccatgctg tgtcccgagg aagtgcaaag ctgagatggt	7860
tggtggagcg gggatacctg cagccctatg gaaaggatcat tgatcttgga tgtggcagag	7920
ggggctggag ttactacgcc gccaccatcc gcaaagttca agaagtgaag ggatacacia	7980
aaggaggccc tggatcatgaa gaacccatgt tgggtgcaaag ctatgggttg aacatagtcc	8040
gtcttaagag tgggggtggac gtctttcata tggcggctga gccgtgtgac acgttgctgt	8100
gtgacatagg tgagtcatca tctagtcttg aagtggaaga agcacggacg ctgagagtcc	8160
tctccatggt gggggatttg cttgaaaaaa gaccaggagc cttttgtgta aaagtgttgt	8220
gccatacac cagcactatg atggaaaccc tggagcgact gcagcgtagg tatgggggag	8280
gactggtcag agtgccactc tcccgcaact ctacacatga gatgtactgg gtctctggag	8340
cgaaaagcaa caccataaaa agtgtgtcca ccacgagcca gctcctcttg gggcgcatgg	8400
acgggcccag gaggccagtg aaatatgagg aggatgtgaa tctcggctct ggcacgcggg	8460
ctgtggtgag ctgcgctgaa gctcccaaca tgaagatcat tggttaaccgc attgaaagga	8520
tccgcagtga gcacgcggaa acgtggttct ttgacgagaa ccaccatat aggacatggg	8580
cttaccatgg aagctatgag gccctacac aagggtcagc gtcctctcta ataaacgggg	8640
ttgtcaggct cctgtcaaaa ccctgggatg tgggtgactgg agtcacagga atagccatga	8700
ccgacaccac accgtatggt cagcaaagag ttttcaagga aaaagtggac accagggtgc	8760
cagaccccca agaaggcact cgtcaggtta tgagcatggt ctcttcctgg ttgtggaaag	8820

agctaggcaa	acacaaacgg	ccacgagtct	gtaccaaaaga	agagttcatc	aacaagggttc	8880
gtagcaatgc	agcattaggg	gcaatatttg	aagaggaaaa	agagtgggaag	accgcagtgg	8940
aagctgtgaa	cgatccaagg	ttctgggctc	tagtggacaa	ggaaagagag	caccacctga	9000
gaggagagtg	ccagagctgt	gtgtacaaca	tgatgggaaa	aagagaaaag	aaacaagggg	9060
aatttgga	ggccaagggc	agccgcgcca	tctggtatat	gtggctaggg	gctagatttc	9120
tagagttcga	agcccttgga	ttcttaaagt	aggatcactg	gatggggaga	gagaactcag	9180
gaggtggtgt	tgaagggtct	ggattacaaa	gactcggata	tgtcctagaa	gagatgagtc	9240
gcataccagg	aggaaggatg	tatgcagatg	acactgctgg	ctgggacacc	cgcatcagca	9300
ggtttgatct	ggagaatgaa	gctttaatac	ccaaccaa	ggagaaagg	cacagggcct	9360
tagcattggc	cataatcaag	tacacatacc	aaaacaaagt	ggtaaagggtc	cttagaccag	9420
ctgaaaaagg	gaagacagtt	atggacatta	tttcaagaca	agaccaaagg	gggagcggac	9480
aagttgtcac	ttacgctctt	aacacattta	ccaacctagt	ggtgcaactc	attcggaata	9540
tggaggctga	ggaagttcta	gagatgcaag	acttgtggct	gctgcggagg	tcagagaaag	9600
tgaccaactg	gttgacagagc	aacggatggg	ataggctcaa	acgaatggca	gtcagtggag	9660
atgattgctg	tgtgaagcca	attgatgata	ggtttgcaca	tgccctcagg	ttcttgaatg	9720
atatgggaaa	agttaggaag	gacacacaag	agtggaaacc	ctcaactgga	tgggacaact	9780
gggaagaagt	tccgttttgt	tcccaccact	tcaacaagct	ccatctcaag	gacgggaggt	9840
ccattgtggt	tccctgccgc	caccaagatg	aactgattgg	ccgggcccgt	gtctctccag	9900
gggcgggatg	gagcatccgg	gagactgctt	gcctagcaaa	gtcatatgcg	caaagtgggc	9960
agctccttta	tttccacaga	agggacctcc	gactgatggc	caatgccatc	tgttcatctg	10020
tgccagttga	ctgggttcca	actgggagaa	ctacctggtc	aatccatgga	aaggggagaat	10080
ggatgaccac	tgaagacatg	cttgtggtgt	ggaacagagt	gtggattgag	gagaacgacc	10140
acatggaaga	caagacccca	gttacgaaat	ggacagacat	tccctatctg	ggaaaaagg	10200
aagacttggt	gtgtggatct	ctcatagggc	acagaccgcg	caccacctgg	gctgagaaca	10260
ttaaaaacac	agtcaacatg	gtgcgcagga	tcataggtga	tgaagaaaag	tacatggact	10320
acctatccac	ccaagtctgc	tacttgggtg	aagaagggtc	tacacctgga	gtgctataag	10380
caccaatctt	agtgttgtca	ggcctgctag	tcagccacag	cttggggaaa	gctgtgcagc	10440
ctgtgacccc	cccaggagag	gctgggaaac	caagcccata	gtcaggccga	gaacgccatg	10500
gcacggaaga	agccatgctg	cctgtgagcc	cctcagagga	cactgagtca	aaaaacccca	10560

cgcgcttgga ggcgcaggat gggaaaagaa ggtggcgacc ttccccaccc ttcaatctgg 10620
ggcctgaact ggagatcagc tgtggatctc cagaagaggg actagtgggtt agaggagacc 10680
ccccggaaaa cgcaaaacag catattgacg ctgggaaaga ccagagactc catgagtttc 10740
caccacgctg gccgccaggc acagatcgcc gaatagcggc ggccggtgtg gggaaatcca 10800
tgggtct 10807

<210> 81
<211> 10755
<212> DNA
<213> Zika virus isolate ARB7701 polyprotein gene, complete cds

<220>
<221> misc_feature
<222> (3606)..(3607)
<223> n is a, c, g, or t

<400> 81
acctgttgat ctgtgtgaat cagactgcga cagttcgagt ttgaagcgag agctaacaac 60
agtatcaaca ggtttaattt ggatttgga gcgagagttt ctgggtcatga aaaacccaaa 120
gaagaaatcc ggaggattcc ggattgtcaa tatgctaaaa cgcgagtag cccgtgtaaa 180
ccccttggga ggtttgaaga ggctgccagc cggacttctg ctgggtcatg gacccatcag 240
aatggttttg gcaataactag cttttttgag atttacagca atcaagccat cactgggcct 300
catcaacaga tggggttctg tggggaaaaa agaggctatg gaaataataa agaagtttaa 360
gaaagatctt gctgccatgt tgagaataat caatgctagg aaggagagga agagacgtgg 420
tgcagacacc agcatcgga tcattggtct cctgctgact acagccatgg cagcggagat 480
taccagacgt ggaagtgcac actacatgta cttggacagg agcgatgctg ggaaggccat 540
ctcctttgct accaacttgg gagttaacaa atgccatgta cagatcatgg atctcgggca 600
catgtgtgac gccaccatga gttatgagtg ccctatgttg gacgagggag tggaaccaga 660
tgatgtcgat tgctggtgca acacgacatc aacttgggtt gtgtacggaa cctgtcatca 720
caaaaaaggt gaagcacggc gatctagaag agctgtgacg ctcccttctc actctacaag 780
gaagttgcaa acgcggtcgc agacctgggtt agaatacaaga gaatacacga agcacctgat 840
caaggttgaa aactggatat ttaggaaccc cgggtttgcg ctgcgagctg ttgccattgc 900
ctggcttttg ggaagctcga cgagccaaaa agtcatatac ttggttatga tactgctgat 960
tgccccggca tacagcatca ggtgcattgg agtcagcaat agagacttcg tggaaggcat 1020
gtcaggtggg acctgggttg atgtcgtctt ggaacatgga ggttgcgta ccgttatggc 1080

acaggacaag ccaacagttg acatagagtt ggtcacgaca acggtttagta acatggccga	1140
ggtaagatcc tactgttatg aggcatacat atcagacatg gcttcggaca gtcgctgccc	1200
aacacaaggt gaagcctacc ttgataagca atcagacacc caatatgtgt gcaaaagaac	1260
attggtggac agaggttggg gaaatgggtg tggacttttt ggcaaaggga gcctggtgac	1320
atgtgccaag ttcacgtgtt ccaagaagat gactgggaag agcattcagc cggagaatct	1380
ggagtatcga ataatgctat cagtgcattg ctcccagcac agcgggatga ttgttaatga	1440
cataggacat gaaactgacg aaaacagagc gaaagtcgag gtcacgcca attcaccaag	1500
agcagaagca accttgggag gctttggaag cttaggactt gattgtgaac caaggacagg	1560
cctggacttt tcagatttgt actacttgac catgaacaac aagcactggg tgggtgcaca	1620
agagtgggtt catgacatcc cattgccttg gcatgctggg gcagataacc gaactccaca	1680
ctggaacaac aaggaggcat tggtagagtt caaagatgcc cacgccaaga ggcaaaccgt	1740
cgttgttcta gggagccagg aaggagccgt tcacacggct cttgctggag ctctggaggc	1800
tgagatggat ggtgcaaaag gaaggctgtt ctccggccat ttgaaatgcc gcttaaaaat	1860
ggacaagctt agattgaagg gcgtgtcata ttccttgtgc accgcagcgt tcacatttac	1920
caaggcccca gctgaaacat tgcattgaac agttacagtg gaggtgcagt atgcagggac	1980
agatggaccc tgcaagggtc cagcccagat ggcgggtggac atgcagaccc tgacccagc	2040
cgggaggctg ataaccgcca accctgtgat tactgaaagc actgagaatt caaagatgat	2100
gttgaggctc gaccacccat ttggggattc ttacattgtc ataggagttg gggacaagaa	2160
aatcacccat cactggcata ggagtggtag caccatcgga aaagcatttg aggccactgt	2220
gagaggtgcc aagagaatgg cagttctggg ggatacagcc tgggacttcg gatcagtcgg	2280
gggcgtgttc aactcatttg gcaaggggtg tcaccagatt tttggagcag ctttcaaate	2340
actgtttgga ggaatgtcct ggttctcaca gatcctcata ggcacgctgc tgggtgtggtt	2400
gggtttgaac acaaagaatg gatccatctc cctcacatgc ttggccctgg ggggagtgat	2460
gatcttcctc tccacggctg tctctgctga cgtgggggtgc tcggtggact tctcaaaaag	2520
agaaacgaga tgtggcacgg ggggtgttcgt ctacaatgat gttgaagcct ggaggacag	2580
gtacaagtac catcctgact cccccgcag attggcagca gcagtcaagc aggcttggga	2640
agaggggatt tgtgggatct cctccgtttc aagaatggaa aacatcatgt ggaaatcagt	2700
ggaaggggag ctcaatgcta tcttagagga gaatggagtt caactgacag ttgtttagg	2760
atctgtaaaa aaccccatgt ggagaggccc acaaagattg ccagtgcctg tgaatgagct	2820

gccccatggc	tggaaagcct	gggggaaatc	atattttgtc	agagcggcaa	agaccaacaa	2880
cagttttgtt	gtcgatggtg	acacactgaa	ggaatgtccg	ctcaaacaca	gagcatggaa	2940
tagtttcctt	gtggaggatc	atgggtttgg	ggtcttccac	accagtgttt	ggctcaaggt	3000
tagagaagac	tactcactag	aatgtgaccc	agccgtcata	ggaacagctg	ttaagggaaa	3060
ggaggccgcc	cacagtgacc	tgggctactg	gattgaaagt	gaaaagaatg	acacatggag	3120
gctgaagagg	gccccatctga	ttgagatgaa	aacatgtgag	tggccaaagt	ctcacactct	3180
gtggacagat	ggagtagaag	aaagtgatct	gatcatacct	aaatcttttag	ctggtccact	3240
cagccaccac	aacactagag	agggttacag	aactcaagca	aaagggccat	ggcatagtga	3300
agagcttgaa	atccggtttg	aggaatgtcc	aggcaccaag	gttcacgtgg	aggagacatg	3360
cggaactaga	ggaccatctc	tgagatcaac	cactgcaagt	ggaaggggtca	ttgaggaatg	3420
gtgctgtaga	gaatgcacaa	tgccccact	atcgtttcga	gcaaaagacg	gctgctggta	3480
tggaatggag	ataaggccca	ggaaagaacc	agagagcaac	ttagtgaggt	caatggtgac	3540
agcgggatca	accgatcaca	tggaccactt	ctctcttgga	gtgcttggtga	ttctactcat	3600
ggtgcnngaa	gggctgaaga	agagaatgac	cacaaagatc	attatgagca	catcaatggc	3660
agtgctggtg	gccatgatcc	tgggaggatt	tttaatgagt	gacttggcta	agcttgatgat	3720
cctgatgggt	gccaccttcg	cagaaatgaa	cactggagga	gatgtggctc	acttggcatt	3780
ggttgcgga	tttaaagtca	gaccagcctt	gctgggtctcc	tttatatttca	gagctaattg	3840
gacacctcgt	gagagcatgc	tgctagccct	ggcttcgtgt	cttttgcaaa	ctgcaatctc	3900
tgctctcgaa	ggtgacttga	tggtcctcgt	caatggattt	gctttggcct	ggttggcaat	3960
acgagcaatg	gccgtgccac	gcactgacaa	cattgctctg	gcaatcctgg	ctgctctgac	4020
accactagcc	cgaggtagac	tgctcgtggc	atggagagcg	ggcctcgcta	cttgtggagg	4080
gtttatgctc	ctctccctga	aagggaaagg	tagtgtgaag	aagaacctgc	catttgatcat	4140
ggccttgga	ttgactgctg	tgaggatagt	agacccatt	aatgtgggtg	gactactgtt	4200
actcacaagg	agtgggaagc	ggagctggcc	ccctagtga	gtgcttacag	ctgttggcct	4260
gatatgtgca	ctggccggag	gctttgcaa	ggcagacatt	gagatggctg	ggcccatggc	4320
tgcagtaggc	ttgctgattg	tcagttatgt	ggtctcagga	aagagtgtgg	atatgtacat	4380
tgaaagagca	ggtgacatca	catgggaaaa	ggacgcggaa	gttactggaa	atagtcctcg	4440
gcttgacgtg	gcactagatg	agagtgggtga	tttctctctg	gtggaggaag	atggtccacc	4500
catgagagag	atcatactca	aggtggctct	gatggccatc	tgtggcatga	acccaatagc	4560

catacccttt gctgcaggag cgtggtatgt gtatgtgaag actggaaaaa ggagtgggtgc	4620
cctctgggat gtgcccgcctc ccaaagaagt gaaaaaagga gagaccacag atgggggtata	4680
cagagtgatg acccgcagac tgctgggttc aacacaggtt ggagtgggag tcatgcaaga	4740
gggagtcttc cacaccatgt ggcacgtcac aaaaggagct gcactgagga gcggtgaagg	4800
gagacttgat ccatactggg gggatgtcaa gcaggactta gtgtcatact gtgggccttg	4860
gaagttggat gcagcttggg atggacttag tgaggtgcag ctcttggcag tcccccccg	4920
agagagggcc agaaacattc agactctgcc tggaaatattc aagacaaagg atggggacat	4980
cggagcagtc gctctggact acccgcagc aacttcagga tccccgatcc tagacaaatg	5040
cggaagagtg ataggacttt atggcaatgg ggttgtgatc aagaatggaa gctatgttag	5100
tgccataacc cagggaaaga gggaggagga gactccggtt gaatgtttcg aaccctcgat	5160
gctgaagaag aagcagctaa ctgtcctgga tctgcatcca ggagccggaa agactaggag	5220
agttcttcct gaaatagtcc gtgaagccat aaaaaagaga ctccgcacag tgattttggc	5280
tccaaccagg gttgtcgctg ctgagatgga ggaagccttg agaggacttc cggtgcgтта	5340
catgacaaca gcagttaacg tcacccactc tgggacagaa atcgttgatt tgatgtgcca	5400
tgccaccttc acctcacgcc tattacaacc catcagagtc cctaattaca atctctacat	5460
catggatgaa gcccathttca cagaccctc aagtatagct gcaagaggat acatatcaac	5520
aagggttgaa atgggcgagg cggctgccat cttcatgaca gccacgccac caggaacccg	5580
agatgcattt ccagactcca actcaccaat catggacaca gaagtggaag tcccagagag	5640
agcctggagc tcaggctttg attgggtgac agaccattct gggaaaacag tttggttcgt	5700
tccaagtgtg agaaatggaa atgaaatcgc agcctgtctg acaaaggctg gaaagcgggt	5760
catacaactc agcaggaaga cttttgagac agagtttcag aaaacaaaaa atcaagagtg	5820
ggactttgtc ataacaactg acatctcaga gatgggcgcg aatttcaaag ctgaccgggt	5880
catagactct aggagatgcc taaagccagt catacttgat ggtgagagag tcatcttggc	5940
tgggcccattg cctgtcacgc atgctagtgc tgctcaaagg agagggcgta taggcaggaa	6000
ccctaacaaa cctggagatg agtacatgta tggaggtgga tgtgcagaga ccgatgaaga	6060
ccatgcacac tggcttgaag caagaatgct tcttgacaac atctacctcc aggatggcct	6120
catagcctcg ctctaccggc ctgaggccga taaggtagct gccattgagg gagagttcaa	6180
gctgaggaca gagcaaagga aaacctttgt ggaacttatg aagagaggag accttcccgt	6240
ttggctagcc tatcaggttg catctgccgg aataacttac acagacagaa gatggtgctt	6300

tgatggcaca	accaacaaca	ccataatgga	agatagtgtg	ccagcagaag	tgtggacaaa	6360
atatggagag	aagagagtgc	tcaaaccaag	atggatggat	gcgaggggtct	gttccgatca	6420
tgctgccctg	aagtcgttca	aagaatttgc	tgccgggaaa	agaggagtgg	ctttaggagt	6480
aatggaggcc	ctgggaacat	tgccaggaca	catgacagag	aggtttcagg	aggccattga	6540
caatctcgct	gtgctcatgc	gagcagagac	tggaagcagg	ccttacaagg	cagcggcagc	6600
ccaactgccg	gagaccctag	agaccatcat	gctcttaggc	ttgttgggaa	cagtttcggt	6660
ggggatcttc	tttgtcttga	tgcggaacaa	gggcatcggg	aagatggggt	ttggaatggg	6720
aactcttggg	gccagtgc	ggctcatgtg	gctttcggaa	attgaaccag	ccagaattgc	6780
atgtgtcctc	attgttgtgt	tcttggtact	ggtggtactc	atacccgagc	cagagaagca	6840
aagatctccc	caggacaacc	agatggcaat	catcatcatg	gtggcagtgg	gccttctggg	6900
tttgataact	gcaaacgaac	ttggatggct	ggaaagaaca	aaaaatgaca	tagctcatct	6960
aatgggaagg	agagaagaag	gagtaactat	gggattctca	atggacatcg	atttgcggcc	7020
agcctccgcc	tgggctatct	atgccgcact	gacaactctc	atcaccccag	ccgtccaaca	7080
cgcggtaacc	acttcataca	acaactactc	cctaattggcg	atggccacac	aagctggagt	7140
gctatttggc	atgggcaaag	ggatgccatt	ttatgcatgg	gactttggag	tcccgtgct	7200
aatgatgggt	tgctactcac	aattaacacc	cctaaccttg	atagtggcta	tcattctgct	7260
tgtggcacac	tatatgtact	tgatcccagg	cctacaggca	gcagcagcgc	gtgctgcca	7320
gaagagaaca	gcagctggca	tcatgaagaa	tcccgttgtg	gatggaatag	tggtactga	7380
cattgacaca	atgacaattg	acccccaagt	ggagaagaag	atgggacaag	tggtacttat	7440
agcagtagcc	atctccagtg	ctgtgctgct	gcggactgct	tggggatggg	gggaggctgg	7500
agctctgatt	actgcagcaa	cctccacctt	gtgggaaggt	tctccaaaca	aatactggaa	7560
ctcctctaca	gccacctcac	tgtgcaacat	cttcagagga	agttacctgg	caggcgcttc	7620
tcttatttat	acagtgacaa	gaaatgctgg	cctagtcaag	agacgtggag	gtggaacggg	7680
agagactcta	ggagagaagt	ggaaagctcg	cctgaatcag	atgtcggccc	tggagttcta	7740
ctcttacaaa	aagtcaggca	tactgaagt	gtgtagagag	gaggctcgcc	gcgccctcaa	7800
ggatggagtg	gccacaggag	gacatgctgt	atcccgggga	agcgcaaagc	tcagatggct	7860
ggtggagaga	ggatacctgc	aaccccatgg	aaaggttgtt	gacctcggat	gtggcagagg	7920
gggttggagc	tattatgccg	ccaccatccg	gaaagtgcag	gaggtgaaag	gatacacaaa	7980
gggaggtccc	ggtcatgaag	aacccatgct	ggtgcaaagc	tatgggtgga	acatcgttcg	8040

tctcaagagt	ggagtggacg	tcttccacat	ggcggccgag	ccgtgtgata	ccttgctgtg	8100
tgacataggt	gagtcatcat	ctagtcctga	agtggaagag	acgcgaacac	tccgagtgct	8160
ctctatggtg	ggggactggc	ttgagaaaag	accggggggc	ttctgtataa	aggtgctgtg	8220
tccatacacc	agcactatga	tggagaccat	ggagcgcctg	caacgtaggt	atgggggagg	8280
attagtcaga	gtgccattgt	ctcgcaactc	cacacatgag	atgtattggg	tctctggagc	8340
aaaaagtaac	gtcataaaaa	gtgtgtccac	cacaagtcag	ctcctcctgg	gacgcatgga	8400
tgggtcccagg	aggccagtga	aatatgagga	agatgtgaac	ctcggctcgg	gcacacgagc	8460
tgtggcaagc	tgtgctgaag	ctcccaacat	gaaggtcatt	ggcaagcgca	ttgagagaat	8520
ccgcagtga	catgcagaaa	catggttctt	tgatgaaaac	catccataca	ggacatgggc	8580
ctaccatggg	agctacgaag	ccccacaca	agggtcagca	tcttccctcg	tgaatggggg	8640
tgttagactc	ctgtcaaagc	cctgggatgt	agtgactgga	gttacaggaa	tagctatgac	8700
tgatacaaca	ccatacggcc	aacaaagagt	cttcaaagaa	aaagtggaca	ccaggggtgcc	8760
agatccccaa	gaaggcactc	gccaggcaat	gaacatggtc	tcttcctggc	tgtggaagga	8820
gttggggaaa	cgcaagcggc	cacgtgtctg	caccaaagaa	gagttcatca	acaaggtgcg	8880
cagcaatgca	gcactgggag	caatatttga	agaggaaaaa	gaatggaaga	cggccgtgga	8940
ggctgtgaat	gatccaaggt	tttgggctct	agtggacaag	gaaagagaac	atcacctgag	9000
aggagagtgc	catagctgtg	tgtacaatat	gatgggaaaa	agagagaaga	agcaaggaga	9060
attcggaaaa	gcaaaaggca	gccgcgccat	ctggtacatg	tggttgggag	ccagattctt	9120
ggagtttgaa	gcccttggat	tcttgaatga	ggaccattgg	atgggaagag	aaaactcagg	9180
aggtggtgtc	gaagggctag	gactgcaaag	acttggatac	attctagaag	aatgaatcg	9240
ggcaccagga	ggaaagatgt	atgcagatga	caccgctggc	tgggacaccc	gcattagtaa	9300
gtttgatctg	gagaatgaag	ccttaattac	caaccaaagt	gaggaagggc	acagagctct	9360
ggcgttggct	gtgattaagt	acacaaaaaa	caaagtgggt	aaggtcctca	gaccagctga	9420
aggagggaaa	acagttatgg	acatcatttc	aagacaggac	cagagaggga	gtggacaagt	9480
tgtcacctat	gctctcaaca	catttaccaa	cttagtggtg	cagcttatcc	ggaatatgga	9540
ggctgaggaa	gtgttagaga	tgcaagactt	atggctgttg	aggaagccag	agaaagtgac	9600
cagatggttg	cagtgcaatg	gatgggacag	actcaaacga	atggcagtca	gtggagatga	9660
ctgcgttgtg	aagccaattg	atgatagggt	tgcgcatgcc	ctcaggttct	taaatgacat	9720
gggaaaagtt	aggaaagaca	cacaggaatg	gaaaccctcg	actggatgga	gcaattggga	9780

agaagtcccg ttctgctccc accatttcaa caagctgcac ctcaaggatg gtagatccat	9840
tgtggtcctt tgccgccacc aagatgaatt gattggccga gcccggtgtat caccaggggc	9900
aggatggagc attcgggaga ctgcctgtct agcaaaatca tatgcacaga tgtggcagct	9960
tctttacttc cacagaagag accttcgact gatggccaat gctatttggt cggctgtgcc	10020
agttgactgg gtaccaaccg ggagaaccac ctggtcaatc cacggaaagg gagaatggat	10080
gactactgag gacatgctca tgggtgtggaa tagagtgtgg attgaggaga acgaccatat	10140
ggaggacaag actcctgtga caaagtggac agacatcccc tatctgggaa aaaggaggga	10200
cttatgggtgt ggatccctta tagggcacag gccccgcacc acttgggctg agaacatcaa	10260
agacacagtc aacatgggtgc gcaggatcat aggtgatgaa gaaaaataca tggactactt	10320
atccaccag gtccgctact tgggtgagga agggccaca cctggagtgt tgtaagcacc	10380
aatttcagtg ttgtcaggcc tgctagccag ccacagtttg gggaaagctg tgcagcctgt	10440
agcccccca ggagaagctg ggaaaccaag ctcatagtca ggccgagaac gccatggcac	10500
ggaagaagcc atgctgcctg tgagcccctc agaggacact gagttaaaaa accccacgcg	10560
cttggaagcg caggatggga aaagaaggtg gcgaccttc ccacccttta atctggggcc	10620
tgaactggag actagctgtg aatctccagc agagggacta gtggttagag gagaccccc	10680
ggaaaacgca aaacagcata ttgacgtgg gaaagaccag agactccatg agtttccacc	10740
acgctggccg ccagg	10755

<210> 82

<211> 10776

<212> DNA

<213> Zika virus isolate ARB15076 polyprotein gene, complete cds

<400> 82

gttgttgatc tgtgtgaatc agactgcgac agttcgagtt tgaagcgaga gctaacaaca	60
gtatcaacag gtttaatttg gatttggaaa cgagagtttc tggatcatgaa aaacccaaag	120
aagaaatccg gaggattccg gattgtcaat atgctaaaac gcggagtagc ccgtgtaaac	180
cccttgggag gtttgaagag gctgccagcc ggactcctgc tgggtcatgg acccatcaga	240
atggtttttg caatactagc ctttttgaga ttacagcaa tcaagccatc actgggcctc	300
atcaacagat ggggttcagt ggggaaaaaa gaggctatgg aaataataaa gaagttaag	360
aaagatcttg ctgccatgtt gagaataatc aatgctagga aggagaggaa gagacgtgg	420
gcagacacca gcacggaat cattggtctc ctgctgacta cagccatggc agcagagatt	480

accagacgtg gaagtgcata ctacatgtac ttggacagga gcgatgctgg gaaggccatc	540
tcctttgcta ccaatttggg agttaacaaa tgccatgtac agatcatgga tctcggggcac	600
atgtgtgacg ccaccatgag ttatgagtgt cctatgttgg acgagggagt ggaaccagat	660
gatgtcgatt gctggtgcaa cacgacatca acttgggttg tgtacggaac ctgtcatcac	720
aaaaaaggtg aagcacggcg atctagaaga gctgtgacgc tccctttctca ctctacaagg	780
aagctgcaaa cgcggtcgca gacttggtta gaatcaagag aatacacgaa gcacttgatc	840
aaggttgaaa actggatatt caggaacccc gggtttgcg ctcgagctgt tgccattgcc	900
tggcttttgg gaagctcgac gagccaaaaa gtcataact ttggtcatgat actgctgatt	960
gccccggcat acagcatcag gtgcattgga gtcagcaata gagacttcgt ggaaggcatg	1020
tcaggtggga cctgggttga tgtcgtcttg gaacatggag gttgcgtcac cgtaatggca	1080
caggacaagc caacagttga catagagttg gtcacgacaa cggtcagtaa catggccgag	1140
gtaagatcct actgttatga ggcataata tcggacatgg cttcggacag tcgctgcca	1200
acacaaggtg aagcctacct tgacaagcaa tcagacactc aatatgtatg caaaagaaca	1260
ttggtggaca gaggttgggg aaatgggtgt ggactttttg gcaaaggag cctggtgaca	1320
tgtgccaagt tcacgtgttc caagaagatg accgggaaga gcattcagcc ggagaatctg	1380
gagtatcgaa taatgctatc agtgcattgg tcccagcaca gcgggatgat tgtaatgac	1440
gaaaataggg cgaaagtcga ggtcacgccc aattcaccaa gagcagaagc aaccttggga	1500
ggcttttgaa gcttaggact tgattgtgaa ccaaggacag gcctggactt ttcagatttg	1560
tactacttga ccatgaacaa taagcactgg ttagtgcaca aagagtgggt tcatgacatc	1620
ccattgccct ggcattgctg ggcagacacc ggaactccac attggaacaa caaggaggca	1680
ttggtagagt tcaaagatgc ccacgctaag aggcaaaccg tcgttggttct agggagccag	1740
gaaggagccg ttcacacggc tcttgctgga gctctggagg ctgagatgga tggtgcaaaa	1800
ggaaggttgt tctccggcca tttgaaatgc cgcttaaaaa tggacaagct tagattgaag	1860
ggcgtgtcat attccttggt caccgcagcg ttcacattca ccaaggcccc agctgaaaca	1920
ttgcatggaa cagttacagt ggaggtgcag tatgcaggga cagatggacc ctgcaaggtc	1980
ccagctcaga tggcgggtgga catgcagacc ctgaccccag tcggaaggct gataaccgcc	2040
aaccccgatg ttactgaaag cactgagaat tcaaagatga tgttgagct cgaccacca	2100
tttggggatt cttacattgt cataggagtt ggggacaaga aaattacca cactggcat	2160
aggagtggta gcaccatcgg aaaagcattt gaggccactg tgagaggtgc caagagaatg	2220

gcagttcttg	gggacacagc	ctgggacttt	ggatcagtcg	ggggcgtggt	taactcattg	2280
ggcaagggca	tccaccagat	ttttggagca	gccttcaa	actgtttg	aggaatgtcc	2340
tggttctcac	agatcctcat	aggcacgctg	ctggtgtggt	tggtttgaa	cacaaagaat	2400
ggatccatct	ccctcacatg	cttggccctg	gggggagtga	tgatcttcct	ctccacggct	2460
gtctctgctg	acgtgggggtg	ctcgggtggac	ttctcaaaaa	gagaaacgag	atgtggcacg	2520
ggggtgttcg	tctacaatga	tgttgaagcc	tggagggaca	ggtacaagta	ccatcctgac	2580
tcccccgca	gattggcagc	agcagtcaag	caggcttggg	aagagggaat	ttgtgggatc	2640
tcctccgttt	caagaatgga	aaacatcatg	tggaaatcag	tggaagggga	gctcaatgct	2700
atcttagagg	agaatggagt	tcaactgaca	gttggtgtag	gatctgtaaa	aaaccccatg	2760
tggagaggtc	cacaaagatt	gccagtgcct	gtgaatgagc	tgcccatgg	ctggaaagcc	2820
tgggggaaat	catattttgt	cagagcggca	aagaccaaca	acaggtttgt	tgtcgatggt	2880
gacacactga	aggaatgtcc	gctcaa	acagcatgga	atagtttcct	tgtggaggat	2940
catgggtttg	gggtcttcca	caccagtgtt	tggcttaagg	ttagagaaga	ttactcacta	3000
gaatgtgacc	cagccgtcat	aggaacagct	gttaagggaa	aggaggccgc	gcacagtgac	3060
ctaggctact	ggattgaaag	tgaaaagaat	gacacatgga	ggctgaagag	ggccacctg	3120
attgagatga	aaacatgtga	gtggccaaag	tctcacactc	tgtggacaga	tggagtagaa	3180
gaaagtgatc	tgatcatacc	taaatcttta	gctggtccac	tcagccacca	caacactaga	3240
gagggttaca	gaactcaagc	aaaagggcca	tggcatagt	aagagcttga	aatccggttt	3300
gaggaatgtc	caggcaccaa	ggttcatgtg	gaggagacat	gcggaactag	aggaccatct	3360
ctgagatcaa	ccactgcaag	tggaagggtc	attgaggaat	ggtgctgtag	agaatgcaca	3420
atgccccac	tatcgtttcg	agcaaaagat	ggctgctggt	atggaatgga	gataaggccc	3480
aggaaagaac	cagagagcaa	cttagtgagg	tcaatggtga	cagcgggatc	aaccgatcac	3540
atggaccact	tctctcttgg	agtgttgtg	attctactca	tgggtgcagga	agggttgaag	3600
aagagaatga	ccacgaagat	cattatgagc	acatcaatgg	cagtgtggt	agccatgatc	3660
ctgggaggat	tttcaatgag	tgacctggct	aagcttgtga	tcctgatggg	tgccaccttc	3720
gcagaaatga	acactggagg	agatgtggct	cacttggcat	tggttgcggc	atttaaagtc	3780
agaccagcct	tgctgggtctc	ctttattttc	agagctaatt	ggacacctcg	tgagagcatg	3840
ctgctagccc	tggcttcgtg	tcttttacia	actgcaatct	ctgctcttga	aggtgacttg	3900
atggtcctcg	tcaatggatt	tgctttggcc	tggttggcaa	tacgagcaat	ggccgtgcca	3960

cgcactgaca	acattgctct	agcagtcctg	gctgctctga	caccactagc	ccgaggcaca	4020
ctgctcgtgg	catggagagc	gggcctcgct	acttgtggag	ggttcatgct	cctttccctg	4080
aaggggaaag	gtagtgtgaa	gaagaacctg	ccatttgtca	tggccttggg	attgaccgct	4140
gtgaggatag	tagaccccat	taatgtggta	ggactactgt	tactcacaag	gagcgggaag	4200
cggagctggc	cccctagtga	agtgcttaca	gctgttggcc	tgatatgtgc	actggccgga	4260
gggtttgcca	aggcagacat	tgagatggct	gggcccattg	ctgcagtagg	cttgctaatt	4320
gtcagttatg	tggctctcagg	aaagagtgtg	gatatgtaca	ttgaaagagc	aggtgacatc	4380
acatgggaaa	aggacgcgga	agttactgga	aatagtcctc	ggcttgacgt	ggcactagat	4440
gagagtgggtg	atctctctct	ggtggaggaa	gatgggtccac	ccatgagaga	gatcatactc	4500
aaggtgggtcc	tgatggccat	ctgtggcatg	aaccaaatag	ccataccctt	tgctgcagga	4560
gcgtggatatg	tgtatgtgaa	gactgggaaa	aggagtgggtg	ccctctggga	tgtgcccgtc	4620
cccaaagaag	tgaaaaaagg	agagaccaca	gatggagtat	acagagtgat	gaccgcgaga	4680
ctgctgggtt	caacacaggt	tggagttgga	gtcatgcaag	agggagtctt	ccacaccatg	4740
tggcacgtca	caaaaggagc	tgcactgagg	agcggcgaag	ggagacttga	tccatactgg	4800
ggggatgtca	agcaggactt	agtgtcatac	tgtgggcctt	ggaagttgga	tgcagcttgg	4860
gatggactta	gtgaggtgca	gctcttggca	gtaccccccg	gagagagggc	cagaaacatt	4920
cagactctgc	ctggaatatt	caagacaaag	gatggggaca	tcggagcagt	tgctctggac	4980
taccccgag	gaacttcagg	atccccgatc	ctagacaaat	gcggaagagt	gataggactt	5040
tatggcaatg	gggttgtgat	caagaatgga	agctatgtta	gtgccataac	ccagggaag	5100
agggaggagg	agactccggt	tgaatgtttc	gaaccctcga	tgctgaagaa	gaagcagcta	5160
actgtcctgg	atctgcatcc	aggagccgga	aagactagga	gagttcttcc	tgaaatagtc	5220
cgtgaagcca	taaaaaagag	actccgcaca	gtgatttttg	ctccaaccag	ggttgctgct	5280
gctgagatgg	aggaagcctt	gagaggactt	ccggtgcgtt	acatgacaac	agcagttaac	5340
gtcacccact	ctgggacaga	aatcgttgat	ttgatgtgcc	atgccacctt	cacttcacgc	5400
ttattacaac	ccatcagagt	ccctaattac	aatctctaca	tcatggatga	agcccatttc	5460
acagaccctt	caagtatagc	tgcaagagga	tacatatcaa	caagggttga	aatgggcgag	5520
gcggctgcca	tctttatgac	agccacgcca	ccaggaaccc	gagatgcatt	tccagactcc	5580
aactcaccaa	tcatggacac	agaagtggaa	gtcccagaga	gagcctggag	ctcaggcttt	5640
gattgggtga	cagaccattc	tggaaaaaca	gtttggtttg	ttccaagtgt	gagaaatgga	5700

aatgaaatcg	cagcctgtct	gacaaaggct	ggaaagcggg	tcatacaact	cagcaggaag	5760
acttttgaga	cagagtttca	gaaaacaaaa	aatcaagagt	gggactttgt	cataacaact	5820
gacatctcag	agatgggtgc	caatttcaag	gctgaccggg	tcatagactc	taggagatgc	5880
ctaaagccag	ttatacttga	tggtgagaga	gtcatcttgg	ctggggcccat	gcctgtcacg	5940
catgctagtg	ctgctcaaag	gagagggcgt	ataggcagga	accctaacaa	acctggagat	6000
gagtacatgt	atggaggtgg	atgtgcagag	accgatgaag	accatgcaca	ctggcttgaa	6060
gcaagaatgc	ttcttgacaa	catctacctc	caggatggcc	tcatagcttc	gctctaccgg	6120
cctgaggccg	acaaggtagc	cgccattgag	ggagagttca	agctgaggac	ggagcaaagg	6180
aaaacctttg	tggaacttat	gaagagagga	gaccttcccg	tttggtggc	ctatcaggtt	6240
gcatctgccg	gaataactta	cacagacaga	agatggtgct	ttgatggcac	aaccaacaac	6300
accataatgg	aagatagtgt	accagcagag	gtgtggacaa	aatatggaga	gaagagagtg	6360
cttaaaccaa	gatggatgga	tgcgagggtc	tgttctgata	atgctgccct	gaagtcgttc	6420
aaagaatttg	ctgccgggaa	aagaggagcg	gctttaggag	taatggaggc	cctgggaaca	6480
ttaccaggac	acatgacaga	gaggtttcag	gaggccattg	acaatctcgc	tgtgcttatg	6540
cgagcagaga	ctggaagtag	gccttacaag	gcagcggcag	cccaactgcc	ggagacccta	6600
gagaccatca	tgctcctagg	tttgctggga	acagtttcgt	tggggatctt	ctttgtcttg	6660
atgcggaaca	agggcatcgg	gaagatgggt	tttggaatgg	taactcttgg	ggccagtgca	6720
tggtctcatgt	ggctttcgga	aattgagcca	gccagaattg	catgtgtcct	cattgtttgtg	6780
ttcttgttac	tggtggtact	catacccgag	ccagagaagc	aaagatctcc	ccaggacaac	6840
cagatggcaa	tcatcatcat	ggtggcagtg	ggccttctgg	gtttgataac	tgcaaacgaa	6900
cttggatggc	tggaagaagc	aaaaaatgac	atagctcatc	taatgggaag	gagagaagaa	6960
ggagtaacta	tgggattctc	aatggacatc	gatttgcggc	cagcctccgc	ctgggctatt	7020
tatgccgcac	tgacaactct	catcacccca	gctgtccaac	acgcggtaac	cacttcatac	7080
aacaactact	ccctaattgg	gatggccaca	caagctggag	tgctatattg	catgggcaaa	7140
gggatgccat	tttatgcatg	ggactttgga	gtcccgtgc	taatggtggg	ttgctactca	7200
caattaacac	ccctaacctt	gatagtggct	atcattctgc	ttgtggcaca	ctacatgtac	7260
ttgatcccag	gcctacaggc	agcagcagcg	cgtgctgcc	agaagagaac	agcagctggc	7320
atcatgaaga	atcccgttgt	ggatggaata	gtggtaactg	acattgacac	aatgacaatt	7380
gacccccaag	tggaagaagaa	gatgggacaa	gtgttactca	tagcagtagc	catctccagt	7440

gctgtgctgc	tgcgaaactgc	ttgggggatgg	ggggaggctg	gagctctgat	cacagcagca	7500
acctccacct	tgtgggaagg	ttctccaaac	aaatactgga	actcctctac	agccacctca	7560
ctgtgcaaca	tcttttagagg	aagttacctg	gcaggcgctt	ctctcattta	tacagtgaca	7620
agaaatgctg	gcctagtcaa	gagacgtgga	ggtggaacgg	gagagactct	aggagagaag	7680
tggaaagctc	gcctgaatca	gatgtcggcc	ctggagttct	actcttaca	aaagtcaggc	7740
atcactgaag	tgtgtagaga	ggaggctcgc	cgcgccctca	agaatggagt	ggccacagga	7800
ggacatgctg	tatccccggg	aagcgcaaag	ctcagatggc	tgggtggagag	aggatacctg	7860
caaccccatg	gaaaggttgt	tgacctcgga	tgtggcagag	ggggttggag	ctattatgcc	7920
gccaccatcc	ggaaagtgca	ggaggtgaaa	ggatacacia	agggagggtcc	tggtcatgaa	7980
gaacccatgc	tggtgcaaag	ctatgggtgg	aacatagttc	gtctcaagag	tggagtggat	8040
gtcttccaca	tggcggccga	gccgtgtgac	accttgctgt	gcgacatagg	tgagtcatca	8100
tctagtcttg	aagtggaaga	gacgcgaaca	ctcagagtgc	tctctatggg	gggggactgg	8160
cttgagaaaa	gaccgggagc	cttctgcata	aagggtgctgt	gccatacac	cagcactatg	8220
atggagacca	tggagcgcct	gcaacgtagg	tatgggggag	gattagtcag	agtgccattg	8280
tctcgcaact	ccacacatga	aatgtattgg	gtctctggag	caaaaagtaa	catcataaaa	8340
agtgtgtcca	ccacaagtca	gtcctcctg	ggacgcatgg	atggccccag	gaggccagtg	8400
aaatatgagg	aagatgtgaa	cctcggtcgc	ggcacacgag	ctgtggcaag	ctgtgctgaa	8460
gctcccaaca	tgaagatcat	tggcaagcgc	attgagagaa	tccgcagtga	acatgcagaa	8520
acatggttct	ttgatgaaaa	ccaccatac	aggacatggg	cctaccatgg	gagctacgaa	8580
gccccaccc	aaggatcagc	gtcttccctc	gtgaatgggg	ttgttagact	cctgtcaaag	8640
ccctgggatg	ttgtgactgg	agttacagga	atagctatga	ctgacactac	accatacggc	8700
caacaaagag	tcttcaaaga	aaaagtggac	accaggggtgc	cagatcctca	agaaggcact	8760
cgcagacaa	tgaacatggg	ttcttcctgg	ctgtggaagg	agctggggaa	acgcaagcgg	8820
ccacgtgtct	gcaccaaaga	agagttcatc	aacaagggtgc	gcagcaatgc	agcactggga	8880
gcaatatattg	aagaggaaaa	agaatggaag	acggccgtgg	aagctgtgaa	tgatccaagg	8940
ttttgggccc	tagtggacaa	ggagagagaa	catcacctga	gaggagagtg	ccatagctgt	9000
gtgtacaata	tgatgggaaa	aagagagaag	aagcaaggag	aattcggaaa	agcaaaaggc	9060
agccgcgcca	tctggtacat	gtggttggga	gccagattct	tggagtttga	agcccttgga	9120
ttcttgaatg	aggaccattg	gatgggaaga	gaaaactcag	gaggtggtgt	cgaagggtca	9180

ggactgcaaa gacttggata cattctagaa gaaatgaatc gagcaccagg aggaaagatg	9240
tatgcagatg acaccgctgg ctgggatacc cgtattagta agtttgatct ggagaatgaa	9300
gccttaatta ccaaccaa at ggaggaaggg catagagctc tagcattggc tgtgattaag	9360
tacacatacc aaaacaaagt ggtgaaggtc ctcagaccag ctgaaggagg gaaaacagtt	9420
atggacatca tttcaagaca agaccagaga gggagtggac aagttgtcac ttatgctctc	9480
aacacattta ccaacttggg ggtgcagctt atccggaaca tggaggctga ggaagtgcta	9540
gagatgcaag acttatggct gctgaggaag ccagagaaag tgaccagatg gttgcagtgc	9600
aatggatggg acagactcaa acgaatggca gtcagtggag atgactgcgt tgtgaagcca	9660
attgatgata ggtttgcaca tgccctcagg ttcttgaatg acatgggaaa agttaggaaa	9720
gacacacagg aatggaaacc ctcgactgga tggagcaatt gggaagaagt cccgttctgc	9780
tcccaccatt tcaacaagct gcacctcaag gatggtagat ccattgtggg cccttgccgc	9840
caccaagatg aattgattgg ccgagcccg gtatcaccag gggcaggatg gagcatccgg	9900
gagactgcct gtctagcaaa atcatatgca cagatgtggc agcttcttta cttccacaga	9960
agagaccttc gactgatggc caatgctatt tgttcggctg tgccagttga ctgggtgcca	10020
accgggagaa ccacctgggc aatccacgga aaggggagaat ggatgactac tgaggacatg	10080
ctcatgggtg ggaatagagt gtggattgag gagaacgacc acatggagga caagactcct	10140
gtgacaaagt ggacagacat cccctatctg ggaaaaaggg aggacttatg gtgtggatcc	10200
cttatagggc acaggccccg caccacttgg gctgagaaca tcaaagacac agtcaacatg	10260
gtgcgagga tcataggtga tgaagaaaaa tacatggact acttatccac ccagggtccgc	10320
tacttgggtg aggaaggggc cacacctgga gtgttgtaag caccaatttc agtgttgtca	10380
ggcctgctag tcagccacag tttggggaaa gctgtgcagc ctgtagcccc cccaggagac	10440
gctgggaaac caagctcata gtcaggccga gaacgccatg gcacggaaga agccatgctg	10500
cctgtgagcc cctcagagga cactgagtca aaaaaccca cgcgcttgga agcgcaggat	10560
gggaaaagaa ggtggcgacc ttccccaccc tttaatctgg ggctgaact ggagactagc	10620
tgtgaatctc cagcagaggg actagtgggt agaggagacc ccccgaaaaa cgcaaacag	10680
catattgacg ctgggaaaga ccagagactc catgagtttc caccacgctg gccgccaggc	10740
acagatcgcc gaacagcggc ggccagtgtg gtggaa	10776

<210> 83
 <211> 10788
 <212> DNA

<213> Zika virus isolate ARB13565 polyprotein gene, complete cds

<400> 83

agttgttgat ctgtgtgaat cagactgcga cagttcgagt ttgaagcgag agctaacaac	60
agtatcaaca ggttttaattt ggatttggaa gcgagagttt ctgggtcatga aaaacccaaa	120
gaagaaatcc ggaggattcc ggattgtcaa tatgctaaaa cgcggagtag cccgtgtaaa	180
ccccttggga ggtttgaaga ggctgccagc cggacttctg ctgggtcatg gacccatcag	240
aatggttttg gcaataactag cttttttgag atttacagca atcaagccat cactgggcct	300
catcaacaga tgggggttctg tggggaaaaa agaggctatg gaaataataa agaagtttaa	360
gaaagatctt gctgccatgt tgagaataat caatgctagg aaggagagga agagacgtgg	420
tgcagacacc agcatcggaa tcattgggtct cctgctgact acagccatgg cagcggagat	480
taccagacgt ggaagtgcac actacatgta cttggacagg agcgatgctg ggaaggccat	540
ctcctttgct accaacttgg gagttaacaa atgccatgta cagatcatgg atctcgggca	600
catgtgtgac gccaccatga gttatgagtg ccctatgttg gacgaggag tggaaccaga	660
tgatgtcgat tgctgggtgca acacgacatc aacttgggtt gtgtacggaa cctgtcatca	720
caaaaaaggt gaagcacggc gatctagaag agctgtgacg ctcccttctc actctacaag	780
gaagttgcaa acgcggtcgc agacctgggtt agaatacaaga gaatacacga agcacctgat	840
caaggttgaa aactggatat ttaggaaccc cgggtttgcg ctgcgagctg ttgccattgc	900
ctggcttttg ggaagctcga cgagccaaaa agtcatatac ttggttatga tactgctgat	960
tgccccggca tacagcatca ggtgcattgg agtcagcaat agagacttcg tggaaggcat	1020
gtcaggtggg acctgggttg atgtcgtctt ggaacatgga ggttgcgta ccgttatggc	1080
acaggacaag ccaacagttg acatagagtt ggtcacgaca acggttagta acatggccga	1140
ggtaagatcc tactgttatg aggcataat atcagacatg gcttcggaca gtcgctgccc	1200
aacacaaggt gaagcctacc ttgataagca atcagacacc caatatgtgt gcaaaagaac	1260
attggtggac agaggttggg gaaatgggtg tggacttttt ggcaaaggga gcctggtgac	1320
atgtgccaag ttcacgtgtt ccaagaagat gactgggaag agcattcagc cggagaatct	1380
ggagtatcga ataatgctat cagtgcattg ctcccagcac agcgggatga ttgttaatga	1440
cataggacat gaaactgacg aaaacagagc gaaagtcgag gtcacgcca attcaccaag	1500
agcagaagca accttgggag gctttggaag cttaggactt gattgtgaac caaggacagg	1560
cctggacttt tcagatttgt actacttgac catgaacaac aagcactggg tgggtgcaca	1620
agagtggttt catgacatcc cattgccttg gcatgctggg gcagataccg gaactccaca	1680

ctggaacaac aaggaggcat tggtagagtt caaagatgcc cacgccaaga ggcaaaccgt	1740
cgttgttcta gggagccagg aaggagccgt tcacacggct cttgctggag ctctggaggc	1800
tgagatggat ggtgcaaaag gaaggctggt ctccggccat ttgaaatgcc gcttaaaaat	1860
ggacaagctt agattgaagg gcgtgtcata ttccttgtag accgcagcgt tcacatttac	1920
caaggthcca gctgaaacat tgcattgaac agttacagt gaggtgcagt atgcaggagc	1980
agatggaccc tgcaagggtc cagcccagat ggcgggtggc atgcagaccc tgaccccagt	2040
cgggaggctg ataaccgcca accctgtgat tactgaaagc actgagaatt caaagatgat	2100
gttgaggctc gaccacccat ttggggattc ttacattgtc ataggagttg gggacaagaa	2160
aatcaccat cactggcata ggagtggtag caccatcgga aaagcatttg aggcactgt	2220
gagaggtgcc aagagaatgg cagttctggg ggatacagcc tgggacttcg gatcagtcgg	2280
gggcgtgttc aactcatttg gcaagggtgt tcaccagatt tttggagcag ctttcaaatc	2340
actgtttgga ggaatgtcct ggttctcaca gatcctcata ggcacgctgc tgggtgtggt	2400
gggtttgaac acaaagaatg gatccatctc cctcacatgc ttggccctgg gggagtgat	2460
gatcttcctc tccacggctg tctctgctga cgtggggtgc tcggtggact tctcaaaaag	2520
agaaacgaga tgtggcacgg ggggtttcgt ctacaatgat gttgaagcct ggaggacag	2580
gtacaagtac catcctgact cccccgcag attggcagca gcagtcaagc aggcttggga	2640
agaggggatt tgtgggatct cctccgtttc aagaatggaa aacatcatgt ggaaatcagt	2700
ggaaggggag ctcaatgcta tcttagagga gaatggagtt caactgacag ttgtttagg	2760
atctgtaaaa aaccccatgt ggagaggccc acaaagattg ccagtgcctg tgaatgagct	2820
gccccatggc tggaaagcct gggggaaatc atattttgtc agagcggcaa agaccaacaa	2880
cagttttgtt gtcgatggtg acacactgaa ggaatgtccg ctcaaacaca gagcatggaa	2940
tagtttcctt gtggaggatc atgggttttg ggtcttcac accagtgttt ggctcaagg	3000
tagagaagac tactcactag aatgtgaccc agccgtcata ggaacagctg ttaagggaaa	3060
ggaggccgcc cacagtgacc tgggctactg gattgaaagt gaaaagaatg acacatggag	3120
gctgaagagg gcccatctga ttgagatgaa aacatgtgag tggccaaagt ctcacactct	3180
gtggacagat ggagtagaag aaagtgatct gatcatacct aaatcttttag ctggtccact	3240
cagccaccac aacactagag agggttacag aactcaagca aaagggccat ggcatagtga	3300
agagcttgaa atccggtttg aggaatgtcc aggcaccaag gttcacgtgg aggagacatg	3360
cggaactaga ggaccatctc tgagatcaac cactgcaagt ggaaggggtca ttgaggaatg	3420

gtgctgtaga	gaatgcacaa	tgccccact	atcgtttcga	gcaaaagacg	gctgctggta	3480
tggaatggag	ataaggccca	ggaaagaacc	agagagcaac	ttagtgaggt	caatggtgac	3540
agcgggatca	accgatcaca	tggaaccactt	ctctcttgga	gtgcttggtga	ttctactcat	3600
ggtgcaggaa	gggctgaaga	agagaatgac	cacaaagatc	attatgagca	catcaatggc	3660
agtgctggtg	gccatgatcc	tgggaggatt	tttaatgagt	gacttggcta	agcttgatg	3720
cctgatgggt	gccaccttcg	cagaaatgaa	cactggagga	gatgtggctc	acttggcatt	3780
ggttgcgga	tttaaagtca	gaccagcctt	gctggctctc	tttattttca	gagctaattg	3840
gacacctcgt	gagagcatgc	tgctagccct	ggcttcgtgt	cttttgcaaa	ctgcaatctc	3900
tgctctcgaa	ggtgacttga	tggtcctcgt	caatggattt	gctttggcct	ggttggcaat	3960
acgagcaatg	gccgtgccac	gcactgacaa	cattgctctg	gcaatcctgg	ctgctctgac	4020
accactagcc	cgaggtacac	tgctcgtggc	atggagagcg	ggcctcgcta	cttgtggagg	4080
gtttatgctc	ctctccctga	aagggaaagg	tagtgtgaag	aagaacctgc	catttgcat	4140
ggccttggga	ttgactgctg	tgaggatagt	agacccatt	aatgtgggtg	gactactgtt	4200
actcacaagg	agtgggaagc	ggagctggcc	ccctagtga	gtgcttacag	ctgttggcct	4260
gatatgtgca	ctggccggag	gctttgcaa	ggcagacatt	gagatggctg	ggcccatggc	4320
tgcaagtagc	ttgctgattg	tcagttatgt	ggtctcagga	aagagtgtgg	atatgtacat	4380
tgaaagagca	ggtgacatca	catgggaaaa	ggacgcggaa	gttactggaa	atagtccctg	4440
gcttgacgtg	gcactagatg	agagtgggtg	tttctctctg	gtggaggaag	atggtccacc	4500
catgagagag	atcatactca	aggtggctct	gatggccatc	tgtggcatga	acccaatagc	4560
catacccttt	gctgcaggag	cgtgggtatg	gtatgtgaag	actggaaaaa	ggagtgggtg	4620
cctctgggat	gtgcccgtc	caaagaagt	gaaaaaagga	gagaccacag	atgggggtata	4680
cagagtgatg	acccgcagac	tgctgggttc	aacacagggt	ggagtgggag	tcatgcaaga	4740
gggagtcttc	cacaccatgt	ggcacgtcac	aaaaggagct	gcactgagga	gcggtgaagg	4800
gagacttgat	ccatactggg	gggatgtcaa	gcaggactta	gtgtcatact	gtgggccttg	4860
gaagttggat	gcagcttggg	atggacttag	tgaggtgcag	ctcttggcag	taccccccg	4920
agagagggcc	agaaacattc	agactctgcc	tggaatatcc	aagacaaagg	atggggacat	4980
cggagcagtc	gctctggact	acccgcagag	aacttcagga	tccccgatcc	tagacaaatg	5040
cgaagagtg	ataggacttt	atggcaatgg	ggttgatgat	aagaatggaa	gctatgttag	5100
tgccataacc	cagggaaaga	gggaggagga	gactccggtt	gaatgtttcg	aaccctcgat	5160

gctgaagaag aagcagctaa ctgtcctgga tctgcatcca ggagccggaa agactaggag	5220
agttcttcct gaaatagtcc gtgaagccat aaaaaagaga ctccgcacag tgattttggc	5280
tccaaccagg gttgtcgctg ctgagatgga ggaagccttg agaggacttc cgggtgcgtta	5340
catgacaaca gcagttaacg tcacccactc tgggacagaa atcgttgatt tgatgtgcca	5400
tgccaccttc acctcacgcc tattacaacc catcagagtc cctaattaca atctctacat	5460
catggatgaa gcccathttca cagaccctc aagtatagct gcaagaggat acatatcaac	5520
aagggttgaa atgggcgagg cggctgccat cttcatgaca gccacgccac caggaacccg	5580
agatgcattt ccagactcca actcaccaat catggacaca gaagtggaag tcccagagag	5640
agcctggagc tcaggctttg attgggtgac agaccattct gggaaaacag tttggttcgt	5700
tccaagtgtg agaaatggaa atgaaatcgc agcctgtctg acaaaggctg gaaagcgggt	5760
catacaactc agcaggaaga cttttgagac agagtttcag aaaacaaaa atcaagagtg	5820
ggactttgtc ataacaactg acatctcaga gatgggcgcg aatttcaaag ctgaccgggt	5880
catagactct aggagatgcc taaagccagt catacttgat ggtgagagag tcactttggc	5940
tgggcccattg cctgtcacgc atgctagtgc tgctcaaagg agagggcgta taggcaggaa	6000
ccctaacaaa cctggagatg agtacatgta tggaggtgga tgtgcagaga ccgatgaaga	6060
ccatgcacac tggcttgaag caagaatgct tcttgacaac atctacctcc aggatggcct	6120
catagcctcg ctctaccggc ctgaggccga taaggtagct gccattgagg gagagttaa	6180
gctgaggaca gagcaaagga aaacctttgt ggaacttatg aagagaggag accttcccgt	6240
ttggctagcc tatcaggttg catctgccgg aataacttac acagacagaa gatggtgctt	6300
tgatggcaca accaacaaca ccataatgga agatagtgta ccagcagaag tgtggacaaa	6360
atatggagag aagagagtgc tcaaaccaag atggatggat gcgaggggtct gttccgatca	6420
tgctgccctg aagtcgttca aagaatttgc tgccgggaaa agaggagtgg ctttaggagt	6480
aatggaggcc ctgggaacat tgccaggaca catgacagag aggtttcagg aggccattga	6540
caatctcgct gtgctcatgc gagcagagac tggaagcagg cttacaagg cagcggcagc	6600
ccaactgccg gagaccctag agaccatcat gctcttaggc ttgttgggaa cagtttcgtt	6660
ggggatcttc tttgtcttga tgcggaacaa gggcatcggg aagatgggtt ttggaatggt	6720
aactcttggg gccagtgc at ggctcatgtg gctttcggaa attgaaccag ccagaattgc	6780
atgtgtcctc attgttgtgt tcttgttact ggtggtactc atacccgagc cagagaagca	6840
aagatctccc caggacaacc agatggcaat catcatcatg gtggcagtgg gccttctggg	6900

tttgataact gcaaacgaac ttggatggct ggaaagaaca aaaaatgaca tagctcatct	6960
aatgggaagg agagaagaag gagtaactat gggatttctca atggacatcg atttgcgggc	7020
agcctccgcc tgggctatct atgccgcact gacaactctc atcaccccag ccgccaaca	7080
cgcggtacc acttcataca acaactactc cctaattggcg atggccacac aagctggagt	7140
gctatttggc atgggcaaag ggatgccatt ttatgcatgg gactttggag tcccgtgct	7200
aatgatgggt tgctactcac aattaacacc cctaaccttg atagtggcta tcattctgct	7260
tgtggcacac tatatgtact tgatcccagg cctacaggca gcagcagcg gtgctgcca	7320
gaagagaaca gcagctggca tcatgaagaa tcccgttgtg gatggaatag tggtaactga	7380
cattgacaca atgacaattg accccaagt ggagaagaag atgggacaag tgttacttat	7440
agcagtagcc atctccagtg ctgtgctgct gcggactgct tggggatggg gggaggctgg	7500
agctctgatt actgcagcaa cctccacctt gtgggaaggt tctccaaaca aatactggaa	7560
ctcctctaca gccacctcac tgtgcaacat cttcagagga agttacctgg caggcgcttc	7620
tcttatttat acagtgacaa gaaatgctgg cctagtcaag agacgtggag gtggaacggg	7680
agagactcta ggagagaagt ggaaagctcg cctgaatcag atgtcggccc tggagtctta	7740
ctcttacaaa aagtcaggca tcaactgaagt gtgtagagag gaggctcgcc gcgccctcaa	7800
ggatggagtg gccacaggag gacatgctgt atcccgggga agcgcaaagc tcagatggct	7860
ggtggagaga ggatacctgc aaccccatgg aaaggttgtt gacctcgat gtggcagagg	7920
gggttggagc tattatgccg ccaccatccg gaaagtgcag gaggtgaaag gatacacaaa	7980
gggaggtccc ggtcatgaag aacccatgct ggtgcaaagc tatgggtgga acatcgttcg	8040
tctcaagagt ggagtggacg tcttcacat ggcgccgag ccgtgtgata ccttgctgtg	8100
tgacataggt gagtcatcat ctagtcctga agtggaagag acgcgaacac tccgagtgct	8160
ctctatggtg ggggactggc ttgagaaaag accgggggcc ttctgtataa aggtgctgtg	8220
tccatacacc agcactatga tggagaccat ggagcgctg caacgtaggt atgggggagg	8280
attagtcaga gtgccattgt ctcgcaactc cacacatgag atgtattggg tctctggagc	8340
aaaaagtaac gtcataaaaa gtgtgtccac cacaagtcag ctctccttg gacgcatgga	8400
tgggtcccagg aggccagtga aatatgagga agatgtgaac ctcggctcgg gcacacgagc	8460
tgtggcaagc tgtgctgaag ctcccaacat gaaggtcatt ggcaagcgca ttgagagaat	8520
ccgcagtga catgcagaaa catggttctt tgatgaaaac catccataca ggacatgggc	8580
ctaccatggg agctacgaag cccccacaca agggtcagca tcttcctcg tgaatgggg	8640

tgtagactc	ctgtcaaagc	cctgggatgt	agtgactgga	gttacaggaa	tagctatgac	8700
tgatacaaca	ccatacggcc	aacaaagagt	cttcaaagaa	aaagtggaca	ccaggggtgcc	8760
agatcccca	gaaggcactc	gccaggcaat	gaacatggtc	tcttcctggc	tgtggaagga	8820
gttggggaaa	cgcaagcggc	cacgtgtctg	caccaaagaa	gagttcatca	acaaggtgcg	8880
cagcaatgca	gcactgggag	caatatttga	agaggaaaaa	gaatggaaga	cggccgtgga	8940
ggctgtgaat	gatccaaggt	tttgggctct	agtggacaag	gaaagagaac	atcacctgag	9000
aggagagtgt	catagctgtg	tgtacaacat	gatgggaaaa	agagagaaga	agcaaggaga	9060
attcggaaaa	gcaaaaggca	gccgcgccat	ctggtacatg	tgggtgggag	ccagattctt	9120
ggagtttgaa	gcccttggat	tcttgaatga	ggaccattgg	atgggaagag	aaaactcagg	9180
aggtggtgtc	gaagggctag	gactgcaaag	acttgatac	attctagaag	aaatgaatcg	9240
ggcaccagga	ggaaagatgt	atgcagatga	caccgctggc	tgggacaccc	gcattagtaa	9300
gtttgatctg	gagaatgaag	ccttaattac	caaccaaagt	gaggaagggc	acagagctct	9360
ggcgttggct	gtgattaagt	acacaaaaaa	caaagtgggt	aaggtcctca	gaccagctga	9420
aggagggaaa	acagttatgg	acatcatttc	aagacaggac	cagagaggga	gtggacaagt	9480
tgtcacctat	gctctcaaca	catttaccaa	cttagtgggt	cagcttatcc	ggaatatgga	9540
ggctgaggaa	gtgttagaga	tgcaagactt	atggctgttg	aggaagccag	agaaagtgac	9600
cagatggttg	cagtgcaatg	gatgggacag	actcaaacga	atggcagtca	gtggagatga	9660
ctgcgttgtg	aagccaattg	atgatagggt	tgcgcatgcc	ctcaggttct	taaatgacat	9720
gggaaaagt	aggaaagaca	cacaggaatg	gaaaccctcg	actggatgga	gcaattggga	9780
agaagtcccg	ttctgctccc	accatttcaa	caagctgcac	ctcaaggatg	gtagatccat	9840
tgtggtccct	tgccgccacc	aagatgaatt	gattggccga	gcccggtgat	caccaggggc	9900
aggatggagc	attcgggaga	ctgcctgtct	agcaaaatca	tatgcacaga	tgtggcagct	9960
tctttacttc	cacagaagag	accttcgact	gatggccaat	gctatttggt	cggctgtgcc	10020
agttgactgg	gtaccaaccg	ggagaaccac	ctggtcaatc	cacggaaagg	gagaatggat	10080
gactactgag	gacatgctca	tggtgtggaa	tagagtgtgg	attgaggaga	acgaccatat	10140
ggaggacaag	actcctgtga	caaagtggac	agacatcccc	tatctgggaa	aaagggagga	10200
cttatggtgt	ggatccctta	tagggcacag	gccccgcacc	acttgggctg	agaacatcaa	10260
agacacagtc	aacatggtgc	gcaggatcat	aggtgatgaa	gaaaaataca	tggactactt	10320
atccaccag	gtccgctact	tgggtgagga	aggtccaca	cctggagtgt	tgtaagcacc	10380

aatttcagtg ttgtcaggcc tgctagccag ccacagtttg gggaaagctg tgcagcctgt	10440
agcccccca ggagaagctg ggaaaccaag ctcatagtca ggccgagaac gccatggcac	10500
ggaagaagcc atgctgcctg tgagcccctc agaggacact gagttaaaaa accccacgcg	10560
cttggaagcg caggatggga aaagaaggtg gcgaccttcc ccacccttta atctggggcc	10620
tgaactggag actagctgtg aatctccagc agagggacta gtggttagag gagaccccc	10680
ggaaaacgca aaacagcata ttgacgttg gaaagaccag agactccatg agtttccacc	10740
acgctggccg ccaggcacag atcgccgaac agcggcggcc agtgtggg	10788

<210> 84

<211> 10254

<212> DNA

<213> Zika virus strain MR 766 polyprotein gene, complete cds

<400> 84

atgaaaaacc caaagaagaa atccggagga ttccggattg tcaatatgct aaaacgcgga	60
gtagcccgtg taaaccctt gggaggtttg aagaggctgc cagccggact tctgctgggt	120
catggacca tcagaatggt tttggcgata ttagcctttt tgagattcac agcaatcaag	180
ccatcactgg gcctcatcaa cagatggggt accgtgggga aaaaagaggc tatggaaata	240
ataaaaaaat ttaagaaaga tcttgctgcc atgttgagaa taatcaatgc taggaaggag	300
aggaagagac gtggcgcaga caccagcatc ggaatcggtg gcctcctggt gactacagcc	360
atggcagcag agatcactag acgtgggagt gcatactaca tgtacttgga taggagcgat	420
gcagggaagg ccatttcttt cgctaccaca ttgggggtga acaaatgcca tgtgcagatc	480
atggacctcg ggcacatgtg tgacgccacc atgagctatg aatgcctat gctggacgag	540
ggggtggaac cagatgacgt cgattgctgg tgcaacacga catcaacttg ggttgtgtac	600
ggaacctgtc atcataaaaa aggtgaagca cggcgatcta gaagagccgt cacgctccca	660
tctcactcca caaggaaatt gcaaacgcgg tcgcagactt ggctagaatc aagagaatac	720
acaaagcacc tgatcaaggt tgaaaattgg atattcagga accctggttt tacgctagtg	780
gctgtcgcca tcgctgggt tttgggaagc tcgacgagcc aaaaagtcac atacttggtc	840
atgatactgc tgattgcccc ggcatacagt atcagggtgca taggagtcag caatagagac	900
ttcgtggagg gcatgtcagg tgggacctgg gttgacgttg tcctggaaca tggaggctgc	960
gtcaccgtga tggcacagga caagccaaca gttgacatag agctggtcac aacaacggtt	1020
agtaacatgg ccgagggtgag atcctattgt tacgaggcat caatatcgga catggcttcg	1080

gacagtcgct	gccaacaca	aggtgaagcc	taccttgaca	agcaatcaga	cactcaatat	1140
gtttgcaaaa	gaacattggt	ggacagaggt	tggggaaatg	ggtgtggact	ctttggcaaa	1200
gggagtttgg	tgacatgtgc	taagttcacg	tgctccaaga	agatgactgg	gaagagcatt	1260
cagccggaga	acctggagta	tcggataatg	ctatcagtgc	atggctccca	gcacagtggg	1320
atgattgtta	atgatgaaaa	cagagcgaag	gtcgaggtta	cgcccaattc	accaagagca	1380
gaagcaacc	tgggaggctt	tggaagctta	ggacttgatt	gtgaaccaag	gacaggcctt	1440
gacttttcag	atctgtatta	cctaaccatg	aataacaagc	attggttggg	gcacaaagag	1500
tggtttcatg	acatcccatt	gccctggcat	gctggggcag	acactggaac	tccacattgg	1560
aacaacaagg	aggcattagt	ggaattcaag	gacgcccacg	ccaagaggca	aaccgtcgtg	1620
gttttgggga	gccaggaagg	agccgtccac	acggctcttg	ctggagctct	agaggctgag	1680
atggatggtg	caaaggggaag	gctattctct	ggccacttga	aatgtcgctt	aaaaatggac	1740
aagcttagat	tgaagggcgt	gtcatattcc	ttgtgcaccg	cggcattcac	attcaccaag	1800
gtcccggctg	aaacactaca	tggaacagtc	acagtggagg	tgacgtatgc	agggacagat	1860
ggaccctgca	aggtcccagc	ccagatggcg	gtggacatgc	agaccttgac	cccagtcgga	1920
aggctgataa	ccgccaaccc	cgtgattact	gaaagcactg	agaattcaaa	gatgatgttg	1980
gagctcgacc	caccatttgg	ggattcttac	attgtcatag	gagttgggga	taagaaaatc	2040
acccatcact	ggcataggag	tggcagcacc	attggaaaag	catttgaagc	cactgtgaga	2100
ggcgctaaga	gaatggcagt	cctgggggac	acagcttggg	actttggatc	agtcggaggt	2160
gtgtttaact	cattgggcaa	gggcattcat	cagatttttg	gagcagcttt	caaatacactg	2220
tttgaggagaa	tgtcctgggt	ctcacagatc	ctcataggca	ctctgctggg	gtggttaggt	2280
ctgaacacaa	agaatgggtc	tatctccctc	acatgcttag	ccctgggggg	agtgatgatc	2340
ttcctctcca	cggctgtttc	tgctgacgtg	gggtgctcgg	tggacttctc	aaaaaaagaa	2400
acgagatgtg	gcacgggggt	gttcgtctac	aatgacgttg	aagcctggag	ggaccggtac	2460
aagtaccatc	ctgactcccc	tcgtagactg	gcagcagccg	ttaagcaagc	ttgggaagag	2520
gggatttgtg	ggatctcctc	tgtttctaga	atggaaaaca	taatgtggaa	atcagtggaa	2580
ggagagctca	atgcaatcct	agaggagaat	ggagtccaac	tgacagttgt	tgtgggatct	2640
gtaaaaaacc	ccatgtggag	aggcccacaa	agattgccag	tgctgtgaa	tgagctgccc	2700
catggctgga	aagcctgggg	gaaatcgtag	tttgttaggg	cggcaaagac	caacaacagt	2760
tttgttgtcg	acggtgacac	attgaaggaa	tgtccgctca	agcacagagc	atggaacagc	2820

ttcctcgtgg	aggatcacgg	gtttgggggc	ttccacacca	gtgtttggct	taaggttaga	2880
gaagattact	cactggagtg	tgaccagcc	gtcataggaa	cagctgttaa	gggaaaggag	2940
gccgcgcaca	gtgatctagg	ctattggatt	gaaagtga	agaatgacac	atggaggctg	3000
aagagggctc	atttgattga	gatgaaaaca	tgtgagtggc	caaagtctca	cacactgtgg	3060
acagatggag	tggaagaaag	tgatctgac	atacccaagt	ctttagctgg	tccactcagc	3120
caccacaaca	ccagagaggg	ttacagaact	caagtgaag	ggccatggca	tagtgaggag	3180
cttgaaatcc	gatttgagga	atgtccaggt	accaaggttc	atgtggagga	gacatgcgga	3240
acgagaggac	catctctgag	atcaaccact	gcaagcggaa	gggtcattga	ggaatgggtgc	3300
tgtagggaat	gcacaatgcc	cccactatcg	ttccgagcaa	aagatggctg	ctggtatgga	3360
atggagataa	ggcctaggaa	agaaccagag	agcaacttag	tgaggtcaat	ggtgacagcg	3420
ggatcaaccg	atcatatgga	tcatttttct	cttgagtg	ttgtgattct	actcatggtg	3480
caggaaggg	tgaagaagag	aatgaccaca	aagatcatca	tgagcacatc	aatggcagtg	3540
ctggtggcca	tgatcttggg	aggattctca	atgagtgacc	tggctaagct	tgtgatcctg	3600
atgggggcca	ctttcgcaga	aatgaacact	ggaggagacg	tagctcactt	ggcattagta	3660
gcggcattta	aagtcagacc	agccttgctg	gtctcattta	tcttcagagc	caactggaca	3720
cctcgtgaga	gcatgctgct	agccttggct	tcgtgtcttc	tgcaaactgc	gatctccgct	3780
cttgaaggcg	acttgatgg	cctcgttaat	ggatttgctt	tggcctgggt	ggcaatacgt	3840
gcaatggccg	tgccacgcac	tgacaacatc	gctctagcaa	ttctggctgc	tctaacacca	3900
ctagcccag	gcacactgct	cgtggcatgg	agagcgggcc	tcgccacttg	tggagggttc	3960
atgctcctct	ccctgaaagg	gaaaggtagt	gtgaagaaga	acctgccatt	cgtcgcggcc	4020
ttgggattga	ccgctgtgag	aatagtggac	cccattaatg	tgggtgggact	actgttactc	4080
acaaggagt	ggaagcggag	ctggccccct	agtgaagtgc	tactgctgt	cggcctgata	4140
tgtgcattgg	ccggaggggt	tgccaaggca	gacatagaga	tggctgggcc	catggcggca	4200
gtgggcctgc	taattgtcag	ttatgtggtc	tcgggaaaga	gtgtagatat	gtacattgaa	4260
agagcaggt	acatcacatg	ggagaaagac	gcggaagtca	ctggaaacag	tcctcggctt	4320
gacgtggcac	tagatgagag	tggtgatttc	tctctggtgg	aggaagatgg	tccacccatg	4380
agagagatca	tacttaaggt	ggtcttgatg	gccatctgtg	gcatgaacct	aatagccata	4440
ccttttgctg	caggagcgtg	gtatgtgtat	gtgaagactg	ggaaaaggag	tgggtgcctc	4500
tgggacgtgc	ctgctccgaa	agaagtga	aaaggagaga	ccacagatgg	agtgtacaga	4560

gtgatgactc	gcagactgct	gggttcaaca	caagttggag	tgggagtcac	gcaggaggga	4620
gtcttccaca	ccatgtggca	cgtcacaaaa	ggggccgcat	tgaggagcgg	tgaagggaga	4680
cttgatccat	actgggggga	tgtcaagcag	gacttggtgt	catattgtgg	gccttggaag	4740
ctggacgcag	cttgggacgg	agttagttag	gtgcagcttc	tggccgtacc	ccctggagag	4800
agagccagaa	acattcagac	tctgcctgga	atattttaaga	caaaggatgg	ggacatcgga	4860
gcagttgctt	tggactatcc	tgcaggaacc	tcaggatctc	cgatcctaga	caaatgcggg	4920
agagtgatag	gactctatgg	caatgggggt	gtgatcaaga	acggaagcta	tgttagtgtt	4980
ataaccagg	gaaagaggga	ggaggagact	ccggttgagt	gttttgaacc	ctcgatgctg	5040
aagaagaagc	agctaactgt	cctggacctg	catccagggg	ctgggaaaac	caggagagtt	5100
cttcctgaaa	tagtccgtga	agctataaag	aagagactcc	gcacggtgat	cttggcacca	5160
accagggtcg	tcgctgctga	gatggaggaa	gccctgagag	gacttccggt	gcgttacatg	5220
acaacagcag	tcaagggtcac	ccattctggg	acagaaatcg	ttgatttgat	gtgccatgcc	5280
accttcactt	cacgcctact	acaaccatt	agagtcccta	attacaacct	ctacatcatg	5340
gatgaagccc	atttcacaga	cccctcaagc	atagctgcaa	gaggatatat	atcaacaagg	5400
gttgagatgg	gcgaggcagc	agccatcttt	atgactgcca	caccaccagg	aaccgcgat	5460
gcgtttccag	attccaactc	accaatcatg	gacacagaag	tggaagtccc	agagagagcc	5520
tggagctcag	gctttgattg	ggtgacggac	cattctggga	aaacagtttg	gttcgttcca	5580
agcgtgagga	atggaaatga	aatcgagccc	tgtctgacaa	aggctggaaa	gcgggttata	5640
cagcttagta	ggaaaacttt	tgagacagag	tttcagaaaa	caaaaaatca	agagtgggac	5700
tttgtcataa	caactgacat	ctcagagatg	ggtgccaaact	tcaaggctga	ccgggttata	5760
gattccagga	gatgcctaaa	gccagttata	cttgatggtg	agagagtcac	cttggctggg	5820
cccatgcctg	tcacgcatgc	tagcgtgct	cagaggagag	gacgtatagg	caggaacccc	5880
aacaagcctg	gagatgagta	catgtatgga	ggtgggtgtg	cggagactga	tgaagaccat	5940
gcacattggc	ttgaagcaag	aatgcttctt	gacaacattt	acctccagga	tggcctcata	6000
gcctcgctct	atcgacctga	ggccgacaag	gtagccgcca	ttgagggaga	gtttaagctg	6060
aggacagagc	aaaggaagac	ctttgtggaa	ctcatgaaga	gaggagatct	tcccgtttgg	6120
ttggcctacc	aggttgcatc	tgccggaata	acttatacag	acagaagatg	gtgttttgat	6180
ggcacaacca	acaacaccat	aatggaagac	agtgtaccag	cagaggtgtg	gaccaagtat	6240
ggagagaaga	gagtgtctca	accaagatgg	atggacgcca	gggtctgctc	agatcatgcg	6300

gccctgaagt	cgttcaaaga	attcgccgct	gggaaaagag	gagcgggcttt	gggagtaatg	6360
gagggccttg	gaacattacc	aggacacatg	acagagaggt	ttcaggaagc	cattgataac	6420
ctcgctgtgc	tcatgcgagc	agagactgga	agcaggccct	acaaggcagc	ggcagcccaa	6480
ttgccggaga	ccctagagac	catcatgctt	ttaggcctgc	tgggaacagt	atcgctgggg	6540
atcttttttg	tcttgatgag	gaacaagggc	atcggaaga	tgggctttga	aatggtaacc	6600
cttggggcca	gcgcatggct	catgtggctc	tcagaaatcg	aaccagccag	aattgcatgt	6660
gtccttattg	ttgtgttttt	attactgggtg	gtgctaatac	cagagccaga	gaagcaaaga	6720
tccccccagg	acaatcagat	ggcaatcatt	attatgggtg	cagtgggcct	tttggggttg	6780
ataactgcaa	atgaacttgg	atggctggag	agaacaaaaa	atgacatagc	tcatctgatg	6840
ggaaagagag	aagagggaac	aaccgtggga	ttctcaatgg	acatcgatct	gcgaccagcc	6900
tccgcatggg	ctatttatgc	cgcattgaca	accctcatca	cccagccgt	ccagcacgcg	6960
gtaactacct	cgtacaacaa	ctactcctta	atggcgatgg	ccacacaagc	tggagtgctg	7020
tttggcattg	gcaaagggat	gccattttat	gcatgggact	taggagtccc	gttgctaattg	7080
atgggctgct	actcacaact	aacacccttg	accctgatag	tagccatcat	tttgcttgtg	7140
gcacattaca	tgtacttgat	cccaggccta	caggcagcag	cagcacgcgc	tgcccagaag	7200
agaacagcag	ccggcatcat	gaagaatccc	gttggtgatg	gaatagtggg	aactgacatt	7260
gacacaatga	caattgaccc	ccaagtggag	aagaagatgg	gacaagtgct	acttatagca	7320
gtggctgtct	ccagtgtgtg	gttgctgcgg	accgcttggg	gatgggggga	ggctggagct	7380
ttgatcacag	cagcaacttc	caccctgtgg	gaaggctccc	caaacaaata	ctggaactcc	7440
tccacagcca	cctcaactgtg	caacatcttc	agaggaagtt	acttggcagg	agcttccttt	7500
atttacacag	tgacaagaaa	tgccggcctg	gttaagagac	gtggaggtgg	aacgggagaa	7560
actctgggag	agaagtggaa	agccgcctg	aatcagatgt	cggccttgga	gttctactct	7620
tacaaaaagt	caggcatcac	tgaagtatgt	agagaggagg	ctcgccgcgc	cctcaaggat	7680
ggagtggcca	caggaggaca	tgctgtatcc	cgaggaagcg	caaaactcag	atggttggtg	7740
gagagaggat	atctgcagcc	ctatggaaag	gttgttgatc	tcggatgcgg	cagagggggc	7800
tggagttatt	atgccgccac	catccgcaaa	gtgcaggagg	tgagaggata	cacaaaggga	7860
ggtcccggtc	atgaagagcc	catgctgggtg	caaagctatg	ggtggaacat	aattcgtctc	7920
aagagtggag	tggacgtctt	ccacatggcg	gctgagtcgt	gtgacacttt	gctgtgtgac	7980
ataggtgagt	catcatccag	tcctgaagtg	gaggagacgc	gaacactcag	agtgtctctc	8040

atggtggggg	actggccttga	gaagagacca	ggggccttct	gcataaaggt	gttatgccca	8100
tacaccagca	ccatgatgga	gaccatggag	cgactgcaac	gtaggtatgg	gggaggacta	8160
gtcagagtgc	cactgtcccc	caattctaca	catgagatgt	attgggtctc	tggagcaaaa	8220
agtaacatca	taaaaagtgt	gtccaccaca	agtcagctcc	tcctgggacg	catggatggg	8280
cccaggaggc	cagtgaagta	tgaggaggat	gtgaacctcg	gctcaggcac	acgagctgtg	8340
gcaagctgtg	ctgaggctcc	caacatgaag	gtcattggta	ggcgcattdga	gagaatccgt	8400
agtgaacatg	cagaaacatg	gttctttgat	gaaaaccatc	catacaggac	atgggcctac	8460
cacgggagct	acgaagcccc	cacgcaaggg	tcagcatctt	ccctcgtgaa	tggggttggt	8520
agactcctgt	caaagccctg	ggatgtgggtg	actggagtta	caggaatagc	tatgactgac	8580
accacaccgt	acggccaaca	aagagtcttc	aaagaaaaag	tggacaccag	ggtgccagac	8640
cctcaagaag	gtactcgcca	ggtaatgaac	atggtcgctt	cctggctgtg	gaaggagctg	8700
ggaaaacgta	agcggccacg	tgtctgcacc	aaagaagagt	tcatcaacaa	ggtgcgcagc	8760
aatgcagcac	tgggagcaat	atttgaagag	gaaaaagaat	ggaagacggc	tgtggaagct	8820
gtgaatgata	caaggttttg	ggccctagt	gataaggaaa	gagaacacca	cctgagagga	8880
gagtgccata	gttgtgtgta	caacatgatg	ggaaaaagag	aaaagaagca	aggggaattc	8940
gggaaagcaa	aaggcagtcg	cgccatctgg	tacatgtggt	tgggagccag	attcttggag	9000
tttgaagccc	ttggattctt	gaacgaggac	cattggatgg	gaagagaaaa	ctcaggaggt	9060
ggtgtcgaag	ggttgggact	gcaaagactt	ggatacgctt	tagaagaaat	gagccgggca	9120
ccaggaggaa	agatgtatgc	agatgacacc	gctggctggg	acaccgcat	tagcaagttt	9180
gatttggaga	atgaagcctt	gattactaac	caaattggatg	aagggcacag	aactctggcg	9240
ttggccgtga	ttaagtacac	ataccaaaac	aaagtgggtga	aggtcctcag	accagctgaa	9300
ggaggaaaaa	cagtcatgga	catcatttca	agacaagacc	agagggggag	cggacaagtt	9360
gtcacttatg	ctctcaacac	atttaccaac	ttggtgggtgc	agctcatccg	gaacatggag	9420
gctgaggaag	tgttagagat	gcaagactta	tggctgttga	ggaagccaga	gaaagtaacc	9480
agatggctgc	agagtagcgg	atgggacaga	ctcaaacgaa	tggcagtcag	tggatgatgac	9540
tgtgttgtaa	agccaattga	tgacaggttt	gcacacgccc	tcaggttctt	gaatgatatg	9600
gggaaagtta	ggaaagacac	acaggaatgg	aaaccctcaa	ctggatggag	caactgggaa	9660
gaagtcccgt	tctgctccca	ccactttaac	aagctgcacc	tcaaagacgg	gagatccatt	9720
gtggtccctt	gccgccacca	agatgaactg	attggccggg	ctcgcgtttc	gccgggggca	9780

ggatggagca tccgggagac tgcctgtctt gcaaaatcat atgcacagat gtggcagctt	9840
ctttatttcc acagaagaga cctccgactg atggccaatg ccatttgctc ggccgtgcca	9900
gttgactggg tcccaactgg gagaactacc tgggtcaatcc atggaaaggg agaatggatg	9960
actactgagg acatgctcat ggtgtggaat agagtgtgga ttgaggagaa tgatcacatg	10020
gaggacaaga cccctgtaac aaaatggaca gacattccct atttgggaaa aaggaggagac	10080
ttatggtgtg gatcccttat aggacacaga cctcgcacca cttgggctga gaacatcaaa	10140
gacacagtca gcatggtgcg cagaatcata ggtgatgaag aaaagtacat ggactaccta	10200
tccactcaag ttcgctactt gggtgaggaa ggggtctacac ctggagtgtc gtaa	10254

<210> 85

<211> 10793

<212> DNA

<213> Zika virus isolate Brazil-ZKV2015, complete genome

<400> 85

ccaatctgtg aatcagactg cgacagttcg agtttgaagc gaaagctagc aacagtatca	60
acaggtttta ttttggattt ggaaacgaga gtttctggtc atgaaaaacc caaaaaagaa	120
atccggagga ttccggattg tcaatatgct aaaacgcgga gtagcccggtg tgagcccctt	180
tgggggcttg aagaggctgc cagccggact tctgctgggt catgggcca tcaggatggt	240
cttggcgatt ctagcctttt tgagattcac ggcaatcaag ccatcactgg gtctcatcaa	300
tagatggggt tcagtgggga aaaaagaggc tatggaaata ataaagaagt tcaagaaaga	360
tctggctgcc atgctgagaa taatcaatgc caggaaggag aagaagagac gaggcgcaga	420
tactagtgtc ggaatcgttg gcctcctgct gaccacagct atggcagcgg aggtcactag	480
acgtgggagt gcatactata tgtacttgga cagaaacgat gctggggagg ccatatcttt	540
tccaaccaca ttggggatga ataagtgtta tatacagatc atggatcttg gacacatgtg	600
tgatgccacc atgagctatg aatgccctat gctggatgag ggggtggaac cagatgacgt	660
cgattgttgg tgcaacacga cgtcaacttg ggttgtgtac ggaacctgcc atcacaaaaa	720
aggtgaagca cggagatcta gaagagctgt gacgctcccc tcccattcca ctaggaagct	780
gcaaacgcgg tcgcaaacct ggttggaatc aagagaatac acaaagcact tgattagagt	840
cgaaaattgg atattcagga accctggctt cgcgttagca gcagctgcca tcgcttggtc	900
tttggaagc tcaacgagcc aaaaagtc atacttggtc atgatactgc tgattgcccc	960
ggcatacagc atcagggtgca taggagtcag caataggagc tttgtggaag gtatgtcagg	1020
tgggacttgg gttgatgttg tcttgaaca tgggggttgt gtcaccgtaa tggcacagga	1080

caaaccgact gtcgacatag agctgggttac aacaacagtc agcaacatgg cggaggtaag	1140
atcctactgc tatgaggcat caatatcaga catggcttcg gacagccgct gcccaacaca	1200
aggtgaagcc taccttgaca agcaatcaga cactcaatat gtctgcaaaa gaacgttagt	1260
ggacagaggc tggggaaatg gatgtggact ttttggcaaa gggagcctgg tgacatgcgc	1320
taagtttgca tgctccaaga aaatgaccgg gaagagcatc cagccagaga atctggagta	1380
ccggataatg ctgtcagttc atggctccca gcacagtggg atgatcgta atgacacagg	1440
acatgaaact gatgagaata gagcgaaggc tgagataacg cccaattcac caagagccga	1500
agccaccctg gggggttttg gaagcttagg acttgattgt gaaccgagga caggccttga	1560
cttttcagat ttgtattact tgactatgaa taacaagcac tggttgggtc acaaggagt	1620
gttccacgac attccattac cttggcacgc tggggcagac accggaactc cacactggaa	1680
caacaaagaa gcactggtag agttcaagga cgcacatgcc aaaaggcaaa ctgtcgtggt	1740
tctagggact caagaaggag cagttcacac ggcccttgct ggagctctgg aggctgagat	1800
ggatggtgca aagggaaggc tgtcctctgg ccacttgaaa tgtcgctga aaatggataa	1860
acttagattg aagggcgtgt catactcctt gtgtaccgca gcgttcacat tcaccaagat	1920
cccggctgaa aactgcacg ggacagtcac agtggaggta cagtacgcag ggacagatgg	1980
accttgcaag gttccagctc agatggcggg ggacatgcaa actctgaccc cagttgggag	2040
gttgataacc gctaaccctg taatcactga aagcactgag aactctaaga tgatgctgga	2100
acttgatcca ccatttgggg actcttacat tgtcatagga gtcggggaga agaagatcac	2160
ccaccactgg cacaggagtg gcagcaccat tggaaaagca tttgaagcca ctgtgagagg	2220
tgccaagaga atggcagtct tgggagacac agcctgggac tttggatcag ttggaggcgc	2280
tctcaactca ttgggcaagg gcatccatca aatttttgga gcagctttca aatcattgtt	2340
tggaggaatg tcctggttct cacaattct cattggaacg ttgctgatgt ggttgggtct	2400
gaacacaaag aatggatcta tttcccttat gtgcttgcc ttagggggag tgttgatctt	2460
cttatccaca gccgtctctg ctgatgtggg gtgctcgtg gacttctcaa agaaggagac	2520
gagatgtggt acaggggtgt tcgtctataa cgacgttgaa gcctggaggg acaggtacaa	2580
gtaccatcct gactctcccc gtagattggc agcagcagtc aagcaagcct gggaagatgg	2640
tatctgcggg atctcctctg tttcaagaat ggaaaacatc atgtggagat cagtagaagg	2700
ggagcttaac gcaatcctgg aagagaatgg agttcaactg acggtcgttg tgggatctgt	2760
aaaaaacccc atgtggagag gtccacagag attgcccgtg cctgtgaacg agctgcccc	2820

cggtctggaag gcttggggga aatcgtactt cgtcagagca gcaaagacaa ataacagctt	2880
tgtcgtggat ggtgacacac tgaaggaatg ccactcaaa catagagcat ggaacagctt	2940
tcttgtggag gatcatgggt tcgggggtatt tcacactagt gtctggctca aggttagaga	3000
agattattca ttagagtgtg atccagccgt tattggaaca gctgttaagg gaaaggaggc	3060
tgtacacagt gatctaggct actggattga gagtgagaag aatgacacat ggaggctgaa	3120
gagggcccat ctgatcgaga tgaaaacatg tgaatggcca aagtcccaca cattgtggac	3180
agatggaata gaagagagtg atctgatcat acccaagtct ttagctgggc cactcagcca	3240
tcacaatacc agagagggct acaggacca aatgaaaggg ccatggcaca gtgaagagct	3300
tgaaattcgg tttgaggaat gcccaggcac taaggccac gtggaggaaa catgtggaac	3360
aagaggacca tctctgagat caaccactgc aagcggagg gtgatcgagg aatgggtctg	3420
cagggagtgc acaatgcccc cactgtcgtt ccgggctaaa gatggctgtt ggtatggaat	3480
ggagataagg ccagggaaag aaccagaaag caacttagta aggtcaatgg tgactgcagg	3540
atcaactgat cacatggatc acttctccct tggagtgcct gtgattctgc tcatggtgca	3600
ggaagggctg aagaagagaa tgaccacaaa gatcatcata agcacatcaa tggcagtgc	3660
ggtagctatg atcctgggag gatcttcaat gagtgacctg gctaagcttg caattttgat	3720
gggtgccacc ttgcgggaaa tgaacactgg aggagatgta gctcatctgg cgctgatagc	3780
ggcattcaaa gtcagaccag cgttgctggt atctttcatc ttcagagcta attggacacc	3840
ccgtgaaagc atgctgctgg ccttggcctc gtgttttttg caaactgcga tctccgcctt	3900
ggaaggcgac ctgatggttc tcatcaatgg ttttgctttg gcctggttgg caatacgagc	3960
gatggttgtt ccacgcactg acaacatcac cttggcaatc ctggctgctc tgacaccact	4020
ggcccggggc aactgcttg tggcgtggag agcaggcctt gctacttgcg gggggttat	4080
gctcctctct ctgaagggaa aaggcagtgt gaagaagaac ttaccatttg tcatggccct	4140
gggactaacc gctgtgaggc tggtcgacct catcaacgtg gtgggactgc tgttgctcac	4200
aaggagtggg aagcggagct ggccccctag cgaagtactc acagctgttg gcctgatatg	4260
cgcattggct ggagggttcg ccaaggcaga tatagagatg gctgggcca tggccgcggt	4320
cggtctgcta attgtcagtt acgtggtctc aggaaagagt gtggacatgt acattgaaag	4380
agcaggtgac atcacatggg aaaaagatgc ggaagtcact ggaaacagtc cccggctcga	4440
tgtggcgcta gatgagagtg gtgacttctc cctggtggag gatgacggtc ccccatgag	4500
agagatcata ctcaaggtgg tcctgatgac catctgtggc atgaaccaa tagccatacc	4560

ctttgcagct ggagcgtggt acgtatacgt gaagactgga aaaaggagtg gtgctctatg	4620
ggatgtgcct gctcccaagg aagtaaaaaa gggggagacc acagatggag tgtacagagt	4680
aatgactcgt agactgctag gttcaacaca agttggagtg ggagttatgc aagaggggggt	4740
ctttcacact atgtggcacg tcacaaaagg atccgcgctg agaagcggtg aaggagagact	4800
tgatccatac tggggagatg tcaagcagga tctggtgtca tactgtggtc catggaagct	4860
agatgccgcc tgggacgggc acagcgaggt gcagctcttg gccgtgcccc ccggagagag	4920
agcgaggaac atccagactc tgcccgaat atttaagaca aaggatgggg acattggagc	4980
ggttgcgctg gattacccag caggaacttc aggatctcca atcctagaca agtgtgggag	5040
agtgatagga ctttatggca atggggtcgt gataaaaaat gggagttatg ttagtgccat	5100
cacccaaggg aggagggagg aagagactcc tgttgagtgc ttcgagcctt cgatgctgaa	5160
gaagaagcag ctaactgtct tagacttgca tcctggagct gggaaaacca ggagagttct	5220
tcctgaaata gtccgtgaag ccataaaaac aagactccgt actgtgatct tagctccaac	5280
cagggttgtc gctgctgaaa tggaggaagc ccttagaggg cttccagtgc gttatatgac	5340
aacagcagtc aatgtcaccc actctggaac agaaatcgtc gacttaatgt gccatgccac	5400
cttcacttca cgtctactac agccaatcag agtccccaac tataatctgt atattatgga	5460
tgaggcccac ttcacagatc cctcaagcat agcagcaaga ggatacattt caacaagggt	5520
tgagatgggc gaggcggctg ccatcttcat gaccgccacg ccaccaggaa cccgtgacgc	5580
atttccggac tccaactcac caattatgga caccgaagtg gaagtcccag agagagcctg	5640
gagctcaggc tttgattggg tgacggatca ttctggaaaa acagtttggg ttgttccaag	5700
cgtgaggaac ggcaatgaga tcgcagcttg tctgacaaag gctggaaaac gggtcataca	5760
gctcagcaga aagacttttg agacagagtt ccagaaaaca aaacatcaag agtgggactt	5820
tgtcgtgaca actgacattt cagagatggg cgccaacttt aaagctgacc gtgtcataga	5880
ttccaggaga tgccataaagc cggtcatact tgatggcgag agagtcattc tggctggacc	5940
catgcctgtc acacatgcca gcgctgcca gaggaggggg cgcataggca ggaatcccaa	6000
caaacctgga gatgagtacc tgtatggagg tgggtgcgca gagactgacg aagaccatgc	6060
acactggctt gaagcaagaa tgctccttga caatatttac ctccaagatg gcctcatagc	6120
ctcgctctat cgacctgagg ccgacaaagt agcagccatt gagggagagt tcaagcttag	6180
gacggagcaa aggaagacct ttgtggaact catgaaaaga ggagatcttc ctgtttggct	6240
ggcctatcag gttgcatctg ccggaataac ctacacagat agaagatggg gctttgatgg	6300

cacgaccaac aacaccataa tggaagacag tgtgccggca gaggtgtgga ccagacacgg	6360
agagaaaaga gtgctcaaac cgaggtggat ggacgccaga gtttgttcag atcatgcggc	6420
cctgaagtca ttcaaggagt ttgccgctgg gaaaagagga gcggccttttg gagtgatgga	6480
agccctggga aactgccag gacacatgac agagagattc caggaagcca ttgacaacct	6540
cgctgtgctc atgcgggcag agactggaag caggccttac aaagccgcgg cgccccaatt	6600
gccggagacc ctagagacca ttatgctttt ggggttgctg ggaacagtct cgctgggaat	6660
ctttttcgtc ttgatgagga acaagggcat agggaagatg ggctttggaa tggtgactct	6720
tggggccagc gcatggctca tgtggctctc ggaaattgag ccagccagaa ttgcatgtgt	6780
cctcattgtt gtgttcctat tgctgggtgt gtcatacct gagccagaaa agcaaagatc	6840
tccccaggac aaccaaattg caatcatcat catggtagca gtaggtcttc tgggcttgat	6900
taccgccaat gaactcggat ggttgagag aacaagagt gacctagcc atctaattgg	6960
aaggagagag gagggggcaa ccataggatt ctcaatggac attgacctgc ggccagcctc	7020
agcttgggcc atctatgctg cttgacaac tttcattacc ccagccgtcc aacatgcagt	7080
gaccacttca tacaacaact actccttaat ggcgatggcc acgcaagctg gagtgttgtt	7140
tgggtatggc aaagggatgc cattctacgc atgggacttt ggagtccgc tgctaattgat	7200
aggttgctac tcacaattaa caccctgac cctaatagtg gccatcattt tgctcgtggc	7260
gcactacatg tacttgatcc cagggtgca ggcagcagct gcgcgtgctg ccagaagag	7320
aacggcagct ggcatcatga agaaccctgt tgtggatgga atagtgggtga ctgacattga	7380
cacaatgaca attgaccccc aagtggagaa aaagatggga caggtgctac tcatagcagt	7440
agccgtctcc agcgccatac tgtcgcgac cgctggggg tggggggagg ctggggccct	7500
gatcacagcc gcaacttcca ctttgtggga aggtctccg aacaagtact ggaactcctc	7560
tacagccact tactgtgta acatttttag gggaagttac ttggctggag cttctcta	7620
ctacacagta acaagaaacg ctggcttgggt caagagacgt gggggtggaa caggagagac	7680
cctgggagag aaatggaagg cccgcttgaa ccagatgtcg gccctggagt tctactccta	7740
caaaaagtca ggcatcaccg aggtgtgcag agaagaggcc cgccgcgcc tcaaggacgg	7800
tgtggcaacg ggaggccatg ctgtgtcccg aggaagtga aagctgagat ggttggtgga	7860
gcggggatac ctgcagccct atggaaagg cattgatctt ggatgtggca gagggggctg	7920
gagttactac gccgccacca tccgcaaagt tcaagaagt aaaggatata caaaaggagg	7980
ccctggtcat gaagaaccg tgttgggtgca aagctatggg tggaacatag tccgtcttaa	8040

gagtggggtg gacgtctttc atatggcggc tgagccgtgt gacacgttgc tgtgtgacat	8100
aggtgagtca tcatctagtc ctgaagtgga agaagcacgg acgctcagag tcctctccat	8160
ggtgggggat tggcttgaaa aaagaccagg agccttttgc ataaaagtgt tgtgcccata	8220
caccagcact atgatggaaa ccctggagcg actgcagcgt aggtatgggg gaggactggt	8280
cagagtgcc a ctctcccgca actctacaca tgagatgtac tgggtctctg gagcgaaaag	8340
caacaccata aaaagtgtgt ccaccacgag ccagctcctc ttggggcgca tggacggggc	8400
taggaggcca gtgaaatatg aggaggatgt gaatctcggc tctggcacgc gggctgtggt	8460
aagctgcgct gaagctccca acatgaagat cattggtaac cgcattgaaa ggatccgcag	8520
tgagcacgcg gaaacgtggt tctttgacga aaaccacca tataggacat gggcttacca	8580
tggaagctat gtggccccc cacaagggtc agcgtcctc ctaataaacg gggttgtcag	8640
gctcctgtca aaaccctggg atgtggtgac tggagtcaca ggaatagcca tgaccgacac	8700
cacaccgtat ggtcagcaaa gagttttcaa ggaaaaagtg gacactaggg tgccagaccc	8760
ccaagaaggc actcgtcagg ttatgagcat ggtctcttcc tggttgtgga aagagctagg	8820
caaacacaaa cgaccacgag tctgtaccaa agaagagttc atcaacaagg ttcgtagcaa	8880
tgcagcatta ggggcaatat ttgaagagga aaaagagtgg aagactgcag tggaagctgt	8940
gaacgatcca aggttctggg ctctagtgga caaggaaaga gagcaccacc tgagaggaga	9000
gtgccagagt tgtgtgtaca acatgatggg aaaaagagaa aagaaacaag ggaatttgg	9060
aaaggccaag ggcagccgcg ccatctggta tatgtggcta ggggctagat ttctagagtt	9120
cgaagccctt ggattcttga acgaggatca ctggatgggg agagagaact caggaggtgg	9180
tgttgaaggg ctgggattac aaagactcgg atatgtccta gaagagatga gtcgcatacc	9240
aggaggaagg atgtatgcag atgacactgc tggctgggac acccgcatca gcaggtttga	9300
tctggagaat gaagctctaa tcaccaacca aatggagaaa gggcacaggg ccttggcatt	9360
ggccataatc aagtacacat accaaaacaa agtggttaaag gtccttagac cagctgaaaa	9420
agggaaaaca gttatggaca ttatttcgag acaagaccaa agggggagcg gacaagttgt	9480
cacttacgct cttaacacat ttaccaacct agtggtgcaa ctcatcggga atatggaggc	9540
tgaggaagtt ctagagatgc aagacttgtg gctgctgcgg aggtcagaga aagtgaccaa	9600
ctggttgcag agcaacggat gggataggct caaacgaatg gcagtcagtg gagatgattg	9660
cgttgtgaag ccaattgatg ataggtttgc acatgccctc aggttcttga atgatatggg	9720
aaaagttagg aaggacacac aagagtggaa accctcaact ggatgggaca actgggaaga	9780

agttccgttt	tgctcccacc	acttcaacaa	gctccatctc	aaggacggga	ggtccattgt	9840
ggttccctgc	cgccaccaag	atgaactgat	tggccggggc	cgcgctctctc	caggggcggg	9900
atggagcatc	cgggagactg	cttgccctagc	aaaatcatat	gcgcaaagt	ggcagctcct	9960
ttattttccac	agaagggacc	tccgactgat	ggccaatgcc	atttgttcat	ctgtgccagt	10020
tgactgggtt	ccaactggga	gaactacctg	gtcaatccat	ggaaagggag	aatggatgac	10080
cactgaagac	atgcttgtgg	tgtggaacag	agtgtggatt	gaggagaacg	accacatgga	10140
agacaagacc	ccagttacga	aatggacaga	cattccctat	ttgggaaaaa	gggaagactt	10200
gtggtgtgga	tctctcatag	ggcacagacc	gcgcaccacc	tgggctgaga	acattaataa	10260
tacagtcaac	atggtgcgca	ggatcatagg	tgatgaagaa	aagtacatgg	actacctatc	10320
cacccaagtt	cgctacttgg	gtgaagaagg	gtctacacct	ggagtgtgtg	gagcaccaat	10380
cttaatgttg	tcaggcctgc	tagtcagcca	cagcttgggg	aaagctgtgc	agcctgtgac	10440
ccctccagga	gaagctgggt	aaccaagcct	atagtcaggc	cgagaacgcc	atggcacgga	10500
agaagccatg	ctgcctgtga	gccctcaga	ggacactgag	tcaaaaaacc	ccacgcgctt	10560
ggaggcgag	gatgggaaaa	gaaggtggcg	accttcccc	cccttcaatc	tggggcctga	10620
actggagatc	agctgtggat	ctccagaaga	gggactagt	gttagaggag	acccccgga	10680
aaacgcaaaa	cagcatattg	acgctgggaa	agaccagaga	ctccatgagt	ttccaccacg	10740
ctggccgcca	ggcacagatc	gccgaatagc	ggcgcccggt	gtggggaaat	cca	10793

<210> 86

<211> 10290

<212> DNA

<213> Spondweni virus strain SM-6 V-1 polyprotein gene, complete cds

<400> 86

atgaaaaacc	caaaaagagc	cggtagcagc	cggcttgtca	atatgctaag	acgcggtgca	60
gcccgtgtca	tccctccagg	aggagggctc	aagaggctgc	ctgtaggatt	gctgttgggt	120
cggggtccga	tcaaatgat	cctggccata	ctggcattcc	tacgatttac	agcaataaaa	180
ccgtccactg	gcctcatcaa	cagatgggga	aaagtgggca	aaaaagaggc	catcaaaatc	240
ctcacaaaat	tcaaggctga	cgtgggcacc	atgctgcgta	tcatcaacaa	tcggaagaca	300
aaaaagagag	gagtcgaaac	tggaattgtg	ttcctggcat	tgctggtgtc	tattgttgct	360
gtggaagtca	caaaaaagg	ggacacctat	tacatgtttg	cggacaagaa	ggacgccgga	420
aaggtggtga	cctttgagac	tgaatctgga	ccaaccgtt	gctccatcca	agcaatggac	480

attggacata	tgtgtccagc	tacaatgagc	tatgaatgtc	ccgtgctgga	accacagtat	540
gagccagagg	atgtcgactg	ttggtgcaac	tcgacagcag	catggattgt	gtatggcaca	600
tgcacccaca	agacaacggg	agagacaaga	cgttccagac	gttcaatcac	cctgccatct	660
catgcctcac	aaaagttgga	gaccagatca	tcgacgtggc	ttgaatcccg	cgaatactcc	720
aaatatctaa	taaaggtgga	aaactggatc	ctccgcaatc	caggatatgc	gttggtggct	780
gcagtgattg	gatggactct	gggcagcagt	cgcagccaga	agatcatctt	tgtcactctg	840
ctcatgttgg	tagccccgc	atacagcatc	agatgcattg	gaattggaaa	cagagacttc	900
attgagggaa	tgtccggtgg	cacctgggtg	gacattgtcc	tggaacatgg	tggttgtgtg	960
acagtaatgt	caaacgacaa	accacattg	gactttgaac	tggtgacaac	gaccgcaagt	1020
aacatggctg	aggtcaggtc	ctactgctat	gaagctaaca	tatccgagat	ggcatcggac	1080
agcaggtgcc	ccacacaggg	ggaagcttat	cttgacaaaa	tggccgactc	ccagtttgtg	1140
tgcaagcgtg	ggtacgttga	caggggctgg	ggaaacggat	gtggactctt	tggaaaagga	1200
agcattgtca	cttgcgctaa	gttcacgtgt	gtgaaaaagc	tcacagggaa	aagcattcaa	1260
ccggagaatc	tcgagtaccg	ggtccttggt	tcggtgcacg	cttcccaaca	tggaggaatg	1320
attaacaatg	acaccaatca	ccaacacgac	aaggagaaca	gagcgcgcat	tgatatcaca	1380
gctagcgctc	cccgtgttga	ggtggaactt	ggctcctttg	gaccttctc	gatggagtgt	1440
gaaccccggg	caggattgaa	ctttggtgac	ctgtattacc	tcaccatgaa	caacaagcat	1500
tggctggtta	atagagattg	gtttcacgat	ctttccttgc	catggcatac	aggagccaca	1560
tcaaacaatc	atcactggaa	caacaaggag	gcgctggtag	aattcagaga	agcccacgca	1620
aagaagcaga	cggctgtggg	cctgggaagt	caggaaggag	ctgttcacgc	agcactggcc	1680
ggcgactgg	aggctgagtc	tgatggacac	aaagcgacta	tctactctgg	acacttgaag	1740
tgtcgcttga	agctagacaa	actgcgcctg	aagggaatgt	catatgcact	ctgcacagga	1800
gcattcacct	tcgctcgcac	cccctctgaa	acaattcacg	gcaccgccac	agtggagctg	1860
caatatgcag	gtgaagatgg	gccgtgcaaa	gttcccatag	taattaccag	tgacaccaat	1920
agcatggcct	cgacaggcag	gctgatcaca	gcgaatccgg	tggtcacgga	aagtggagca	1980
aactcaaaga	tgatggtcga	gattgaccct	ccgtttggtg	attcttacat	tattgtgggc	2040
actggcacia	caaaaattac	ccaccattgg	cacagagccg	gtagttcaat	tggaactgca	2100
tttgaggcta	ccatgagagg	agcaaacggg	atggcggtcc	tcggcgacac	cgcttgggac	2160
tttggtctctg	ttgggggcat	gttcaactcc	gttggaaggt	ttgtccacca	ggtgtttgga	2220

tcagcattta aggcattggt tggaggcatg tcctggttca cacagctcct gataggattt	2280
ctgctcatat ggatggggtt gaacgcacgc ggtggaaccg tggccatgag cttcatgggc	2340
attggggcta tgctgatttt cctagccacc tcggtgtcag gagacacagg atgctcggtt	2400
gacatatcca gaagggaaat gcggtgcggg agcggcatat tcgtgtacaa tgacgttgac	2460
gcatggcgaa gccgctacaa ataccatcct gaaaccccca gagctttggc cgctgccgtg	2520
aaaacggctt gggaagaagg gacctgtggc attacctcag tgagcagaat ggaaaacctg	2580
atgtggagct ctgtggctgg agagtgaat gcaatccttg aggacaattc agtgccattg	2640
acagtcgtcg ttggcgagcc aaaatatcca ctgtacaatg ctccaaagag gctgaaacca	2700
ccagcatcag agttaccgca ggggtggaag tcctggggaa agtcatactt tgtctcagcc	2760
gcaaaaaaca acaactcctt tgtggtagat ggtgacacca tgaaggaatg cccaagacag	2820
aagcgagcat ggaacagctt gagaatagag gatcatgggt tcggagtctt ccacactagc	2880
atctggctga aattccatga ggacaactcc accgaatgtg acacagctat cataggaacg	2940
gcggttcgcg ggaaggaagc cgttcatagt gacttgggct actggataga gagtgagcgc	3000
aatgacacat ggaggctctc tcgagcgcac ctgatcgaag caaagacatg tgaatggcca	3060
cggtcgcaca cactgtggac ggacggagtg gaagagagcg agctgatcat tccacgtggc	3120
ttagccggtc ctttcagcca tcataacacg cgtgctggct acaagactca gaataaaggt	3180
ccctggcatt taggtgatgt tgaaattcag ttccgccacgt gccccggaac aaccgtggtc	3240
caggaccaag agtgcaggga caggggcgct tctctacgca cgaccacagc tagtggaagg	3300
gtaatcaatg aatggtgctg caggtcgtgc accatgcctc cactcagttt caagacaaaa	3360
gatggatgtt ggtatgcaat ggagatacgt cctgtgaaag aacaagagtc aaacctcgtg	3420
cgatcgcacg tcaactgccg aagcacagac cacatggacc atttctctct cggattagta	3480
gtggtcatgt tgatggtgca agaaggtatg aagaagagaa tgacatcaaa agcaataatc	3540
acctcagcgg cttttctcct ggcggttatg atagtgggag gtttcacgta ccaggatttt	3600
gggaggctgg tggatttggg ggggtgctgca tttgctgaga tgaacactgg aggtgacgtt	3660
gcgcacctgg cgctgggtggc agcgtttaaa gtgaggccag cgatgctggg ctcatlcatg	3720
ttcagagcct tgtggacccc cagggagtca ctgcttttag ctctggctgc ctgcctcctg	3780
caggtgtcag tgacaccact ggatcattcc atcatgatcg tggttgatgg gattgcgctg	3840
tcctggttgt gtctgaaagc catcttggtg ccgcgtaccc caaacatagc ctttctctt	3900
ctcgctatgc tgtcacccat gctccaaggt accaccattg tggcatggcg agctatgatg	3960

gcggccctgg	ctgtcataac	cttggcttcc	atgaagcatg	gaaggggtgt	aaaaaagacg	4020
tttccctaca	ccatcggatg	catccttggc	agcatgggct	tagttgaaaa	cttgggggttg	4080
gttggcctcc	tcttgttgac	agcctcaaaa	aagaggagtt	ggcctccgag	tgaggtgatg	4140
acggctgtcg	gactgatctg	tgcaattgtg	ggcggactaa	ccaagaccga	cattgacatg	4200
gcgggaccca	tggcagccat	aggactgctg	gtggtgagct	atgtggtttc	tggcaagagt	4260
gtggacatgt	acattgaaaa	ggtgtgtgac	atatcatggg	acaaggacgc	tgaataaca	4320
ggcacaagtc	cgcggttga	tgtggctctc	gacgacagt	gagatttctc	acttatccag	4380
gatgacgggc	ccccactcg	agagattgtg	ttgaagggtg	ttctgatgtg	tgtttgcggt	4440
gtcagcccca	tagccatccc	ctttgcagcc	gctgcttgg	tcgtgtacat	taaatcagg	4500
aaaagaagcg	gcgccatgtg	ggacattcca	tccccaaag	aagtgaaaa	aggggaaaca	4560
acggctggag	tgtacagaat	catgacgcgt	aaattgctgg	gcagcacaca	ggtgggagcc	4620
ggagtaatgc	atgaagggtg	ttttcacaca	atgtggcacg	tcacaaaagg	ttcggccctt	4680
cggagtgggtg	agggacgcct	agatccatac	tggggaaacg	tgaagcagga	tttgatctct	4740
tactgcggac	catggaaact	ggatgggaaa	tgggacggcg	tgtcgggaagt	ccaactgata	4800
gcggtcgccc	caggtgagcg	cgccagaaat	gtgcagacaa	aaccaggagt	gttcaagacc	4860
actgatgggg	aaatcggggc	cttggccctt	gacttcccag	gcggaagttc	aggctccccg	4920
ataattgaca	aaaatggaca	tgtaatggc	ctgtatggaa	atggtgtcgt	ggtcaagagt	4980
ggaagctacg	tgagtgccat	catgcagaca	gagaagatgg	aggaaccgc	agttgactgc	5040
tttgaggagg	acatgctgag	aaaaaagaag	ctgacggtgc	tcgacctcca	tccaggagct	5100
ggaaaaactc	gaagagtgt	ccctcagatc	gtcaaggctg	caattaagaa	acgcctacgc	5160
acggtaatcc	tggcacccac	ccgagtgggtg	gcagctgaga	tggctgaggc	actaaaagac	5220
cttccaataa	ggtacatgac	tccggcagtt	tcagccaccc	atgatggcaa	tgagattgtt	5280
gaccttatgt	gccacgccac	ttttacatca	aggctaattg	aaccaattag	ggtgccta	5340
tacaatctat	atataatgga	tgaggccac	ttcacagatc	ctgcaagcat	cgctgcaaga	5400
gggtacatag	caacaagagt	ggacatggga	gacgccgcgg	ccatcttcat	gacggccacc	5460
cctcctggca	gcactgaagc	tttcccggat	tcaaacgccc	ccatcacaga	tgttgaaaca	5520
gaggttcctg	acaaggcgtg	gaattctgga	tttgaatgga	tcactgatta	cccagggaaa	5580
accgttttgt	ttgtccctag	tgtcagaatg	ggcaatgaga	tctcggcctg	cctcacaaaa	5640
gccggcaaat	cggttatcca	actcagccgg	aaaacctttg	aaacagagta	ccagaagaca	5700

aagaatggtg agtgggactt tgtcgtgacc actgacatct cagaaatggg agccaacttc	5760
aaggccgaca gagtcataga ctcacggaaa tgcttgaagc cagtgattct ggatgacatg	5820
gaagagagag ttgtttcttg cgggccgatg gcagtaacac catccagcgc agctcaacgc	5880
agaggaagaa ttggaagaaa cccaacaaa actggagatg agttctatta cggggggggc	5940
tgtgccgcaa cggatgatga ccatgctcat tgggtagagg ctaggatgct gcttgacaac	6000
atctacctcc aggacaacct cgttgcatct ctgtacaagc cagaacaagg aaaggtctcg	6060
gcaatagaag gggagttcaa actgagagga gaacagagga aaaccttcgt ggagctgatg	6120
aagagagggg acttgccagt gtggttgta tatcaagtgg cggcctccgg actcagctat	6180
actgaccggc gctggtgctt tgatggaaaa aacaacaaca ccatcctgga ggactgcgtc	6240
cccgtcgagg tgtggacaaa atttggagag aaaaagattc tgaagcccag atggatggac	6300
gctcggatct gctctgatca tgcctctttg aagtctttca aggagtttgc tgcaggaaag	6360
agaacaatag cactggctt aattgaggct tttgggatgc ttcccgggca catgactgag	6420
agattccagg aggccgtcga caatttgcc gtgttgatga gggccgaggc aggctctagg	6480
gcacacagaa tggctgcagc acagctccct gagacaatgg aaaccatcct gctcctcagc	6540
ctgctggcat tcgtgtcact tgggtgtattt tttgtactga tgagggcaaa agggttagga	6600
aaaatggggc ccggcatgat cgtgctggca ggaagtggct ggctcatgtg gatgtctgag	6660
gtggaaccag cccgcatagc ttgtgtggtg atcatagtgt ttctgctaata ggtcgttctg	6720
attccggaac cggagaagca gcgctctccc caggacaatc agctggctct aattatcttg	6780
atcgcgacgg gcctcatcac gctcatcgcg gccaatgagc tgggttggtt agaaagaaca	6840
aagagtgacc tcaccaggct gttttggaga gaacacgctg agccaacagg agggagaggg	6900
ttttccttct cgctggacat tgacctgcgg ccggcatcgg cctgggcaat atatgccgct	6960
atgacaacct tgatcacacc gacagtccaa cacgctgtga ccacatcgta caacaactac	7020
tctctcatgg ctatggccac tcaggccgga gttctttttg gcatgggacg gggggtgcct	7080
ttttacaaat gggacttttg cgtgccactc cttatgctgg gctgctactc acaacttacc	7140
ccactcacc tgatcgtggc tctcgtgatg ctagccgctc actatctcta tctcatcccc	7200
gggctccagg caacggccgc cagggccgcc caacgaagga cggctgctgg aataatgaaa	7260
aaccagtggt tggatggaat tgtggtaact gacatagacc caatccaaat cgatccaaat	7320
gtcgaaaaga agatgggcca ggtcatgctc atctttgtgg ctttggcgag cgcggttctc	7380
atgagaacgg catgggggtg gggagaggct ggtgcccttg catcggcagc agctgccacc	7440

ctatgggaag	gggctcccaa	caagtactgg	aattcatcaa	cggctacatc	cttgtgcaac	7500
atatttcggg	gaagttatct	ggcaggtccc	tccctcatct	acaccgtcac	acgcaatgca	7560
ggtatcatga	agaaaagggg	cggtggaaat	ggagaaacgg	tgggcgagaa	atggaaggag	7620
cgcttgaatc	ggatgaccgc	gcttgaattc	tacgcctaca	agcggtcagg	aataactgaa	7680
gtgtgcagag	aaccgcgcag	aagagccttg	aaggatggag	tcgtcacagg	aggacacgct	7740
gtctcccgcg	gaagcgcaaa	gctgcatggg	atggtggaac	gtggccacgt	caatctagtg	7800
ggacgcgttg	tcgacctcgg	atgtggaagg	ggtggctgga	gttactacgc	cgcattctcaa	7860
aagcaagtcc	tcgaggtgag	aggctacaca	aaagggggag	cgggccacga	ggagcccatg	7920
aatgtccaaa	gttatgggtg	gaacatagtg	cgactcaaga	gtggagtgga	cgttttttat	7980
ctaccatcag	aaccatgtga	cacgctgctc	tgtgacattg	gagagtcatc	ctcgagccca	8040
gcagtggaag	aagcccggac	tctgagagtg	ctcgggatgg	ttgaaacctg	gctggaacgg	8100
ggcgtaaaga	acttctgcat	caaagtgctc	tgcccgtaca	ccagtgccat	gattgagcgg	8160
ctggaagccc	tccagcgtcg	ctacggagga	ggcctggtga	gggttccact	ctccagaaat	8220
tccaccacag	aaatgtactg	ggtctctgga	gcaaaatcaa	acatcatcag	gagtgtgaat	8280
gccaccagcc	agctgctcat	gcacagaatg	gacatcccca	cgcggaaaac	aaagtttgaa	8340
gaagacgtca	atctggggac	cggaaccagg	gcagttgaaa	gcagagctga	ccctcccgac	8400
atgaaaaaac	taggcagccg	gattgagcgg	ttgagaaagg	aatatggatc	cacttggcac	8460
tacgatgaaa	accacccta	caggacatgg	cattaccacg	gcagttatga	ggctgacacg	8520
caaggctccg	cctcctcaat	ggtcaacggc	gtggtgctgc	tcctctcaaa	accatgggat	8580
gcattgagct	cggtcaccaa	cattgctatg	acggacacaa	ctcgttttgg	acagcagcgg	8640
gtgttcaagg	agaaagtgga	caccgggact	ccagacccca	agcagggcac	gcaaagagtc	8700
atggccataa	catcacaatg	gctgtgggac	cgcctagcaa	gaaacaagac	ccctcggatg	8760
tgcacgcgac	aggaattcat	aaacaaggtc	aacagtcacg	cggcgttggg	acccgttttt	8820
agagaacagc	agggatgggg	ttcagcggcc	gaagcggtgg	tagatcctag	gttttgggag	8880
ctcgttgaca	atgaaagaga	agcccatttg	agaggggagt	gcttgacctg	tgtctacaac	8940
atgatgggga	aaagagaaaa	gaagctcggg	gaattcggga	aggcaaaagg	cagcagagcc	9000
atttggtaca	tgtggctggg	agcccgttgc	ctcgagttcg	aggccctggg	cttcctcaat	9060
gaagaccact	ggttaagcag	agagaactct	ggagggggag	ttgagggcct	gggcctccaa	9120
aaacttgat	acatccttga	agagatcagc	aggaggccag	gaggcaaaat	gtatgccgat	9180

gacacggctg gctgggacac ccgcatcacg aaatgcgacc tagaaaatga ggcgcgcatt	9240
ttggaaaaaa tggacgggat ccacaaaaaa ctcgcacggg ccgtcatcga gttgacatac	9300
aagcataagg ttgtgagagt cttgagacca gcaccacaag ggaaggtcgt tatggacatc	9360
atctccaggc cagaccaaag ggggagtggg cagggtggtta cttatgccct caacacctat	9420
acaaacttgg tggatgcagct gatccgtaac atggaagcag aggctgtcat caatgaaaga	9480
gacatggagg agctccaaaa cccatggaaa gtcatacaatt ggctagaagg aaatggatgg	9540
gacagactcc gctcgatggc agtgagtggg gatgactgtg tcgtgaaacc aatggatgat	9600
aggttcgcct atgcactgaa tttcctcaat gacatgggca aggtcagaaa agatgtccag	9660
gaatggaagc cctcgccggg gtggacaaac tgggaagaag tgcccttttg ctcccaccac	9720
ttcaacaagc tcccgatgaa ggatggaaga acaataatag ttccctgccg gcaccaagat	9780
gagttgatag gcagggctag agtttctcca ggaaaaggct ggtcactcag tgaaacagca	9840
tgcttgggca agtcttatgc ccagatgtgg ctactgttgt actttcacag gagagatctc	9900
cgactcatgg caaacgcaat ctgctctgct gtaccgggtga gttgggtgcc cacggggaga	9960
acaacctggc ccatccatgg gcgtggagag tggatgacaa cagaggacat gctagaggta	10020
tggaaacagag tgtggatcat agagaatgag tacatggagg acaagacccc tgtcacagag	10080
tggaccgatg ttccatactt gggaaagaga gaagacttgt ggtgcggctc ccttattgga	10140
cacaggccaa gaagcacatg ggcagagaac atctgggctg ccatttatca agtgcgccga	10200
gcaatcggcg aaactgaaga atatagagac tacatgagca cacagggtccg ctatggctcg	10260
gaggaagggc caagcgctgg tgtgttgtaa	10290

<210> 87

<211> 10290

<212> DNA

<213> Spondweni virus, complete genome NCBI Reference Sequence:
NC_029055.1

<400> 87

atgaaaaacc caaaaagagc cggtagcagc cggcttgtca atatgctaag acgcggtgca	60
gcccgtgtca tccctccagg aggagggctc aagaggctgc ctgtaggatt gctgttgggt	120
cggggtccga tcaaaatgat cctggccata ctggcattcc tacgatttac agcaataaaa	180
ccgtccactg gcctcatcaa cagatgggga aaagtgggca aaaaagaggc catcaaaatc	240
ctcacaaaat tcaaggctga cgtgggcacc atgctgcgta tcatcaacaa tcggaagaca	300
aaaaagagag gagtcgaaac tggaattgtg ttccctggcat tgctggtgtc tattgttgct	360

gtggaagtca caaaaaaggg ggacacctat tacatgtttg cggacaagaa ggacgccgga	420
aaggtggtga cttttgagac tgaatctgga cccaaccgtt gtcctatcca agcaatggac	480
attggacata tgtgtccagc tacaatgagc tatgaatgtc ccgtgctgga accacagtat	540
gagccagagg atgtcgactg ttggtgcaac tcgacagcag catggattgt gtatggcaca	600
tgcaccaca agacaacggg agagacaaga cgttccagac gttcaatcac cctgccatct	660
catgcctcac aaaagttgga gaccagatca tcgacgtggc ttgaatcccg cgaatactcc	720
aaatatctaa taaaggtgga aaactggatc ctccgcaatc caggatatgc gttggtggct	780
gcagtgattg gatggactct gggcagcagt cgcagccaga agatcatctt tgtcactctg	840
ctcatgttgg tagccccgc atacagcatc agatgcattg gaattggaaa cagagacttc	900
attgagggaa tgtccggtgg cacctgggtg gacattgtcc tggaacatgg tggttgtgtg	960
acagtaatgt caaacgacaa acccacattg gactttgaac tggtgacaac gaccgcaagt	1020
aacatggctg aggtcaggtc ctactgctat gaagctaaca tatccgagat ggcacggac	1080
agcaggtgcc ccacacaggg ggaagcttat cttgacaaaa tggccgactc ccagtttgtg	1140
tgcaagcgtg ggtacgttga caggggctgg ggaaacggat gtggactctt tggaaaagga	1200
agcattgtca cttgcgctaa gttcacgtgt gtgaaaaagc tcacagggaa aagcattcaa	1260
ccggagaatc tcgagtaccg ggtccttggt tcggtgcacg cttcccaaca tggaggaatg	1320
attaacaatg acaccaatca ccaacacgac aaggagaaca gagcgcgcat tgatatcaca	1380
gctagcgtc cccgtgttga ggtggaactt ggctcctttg gatccttctc gatggagtgt	1440
gaaccccggt caggattgaa ctttggtgac ctgtattacc tcaccatgaa caacaagcat	1500
tggctggtta atagagattg gtttcacgat ctttccttgc catggcatac aggagccaca	1560
tcaaacaatc atcactggaa caacaaggag gcgctggtag aattcagaga agcccacgca	1620
aagaagcaga cggctgtggt cctgggaagt caggaaggag ctgttcacgc agcactggcc	1680
ggcgactgg aggctgagtc tgatggacac aaagcgacta tctactctgg acacttgaag	1740
tgtcgcttga agctagacaa actgcgcctg aagggaatgt catatgcact ctgcacagga	1800
gcattcacct tcgctcgac cccctctgaa acaattcacg gcaccgccac agtggagctg	1860
caatatgcag gtgaagatgg gccgtgcaaa gttcccatag taattaccag tgacaccaat	1920
agcatggcct cgacaggcag gctgatcaca gcgaatccgg tggtcacgga aagtggagca	1980
aactcaaaga tgatggtcga gattgaccct ccgtttggtg attcttacat tattgtgggc	2040
actggcacia caaaaattac ccaccattgg cacagagccg gtagttcaat tggacgtgca	2100

tttgaggcta	ccatgagagg	agcaaaacgg	atggcggtcc	tcggcgacac	cgcttgggac	2160
tttggtcttg	ttgggggcat	gttcaactcc	gttggaagt	ttgtccacca	ggtgtttgga	2220
tcagcattta	aggcattggt	tggaggcatg	tcctggttca	cacagctcct	gataggattt	2280
ctgctcatat	ggatgggttt	gaacgcacgc	ggtggaaccg	tggccatgag	cttcatgggc	2340
attggggcta	tgctgatttt	cctagccacc	tcggtgtcag	gagacacagg	atgctcggtt	2400
gacatatcca	gaagggaaat	gcggtgcggg	agcggcatat	tcgtgtacaa	tgacgttgac	2460
gcatggcgaa	gccgctacaa	ataccatcct	gaaaccccca	gagctttggc	cgctgccgtg	2520
aaaacggctt	gggaagaagg	gacctgtggc	attacctcag	tgagcagaat	ggaaaacctg	2580
atgtggagct	ctgtggctgg	agagttgaat	gcaatccttg	aggacaattc	agtgccattg	2640
acagtctctg	ttggcgagcc	aaaatatcca	ctgtacaatg	ctccaaagag	gctgaaacca	2700
ccagcatcag	agttaccgca	ggggtggaag	tcctggggaa	agtcatactt	tgtctcagcc	2760
gcaaaaaaca	acaactcctt	tgtggtagat	ggtgacacca	tgaaggaatg	ccaagacag	2820
aagcgagcat	ggaacagctt	gagaatagag	gatcatgggt	tcggagtctt	ccacactagc	2880
atctggctga	aattccatga	ggacaactcc	accgaatgtg	acacagctat	cataggaacg	2940
gcggttcgcg	ggaaggaagc	cgttcatagt	gacttgggct	actggataga	gagtgagcgc	3000
aatgacacat	ggaggctctc	tcgagcgcac	ctgatcgaag	caaagacatg	tgaatggcca	3060
cggtcgcaca	cactgtggac	ggacggagtg	gaagagagcg	agctgatcat	tccacgtggc	3120
ttagccggtc	ctttcagcca	tcataacacg	cgtgctggct	acaagactca	gaataaaggt	3180
ccctggcatt	taggtgatgt	tgaattcag	ttcgccacgt	gccccggaac	aaccgtggtc	3240
caggaccaag	agtgcaggga	caggggcgct	tctctacgca	cgaccacagc	tagtggaagg	3300
gtaatcaatg	aatggtgctg	caggtcgtgc	accatgcctc	cactcagttt	caagacaaaa	3360
gatggatggt	ggtatgcaat	ggagatacgt	cctgtgaaag	aacaagagtc	aaacctcgtg	3420
cgatcgcacg	tactgccgg	aagcacagac	cacatggacc	atttctctct	cggattagta	3480
gtggtcatgt	tgatggtgca	agaaggtatg	aagaagagaa	tgacatcaaa	agcaataatc	3540
acctcagcgg	cctttctcct	ggcggttatg	atagtgggag	gtttcacgta	ccaggatttt	3600
gggaggctgg	tggtattggt	gggtgctgca	tttgctgaga	tgaacactgg	aggtgacgtt	3660
gcgcacctgg	cgctgggtggc	agcgtttaaa	gtgaggccag	cgatgctggg	ctcattcatg	3720
ttcagagcct	tgtggacccc	cagggagtca	ctgcttttag	ctctggctgc	ctgcctcctg	3780
caggtgtcag	tgacaccact	ggatcattcc	atcatgatcg	tggttgatgg	gattgcgctg	3840

tcctggttgt	gtctgaaagc	catcttggtg	ccgcgtaccc	caaacatagc	ccttcctctt	3900
ctcgctatgc	tgtcacccat	gctccaaggt	accaccattg	tggcatggcg	agctatgatg	3960
gcggccctgg	ctgtcataac	cttggtcttc	atgaagcatg	gaaggggtgt	aaaaagacg	4020
tttccctaca	ccatcggatg	catccttggc	agcatgggct	tagttgaaaa	cttggggttg	4080
gttggcctcc	tcttgttgac	agcctcaaaa	aagaggagtt	ggcctccgag	tgaggtgatg	4140
acggctgtcg	gactgatctg	tgcaattgtg	ggcggactaa	ccaagaccga	cattgacatg	4200
gcgggaccca	tggcagccat	aggactgctg	gtggtgagct	atgtggtttc	tggcaagagt	4260
gtggacatgt	acattgaaaa	ggtgtgtgac	atatcatggg	acaaggacgc	tgaaataaca	4320
ggcacaagtc	cgcggttgga	tgtggctctc	gacgacagtg	gagatttctc	acttatccag	4380
gatgacgggc	ccccactcg	agagattgtg	ttgaagggtg	ttctgatgtg	tgtttgcggt	4440
gtcagcccca	tagccatccc	ctttgcagcc	gctgcttggg	tcgtgtacat	taaatcaggg	4500
aaaagaagcg	gcgccatgtg	ggacattcca	tccccaagag	aagtgaaaaa	aggggaaaca	4560
acggctggag	tgtacagaat	catgacgcgt	aaattgctgg	gcagcacaca	ggtgggagcc	4620
ggagtaatgc	atgaagggtg	ttttcacaca	atgtggcacg	tcacaaaagg	ttcggccctt	4680
cggagtgggtg	agggacgcct	agatccatac	tggggaaacg	tgaagcagga	tttgatctct	4740
tactgcggac	catggaaaact	ggatgggaaa	tgggacggcg	tgtcgggaagt	ccaactgata	4800
gcggtcggcc	caggtgagcg	cgccagaaat	gtgcagacaa	aaccaggagt	gttcaagacc	4860
actgatgggg	aaatcggggc	cttggccctt	gacttcccag	gcggaagttc	aggctccccg	4920
ataattgaca	aaaatggaca	tgtaattggc	ctgtatggaa	atggtgtcgt	ggtcaagagt	4980
ggaagctacg	tgagtgccat	catgcagaca	gagaagatgg	aggaaccgcg	agttgactgc	5040
tttgaggagg	acatgctgag	aaaaaagaag	ctgacggtgc	tcgacctcca	tccaggagct	5100
ggaaaaactc	gaagagtgtc	ccctcagatc	gtcaaggctg	caattaagaa	acgcctacgc	5160
acggtaatcc	tggcaccac	ccgagtgggtg	gcagctgaga	tggctgaggc	actaaaagac	5220
cttccaataa	ggtacatgac	tccggcagtt	tcagccaccc	atgatggcaa	tgagattgtt	5280
gaccttatgt	gccacgccac	ttttacatca	aggctaattg	aaccaattag	ggtgccta	5340
tacaatctat	atataatgga	tgaggccac	ttcacagatc	ctgcaagcat	cgctgcaaga	5400
gggtacatag	caacaagagt	ggacatggga	gacgccgcgg	ccatcttcat	gacggccacc	5460
cctcctggca	gcactgaagc	tttcccggat	tcaaacgccc	ccatcacaga	tgttgaaaca	5520
gaggttcctg	acaaggcgtg	gaattctgga	tttgaatgga	tcactgatta	cccagggaaa	5580

accgtttggt	ttgtccctag	tgtcagaatg	ggcaatgaga	tctcggcctg	cctcacaaaa	5640
gccggcaaat	cggttatcca	actcagccgg	aaaacctttg	aaacagagta	ccagaagaca	5700
aagaatggtg	agtgggactt	tgtcgtgacc	actgacatct	cagaaatggg	agccaacttc	5760
aaggccgaca	gagtcataga	ctcacggaaa	tgcttgaagc	cagtgattct	ggatgacatg	5820
gaagagagag	ttgttcttgc	cgggccgatg	gcagtaacac	catccagcgc	agctcaacgc	5880
agaggaagaa	ttggaagaaa	ccccaacaaa	actggagatg	agttctatta	cggggggggc	5940
tgtgccgcaa	cggatgatga	ccatgctcat	tgggtagagg	ctaggatgct	gcttgacaac	6000
atctacctcc	aggacaacct	cgttgcatct	ctgtacaagc	cagaacaagg	aaaggtctcg	6060
gcaatagaag	gggagttcaa	actgagagga	gaacagagga	aaaccttcgt	ggagctgatg	6120
aagagagggg	acttgccagt	gtggttgtca	tatcaagtgg	cggcctccgg	actcagctat	6180
actgaccggc	gctggtgctt	tgatggaaaa	aacaacaaca	ccatcctgga	ggactgcgtc	6240
cccgctcgagg	tgtggacaaa	atttgagag	aaaaagattc	tgaagcccag	atggatggac	6300
gctcggatct	gctctgatca	tgctcttttg	aagtctttca	aggagtttgc	tgcaggaaaag	6360
agaacaatag	ccactgggctt	aattgaggct	tttgggatgc	ttcccgggca	catgactgag	6420
agattccagg	aggccgctga	caatttggcc	gtggtgatga	gggccgaggc	aggctctagg	6480
gcacacagaa	tggctgcagc	acagctccct	gagacaatgg	aaaccatcct	gctcctcagc	6540
ctgctggcat	tcgtgtcact	tgggtgtattt	tttgtactga	tgagggcaaa	agggttagga	6600
aaaatggggg	ccggcatgat	cgtgctggca	ggaagtggct	ggctcatgtg	gatgtctgag	6660
gtggaaccag	cccgcatagc	ttgtgtggtg	atcatagtgt	ttctgctaat	ggtcgttctg	6720
attccggaac	cggagaagca	gcgctctccc	caggacaatc	agctggctct	aattatcttg	6780
atcgcgacgg	gcctcatcac	gctcatcgcg	gccaatgagc	tgggttggtt	agaaagaaca	6840
aagagtgacc	tcaccaggct	gttttgagag	gaacacgctg	agccaacagg	agggagaggg	6900
ttttccttct	cgctggacat	tgacctgcgg	ccggcatcgg	cctgggcaat	atatgccgct	6960
atgacaaccc	tgatcacacc	gacagtccaa	cacgctgtga	ccacatcgta	caacaactac	7020
tctctcatgg	ctatggccac	tcaggccgga	gttctttttg	gcatgggacg	gggggtgcct	7080
ttttacaaat	gggacttttg	cgtgccactc	cttatgctgg	gctgctactc	acaacttacc	7140
ccactcacc	tgatcgtggc	tctcgtgatg	ctagccgctc	actatctcta	tctcatcccc	7200
gggctccagg	caacggccgc	cagggccgcc	caacgaagga	cggctgctgg	aataatgaaa	7260
aaccagtg	tggtatggaat	tgtggtaact	gacatagacc	caatccaaat	cgatccaaat	7320

gtcgaaaaga agatgggcca ggtcatgctc atctttgtgg ctttggcgag cgcggttctc	7380
atgagaacgg catgggggttg gggagaggct ggtgcccttg catcggcagc agctgccacc	7440
ctatgggaag gggctcccaa caagtactgg aattcatcaa cggctacatc cttgtgcaac	7500
atatttcggg gaagttatct ggcaggctcc tccctcatct acaccgtcac acgcaatgca	7560
ggtatcatga agaaaagggg cggtggaat ggagaaacgg tgggcgagaa atggaaggag	7620
cgcttgaatc ggatgaccgc gcttgaattc tacgcctaca agcggtcagg aataactgaa	7680
gtgtgcagag aaccgccag aagagccttg aaggatggag tcgtcacagg aggacacgct	7740
gtctcccgcg gaagcgcaaa gctgcatgg atggtggaac gtggccacgt caatctagt	7800
ggacgcgttg tcgacctcg atgtggaagg ggtggctgga gttactacgc cgcattctca	7860
aagcaagtcc tcgagggtgag aggctacaca aaagggggag cgggccacga ggagcccatg	7920
aatgtccaaa gttatggttg gaacatagtg cgactcaaga gtggagtgga cgttttttat	7980
ctaccatcag aaccatgtga cacgctgctc tgtgacattg gagagtcac ctcgagccca	8040
gcagtggaag aagcccggac tctgagagt ctcgggatgg ttgaaacctg gctggaacgg	8100
ggcgtaaaga acttctgcat caaagtgctc tgcccgtaca ccagtgccat gattgagcgg	8160
ctggaagccc tccagcgctc ctacggagga ggcctggtga gggttccact ctccagaaat	8220
tccaccacag aaatgtactg ggtctctgga gcaaaatcaa acatcatcag gagtgtgaat	8280
gccaccagcc agctgctcat gcacagaatg gacatcccca cgcggaaaac aaagtttgaa	8340
gaagacgtca atctggggac cggaaccagg gcagttgaaa gcagagctga ccctcccgac	8400
atgaaaaaac taggcagccg gattgagcgg ttgagaaagg aatatggatc cacttggcac	8460
tacgatgaaa accacccta caggacatgg cattaccacg gcagttatga ggctgacacg	8520
caaggctccg cctcctcaat ggtcaacggc gtggtgctc tcctctcaaa accatgggat	8580
gcattgagct cggtcaccaa cattgctatg acggacacaa ctccgttttg acagcagcgg	8640
gtgttcaagg agaaagtgga caccggact ccagaccca agcagggcac gcaaagagtc	8700
atggccataa catcacaatg gctgtgggac cgcctagcaa gaaacaagac ccctcggatg	8760
tgcacgcgac aggaattcat aaacaaggtc aacagtcacg cggcgttggg acccgttttt	8820
agagaacagc agggatgggg ttcagcggcc gaagcggtgg tagatcctag gttttgggag	8880
ctcgttgaca atgaaagaga agcccatttg agaggggagt gcttgacctg tgtctacaac	8940
atgatgggga aaagagaaaa gaagctcggg gaattcggga aggcaaaagg cagcagagcc	9000
atttggtaca tgtggctggg agcccgttc ctcgagttcg aggccctggg cttcctcaat	9060

gaagaccact ggttaagcag agagaactct ggagggggag ttgagggcctt gggcctccaa 9120
 aaacttgat acatccttga agagatcagc aggaggccag gaggcaaaat gtatgccgat 9180
 gacacggctg gctgggacac ccgcatcacg aaatgcgacc tagaaaatga ggcgcgcatt 9240
 ttggaaaaaa tggacgggat ccacaaaaaa ctcgcacggg ccgtcatcga gttgacatac 9300
 aagcataagg ttgtgagagt cttgagacca gcaccacaag ggaaggtcgt tatggacatc 9360
 atctccaggc cagaccaaag ggggagtggg caggtgggta cttatgccct caacacctat 9420
 acaaacttgg tgggtgcagct gatccgtaac atggaagcag aggctgtcat caatgaaaga 9480
 gacatggagg agctccaaaa cccatggaaa gtcatacaatt ggctagaagg aaatggatgg 9540
 gacagactcc gctcgatggc agtgagtgga gatgactgtg tcgtgaaacc aatggatgat 9600
 aggttcgcct atgcactgaa tttcctcaat gacatgggca aggtcagaaa agatgtccag 9660
 gaatggaagc cctcgccggg gtggacaaac tgggaagaag tgcctttttg ctcccaccac 9720
 ttcaacaagc tcccgatgaa ggatggaaga acaataatag ttccctgccg gcaccaagat 9780
 gagttgatag gcagggctag agtttctcca ggaaaaggct ggtcactcag tgaaacagca 9840
 tgcttgggca agtcttatgc ccagatgtgg ctactgttgt actttcacag gagagatctc 9900
 cgactcatgg caaacgcaat ctgctctgct gtaccgggtga gttgggtgcc cacggggaga 9960
 acaacctggc ccatccatgg gcgtggagag tggatgacaa cagaggacat gctagaggta 10020
 tggaacagag tgtggatcat agagaatgag tacatggagg acaagacccc tgtcacagag 10080
 tggaccgatg ttccatactt gggaaagaga gaagacttgt ggtgcggctc ccttattgga 10140
 cacaggccaa gaagcacatg ggcagagaac atctgggctg ccatttatca agtgcgccga 10200
 gcaatcggcg aaactgaaga atatagagac tacatgagca cacaggtccg ctatggctcg 10260
 gaggaagggc caagcgctgg tgtgttgtaa 10290

<210> 88
 <211> 3423
 <212> PRT
 <213> Zika virus isolate GD01 polyprotein

<400> 88

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Glu Thr Ser Val Gly Ile
 100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
 130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
 145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
 165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
 180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
 195 200 205

Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
 210 215 220

Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr
 225 230 235 240

Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly
 245 250 255

Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr
 260 265 270

Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
275 280 285

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
290 295 300

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
305 310 315 320

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
325 330 335

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
340 345 350

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
355 360 365

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
370 375 380

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
385 390 395 400

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Gly Thr Gly His
435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln	Ile	Phe	Gly	Ala	Ala	Phe	Lys	Ser	Leu	Phe	Gly	Gly	Met	Ser	Trp	740	745	750
Phe	Ser	Gln	Ile	Leu	Ile	Gly	Thr	Leu	Leu	Met	Trp	Leu	Gly	Leu	Asn	755	760	765
Thr	Lys	Asn	Gly	Ser	Ile	Ser	Leu	Met	Cys	Leu	Ala	Leu	Gly	Gly	Val	770	775	780
Leu	Ile	Phe	Leu	Ser	Thr	Ala	Val	Ser	Ala	Asp	Val	Gly	Cys	Ser	Val	785	790	795
Asp	Phe	Ser	Lys	Lys	Glu	Thr	Arg	Cys	Gly	Thr	Gly	Val	Phe	Val	Tyr	805	810	815
Asn	Asp	Val	Glu	Ala	Trp	Arg	Asp	Arg	Tyr	Lys	Tyr	His	Pro	Asp	Ser	820	825	830
Pro	Arg	Arg	Leu	Ala	Ala	Ala	Val	Lys	Gln	Ala	Trp	Glu	Asp	Gly	Ile	835	840	845
Cys	Gly	Ile	Ser	Ser	Val	Ser	Arg	Met	Glu	Asn	Ile	Met	Trp	Arg	Ser	850	855	860
Val	Glu	Gly	Glu	Leu	Asn	Ala	Ile	Leu	Glu	Glu	Asn	Gly	Val	Gln	Leu	865	870	875
Thr	Val	Val	Val	Gly	Ser	Val	Lys	Asn	Pro	Met	Trp	Arg	Gly	Pro	Gln	885	890	895
Arg	Leu	Pro	Val	Pro	Val	Asn	Glu	Leu	Pro	His	Gly	Trp	Lys	Ala	Trp	900	905	910
Gly	Lys	Ser	Tyr	Phe	Val	Arg	Ala	Ala	Lys	Thr	Asn	Asn	Ser	Phe	Val	915	920	925
Val	Asp	Gly	Asp	Thr	Leu	Lys	Glu	Cys	Pro	Leu	Lys	His	Arg	Ala	Trp	930	935	940
Asn	Ser	Phe	Leu	Val	Glu	Asp	His	Gly	Phe	Gly	Val	Phe	His	Thr	Ser	945	950	955

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro
1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
1040 1045 1050

Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu
1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
1100 1105 1110

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu
1115 1120 1125

Ile Arg Pro Arg Lys Glu Pro Glu Ser Asn Leu Val Arg Ser Met
1130 1135 1140

Val Thr Ala Gly Ser Thr Asp His Met Asp His Phe Ser Leu Gly
1145 1150 1155

Val Leu Val Ile Leu Leu Met Val Gln Glu Gly Leu Lys Lys Arg
1160 1165 1170

Met Thr Thr Lys Ile Ile Ile Ser Thr Ser Met Ala Val Leu Val
1175 1180 1185

Ala Met	Ile Leu Gly Gly	Phe	Ser Met Ser Asp	Leu	Ala Lys Leu
1190		1195		1200	
Ala Ile	Leu Met Gly Ala	Thr	Phe Ala Glu Met	Asn	Thr Gly Gly
1205		1210		1215	
Asp Val	Ala His Leu Ala	Leu	Ile Ala Ala Phe	Lys	Val Arg Pro
1220		1225		1230	
Ala Leu	Leu Val Ser Phe	Ile	Phe Arg Ala Asn	Trp	Thr Pro Arg
1235		1240		1245	
Glu Ser	Met Leu Leu Ala	Leu	Ala Ser Cys Leu	Leu	Gln Thr Ala
1250		1255		1260	
Ile Ser	Ala Leu Glu Gly	Asp	Leu Met Val Leu	Ile	Asn Gly Phe
1265		1270		1275	
Ala Leu	Ala Trp Leu Ala	Val	Arg Ala Met Val	Val	Pro Arg Thr
1280		1285		1290	
Asp Asn	Ile Thr Leu Ala	Ile	Leu Ala Ala Leu	Thr	Pro Leu Ala
1295		1300		1305	
Arg Gly	Thr Leu Leu Val	Ala	Trp Arg Ala Gly	Leu	Ala Thr Cys
1310		1315		1320	
Gly Gly	Phe Met Leu Leu	Ser	Leu Lys Gly Lys	Gly	Ser Val Lys
1325		1330		1335	
Lys Asn	Leu Pro Phe Val	Met	Ala Leu Gly Leu	Thr	Ala Val Arg
1340		1345		1350	
Leu Val	Asp Pro Ile Asn	Val	Val Gly Leu Leu	Leu	Leu Thr Arg
1355		1360		1365	
Ser Gly	Lys Arg Ser Trp	Pro	Pro Ser Glu Val	Leu	Thr Ala Val
1370		1375		1380	
Gly Leu	Ile Cys Ala Leu	Ala	Gly Gly Phe Ala	Lys	Ala Asp Ile
1385		1390		1395	

Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
1460						1465					1470			
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			

Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			

Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			

Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			

Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			

Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
2510						2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
2525						2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			

Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Ile	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			

Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			

Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			
Ser	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3305						3310					3315			
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Val
3320						3325					3330			
Val	Trp	Asn	Arg	Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp
3335						3340					3345			
Lys	Thr	Pro	Val	Thr	Lys	Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys
3350						3355					3360			

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg
 3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 89

<211> 3423

<212> PRT

<213> Zika virus strain MRS_OPY_Martinique_PaRi_2015 polyprotein

<400> 89

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Glu Thr Ser Val Gly Ile
 100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala

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

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
 370 375 380

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
 385 390 395 400

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
 405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
 420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
 435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
 450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
 465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
 485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
 500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
 515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
 530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
 545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
 565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
 580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro

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

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro
1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
1040 1045 1050

Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu

1055	1060	1065
Ile Arg Phe Glu Glu Cys 1070	Pro Gly Thr Lys Val 1075	His Val Glu Glu 1080
Thr Cys Gly Thr Arg Gly 1085	Pro Ser Leu Arg Ser 1090	Thr Thr Ala Ser 1095
Gly Arg Val Ile Glu Glu 1100	Trp Cys Cys Arg Glu 1105	Cys Thr Met Pro 1110
Pro Leu Ser Phe Trp Ala 1115	Lys Asp Gly Cys Trp 1120	Tyr Gly Met Glu 1125
Ile Arg Pro Arg Lys Glu 1130	Pro Glu Ser Asn Leu 1135	Val Arg Ser Met 1140
Val Thr Ala Gly Ser Thr 1145	Asp His Met Asp His 1150	Phe Ser Leu Gly 1155
Val Leu Val Ile Leu Leu 1160	Met Val Gln Glu Gly 1165	Leu Lys Lys Arg 1170
Met Thr Thr Lys Ile Ile 1175	Ile Ser Thr Ser Met 1180	Ala Val Leu Val 1185
Ala Met Ile Leu Gly Gly 1190	Phe Ser Met Ser Asp 1195	Leu Ala Lys Leu 1200
Ala Ile Leu Met Gly Ala 1205	Thr Phe Ala Glu Met 1210	Asn Thr Gly Gly 1215
Asp Val Ala His Leu Ala 1220	Leu Thr Ala Ala Phe 1225	Lys Val Arg Pro 1230
Ala Leu Leu Val Ser Phe 1235	Ile Phe Arg Ala Asn 1240	Trp Thr Pro Arg 1245
Glu Ser Met Leu Leu Ala 1250	Leu Ala Ser Cys Leu 1255	Leu Gln Thr Ala 1260
Ile Ser Ala Leu Glu Gly 1265	Asp Leu Met Val Leu 1270	Ile Asn Gly Phe 1275

Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
1460						1465					1470			
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser

1490						1495						1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly	
1505						1510					1515				
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu	
1520						1525					1530				
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe	
1535						1540					1545				
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly	
1550						1555					1560				
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu	
1565						1570					1575				
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly	
1580						1585					1590				
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala	
1595						1600					1605				
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly	
1610						1615					1620				
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly	
1625						1630					1635				
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly	
1640						1645					1650				
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr	
1655						1660					1665				
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro	
1670						1675					1680				
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro	
1685						1690					1695				
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu	
1700						1705					1710				

Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp

1925						1930						1935			
Gly 1940	Glu	Arg	Val	Ile	Leu	Ala 1945	Gly	Pro	Met	Pro	Val 1950	Thr	His	Ala	
Ser 1955	Ala	Ala	Gln	Arg	Arg	Gly 1960	Arg	Ile	Gly	Arg	Asn 1965	Pro	Asn	Lys	
Pro 1970	Gly	Asp	Glu	Tyr	Leu	Tyr 1975	Gly	Gly	Gly	Cys	Ala 1980	Glu	Thr	Asp	
Glu 1985	Asp	His	Ala	His	Trp	Leu 1990	Glu	Ala	Arg	Met	Leu 1995	Leu	Asp	Asn	
Ile 2000	Tyr	Leu	Gln	Asp	Gly	Leu 2005	Ile	Ala	Ser	Leu	Tyr 2010	Arg	Pro	Glu	
Ala 2015	Asp	Lys	Val	Ala	Ala	Ile 2020	Glu	Gly	Glu	Phe	Lys 2025	Leu	Arg	Thr	
Glu 2030	Gln	Arg	Lys	Thr	Phe	Val 2035	Glu	Leu	Met	Lys	Arg 2040	Gly	Asp	Leu	
Pro 2045	Val	Trp	Leu	Ala	Tyr	Gln 2050	Val	Ala	Ser	Ala	Gly 2055	Ile	Thr	Tyr	
Thr 2060	Asp	Arg	Arg	Trp	Cys	Phe 2065	Asp	Gly	Thr	Thr	Asn 2070	Asn	Thr	Ile	
Met 2075	Glu	Asp	Ser	Val	Pro	Ala 2080	Glu	Val	Trp	Thr	Arg 2085	His	Gly	Glu	
Lys 2090	Arg	Val	Leu	Lys	Pro	Arg 2095	Trp	Met	Asp	Ala	Arg 2100	Val	Cys	Ser	
Asp 2105	His	Ala	Ala	Leu	Lys	Ser 2110	Phe	Lys	Glu	Phe	Ala 2115	Ala	Gly	Lys	
Arg 2120	Gly	Ala	Ala	Phe	Gly	Val 2125	Met	Glu	Ala	Leu	Gly 2130	Thr	Leu	Pro	
Gly 2135	His	Met	Thr	Glu	Arg	Phe 2140	Gln	Glu	Ala	Ile	Asp 2145	Asn	Leu	Ala	

Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu

2360						2365						2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His	
2375						2380					2385				
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala	
2390						2395					2400				
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val	
2405						2410					2415				
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro	
2420						2425					2430				
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala	
2435						2440					2445				
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu	
2450						2455					2460				
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly	
2465						2470					2475				
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys	
2480						2485					2490				
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr	
2495						2500					2505				
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly	
2510						2515					2520				
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln	
2525						2530					2535				
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr	
2540						2545					2550				
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val	
2555						2560					2565				
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg	
2570						2575					2580				

Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu

2795						2800						2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr	
2810						2815					2820				
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala	
2825						2830					2835				
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp	
2840						2845					2850				
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr	
2855						2860					2865				
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg	
2870						2875					2880				
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val	
2885						2890					2895				
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg	
2900						2905					2910				
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala	
2915						2920					2925				
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	
2930						2935					2940				
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys	
2945						2950					2955				
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr	
2960						2965					2970				
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys	
2975						2980					2985				
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg	
2990						2995					3000				
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp	
3005						3010					3015				

Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
	3020					3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
	3035					3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
	3050					3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
	3065					3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
	3080					3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
	3095					3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
	3110					3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
	3125					3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
	3140					3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
	3155					3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
	3170					3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
	3185					3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
	3200					3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
	3215					3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly

3230		3235		3240
Arg Ser Ile Val Val Pro Cys Arg His Gln Asp Glu Leu Ile Gly				
3245		3250		3255
Arg Ala Arg Val Ser Pro Gly Ala Gly Trp Ser Ile Arg Glu Thr				
3260		3265		3270
Ala Cys Leu Ala Lys Ser Tyr Ala Gln Met Trp Gln Leu Leu Tyr				
3275		3280		3285
Phe His Arg Arg Asp Leu Arg Leu Met Ala Asn Ala Ile Cys Ser				
3290		3295		3300
Ser Val Pro Val Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser				
3305		3310		3315
Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val				
3320		3325		3330
Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp				
3335		3340		3345
Lys Thr Pro Val Ala Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys				
3350		3355		3360
Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg				
3365		3370		3375
Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg				
3380		3385		3390
Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr				
3395		3400		3405
Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu				
3410		3415		3420

<210> 90
 <211> 3423
 <212> PRT
 <213> Zika virus strain H/PF/2013 polyprotein

<400> 90

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

Thr	Lys	His	Leu	Ile	Arg	Val	Glu	Asn	Trp	Ile	Phe	Arg	Asn	Pro	Gly	245	250	255
Phe	Ala	Leu	Ala	Ala	Ala	Ala	Ile	Ala	Trp	Leu	Leu	Gly	Ser	Ser	Thr	260	265	270
Ser	Gln	Lys	Val	Ile	Tyr	Leu	Val	Met	Ile	Leu	Leu	Ile	Ala	Pro	Ala	275	280	285
Tyr	Ser	Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	290	295	300
Met	Ser	Gly	Gly	Thr	Trp	Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys	305	310	315
Val	Thr	Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val	325	330	335
Thr	Thr	Thr	Val	Ser	Asn	Met	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Glu	340	345	350
Ala	Ser	Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	Gly	355	360	365
Glu	Ala	Tyr	Leu	Asp	Lys	Gln	Ser	Asp	Thr	Gln	Tyr	Val	Cys	Lys	Arg	370	375	380
Thr	Leu	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	385	390	395
Gly	Ser	Leu	Val	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Lys	Lys	Met	Thr	405	410	415
Gly	Lys	Ser	Ile	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu	Ser	420	425	430
Val	His	Gly	Ser	Gln	His	Ser	Gly	Met	Ile	Val	Asn	Asp	Thr	Gly	His	435	440	445
Glu	Thr	Asp	Glu	Asn	Arg	Ala	Lys	Val	Glu	Ile	Thr	Pro	Asn	Ser	Pro	450	455	460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
 465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
 485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
 500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
 515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
 530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
 545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
 565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
 580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
 595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
 610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
 625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
 645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
 660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
 675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
 690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
770 775 780

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val	Asp	Gly	Asp	Thr	Leu	Lys	Glu	Cys	Pro	Leu	Lys	His	Arg	Ala	Trp
930						935					940				
Asn	Ser	Phe	Leu	Val	Glu	Asp	His	Gly	Phe	Gly	Val	Phe	His	Thr	Ser
945					950					955					960
Val	Trp	Leu	Lys	Val	Arg	Glu	Asp	Tyr	Ser	Leu	Glu	Cys	Asp	Pro	Ala
				965					970					975	
Val	Ile	Gly	Thr	Ala	Val	Lys	Gly	Lys	Glu	Ala	Val	His	Ser	Asp	Leu
			980					985					990		
Gly	Tyr	Trp	Ile	Glu	Ser	Glu	Lys	Asn	Asp	Thr	Trp	Arg	Leu	Lys	Arg
	995						1000					1005			
Ala	His	Leu	Ile	Glu	Met	Lys	Thr	Cys	Glu	Trp	Pro	Lys	Ser	His	
1010						1015					1020				
Thr	Leu	Trp	Thr	Asp	Gly	Ile	Glu	Glu	Ser	Asp	Leu	Ile	Ile	Pro	
1025						1030					1035				
Lys	Ser	Leu	Ala	Gly	Pro	Leu	Ser	His	His	Asn	Thr	Arg	Glu	Gly	
1040						1045					1050				
Tyr	Arg	Thr	Gln	Met	Lys	Gly	Pro	Trp	His	Ser	Glu	Glu	Leu	Glu	
1055						1060					1065				
Ile	Arg	Phe	Glu	Glu	Cys	Pro	Gly	Thr	Lys	Val	His	Val	Glu	Glu	
1070						1075					1080				
Thr	Cys	Gly	Thr	Arg	Gly	Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser	
1085						1090					1095				
Gly	Arg	Val	Ile	Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro	
1100						1105					1110				
Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu	
1115						1120					1125				
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met	
1130						1135					1140				
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly	
1145						1150					1155				

Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			

Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
1460						1465					1470			
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			

His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			

Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			

Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			

Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			

Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
2510						2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
2525						2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			

Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			

Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			

Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			
Ser	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3305						3310					3315			
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Val
3320						3325					3330			

Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp
 3335 3340 3345

Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
 3350 3355 3360

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg
 3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 91

<211> 3423

<212> PRT

<213> Zika virus strain MR 766 polyprotein

<400> 91

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Asn Pro Leu Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

Ala Arg Lys Glu Arg Lys Arg Arg Gly Ala Asp Thr Ser Ile Gly Ile

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
 340 345 350

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
 355 360 365

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
 370 375 380

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
 385 390 395 400

Gly Ser Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr
 405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
 420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly Tyr
 435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro
 450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
 465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
 485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
 500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
 515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
 530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
 545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Lys Leu Phe Ser

565

570

575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
 580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro
 595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
 610 615 620

Thr Asp Gly Pro Cys Lys Ile Pro Val Gln Met Ala Val Asp Met Gln
 625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
 645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
 660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His
 675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
 690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
 705 710 715 720

Phe Gly Ser Val Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Ile His
 725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
 740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn
 755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val
 770 775 780

Met Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
 785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Ile Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Glu Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Lys Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Glu His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Arg Glu Ala Ala His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Val Glu Glu Ser Asp Leu Ile Ile Pro

1025						1030						1035			
Lys	Ser	Leu	Ala	Gly	Pro	Leu	Ser	His	His	Asn	Thr	Arg	Glu	Gly	
1040						1045					1050				
Tyr	Arg	Thr	Gln	Val	Lys	Gly	Pro	Trp	His	Ser	Glu	Glu	Leu	Glu	
1055						1060					1065				
Ile	Arg	Phe	Glu	Glu	Cys	Pro	Gly	Thr	Lys	Val	Tyr	Val	Glu	Glu	
1070						1075					1080				
Thr	Cys	Gly	Thr	Arg	Gly	Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser	
1085						1090					1095				
Gly	Arg	Val	Ile	Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro	
1100						1105					1110				
Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu	
1115						1120					1125				
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met	
1130						1135					1140				
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly	
1145						1150					1155				
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg	
1160						1165					1170				
Met	Thr	Thr	Lys	Ile	Ile	Met	Ser	Thr	Ser	Met	Ala	Val	Leu	Val	
1175						1180					1185				
Val	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu	
1190						1195					1200				
Val	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly	
1205						1210					1215				
Asp	Val	Ala	His	Leu	Ala	Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro	
1220						1225					1230				
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg	
1235						1240					1245				

Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Ala	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Ala	Leu	Pro	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Ile	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Val	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Val	Glu	Glu	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val

1460							1465					1470				
Val	Leu	Met	Ala	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe		
1475						1480					1485					
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser		
1490						1495					1500					
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly		
1505						1510					1515					
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu		
1520						1525					1530					
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe		
1535						1540					1545					
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ala	Ala	Leu	Arg	Ser	Gly		
1550						1555					1560					
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu		
1565						1570					1575					
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly		
1580						1585					1590					
Leu	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala		
1595						1600					1605					
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly		
1610						1615					1620					
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly		
1625						1630					1635					
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly		
1640						1645					1650					
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr		
1655						1660					1665					
Gln	Gly	Lys	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro		
1670						1675					1680					

Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Lys	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	Asn	Gln	Glu	Trp	Asp	Phe	Val

1895						1900						1905			
Ile Thr Thr Asp Ile Ser Glu Met Gly Ala Asn Phe Lys Ala Asp															
1910						1915						1920			
Arg Val Ile Asp Ser Arg Arg Cys Leu Lys Pro Val Ile Leu Asp						1930						1935			
1925															
Gly Glu Arg Val Ile Leu Ala Gly Pro Met Pro Val Thr His Ala						1945						1950			
1940															
Ser Ala Ala Gln Arg Arg Gly Arg Ile Gly Arg Asn Pro Asn Lys						1960						1965			
1955															
Pro Gly Asp Glu Tyr Met Tyr Gly Gly Gly Cys Ala Glu Thr Asp						1975						1980			
1970															
Glu Gly His Ala His Trp Leu Glu Ala Arg Met Leu Leu Asp Asn						1990						1995			
1985															
Ile Tyr Leu Gln Asp Gly Leu Ile Ala Ser Leu Tyr Arg Pro Glu						2005						2010			
2000															
Ala Asp Lys Val Ala Ala Ile Glu Gly Glu Phe Lys Leu Arg Thr						2020						2025			
2015															
Glu Gln Arg Lys Thr Phe Val Glu Leu Met Lys Arg Gly Asp Leu						2035						2040			
2030															
Pro Val Trp Leu Ala Tyr Gln Val Ala Ser Ala Gly Ile Thr Tyr						2050						2055			
2045															
Thr Asp Arg Arg Trp Cys Phe Asp Gly Thr Thr Asn Asn Thr Ile						2065						2070			
2060															
Met Glu Asp Ser Val Pro Ala Glu Val Trp Thr Lys Tyr Gly Glu						2080						2085			
2075															
Lys Arg Val Leu Lys Pro Arg Trp Met Asp Ala Arg Val Cys Ser						2095						2100			
2090															
Asp His Ala Ala Leu Lys Ser Phe Lys Glu Phe Ala Ala Gly Lys						2110						2115			
2105															

Arg	Gly	Ala	Ala	Leu	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Asn	Asp	Ile	Ala
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Met	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Leu	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala

2330						2335						2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp	
2345						2350					2355				
Asp	Leu	Gly	Val	Pro	Leu	Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu	
2360						2365					2370				
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His	
2375						2380					2385				
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala	
2390						2395					2400				
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val	
2405						2410					2415				
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro	
2420						2425					2430				
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala	
2435						2440					2445				
Ile	Ser	Ser	Ala	Val	Leu	Leu	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu	
2450						2455					2460				
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly	
2465						2470					2475				
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys	
2480						2485					2490				
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr	
2495						2500					2505				
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly	
2510						2515					2520				
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln	
2525						2530					2535				
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr	
2540						2545					2550				

Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Val
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Arg	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Thr	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Met	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	His	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Ile	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn

2765						2770						2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro	
2780						2785					2790				
Asn	Met	Lys	Ile	Ile	Gly	Arg	Arg	Ile	Glu	Arg	Ile	Arg	Asn	Glu	
2795						2800					2805				
His	Ala	Glu	Thr	Trp	Phe	Leu	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr	
2810						2815					2820				
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala	
2825						2830					2835				
Ser	Ser	Leu	Val	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp	
2840						2845					2850				
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr	
2855						2860					2865				
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg	
2870						2875					2880				
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Asn	Ile	Val	
2885						2890					2895				
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg	
2900						2905					2910				
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala	
2915						2920					2925				
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	
2930						2935					2940				
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Arg	
2945						2950					2955				
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr	
2960						2965					2970				
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys	
2975						2980					2985				

Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Ile	Leu	Glu	Glu	Met	Asn	Arg	Ala	Pro	Gly
3035						3040					3045			
Gly	Lys	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Lys	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Glu	Gly	His	Arg	Thr	Leu	Ala	Leu	Ala	Val	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Gly	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Lys	Val	Thr	Arg	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr

3200							3205								3210
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val	
3215						3220					3225				
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	Tyr	Leu	Lys	Asp	Gly	
3230						3235					3240				
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly	
3245						3250					3255				
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr	
3260						3265					3270				
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr	
3275						3280					3285				
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser	
3290						3295					3300				
Ala	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser	
3305						3310					3315				
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Met	
3320						3325					3330				
Val	Trp	Asn	Arg	Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp	
3335						3340					3345				
Lys	Thr	Pro	Val	Thr	Lys	Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys	
3350						3355					3360				
Arg	Glu	Asp	Leu	Trp	Cys	Gly	Ser	Leu	Ile	Gly	His	Arg	Pro	Arg	
3365						3370					3375				
Thr	Thr	Trp	Ala	Glu	Asn	Ile	Lys	Asp	Thr	Val	Asn	Met	Val	Arg	
3380						3385					3390				
Arg	Ile	Ile	Gly	Asp	Glu	Glu	Lys	Tyr	Met	Asp	Tyr	Leu	Ser	Thr	
3395						3400					3405				
Gln	Val	Arg	Tyr	Leu	Gly	Glu	Glu	Gly	Ser	Thr	Pro	Gly	Val	Leu	
3410						3415					3420				

<210> 92
 <211> 3423
 <212> PRT
 <213> Zika virus strain 8375 polyprotein

<400> 92

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
 100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
 130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
 145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
 165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
 180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
 195 200 205

Glu	Ala	Arg	Arg	Ser	Arg	Arg	Ala	Val	Thr	Leu	Pro	Ser	His	Ser	Thr			
	210						215				220							
Arg	Lys	Leu	Gln	Thr	Arg	Ser	Gln	Thr	Trp	Leu	Glu	Ser	Arg	Glu	Tyr			
225					230					235					240			
Thr	Lys	His	Leu	Ile	Arg	Val	Glu	Asn	Trp	Ile	Phe	Arg	Asn	Pro	Gly			
				245					250					255				
Phe	Ala	Leu	Ala	Ala	Ala	Ala	Ile	Ala	Trp	Leu	Leu	Gly	Ser	Ser	Thr			
			260					265					270					
Ser	Gln	Lys	Val	Ile	Tyr	Leu	Val	Met	Ile	Leu	Leu	Ile	Ala	Pro	Ala			
		275					280					285						
Tyr	Ser	Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly			
	290					295					300							
Met	Ser	Gly	Gly	Thr	Trp	Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys			
305					310					315					320			
Val	Thr	Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val			
				325					330					335				
Thr	Thr	Thr	Val	Ser	Asn	Met	Ala	Glu	Ile	Arg	Ser	Tyr	Cys	Tyr	Glu			
			340					345					350					
Ala	Ser	Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	Gly			
		355					360					365						
Glu	Ala	Tyr	Leu	Asp	Lys	Gln	Ser	Asp	Thr	Gln	Tyr	Val	Cys	Lys	Arg			
	370					375					380							
Thr	Leu	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys			
385					390					395					400			
Gly	Ser	Leu	Val	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Lys	Lys	Met	Thr			
				405					410					415				
Gly	Lys	Ser	Ile	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu	Ser			
			420					425					430					

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
770 775 780

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Ala Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
 900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
 915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
 930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
 945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
 965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu
 980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
 995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
 1010 1015 1020

Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro
 1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
 1040 1045 1050

Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu
 1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
 1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
 1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
 1100 1105 1110

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu
 1115 1120 1125

Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met
1130						1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			

Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
1460						1465					1470			
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			

Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			

Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			

Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Leu	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			

Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			

Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
2510						2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
2525						2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			

Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Arg	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			

Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Cys	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			

Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			

Ser Val Pro Val Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser
 3305 3310 3315

Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val
 3320 3325 3330

Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp
 3335 3340 3345

Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
 3350 3355 3360

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg
 3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 93
 <211> 3423
 <212> PRT
 <213> Zika virus strain 103344 polyprotein

<400> 93

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile

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

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
305 310 315 320

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
325 330 335

Thr Thr Thr Val Ser Asn Met Ala Glu Ile Arg Ser Tyr Cys Tyr Glu
340 345 350

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
355 360 365

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
370 375 380

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
385 390 395 400

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr

530																
Val	Val	Val	Leu	Gly	Ser	Gln	Glu	Gly	Ala	Val	His	Thr	Ala	Leu	Ala	
545					550					555					560	
Gly	Ala	Leu	Glu	Ala	Glu	Met	Asp	Gly	Ala	Lys	Gly	Arg	Leu	Ser	Ser	
				565					570					575		
Gly	His	Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Arg	Leu	Lys	Gly	
			580					585					590			
Val	Ser	Tyr	Ser	Leu	Cys	Thr	Ala	Ala	Phe	Thr	Phe	Thr	Lys	Ile	Pro	
		595					600						605			
Ala	Glu	Thr	Leu	His	Gly	Thr	Val	Thr	Val	Glu	Val	Gln	Tyr	Ala	Gly	
	610					615						620				
Thr	Asp	Gly	Pro	Cys	Lys	Val	Pro	Ala	Gln	Met	Ala	Val	Asp	Met	Gln	
625					630					635					640	
Thr	Leu	Thr	Pro	Val	Gly	Arg	Leu	Ile	Thr	Ala	Asn	Pro	Val	Ile	Thr	
				645					650					655		
Glu	Ser	Thr	Glu	Asn	Ser	Lys	Met	Met	Leu	Glu	Leu	Asp	Pro	Pro	Phe	
			660					665					670			
Gly	Asp	Ser	Tyr	Ile	Val	Ile	Gly	Val	Gly	Glu	Lys	Lys	Ile	Thr	His	
		675					680					685				
His	Trp	His	Arg	Ser	Gly	Ser	Thr	Ile	Gly	Lys	Ala	Phe	Glu	Ala	Thr	
	690					695					700					
Val	Arg	Gly	Ala	Lys	Arg	Met	Ala	Val	Leu	Gly	Asp	Thr	Ala	Trp	Asp	
705					710					715					720	
Phe	Gly	Ser	Val	Gly	Gly	Ala	Leu	Asn	Ser	Leu	Gly	Lys	Gly	Ile	His	
				725					730					735		
Gln	Ile	Phe	Gly	Ala	Ala	Phe	Lys	Ser	Leu	Phe	Gly	Gly	Met	Ser	Trp	
			740					745					750			
Phe	Ser	Gln	Ile	Leu	Ile	Gly	Thr	Leu	Leu	Met	Trp	Leu	Gly	Leu	Asn	
		755					760					765				

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
770 775 780

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Ala Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg

995					1000					1005				
Ala	His	Leu	Ile	Glu	Met	Lys	Thr	Cys	Glu	Trp	Pro	Lys	Ser	His
1010						1015					1020			
Thr	Leu	Trp	Thr	Asp	Gly	Ile	Glu	Glu	Ser	Asp	Leu	Ile	Ile	Pro
1025						1030					1035			
Lys	Ser	Leu	Ala	Gly	Pro	Leu	Ser	His	His	Asn	Thr	Arg	Glu	Gly
1040						1045					1050			
Tyr	Arg	Thr	Gln	Met	Lys	Gly	Pro	Trp	His	Ser	Glu	Glu	Leu	Glu
1055						1060					1065			
Ile	Arg	Phe	Glu	Glu	Cys	Pro	Gly	Thr	Lys	Val	His	Val	Glu	Glu
1070						1075					1080			
Thr	Cys	Gly	Thr	Arg	Gly	Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser
1085						1090					1095			
Gly	Arg	Val	Ile	Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro
1100						1105					1110			
Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu
1115						1120					1125			
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met
1130						1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			

Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser

1430						1435						1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu	
1445						1450					1455				
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val	
1460						1465					1470				
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe	
1475						1480					1485				
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser	
1490						1495					1500				
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly	
1505						1510					1515				
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu	
1520						1525					1530				
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe	
1535						1540					1545				
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly	
1550						1555					1560				
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu	
1565						1570					1575				
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly	
1580						1585					1590				
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala	
1595						1600					1605				
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly	
1610						1615					1620				
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly	
1625						1630					1635				
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly	
1640						1645					1650				

Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu

1865		1870		1875
Thr Lys 1880	Ala Gly Lys Arg	Val 1885	Ile Gln Leu Ser	Arg Lys Thr Phe 1890
Glu Thr 1895	Glu Phe Gln Lys	Thr 1900	Lys His Gln Glu	Trp Asp Phe Val 1905
Val Thr 1910	Thr Asp Ile Ser	Glu 1915	Met Gly Ala Asn	Phe Lys Ala Asp 1920
Arg Val 1925	Ile Asp Ser Arg	Arg 1930	Cys Leu Lys Pro	Val Ile Leu Asp 1935
Gly Glu 1940	Arg Val Ile Leu	Ala 1945	Gly Pro Met Pro	Val Thr His Ala 1950
Ser Ala 1955	Ala Gln Arg Arg	Gly 1960	Arg Ile Gly Arg	Asn Pro Asn Lys 1965
Pro Gly 1970	Asp Glu Tyr Leu	Tyr 1975	Gly Gly Gly Cys	Ala Glu Thr Asp 1980
Glu Asp 1985	His Ala His Trp	Leu 1990	Glu Ala Arg Met	Leu Leu Asp Asn 1995
Ile Tyr 2000	Leu Gln Asp Gly	Leu 2005	Ile Ala Ser Leu	Tyr Arg Pro Glu 2010
Ala Asp 2015	Lys Val Ala Ala	Ile 2020	Glu Gly Glu Phe	Lys Leu Arg Thr 2025
Glu Gln 2030	Arg Lys Thr Phe	Val 2035	Glu Leu Met Lys	Arg Gly Asp Leu 2040
Pro Val 2045	Trp Leu Ala Tyr	Gln 2050	Val Ala Ser Ala	Gly Ile Thr Tyr 2055
Thr Asp 2060	Arg Arg Trp Cys	Phe 2065	Asp Gly Thr Thr	Asn Asn Thr Ile 2070
Leu Glu 2075	Asp Ser Val Pro	Ala 2080	Glu Val Trp Thr	Arg His Gly Glu 2085

Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala

2300		2305		2310
Ala Leu Thr Thr Phe Ile Thr Pro Ala Val Gln His Ala Val Thr				
2315		2320		2325
Thr Ser Tyr Asn Asn Tyr Ser Leu Met Ala Met Ala Thr Gln Ala				
2330		2335		2340
Gly Val Leu Phe Gly Met Gly Lys Gly Met Pro Phe Tyr Ala Trp				
2345		2350		2355
Asp Phe Gly Val Pro Leu Leu Met Ile Gly Cys Tyr Ser Gln Leu				
2360		2365		2370
Thr Pro Leu Thr Leu Ile Val Ala Ile Ile Leu Leu Val Ala His				
2375		2380		2385
Tyr Met Tyr Leu Ile Pro Gly Leu Gln Ala Ala Ala Ala Arg Ala				
2390		2395		2400
Ala Gln Lys Arg Thr Ala Ala Gly Ile Met Lys Asn Pro Val Val				
2405		2410		2415
Asp Gly Ile Val Val Thr Asp Ile Asp Thr Met Thr Ile Asp Pro				
2420		2425		2430
Gln Val Glu Lys Lys Met Gly Gln Val Leu Leu Ile Ala Val Ala				
2435		2440		2445
Val Ser Ser Ala Ile Leu Ser Arg Thr Ala Trp Gly Trp Gly Glu				
2450		2455		2460
Ala Gly Ala Leu Ile Thr Ala Ala Thr Ser Thr Leu Trp Glu Gly				
2465		2470		2475
Ser Pro Asn Lys Tyr Trp Asn Ser Ser Thr Ala Thr Ser Leu Cys				
2480		2485		2490
Asn Ile Phe Arg Gly Ser Tyr Leu Ala Gly Ala Ser Leu Ile Tyr				
2495		2500		2505
Thr Val Thr Arg Asn Ala Gly Leu Val Lys Arg Arg Gly Gly Gly				
2510		2515		2520

Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
	2525					2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
	2540					2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
	2555					2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
	2570					2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
	2585					2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
	2600					2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
	2615					2620					2625			
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
	2630					2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
	2645					2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
	2660					2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
	2675					2680					2685			
Gly	Asp	Trp	Leu	Glu	Arg	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
	2690					2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
	2705					2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
	2720					2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn

2735						2740						2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg	
2750						2755					2760				
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn	
2765						2770					2775				
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro	
2780						2785					2790				
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu	
2795						2800					2805				
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr	
2810						2815					2820				
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala	
2825						2830					2835				
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp	
2840						2845					2850				
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr	
2855						2860					2865				
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg	
2870						2875					2880				
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val	
2885						2890					2895				
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg	
2900						2905					2910				
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala	
2915						2920					2925				
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	
2930						2935					2940				
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys	
2945						2950					2955				

Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Cys	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser

3170							3175								3180
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His	
3185						3190					3195				
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr	
3200						3205					3210				
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val	
3215						3220					3225				
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly	
3230						3235					3240				
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly	
3245						3250					3255				
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr	
3260						3265					3270				
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr	
3275						3280					3285				
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser	
3290						3295					3300				
Ser	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser	
3305						3310					3315				
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Val	
3320						3325					3330				
Val	Trp	Asn	Arg	Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp	
3335						3340					3345				
Lys	Thr	Pro	Val	Thr	Lys	Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys	
3350						3355					3360				
Arg	Glu	Asp	Leu	Trp	Cys	Gly	Ser	Leu	Ile	Gly	His	Arg	Pro	Arg	
3365						3370					3375				
Thr	Thr	Trp	Ala	Glu	Asn	Ile	Lys	Asn	Thr	Val	Asn	Met	Val	Arg	
3380						3385					3390				

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 94

<211> 3423

<212> PRT

<213> Zika virus strain ArD158084 polyprotein

<400> 94

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Asn Pro Leu Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

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

Ile Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Ile Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Ser Asp Ala Gly Lys Ala
 130 135 140

Ile Ser Phe Ala Thr Thr Leu Gly Val Asn Lys Cys His Val Gln Ile
 145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
 165 170 175

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

Gly Ser Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr
405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Ile Gly His
435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro
450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

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

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Gly Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Arg Glu Ala Ala His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Val Glu Glu Ser Asp Leu Ile Ile Pro
1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
1040 1045 1050

Tyr Arg Thr Gln Val Lys Gly Pro Trp His Ser Glu Glu Leu Glu
1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
1085 1090 1095

Gly	Arg	Val	Ile	Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro
1100						1105					1110			
Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu
1115						1120					1125			
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met
1130						1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Met	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Val	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Val	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Leu	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Val	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Ala	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Ala	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			

Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
	1310					1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
	1325					1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
	1340					1345					1350			
Val	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
	1355					1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
	1370					1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
	1385					1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
	1400					1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
	1415					1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
	1430					1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
	1445					1450					1455			
Val	Glu	Glu	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
	1460					1465					1470			
Val	Leu	Met	Ala	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
	1475					1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
	1490					1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
	1505					1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
	1520					1525					1530			

Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ala	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
Leu	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Lys	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Lys	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			

Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Asn	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	Asn	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Ile	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			

Pro 1970	Gly	Asp	Glu	Tyr	Met	Tyr 1975	Gly	Gly	Gly	Cys	Ala 1980	Glu	Thr	Asp
Glu 1985	Gly	His	Ala	His	Trp	Leu 1990	Glu	Ala	Arg	Met	Leu 1995	Leu	Asp	Asn
Ile 2000	Tyr	Leu	Gln	Asp	Gly	Leu 2005	Ile	Ala	Ser	Leu	Tyr 2010	Arg	Pro	Glu
Ala 2015	Asp	Lys	Val	Ala	Ala	Ile 2020	Glu	Gly	Glu	Phe	Lys 2025	Leu	Arg	Thr
Glu 2030	Gln	Arg	Lys	Thr	Phe	Val 2035	Glu	Leu	Met	Lys	Arg 2040	Gly	Asp	Leu
Pro 2045	Val	Trp	Leu	Ala	Tyr	Gln 2050	Val	Ala	Ser	Ala	Gly 2055	Ile	Thr	Tyr
Thr 2060	Asp	Arg	Arg	Trp	Cys	Phe 2065	Asp	Gly	Thr	Thr	Asn 2070	Asn	Thr	Ile
Met 2075	Glu	Asp	Ser	Val	Pro	Ala 2080	Glu	Val	Trp	Thr	Lys 2085	Tyr	Gly	Glu
Lys 2090	Arg	Val	Leu	Lys	Pro	Arg 2095	Trp	Met	Asp	Ala	Arg 2100	Val	Cys	Ser
Asp 2105	His	Ala	Ala	Leu	Lys	Ser 2110	Phe	Lys	Glu	Phe	Ala 2115	Ala	Gly	Lys
Arg 2120	Gly	Ala	Ala	Leu	Gly	Val 2125	Met	Glu	Ala	Leu	Gly 2130	Thr	Leu	Pro
Gly 2135	His	Met	Thr	Glu	Arg	Phe 2140	Gln	Glu	Ala	Ile	Asp 2145	Asn	Leu	Ala
Val 2150	Leu	Met	Arg	Ala	Glu	Thr 2155	Gly	Ser	Arg	Pro	Tyr 2160	Lys	Ala	Ala
Ala 2165	Ala	Gln	Leu	Pro	Glu	Thr 2170	Leu	Glu	Thr	Ile	Met 2175	Leu	Leu	Gly

Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Asn	Asp	Ile	Ala
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Met	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Leu	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			

Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Ile	Ser	Ser	Ala	Val	Leu	Leu	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
2510						2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
2525						2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	His	Gly	Lys	Val	Val
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			

Ile	Arg	Lys	Val	Gln	Glu	Val	Arg	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
	2615					2620					2625			
Gly	His	Glu	Glu	Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
	2630					2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
	2645					2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
	2660					2665					2670			
Pro	Glu	Val	Glu	Glu	Thr	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
	2675					2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
	2690					2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Met	Glu	Arg	Leu
	2705					2710					2715			
Gln	Arg	Arg	His	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
	2720					2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
	2735					2740					2745			
Ile	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
	2750					2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
	2765					2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro
	2780					2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Arg	Arg	Ile	Glu	Arg	Ile	Arg	Asn	Glu
	2795					2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Leu	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
	2810					2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
	2825					2830					2835			

Ser	Ser	Leu	Val	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Asn	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Arg
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Gln	Ala	Pro	Gly
3035						3040					3045			

Gly	Lys	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Lys	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Glu	Gly	His	Arg	Thr	Leu	Ala	Leu	Ala	Val	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Gly	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Lys	Val	Thr	Arg	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Gly	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	Tyr	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			

Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			
Ala	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3305						3310					3315			
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Met
3320						3325					3330			
Val	Trp	Asn	Arg	Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp
3335						3340					3345			
Lys	Thr	Pro	Val	Thr	Lys	Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys
3350						3355					3360			
Arg	Glu	Asp	Leu	Trp	Cys	Gly	Ser	Leu	Ile	Gly	His	Arg	Pro	Arg
3365						3370					3375			
Thr	Thr	Trp	Ala	Glu	Asn	Ile	Lys	Asp	Thr	Val	Asn	Met	Val	Arg
3380						3385					3390			
Arg	Ile	Ile	Gly	Asp	Glu	Glu	Lys	Tyr	Met	Asp	Tyr	Leu	Ser	Thr
3395						3400					3405			
Gln	Val	Arg	Tyr	Leu	Gly	Glu	Glu	Gly	Ser	Thr	Pro	Gly	Val	Leu
3410						3415					3420			

<210> 95
 <211> 3423
 <212> PRT
 <213> Zika virus strain ArD157995 polyprotein

<220>
 <221> misc_feature
 <222> (904)..(904)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (2829)..(2829)
 <223> Xaa can be any naturally occurring amino acid

<400> 95

Met Lys Asn Pro Lys Lys Lys Ser Gly Arg Phe Arg Ile Val Asn Met
1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Asn Pro Leu Gly Gly Leu Lys Arg
20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
85 90 95

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

Ile Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Ile Thr Arg Arg
115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Ser Asp Ala Gly Lys Ala
130 135 140

Ile Ser Phe Ala Thr Thr Leu Gly Val Asn Lys Cys His Val Gln Ile
145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
195 200 205

Glu Thr Arg Arg Ser Arg Arg Ser Val Ser Leu Arg Tyr His Tyr Thr
210 215 220

Arg	Lys	Leu	Gln	Thr	Arg	Ser	Gln	Thr	Trp	Leu	Glu	Ser	Arg	Glu	Tyr	225	230	235	240
Lys	Lys	His	Leu	Ile	Met	Val	Glu	Asn	Trp	Ile	Phe	Arg	Asn	Pro	Gly	245	250	255	
Phe	Ala	Ile	Val	Ser	Val	Ala	Ile	Thr	Trp	Leu	Met	Gly	Ser	Leu	Thr	260	265	270	
Ser	Gln	Lys	Val	Ile	Tyr	Leu	Val	Met	Ile	Val	Leu	Ile	Val	Pro	Ala	275	280	285	
Tyr	Ser	Ile	Ser	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Leu	Val	Glu	Gly	290	295	300	
Met	Ser	Gly	Gly	Thr	Trp	Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys	305	310	315	320
Val	Thr	Glu	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val	325	330	335	
Thr	Met	Thr	Val	Ser	Asn	Met	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Glu	340	345	350	
Ala	Ser	Leu	Ser	Asp	Met	Ala	Ser	Ala	Ser	Arg	Cys	Pro	Thr	Gln	Gly	355	360	365	
Glu	Pro	Ser	Leu	Asp	Lys	Gln	Ser	Asp	Thr	Gln	Ser	Val	Cys	Lys	Arg	370	375	380	
Thr	Leu	Gly	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Ile	Phe	Gly	Lys	385	390	395	400
Gly	Ser	Leu	Val	Thr	Cys	Ser	Lys	Phe	Thr	Cys	Cys	Lys	Lys	Met	Pro	405	410	415	
Gly	Lys	Ser	Ile	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu	Pro	420	425	430	
Val	His	Gly	Ser	Gln	His	Ser	Gly	Met	Ile	Val	Asn	Asp	Ile	Gly	His	435	440	445	
Glu	Thr	Asp	Glu	Asn	Arg	Ala	Lys	Val	Glu	Val	Thr	Pro	Asn	Ser	Pro	450	455	460	

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
 465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
 485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
 500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
 515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
 530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
 545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser
 565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
 580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro
 595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Ser Ala Gly
 610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
 625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
 645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
 660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His
 675 680 685

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

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
 930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
 945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
 965 970 975

Val Ile Gly Thr Ala Val Lys Gly Arg Glu Ala Ala His Ser Asp Leu
 980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
 995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
 1010 1015 1020

Thr Leu Trp Thr Asp Gly Val Glu Glu Ser Asp Leu Ile Ile Pro
 1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
 1040 1045 1050

Tyr Arg Thr Gln Val Lys Gly Pro Trp His Ser Glu Glu Leu Glu
 1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
 1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
 1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
 1100 1105 1110

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu
 1115 1120 1125

Ile Arg Pro Arg Lys Glu Pro Glu Ser Asn Leu Val Arg Ser Met
 1130 1135 1140

Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Met	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Val	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Val	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Leu	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Val	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Ala	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Ala	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Val	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			

Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
	1370					1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
	1385					1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
	1400					1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
	1415					1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
	1430					1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
	1445					1450					1455			
Val	Glu	Glu	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
	1460					1465					1470			
Val	Leu	Met	Ala	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
	1475					1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
	1490					1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
	1505					1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
	1520					1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
	1535					1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ala	Ala	Leu	Arg	Ser	Gly
	1550					1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
	1565					1570					1575			

Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
Leu	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Lys	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Lys	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Pro
1715						1720					1725			
Val	Glu	Arg	Ser	Tyr	Ser	Arg	Trp	Ser	Leu	Trp	Pro	Ser	Val	Ala
1730						1735					1740			
Arg	Thr	Gln	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Asn	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			

Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Ser	Gly	Glu	Glu	Ser	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	Asn	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Ile	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Met	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			

Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Lys	Tyr	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Leu	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			

Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Asn	Asp	Ile	Ala
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Met	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Leu	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Met	His	Gly
2345						2350					2355			
Asp	Leu	Gly	Val	Pro	Leu	Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			

Ile	Ser	Ser	Ala	Val	Leu	Leu	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
	2450					2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
	2465					2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
	2480					2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
	2495					2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
	2510					2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
	2525					2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
	2540					2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
	2555					2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
	2570					2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	His	Gly	Lys	Val	Val
	2585					2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
	2600					2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Arg	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
	2615					2620					2625			
Gly	His	Glu	Glu	Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
	2630					2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
	2645					2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
	2660					2665					2670			

Pro	Glu	Val	Glu	Glu	Thr	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Met	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	His	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Ile	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Arg	Arg	Ile	Glu	Arg	Ile	Arg	Asn	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Leu	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Xaa	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Val	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			

Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Asn	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Arg
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ser	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Gln	Ala	Pro	Gly
3035						3040					3045			
Gly	Lys	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Lys	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Glu	Gly	His	Arg	Thr	Leu	Ala	Leu	Ala	Val	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Gly	Gly
3095						3100					3105			

Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Lys	Val	Thr	Arg	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	Tyr	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			
Ala	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3305						3310					3315			

Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Met
 3320 3325 3330

Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp
 3335 3340 3345

Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
 3350 3355 3360

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asp Thr Val Asn Met Val Arg
 3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 96
 <211> 3423
 <212> PRT
 <213> Zika virus strain ArD128000 polyprotein

<220>
 <221> misc_feature
 <222> (442)..(446)
 <223> Xaa can be any naturally occurring amino acid

<400> 96

Met Lys Asn Pro Lys Arg Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Asn Pro Leu Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile

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

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
305 310 315 320

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
325 330 335

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
340 345 350

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
355 360 365

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
370 375 380

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
385 390 395 400

Gly Ser Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr
405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
420 425 430

Val His Gly Ser Gln His Ser Gly Met Xaa Xaa Xaa Xaa Xaa Gly His
435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro
450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
485 490 495

Asn Asn Lys His Arg Leu Val Arg Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr

530					535					540					
Val 545	Val	Val	Leu	Gly	Ser 550	Gln	Glu	Gly	Ala	Val 555	His	Thr	Ala	Leu	Ala 560
Gly	Ala	Leu	Glu	Ala 565	Glu	Met	Asp	Gly	Ala 570	Lys	Gly	Arg	Leu	Phe	Ser 575
Gly	His	Leu	Lys 580	Cys	Arg	Leu	Lys	Met 585	Asp	Lys	Leu	Arg	Leu 590	Lys	Gly
Val	Ser	Tyr 595	Ser	Leu	Cys	Thr	Ala	Ala 600	Phe	Thr	Phe	Thr 605	Lys	Val	Pro
Ala	Glu 610	Thr	Leu	His	Gly	Thr 615	Val	Thr	Val	Glu	Val 620	Gln	Tyr	Ala	Gly
Thr 625	Asp	Gly	Pro	Cys	Lys 630	Val	Pro	Ala	Gln	Met 635	Ala	Val	Asp	Met	Gln 640
Thr	Leu	Thr	Pro	Val 645	Gly	Arg	Leu	Ile	Thr 650	Ala	Asn	Pro	Val	Ile 655	Thr
Glu	Ser	Thr	Glu 660	Asn	Ser	Lys	Met	Met 665	Leu	Glu	Leu	Asp	Pro 670	Pro	Phe
Gly	Asp	Ser 675	Tyr	Ile	Val	Ile	Gly 680	Val	Gly	Asp	Lys	Lys 685	Ile	Thr	His
His 690	Trp	Leu	Lys	Lys	Gly	Ser 695	Ser	Ile	Gly	Lys	Ala 700	Phe	Glu	Ala	Thr
Val 705	Arg	Gly	Ala	Lys	Arg 710	Met	Ala	Val	Leu	Gly 715	Asp	Thr	Ala	Trp	Asp 720
Phe	Gly	Ser	Val	Gly 725	Gly	Val	Phe	Asn	Ser 730	Leu	Gly	Lys	Gly	Val 735	His
Gln	Ile	Phe	Gly 740	Ala	Ala	Phe	Lys	Ser 745	Leu	Phe	Gly	Gly	Met 750	Ser	Trp
Phe	Ser	Gln 755	Ile	Leu	Ile	Gly	Thr 760	Leu	Leu	Val	Trp	Leu 765	Gly	Leu	Asn

Thr Lys Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val
770 775 780

Met Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Glu Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Lys Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Ile Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Ala His Ser Asp Leu
980 985 990

Cys Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Arg Arg

995						1000					1005			
Ala	His	Leu	Ile	Glu	Met	Lys	Thr	Cys	Glu	Trp	Pro	Lys	Ser	His
1010						1015					1020			
Thr	Leu	Trp	Thr	Asp	Gly	Val	Glu	Glu	Ser	Asp	Leu	Ile	Ile	Pro
1025						1030					1035			
Lys	Ser	Leu	Ala	Gly	Pro	Leu	Ser	His	His	Asn	Thr	Arg	Glu	Gly
1040						1045					1050			
Tyr	Arg	Thr	Gln	Val	Lys	Gly	Pro	Trp	His	Ser	Glu	Glu	Leu	Glu
1055						1060					1065			
Ile	Arg	Phe	Glu	Glu	Cys	Pro	Gly	Thr	Lys	Val	Tyr	Val	Glu	Glu
1070						1075					1080			
Thr	Cys	Gly	Thr	Arg	Gly	Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser
1085						1090					1095			
Gly	Arg	Val	Ile	Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro
1100						1105					1110			
Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu
1115						1120					1125			
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met
1130						1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Met	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Val	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Val	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			

Asp	Val	Ala	His	Leu	Ala	Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Glu	Leu	Met	Val	Leu	Val	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Ala	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Ala	Leu	Ala	Thr	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Ala	Ala	Val	Arg
1340						1345					1350			
Ile	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser

1430						1435						1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu	
1445						1450					1455				
Val	Glu	Glu	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val	
1460						1465					1470				
Val	Leu	Met	Ala	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe	
1475						1480					1485				
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser	
1490						1495					1500				
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly	
1505						1510					1515				
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu	
1520						1525					1530				
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe	
1535						1540					1545				
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ala	Ala	Leu	Arg	Ser	Gly	
1550						1555					1560				
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu	
1565						1570					1575				
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Thr	Trp	Asp	Gly	
1580						1585					1590				
Leu	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala	
1595						1600					1605				
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly	
1610						1615					1620				
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly	
1625						1630					1635				
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly	
1640						1645					1650				

Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Lys	Arg	Glu	Glu	Glu	Ala	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Arg	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Lys	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Asn	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Ile	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu

1865						1870						1875			
Thr Lys	Ala Gly	Lys Arg	Val	Ile Gln	Leu Ser	Arg	Lys Thr	Phe							
1880			1885			1890									
Glu Thr	Glu Phe	Gln Lys	Thr	Lys Asn	Gln Glu	Trp	Asp Phe	Val							
1895			1900			1905									
Ile Thr	Thr Asp	Ile Ser	Glu	Met Gly	Ala Asn	Phe	Lys Ala	Asp							
1910			1915			1920									
Arg Val	Ile Asp	Ser Arg	Arg	Cys Leu	Lys Pro	Val	Ile Leu	Asp							
1925			1930			1935									
Gly Glu	Arg Val	Ile Leu	Ala	Gly Pro	Met Pro	Val	Thr His	Ala							
1940			1945			1950									
Ser Ala	Ala Gln	Arg Arg	Gly	Arg Ile	Gly Arg	Asn	Pro Asn	Lys							
1955			1960			1965									
Pro Gly	Asp Glu	Tyr Met	Tyr	Gly Gly	Gly Cys	Ala	Glu Thr	Asp							
1970			1975			1980									
Glu Asp	His Ala	His Trp	Leu	Glu Ala	Arg Met	Leu	Leu Asp	Asn							
1985			1990			1995									
Ile Tyr	Leu Gln	Asp Gly	Leu	Ile Ala	Ser Leu	Tyr	Arg Pro	Glu							
2000			2005			2010									
Ala Asp	Lys Val	Ala Ala	Ile	Glu Gly	Glu Phe	Lys	Leu Arg	Thr							
2015			2020			2025									
Glu Gln	Arg Lys	Thr Phe	Val	Glu Leu	Met Lys	Arg	Gly Asp	Leu							
2030			2035			2040									
Pro Val	Trp Leu	Ala Tyr	Gln	Val Ala	Ser Ala	Gly	Ile Thr	Tyr							
2045			2050			2055									
Thr Asp	Arg Arg	Trp Cys	Phe	Asp Gly	Thr Thr	Asn	Asn Thr	Ile							
2060			2065			2070									
Met Glu	Asp Ser	Val Pro	Ala	Glu Val	Trp Thr	Lys	Tyr Gly	Glu							
2075			2080			2085									

Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Leu	Gly	Val	Met	Asp	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Ile	Ala
2270						2275					2280			
Tyr	Leu	Met	Gly	Arg	Lys	Glu	Glu	Gly	Thr	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala

2300		2305		2310
Ala Leu Thr Thr Leu Ile Thr	Pro Ala Val Gln His	Ala Val Thr		
2315	2320	2325		
Thr Ser Tyr Asn Asn Tyr Ser	Leu Met Ala Met Ala	Thr Gln Ala		
2330	2335	2340		
Gly Val Leu Phe Gly Met Gly	Lys Gly Met Pro Phe	Tyr Ala Trp		
2345	2350	2355		
Asp Phe Gly Val Pro Leu Leu	Met Ile Gly Cys Tyr	Ser Gln Leu		
2360	2365	2370		
Thr Pro Leu Thr Leu Ile Val	Ala Ile Ile Leu Leu	Val Ala His		
2375	2380	2385		
Tyr Met Tyr Leu Ile Pro Gly	Leu Gln Ala Ala Ala	Ala Arg Ala		
2390	2395	2400		
Ala Gln Lys Arg Thr Ala Ala	Gly Ile Met Lys Asn	Pro Val Val		
2405	2410	2415		
Asp Gly Ile Val Val Thr Asp	Ile Asp Thr Met Thr	Ile Asp Pro		
2420	2425	2430		
Gln Val Glu Lys Lys Met Gly	Gln Val Leu Leu Ile	Ala Val Ala		
2435	2440	2445		
Val Ser Ser Ala Val Leu Leu	Arg Thr Ala Gly Gly	Trp Gly Glu		
2450	2455	2460		
Ala Gly Ala Leu Ile Thr Ala	Ala Thr Ser Thr Leu	Trp Glu Gly		
2465	2470	2475		
Ser Pro Asn Lys Tyr Trp Asn	Ser Ser Thr Ala Thr	Ser Leu Cys		
2480	2485	2490		
Asn Ile Phe Arg Gly Ser Tyr	Leu Ala Gly Ala Ser	Leu Ile Tyr		
2495	2500	2505		
Thr Val Thr Arg Asn Ala Gly	Leu Val Lys Arg Arg	Gly Gly Gly		
2510	2515	2520		

Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
	2525					2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
	2540					2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
	2555					2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
	2570					2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	His	Gly	Lys	Val	Val
	2585					2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
	2600					2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Arg	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
	2615					2620					2625			
Gly	His	Glu	Glu	Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
	2630					2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
	2645					2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
	2660					2665					2670			
Pro	Glu	Val	Glu	Glu	Thr	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
	2675					2680					2685			
Glu	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
	2690					2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Met	Glu	Arg	Leu
	2705					2710					2715			
Gln	Arg	Arg	His	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
	2720					2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn

2735						2740						2745			
Ile	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg	
2750						2755					2760				
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn	
2765						2770					2775				
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro	
2780						2785					2790				
Asn	Met	Lys	Ile	Ile	Gly	Arg	Arg	Ile	Glu	Arg	Ile	Arg	Asn	Glu	
2795						2800					2805				
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr	
2810						2815					2820				
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala	
2825						2830					2835				
Ser	Ser	Leu	Val	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp	
2840						2845					2850				
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr	
2855						2860					2865				
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg	
2870						2875					2880				
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Asn	Ile	Val	
2885						2890					2895				
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg	
2900						2905					2910				
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala	
2915						2920					2925				
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	
2930						2935					2940				
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys	
2945						2950					2955				

Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Ile	Leu	Glu	Glu	Met	Asn	Arg	Ala	Pro	Gly
3035						3040					3045			
Gly	Lys	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Lys	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Glu	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Val	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Gly	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
His	Asp	Leu	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Lys	Val	Thr	Arg	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser

3170							3175								3180
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His	
3185						3190					3195				
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr	
3200						3205					3210				
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val	
3215						3220					3225				
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly	
3230						3235					3240				
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly	
3245						3250					3255				
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr	
3260						3265					3270				
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr	
3275						3280					3285				
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser	
3290						3295					3300				
Ala	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser	
3305						3310					3315				
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Met	
3320						3325					3330				
Val	Trp	Asn	Arg	Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp	
3335						3340					3345				
Lys	Thr	Pro	Val	Pro	Lys	Trp	Thr	Glu	Ile	Pro	Tyr	Leu	Gly	Lys	
3350						3355					3360				
Arg	Glu	Ser	Leu	Trp	Cys	Gly	Tyr	Ile	Ile	Gly	His	Arg	Pro	Arg	
3365						3370					3375				
Thr	Thr	Trp	Ala	Glu	Asn	Ile	Lys	Asp	Thr	Val	Asn	Met	Val	Leu	
3380						3385					3390				

Arg Leu Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 97
 <211> 3423
 <212> PRT
 <213> Zika virus strain ArD7117 polyprotein

<220>
 <221> misc_feature
 <222> (1437)..(1437)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (1742)..(1742)
 <223> Xaa can be any naturally occurring amino acid

<400> 97

Met Lys Asn Pro Lys Lys Arg Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Asn Pro Leu Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

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

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Ile Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Ser Asp Ala Gly Lys Ala
130 135 140

Ile Ser Phe Ala Thr Thr Leu Gly Val Asn Lys Cys His Val Gln Ile
145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys Gln His Lys Lys Gly
195 200 205

Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
210 215 220

Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr
225 230 235 240

Thr Lys His Leu Ile Lys Val Glu Asn Trp Ile Phe Arg Asn Pro Gly
245 250 255

Phe Ala Leu Val Ala Val Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr
260 265 270

Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
275 280 285

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
290 295 300

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
305 310 315 320

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
325 330 335

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
340 345 350

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly

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

Val Ser Tyr Ser Leu Cys Thr Ala Val Cys Thr Ala Ala Lys Val Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val
770 775 780

Met Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser

820	825	830
Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Glu Gly Ile		
835	840	845
Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Lys Ser		
850	855	860
Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu		
865	870	875
Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln		
	885	890
Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp		
	900	905
Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val		
	915	920
Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp		
	930	935
Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Ile Phe His Thr Ser		
945	950	955
Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala		
	965	970
Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Ala His Ser Asp Leu		
	980	985
Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Arg Arg		
	995	1000
Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His		
	1010	1015
Thr Leu Trp Thr Asp Gly Val Glu Glu Ser Asp Leu Ile Ile Pro		
	1025	1030
Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly		
	1040	1045
		1050

Tyr	Arg	Thr	Gln	Val	Lys	Gly	Pro	Trp	His	Ser	Glu	Glu	Leu	Glu
1055						1060					1065			
Ile	Arg	Phe	Glu	Glu	Cys	Pro	Gly	Thr	Lys	Val	His	Val	Glu	Glu
1070						1075					1080			
Thr	Cys	Gly	Thr	Arg	Gly	Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser
1085						1090					1095			
Gly	Arg	Val	Ile	Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro
1100						1105					1110			
Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu
1115						1120					1125			
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met
1130						1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Met	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Val	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Val	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Glu	Leu	Met	Val	Leu	Val	Asn	Gly	Phe

1265		1270		1275
Ala Leu Ala Trp Leu Ala Ile Arg Ala Met Ala Val Pro Arg Thr				
1280		1285		1290
Asp Asn Ile Ala Leu Ala Ile Leu Ala Ala Leu Thr Pro Leu Ala				
1295		1300		1305
Arg Gly Thr Leu Leu Val Ala Trp Arg Ala Gly Leu Ala Thr Cys				
1310		1315		1320
Gly Gly Phe Met Leu Leu Ser Leu Lys Gly Lys Gly Ser Val Lys				
1325		1330		1335
Lys Asn Leu Pro Phe Val Met Ala Leu Gly Leu Thr Ala Val Arg				
1340		1345		1350
Ile Val Asp Pro Ile Asn Val Val Gly Leu Leu Leu Leu Thr Arg				
1355		1360		1365
Ser Gly Lys Arg Ser Trp Pro Pro Ser Glu Val Leu Thr Ala Val				
1370		1375		1380
Gly Leu Ile Cys Ala Leu Ala Gly Gly Phe Ala Lys Ala Asp Ile				
1385		1390		1395
Glu Met Ala Gly Pro Met Ala Ala Val Gly Leu Leu Ile Val Ser				
1400		1405		1410
Tyr Val Val Ser Gly Lys Ser Val Asp Met Tyr Ile Glu Arg Ala				
1415		1420		1425
Gly Asp Ile Thr Trp Glu Lys Asp Xaa Glu Val Thr Gly Asn Ser				
1430		1435		1440
Pro Arg Leu Asp Val Ala Leu Asp Glu Ser Gly Asp Phe Ser Leu				
1445		1450		1455
Val Glu Glu Asp Gly Pro Pro Met Arg Glu Ile Ile Leu Lys Val				
1460		1465		1470
Val Leu Met Ala Ile Cys Gly Met Asn Pro Ile Ala Ile Pro Phe				
1475		1480		1485

Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ala	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
Leu	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Lys	Arg	Glu	Glu	Glu	Ala	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Arg	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu

1700		1705		1710
Ala Ile Lys Lys Arg Leu Arg Thr Leu Ile Leu Ala Pro Thr Arg				
1715		1720		1725
Val Val Ala Ala Glu Met Glu Glu Ala Leu Arg Gly Leu Xaa Val				
1730		1735		1740
Arg Tyr Met Thr Thr Ala Val Asn Val Thr His Ser Gly Thr Glu				
1745		1750		1755
Ile Val Asp Leu Met Cys His Ala Thr Phe Thr Ser Arg Leu Leu				
1760		1765		1770
Gln Pro Ile Arg Val Pro Asn Tyr Asn Leu Asn Ile Met Asp Glu				
1775		1780		1785
Ala His Phe Thr Asp Pro Ser Ser Ile Ala Ala Arg Gly Tyr Ile				
1790		1795		1800
Ser Thr Arg Val Glu Met Gly Glu Ala Ala Ala Ile Phe Met Thr				
1805		1810		1815
Ala Thr Pro Pro Gly Thr Arg Asp Ala Phe Pro Asp Ser Asn Ser				
1820		1825		1830
Pro Ile Met Asp Thr Glu Val Glu Val Pro Glu Arg Ala Trp Ser				
1835		1840		1845
Ser Gly Phe Asp Trp Val Thr Asp His Ser Gly Lys Thr Ile Trp				
1850		1855		1860
Phe Val Pro Ser Val Arg Ser Gly Glu Glu Ser Ala Ala Cys Leu				
1865		1870		1875
Thr Lys Ala Gly Lys Arg Val Ile Gln Leu Ser Arg Lys Thr Phe				
1880		1885		1890
Glu Thr Glu Phe Gln Lys Thr Lys Asn Gln Glu Trp Asp Phe Val				
1895		1900		1905
Ile Thr Thr Asp Ile Ser Glu Met Gly Ala Asn Phe Lys Ala Asp				
1910		1915		1920

Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Met	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Lys	Tyr	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Leu	Gly	Val	Met	Asp	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala

2135		2140		2145
Val Leu Met Arg Ala Glu Thr Gly Ser Arg Pro Tyr Lys Ala Ala				
2150		2155		2160
Ala Ala Gln Leu Pro Glu Thr Leu Glu Thr Ile Met Leu Leu Gly				
2165		2170		2175
Leu Leu Gly Thr Val Ser Leu Gly Ile Phe Phe Val Leu Met Arg				
2180		2185		2190
Asn Lys Gly Ile Gly Lys Met Gly Phe Gly Met Val Thr Leu Gly				
2195		2200		2205
Ala Ser Ala Trp Leu Met Trp Leu Ser Glu Ile Glu Pro Ala Arg				
2210		2215		2220
Ile Ala Cys Val Leu Ile Val Val Phe Leu Leu Leu Val Val Leu				
2225		2230		2235
Ile Pro Glu Pro Glu Lys Gln Arg Ser Pro Gln Asp Asn Gln Met				
2240		2245		2250
Ala Ile Ile Ile Met Val Ala Val Gly Leu Leu Gly Leu Ile Thr				
2255		2260		2265
Ala Asn Glu Leu Gly Trp Leu Glu Arg Thr Lys Ser Asp Ile Ala				
2270		2275		2280
His Leu Met Gly Arg Lys Glu Glu Gly Thr Thr Ile Gly Phe Ser				
2285		2290		2295
Met Asp Ile Asp Leu Arg Pro Ala Ser Ala Trp Ala Ile Tyr Ala				
2300		2305		2310
Ala Leu Thr Thr Leu Ile Thr Pro Ala Val Gln His Ala Val Thr				
2315		2320		2325
Thr Ser Tyr Asn Asn Tyr Ser Leu Met Ala Met Ala Thr Gln Ala				
2330		2335		2340
Gly Val Leu Phe Gly Met Gly Lys Gly Met Pro Phe Tyr Ala Trp				
2345		2350		2355

Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu
	2360					2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
	2375					2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
	2390					2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
	2405					2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
	2420					2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
	2435					2440					2445			
Val	Ser	Ser	Ala	Val	Leu	Leu	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
	2450					2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
	2465					2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
	2480					2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
	2495					2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
	2510					2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
	2525					2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
	2540					2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
	2555					2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg

2570							2575								2580
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	His	Gly	Lys	Val	Val	
2585						2590					2595				
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr	
2600						2605					2610				
Ile	Arg	Lys	Val	Gln	Glu	Val	Arg	Gly	Tyr	Thr	Lys	Gly	Gly	Pro	
2615						2620					2625				
Gly	His	Glu	Glu	Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile	
2630						2635					2640				
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu	
2645						2650					2655				
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser	
2660						2665					2670				
Pro	Glu	Val	Glu	Glu	Thr	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val	
2675						2680					2685				
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val	
2690						2695					2700				
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Met	Glu	Arg	Leu	
2705						2710					2715				
Gln	Arg	Arg	His	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg	
2720						2725					2730				
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn	
2735						2740					2745				
Ile	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg	
2750						2755					2760				
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn	
2765						2770					2775				
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro	
2780						2785					2790				

Asn	Met	Lys	Ile	Ile	Gly	Arg	Arg	Ile	Glu	Arg	Ile	Arg	Asn	Glu
	2795					2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
	2810					2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
	2825					2830					2835			
Ser	Ser	Leu	Val	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
	2840					2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
	2855					2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
	2870					2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Asn	Met	Val
	2885					2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg
	2900					2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
	2915					2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
	2930					2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
	2945					2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr
	2960					2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
	2975					2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
	2990					2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp

3005						3010					3015				
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu	
	3020					3025					3030				
Gln	Arg	Leu	Gly	Tyr	Ile	Leu	Glu	Glu	Met	Asn	Arg	Ala	Pro	Gly	
	3035					3040					3045				
Gly	Lys	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile	
	3050					3055					3060				
Ser	Lys	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met	
	3065					3070					3075				
Glu	Glu	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Val	Ile	Lys	Tyr	Thr	
	3080					3085					3090				
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Gly	Gly	
	3095					3100					3105				
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser	
	3110					3115					3120				
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val	
	3125					3130					3135				
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met	
	3140					3145					3150				
His	Asp	Leu	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Lys	Val	Thr	Arg	Trp	
	3155					3160					3165				
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser	
	3170					3175					3180				
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His	
	3185					3190					3195				
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr	
	3200					3205					3210				
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val	
	3215					3220					3225				

Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
	3230					3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
	3245					3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
	3260					3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
	3275					3280					3285			
Phe	His	Lys	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
	3290					3295					3300			
Ala	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
	3305					3310					3315			
Ile	His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Met
	3320					3325					3330			
Val	Trp	Asn	Arg	Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp
	3335					3340					3345			
Lys	Thr	Pro	Val	Thr	Lys	Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys
	3350					3355					3360			
Arg	Glu	Asp	Leu	Trp	Cys	Gly	Ser	Leu	Ile	Gly	His	Arg	Pro	Arg
	3365					3370					3375			
Thr	Thr	Trp	Ala	Glu	Asn	Ile	Lys	Asp	Thr	Val	Asn	Met	Val	Arg
	3380					3385					3390			
Arg	Ile	Ile	Gly	Asp	Glu	Glu	Lys	Tyr	Met	Asp	Tyr	Leu	Ser	Thr
	3395					3400					3405			
Gln	Val	Arg	Tyr	Leu	Gly	Glu	Glu	Gly	Ser	Thr	Pro	Gly	Val	Leu
	3410					3415					3420			

<210> 98
 <211> 3423
 <212> PRT
 <213> Zika virus strain ArB1362 polyprotein

<220>
 <221> misc_feature
 <222> (446)..(452)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (1742)..(1742)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (2983)..(2983)
 <223> Xaa can be any naturally occurring amino acid

<400> 98

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Asn Pro Leu Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

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

Ile Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Ile Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Ser Asp Ala Gly Lys Ala
 130 135 140

Ile Ser Phe Ala Thr Thr Leu Gly Val Asn Lys Cys His Val Gln Ile
 145 150 155 160

Met	Asp	Leu	Gly	His	Met	Cys	Asp	Ala	Thr	Met	Ser	Tyr	Glu	Cys	Pro	
				165					170					175		
Met	Leu	Asp	Glu	Gly	Val	Glu	Pro	Asp	Asp	Val	Asp	Cys	Trp	Cys	Asn	
			180					185					190			
Thr	Thr	Ser	Thr	Trp	Val	Val	Tyr	Gly	Thr	Cys	His	His	Lys	Lys	Gly	
		195					200					205				
Glu	Ala	Arg	Arg	Ser	Arg	Arg	Ala	Val	Thr	Leu	Pro	Ser	His	Ser	Thr	
	210					215					220					
Arg	Lys	Leu	Gln	Thr	Arg	Ser	Gln	Thr	Trp	Leu	Glu	Ser	Arg	Glu	Tyr	
225					230					235					240	
Thr	Lys	His	Leu	Ile	Lys	Val	Glu	Asn	Trp	Ile	Phe	Arg	Asn	Pro	Gly	
				245					250					255		
Phe	Ala	Leu	Ala	Ala	Val	Ala	Ile	Ala	Trp	Leu	Leu	Gly	Ser	Ser	Thr	
			260					265					270			
Ser	Gln	Lys	Val	Ile	Tyr	Leu	Ile	Met	Ile	Leu	Leu	Ile	Ala	Pro	Ala	
		275					280					285				
Tyr	Ser	Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	
	290					295					300					
Met	Ser	Gly	Gly	Thr	Trp	Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys	
305					310					315					320	
Val	Thr	Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val	
				325					330					335		
Thr	Thr	Thr	Val	Ser	Asn	Met	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Glu	
			340					345					350			
Ala	Ser	Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	Gly	
		355					360					365				
Glu	Ala	Tyr	Leu	Asp	Lys	Gln	Ser	Asp	Thr	Gln	Tyr	Val	Cys	Lys	Arg	
	370					375					380					
Thr	Leu	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	
385					390					395					400	

Gly Ser Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr
405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Xaa Xaa Xaa
435 440 445

Xaa Xaa Xaa Xaa Asn Arg Ala Glu Val Glu Val Thr Pro Asn Ser Pro
450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val
770 775 780

Met Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Arg Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Glu Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Lys Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Ala His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Val Glu Glu Ser Asp Leu Ile Ile Pro
1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
1040 1045 1050

Tyr Arg Thr Gln Ala Lys Gly Pro Trp His Ser Glu Glu Leu Glu
1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
1070 1075 1080

Thr	Cys	Gly	Thr	Arg	Gly	Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser
1085						1090					1095			
Gly	Arg	Val	Ile	Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro
1100						1105					1110			
Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu
1115						1120					1125			
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met
1130						1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Val	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Val	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Val	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Ala	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Ala	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			

Arg Gly	Thr Leu Leu Val	Ala	Trp Arg Ala Gly	Leu	Ala Thr Cys
1310		1315		1320	
Gly Gly	Phe Met Leu Leu Ser	Leu Lys Gly Lys	Gly	Ser Val Lys	
1325		1330		1335	
Lys Asn	Leu Pro Phe Val Met	Ala Leu Gly Met	Thr	Ala Val Arg	
1340		1345		1350	
Ile Val	Asp Pro Ile Asn Val	Val Gly Leu Leu	Leu	Leu Thr Arg	
1355		1360		1365	
Ser Gly	Lys Arg Ser Trp Pro	Pro Ser Glu Val	Leu	Thr Ala Val	
1370		1375		1380	
Gly Leu	Ile Cys Ala Leu Ala	Gly Gly Phe Ala	Lys	Ala Asp Ile	
1385		1390		1395	
Glu Met	Ala Gly Pro Met Ala	Ala Val Gly Leu	Leu	Ile Val Ser	
1400		1405		1410	
Tyr Val	Val Ser Gly Lys Ser	Val Asp Met Tyr	Ile	Glu Arg Ala	
1415		1420		1425	
Gly Asp	Ile Thr Trp Glu Lys	Asp Ala Glu Val	Thr	Gly Asn Ser	
1430		1435		1440	
Pro Arg	Leu Asp Val Ala Leu	Asp Glu Ser Gly	Asp	Phe Ser Leu	
1445		1450		1455	
Val Glu	Glu Asp Gly Pro Pro	Met Arg Glu Ile	Ile	Leu Lys Val	
1460		1465		1470	
Val Leu	Met Ala Ile Cys Gly	Met Asn Pro Ile	Ala	Ile Pro Phe	
1475		1480		1485	
Ala Ala	Gly Ala Trp Tyr Val	Tyr Val Lys Thr	Gly	Lys Arg Ser	
1490		1495		1500	
Gly Ala	Leu Trp Asp Val Pro	Ala Pro Lys Glu	Val	Lys Lys Gly	
1505		1510		1515	

Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ala	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
Leu	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Lys	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Lys	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Xaa	Val
1730						1735					1740			

Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Asn	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Thr	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	Asn	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Ile	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			

Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Met	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Lys	Tyr	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Leu	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Pro	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			

Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Asn	Asp	Ile	Ala
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Val	Thr	Met	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Leu	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			

Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Ile	Ser	Ser	Ala	Val	Leu	Leu	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
2510						2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
2525						2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	His	Gly	Lys	Val	Val
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			

Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Thr	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Met	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Ile	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Lys	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			

Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Val	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Thr	Met	Asn	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Xaa	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ser	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Ile	Leu	Glu	Glu	Met	Asn	Arg	Ala	Pro	Gly
3035						3040					3045			

Gly	Lys	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Lys	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Glu	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Val	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Gly	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Lys	Val	Thr	Arg	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	Cys
3185						3190					3195			
Cys	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			

Arg Ala Arg Val Ser Pro Gly Ala Gly Trp Ser Ile Arg Glu Thr
 3260 3265 3270
 Ala Cys Leu Ala Lys Ser Tyr Ala Gln Met Trp Gln Leu Leu Tyr
 3275 3280 3285
 Phe His Arg Arg Asp Leu Arg Leu Met Ala Asn Ala Ile Cys Ser
 3290 3295 3300
 Ala Val Pro Val Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser
 3305 3310 3315
 Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Met
 3320 3325 3330
 Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp
 3335 3340 3345
 Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
 3350 3355 3360
 Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375
 Thr Thr Trp Ala Glu Asn Ile Lys Asp Thr Val Asn Met Val Arg
 3380 3385 3390
 Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405
 Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 99
 <211> 3423
 <212> PRT
 <213> ZIKA VIRUS POLYPROTEIN GENBANK: EU545988.1

<220>
 <221> misc_feature
 <222> (845)..(845)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (2121)..(2121)

<223> Xaa can be any naturally occurring amino acid

<400> 99

Met Lys Asn Pro Lys Glu Glu Ile Arg Arg Ile Arg Ile Val Asn Met
1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Thr Asp Thr Ser Val Gly Ile
100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Val Glu Val Thr Arg Arg
115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Ser Asp Ala Gly Glu Ala
130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
195 200 205

Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
210 215 220

Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr
 225 230 235 240

Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly
 245 250 255

Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr
 260 265 270

Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
 275 280 285

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
 290 295 300

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
 305 310 315 320

Val Thr Val Met Ala Gln Asp Lys Pro Ala Val Asp Ile Glu Leu Val
 325 330 335

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
 340 345 350

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
 355 360 365

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
 370 375 380

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
 385 390 395 400

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
 405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
 420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
 435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
 450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
 465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
 485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
 500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
 515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
 530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
 545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
 565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
 580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
 595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
 610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
 625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
 645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
 660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
 675 680 685

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

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
 915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
 930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
 945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
 965 970 975

Val Ile Gly Thr Ala Ala Lys Gly Lys Glu Ala Val His Ser Asp Leu
 980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
 995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
 1010 1015 1020

Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro
 1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
 1040 1045 1050

Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu
 1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
 1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
 1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
 1100 1105 1110

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu
 1115 1120 1125

Ile Arg Pro Arg Lys Glu Pro Glu Ser Asn Leu Val Arg Ser Met
 1130 1135 1140

Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Thr	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			

Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
1460						1465					1470			
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			

Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Pro	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			

Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Leu	Lys	Thr	Lys	Asn	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			

Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Lys	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	Tyr	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Xaa	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Glu	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			

Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Ile	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	His
2420						2425					2430			
Arg	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			

Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
	2450					2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
	2465					2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
	2480					2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
	2495					2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
	2510					2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
	2525					2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
	2540					2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
	2555					2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
	2570					2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
	2585					2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
	2600					2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
	2615					2620					2625			
Gly	His	Glu	Glu	Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
	2630					2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
	2645					2650					2655			

Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
	2660					2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
	2675					2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
	2690					2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
	2705					2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
	2720					2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
	2735					2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
	2750					2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
	2765					2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
	2780					2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
	2795					2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
	2810					2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
	2825					2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
	2840					2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
	2855					2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
	2870					2875					2880			

Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			

Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser
3290						3295					3300			
Ser	Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser
3305						3310					3315			

Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val
 3320 3325 3330

Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp
 3335 3340 3345

Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
 3350 3355 3360

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Met Arg
 3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 100

<211> 3423

<212> PRT

<213> Zika virus isolate Zika virus/H.sapiens-tc/PHL/2012/CPC-0740

<400> 100

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn

85

90

95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
 100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Val Glu Val Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Ser Asp Ala Gly Glu Ala
 130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
 145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
 165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
 180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
 195 200 205

Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
 210 215 220

Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr
 225 230 235 240

Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe Arg Asn Pro Gly
 245 250 255

Phe Ala Leu Ala Ala Ala Val Ile Ala Trp Leu Leu Gly Ser Ser Thr
 260 265 270

Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala
 275 280 285

Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly
 290 295 300

Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys
 305 310 315 320

Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val
325 330 335

Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu
340 345 350

Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly
355 360 365

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
370 375 380

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
385 390 395 400

Gly Ser Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr
405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala

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

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Ala Lys Gly Lys Glu Ala Val His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His

1010						1015					1020			
Thr	Leu	Trp	Thr	Asp	Gly	Val	Glu	Glu	Ser	Asp	Leu	Ile	Ile	Pro
1025						1030					1035			
Lys	Ser	Leu	Ala	Gly	Pro	Leu	Ser	His	His	Asn	Thr	Arg	Glu	Gly
1040						1045					1050			
Tyr	Arg	Thr	Gln	Met	Lys	Gly	Pro	Trp	His	Ser	Glu	Glu	Leu	Glu
1055						1060					1065			
Ile	Arg	Phe	Glu	Glu	Cys	Pro	Gly	Thr	Lys	Val	His	Val	Glu	Glu
1070						1075					1080			
Thr	Cys	Gly	Thr	Arg	Gly	Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser
1085						1090					1095			
Gly	Arg	Val	Ile	Glu	Glu	Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro
1100						1105					1110			
Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu
1115						1120					1125			
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met
1130						1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Ile	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			

Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			
Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
1325						1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Ile	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu

1445						1450						1455			
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val	
1460						1465					1470				
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe	
1475						1480					1485				
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser	
1490						1495					1500				
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly	
1505						1510					1515				
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu	
1520						1525					1530				
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe	
1535						1540					1545				
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly	
1550						1555					1560				
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu	
1565						1570					1575				
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly	
1580						1585					1590				
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala	
1595						1600					1605				
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Thr	Phe	Lys	Thr	Lys	Asp	Gly	
1610						1615					1620				
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly	
1625						1630					1635				
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly	
1640						1645					1650				
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr	
1655						1660					1665				

Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
	1670					1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
	1685					1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
	1700					1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
	1715					1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
	1730					1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
	1745					1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
	1760					1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
	1775					1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
	1790					1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
	1805					1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
	1820					1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
	1835					1840					1845			
Thr	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
	1850					1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
	1865					1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe

1880						1885						1890			
Glu Thr 1895	Glu Phe	Gln Lys				Thr Lys	Asn Gln	Glu Trp	Asp Phe	Val					
Val Thr 1910	Thr Asp	Ile Ser				Glu Met	Gly Ala	Asn Phe	Lys Ala	Asp					
Arg Val 1925	Ile Asp	Ser Arg				Arg Cys	Leu Lys	Pro Val	Ile Leu	Asp					
Gly Glu 1940	Arg Val	Ile Leu				Ala Gly	Pro Met	Pro Val	Thr His	Ala					
Ser Ala 1955	Ala Gln	Arg Arg				Gly Arg	Ile Gly	Arg Asn	Pro Asn	Lys					
Pro Gly 1970	Asp Glu	Tyr Leu				Tyr Gly	Gly Gly	Cys Ala	Glu Thr	Asp					
Glu Asp 1985	His Ala	His Trp				Leu Glu	Ala Arg	Met Leu	Leu Asp	Asn					
Ile Tyr 2000	Leu Gln	Asp Gly				Leu Ile	Ala Ser	Leu Tyr	Arg Pro	Glu					
Ala Asp 2015	Lys Val	Ala Ala				Ile Glu	Gly Glu	Phe Lys	Leu Arg	Thr					
Glu Gln 2030	Arg Lys	Thr Phe				Val Glu	Leu Met	Lys Arg	Gly Asp	Leu					
Pro Val 2045	Trp Leu	Ala Tyr				Gln Val	Ala Ser	Ala Gly	Ile Thr	Tyr					
Thr Asp 2060	Arg Arg	Trp Cys				Phe Asp	Gly Met	Thr Asn	Asn Thr	Ile					
Met Glu 2075	Asp Ser	Val Pro				Ala Glu	Val Trp	Thr Arg	Tyr Gly	Glu					
Lys Arg 2090	Val Leu	Lys Pro				Arg Trp	Met Asp	Ala Arg	Val Cys	Ser					

Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Ile	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			
Asn	Lys	Gly	Met	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Thr	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr

2315						2320						2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala	
2330						2335					2340				
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp	
2345						2350					2355				
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu	
2360						2365					2370				
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His	
2375						2380					2385				
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala	
2390						2395					2400				
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val	
2405						2410					2415				
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro	
2420						2425					2430				
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala	
2435						2440					2445				
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu	
2450						2455					2460				
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly	
2465						2470					2475				
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys	
2480						2485					2490				
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr	
2495						2500					2505				
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly	
2510						2515					2520				
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln	
2525						2530					2535				

Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			
Gly	His	Glu	Glu	Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg

2750						2755						2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn	
	2765					2770						2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro	
	2780					2785						2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu	
	2795					2800						2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr	
	2810					2815					2820				
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala	
	2825					2830					2835				
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp	
	2840					2845					2850				
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr	
	2855					2860					2865				
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg	
	2870					2875					2880				
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val	
	2885					2890					2895				
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg	
	2900					2905					2910				
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala	
	2915					2920					2925				
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	
	2930					2935					2940				
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys	
	2945					2950					2955				
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr	
	2960					2965					2970				

Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Pro	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His

3185		3190		3195
Ala Leu Arg Phe Leu Asn Asp Met Gly Lys Val Arg Lys Asp Thr				
3200		3205		3210
Gln Glu Trp Lys Pro Ser Thr Gly Trp Asp Asn Trp Glu Glu Val				
3215		3220		3225
Pro Phe Cys Ser His His Phe Asn Lys Leu His Leu Lys Asp Gly				
3230		3235		3240
Arg Ser Ile Val Val Pro Cys Arg His Gln Asp Glu Leu Ile Gly				
3245		3250		3255
Arg Ala Arg Val Ser Pro Gly Ala Gly Trp Ser Ile Arg Glu Thr				
3260		3265		3270
Ala Cys Leu Ala Lys Ser Tyr Ala Gln Met Trp Gln Leu Leu Tyr				
3275		3280		3285
Phe His Arg Arg Asp Leu Arg Leu Met Ala Asn Ala Ile Cys Ser				
3290		3295		3300
Ser Val Pro Val Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser				
3305		3310		3315
Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val				
3320		3325		3330
Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp				
3335		3340		3345
Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys				
3350		3355		3360
Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg				
3365		3370		3375
Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Met Arg				
3380		3385		3390
Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr				
3395		3400		3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 101

<211> 3423

<212> PRT

<213> Zika virus isolate Zika virus/H.sapiens-tc/THA/2014/SV0127- 14

<400> 101

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Thr Asp Thr Ser Val Gly Ile
 100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Ser Asp Ala Gly Glu Ala
 130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
 145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
 165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
 180 185 190

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

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Thr Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Gly Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Val Leu Asn Ser Leu Gly Lys Gly Ile His
725 730 735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val
770 775 780

Leu Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Lys Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Val Val Lys Gln Ala Trp Glu Asp Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Arg Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
 885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
 900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
 915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
 930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
 945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
 965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu
 980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Arg Arg
 995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
 1010 1015 1020

Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro
 1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
 1040 1045 1050

Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu
 1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
 1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
 1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
 1100 1105 1110

Pro	Leu	Ser	Phe	Arg	Ala	Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu
1115						1120					1125			
Ile	Arg	Pro	Arg	Lys	Glu	Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met
1130						1135					1140			
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly
1145						1150					1155			
Val	Leu	Val	Ile	Leu	Leu	Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg
1160						1165					1170			
Met	Thr	Thr	Lys	Ile	Ile	Ile	Ser	Thr	Ser	Met	Ala	Val	Leu	Val
1175						1180					1185			
Ala	Met	Ile	Leu	Gly	Gly	Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu
1190						1195					1200			
Ala	Ile	Leu	Met	Gly	Ala	Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly
1205						1210					1215			
Asp	Val	Ala	His	Leu	Ala	Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Leu	Leu	Val	Ser	Phe	Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Met	Leu	Leu	Ala	Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala
1250						1255					1260			
Ile	Ser	Ala	Leu	Glu	Gly	Asp	Leu	Met	Val	Leu	Ile	Asn	Gly	Phe
1265						1270					1275			
Ala	Leu	Ala	Trp	Leu	Ala	Ile	Arg	Ala	Met	Val	Val	Pro	Arg	Thr
1280						1285					1290			
Asp	Asn	Ile	Thr	Leu	Ala	Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala
1295						1300					1305			
Arg	Gly	Thr	Leu	Leu	Val	Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys
1310						1315					1320			

Gly	Gly	Phe	Met	Leu	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys
	1325					1330					1335			
Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
	1340					1345					1350			
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
	1355					1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
	1370					1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
	1385					1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
	1400					1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
	1415					1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
	1430					1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
	1445					1450					1455			
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
	1460					1465					1470			
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
	1475					1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
	1490					1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
	1505					1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
	1520					1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
	1535					1540					1545			

His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly
1580						1585					1590			
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly
1610						1615					1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr
1655						1660					1665			
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro
1670						1675					1680			
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu
1700						1705					1710			
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val
1730						1735					1740			
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu
1745						1750					1755			

Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			

Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr
2045						2050					2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Met	Thr	Asn	Asn	Thr	Ile
2060						2065					2070			
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu
2075						2080					2085			
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser
2090						2095					2100			
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys
2105						2110					2115			
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro
2120						2125					2130			
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala
2135						2140					2145			
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala
2150						2155					2160			
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly
2165						2170					2175			
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg
2180						2185					2190			

Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly
2195						2200					2205			
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			

Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys
2480						2485					2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr
2495						2500					2505			
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly
2510						2515					2520			
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln
2525						2530					2535			
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr
2540						2545					2550			
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val
2555						2560					2565			
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg
2570						2575					2580			
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile
2585						2590					2595			
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr
2600						2605					2610			
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro
2615						2620					2625			

Gly	His	Glu	Glu	Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile
2630						2635					2640			
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Val	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			

Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala
2915						2920					2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala
2930						2935					2940			
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys
2945						2950					2955			
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr
2960						2965					2970			
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys
2975						2980					2985			
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg
2990						2995					3000			
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp
3005						3010					3015			
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu
3020						3025					3030			
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly
3035						3040					3045			
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile
3050						3055					3060			

Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met
3065						3070					3075			
Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			

Phe His Arg Arg Asp Leu Arg Leu Met Ala Asn Ala Ile Cys Ser
 3290 3295 3300

Ser Val Pro Val Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser
 3305 3310 3315

Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val
 3320 3325 3330

Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp
 3335 3340 3345

Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys
 3350 3355 3360

Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg
 3365 3370 3375

Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg
 3380 3385 3390

Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr
 3395 3400 3405

Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu
 3410 3415 3420

<210> 102
 <211> 3422
 <212> PRT
 <213> Zika virus isolate ARB7701 polyprotein

<220>
 <221> misc_feature
 <222> (1167)..(1167)
 <223> Xaa can be any naturally occurring amino acid

<400> 102

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Asn Pro Leu Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

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

Ile Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Ile Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Ser Asp Ala Gly Lys Ala
 130 135 140

Ile Ser Phe Ala Thr Asn Leu Gly Val Asn Lys Cys His Val Gln Ile
 145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
 165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
 180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly
 195 200 205

Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro Ser His Ser Thr
 210 215 220

Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr
 225 230 235 240

Thr Lys His Leu Ile Lys Val Glu Asn Trp Ile Phe Arg Asn Pro Gly
 245 250 255

Phe Ala Leu Ala Ala Val Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr

260	265	270
Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu Ile Ala Pro Ala		
275	280	285
Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly		
290	295	300
Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys		
305	310	315
Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val		
325	330	335
Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu		
340	345	350
Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly		
355	360	365
Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg		
370	375	380
Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys		
385	390	395
Gly Ser Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr		
405	410	415
Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser		
420	425	430
Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Ile Gly His		
435	440	445
Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro		
450	455	460
Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys		
465	470	475
Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met		
485	490	495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His
675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr
690 695 700

Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Val His

725

730

735

Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn
755 760 765

Thr Lys Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val
770 775 780

Met Ile Phe Leu Ser Thr Ala Val Ser Ala Asp Val Gly Cys Ser Val
785 790 795 800

Asp Phe Ser Lys Arg Glu Thr Arg Cys Gly Thr Gly Val Phe Val Tyr
805 810 815

Asn Asp Val Glu Ala Trp Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser
820 825 830

Pro Arg Arg Leu Ala Ala Ala Val Lys Gln Ala Trp Glu Glu Gly Ile
835 840 845

Cys Gly Ile Ser Ser Val Ser Arg Met Glu Asn Ile Met Trp Lys Ser
850 855 860

Val Glu Gly Glu Leu Asn Ala Ile Leu Glu Glu Asn Gly Val Gln Leu
865 870 875 880

Thr Val Val Val Gly Ser Val Lys Asn Pro Met Trp Arg Gly Pro Gln
885 890 895

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Ala His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Val Glu Glu Ser Asp Leu Ile Ile Pro
1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
1040 1045 1050

Tyr Arg Thr Gln Ala Lys Gly Pro Trp His Ser Glu Glu Leu Glu
1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
1100 1105 1110

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu
1115 1120 1125

Ile Arg Pro Arg Lys Glu Pro Glu Ser Asn Leu Val Arg Ser Met
1130 1135 1140

Val Thr Ala Gly Ser Thr Asp His Met Asp His Phe Ser Leu Gly
1145 1150 1155

Val Leu Val Ile Leu Leu Met Val Xaa Glu Gly Leu Lys Lys Arg
1160 1165 1170

Met Thr Thr Lys Ile Ile Met Ser Thr Ser Met Ala Val Leu Val

1175		1180		1185
Ala Met Ile Leu Gly Gly Phe Leu Met Ser Asp Leu Ala Lys Leu	1190	1195	1200	
Val Ile Leu Met Gly Ala Thr Phe Ala Glu Met Asn Thr Gly Gly	1205	1210	1215	
Asp Val Ala His Leu Ala Leu Val Ala Ala Phe Lys Val Arg Pro	1220	1225	1230	
Ala Leu Leu Val Ser Phe Ile Phe Arg Ala Asn Trp Thr Pro Arg	1235	1240	1245	
Glu Ser Met Leu Leu Ala Leu Ala Ser Cys Leu Leu Gln Thr Ala	1250	1255	1260	
Ile Ser Ala Leu Glu Gly Asp Leu Met Val Leu Val Asn Gly Phe	1265	1270	1275	
Ala Leu Ala Trp Leu Ala Ile Arg Ala Met Ala Val Pro Arg Thr	1280	1285	1290	
Asp Asn Ile Ala Leu Ala Ile Leu Ala Ala Leu Thr Pro Leu Ala	1295	1300	1305	
Arg Gly Thr Leu Leu Val Ala Trp Arg Ala Gly Leu Ala Thr Cys	1310	1315	1320	
Gly Gly Phe Met Leu Leu Ser Leu Lys Gly Lys Gly Ser Val Lys	1325	1330	1335	
Lys Asn Leu Pro Phe Val Met Ala Leu Gly Leu Thr Ala Val Arg	1340	1345	1350	
Ile Val Asp Pro Ile Asn Val Val Gly Leu Leu Leu Leu Thr Arg	1355	1360	1365	
Ser Gly Lys Arg Ser Trp Pro Pro Ser Glu Val Leu Thr Ala Val	1370	1375	1380	
Gly Leu Ile Cys Ala Leu Ala Gly Gly Phe Ala Lys Ala Asp Ile	1385	1390	1395	

1610						1615						1620			
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly	
1625						1630					1635				
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly	
1640						1645					1650				
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr	
1655						1660					1665				
Gln	Gly	Lys	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro	
1670						1675					1680				
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro	
1685						1690					1695				
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu	
1700						1705					1710				
Ala	Ile	Lys	Lys	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg	
1715						1720					1725				
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val	
1730						1735					1740				
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu	
1745						1750					1755				
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu	
1760						1765					1770				
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu	
1775						1780					1785				
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	
1790						1795					1800				
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	
1805						1810					1815				
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser	
1820						1825					1830				

Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	Asn	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Ile	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Met	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr
2015						2020					2025			
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu
2030						2035					2040			
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr

2045						2050						2055			
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile	
2060						2065					2070				
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Lys	Tyr	Gly	Glu	
2075						2080					2085				
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser	
2090						2095					2100				
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys	
2105						2110					2115				
Arg	Gly	Val	Ala	Leu	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro	
2120						2125					2130				
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala	
2135						2140					2145				
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala	
2150						2155					2160				
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly	
2165						2170					2175				
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg	
2180						2185					2190				
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly	
2195						2200					2205				
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg	
2210						2215					2220				
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu	
2225						2230					2235				
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met	
2240						2245					2250				
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr	
2255						2260					2265				

Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Asn	Asp	Ile	Ala
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Val	Thr	Met	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Leu	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
2420						2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
2435						2440					2445			
Ile	Ser	Ser	Ala	Val	Leu	Leu	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu
2450						2455					2460			
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly
2465						2470					2475			
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys

2480						2485						2490			
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr	
2495						2500					2505				
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly	
2510						2515					2520				
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln	
2525						2530					2535				
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr	
2540						2545					2550				
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val	
2555						2560					2565				
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg	
2570						2575					2580				
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	His	Gly	Lys	Val	Val	
2585						2590					2595				
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr	
2600						2605					2610				
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro	
2615						2620					2625				
Gly	His	Glu	Glu	Pro	Met	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile	
2630						2635					2640				
Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu	
2645						2650					2655				
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser	
2660						2665					2670				
Pro	Glu	Val	Glu	Glu	Thr	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val	
2675						2680					2685				
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val	
2690						2695					2700				

Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Met	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Val	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Val	Ile	Gly	Lys	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Val	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
2855						2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
2870						2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Ala	Met	Asn	Met	Val
2885						2890					2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg
2900						2905					2910			
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala

2915						2920						2925			
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	
2930						2935					2940				
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys	
2945						2950					2955				
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr	
2960						2965					2970				
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys	
2975						2980					2985				
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg	
2990						2995					3000				
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp	
3005						3010					3015				
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu	
3020						3025					3030				
Gln	Arg	Leu	Gly	Tyr	Ile	Leu	Glu	Glu	Met	Asn	Arg	Ala	Pro	Gly	
3035						3040					3045				
Gly	Lys	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile	
3050						3055					3060				
Ser	Lys	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met	
3065						3070					3075				
Glu	Glu	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Val	Ile	Lys	Tyr	Thr	
3080						3085					3090				
Lys	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Gly	Gly	Lys	
3095						3100					3105				
Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser	Gly	
3110						3115					3120				
Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val	Val	
3125						3130					3135				

Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met	Gln
3140						3145					3150			
Asp	Leu	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Lys	Val	Thr	Arg	Trp	Leu
3155						3160					3165			
Gln	Cys	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser	Gly
3170						3175					3180			
Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His	Ala
3185						3190					3195			
Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr	Gln
3200						3205					3210			
Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val	Pro
3215						3220					3225			
Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly	Arg
3230						3235					3240			
Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly	Arg
3245						3250					3255			
Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr	Ala
3260						3265					3270			
Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr	Phe
3275						3280					3285			
His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser	Ala
3290						3295					3300			
Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser	Ile
3305						3310					3315			
His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Met	Val
3320						3325					3330			
Trp	Asn	Arg	Val	Trp	Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp	Lys
3335						3340					3345			
Thr	Pro	Val	Thr	Lys	Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys	Arg

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

Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg
 370 375 380

Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys
 385 390 395 400

Gly Ser Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr
 405 410 415

Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser
 420 425 430

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Glu Asn Arg
 435 440 445

Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu
 450 455 460

Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu
 465 470 475 480

Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu
 485 490 495

Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly
 500 505 510

Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu
 515 520 525

Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser
 530 535 540

Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu
 545 550 555 560

Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His Leu Lys Cys Arg
 565 570 575

Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys
 580 585 590

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

Ala Val Lys Gln Ala Trp Glu Glu Gly Ile Cys Gly Ile Ser Ser Val
835 840 845

Ser Arg Met Glu Asn Ile Met Trp Lys Ser Val Glu Gly Glu Leu Asn
850 855 860

Ala Ile Leu Glu Glu Asn Gly Val Gln Leu Thr Val Val Val Gly Ser
865 870 875 880

Val Lys Asn Pro Met Trp Arg Gly Pro Gln Arg Leu Pro Val Pro Val
885 890 895

Asn Glu Leu Pro His Gly Trp Lys Ala Trp Gly Lys Ser Tyr Phe Val
900 905 910

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

Lys Glu Cys Pro Leu Lys His Arg Ala Trp Asn Ser Phe Leu Val Glu
930 935 940

Asp His Gly Phe Gly Val Phe His Thr Ser Val Trp Leu Lys Val Arg
945 950 955 960

Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala Val Ile Gly Thr Ala Val
965 970 975

Lys Gly Lys Glu Ala Ala His Ser Asp Leu Gly Tyr Trp Ile Glu Ser
980 985 990

Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg Ala His Leu Ile Glu Met
995 1000 1005

Lys Thr Cys Glu Trp Pro Lys Ser His Thr Leu Trp Thr Asp Gly
1010 1015 1020

Val Glu Glu Ser Asp Leu Ile Ile Pro Lys Ser Leu Ala Gly Pro
1025 1030 1035

Leu Ser His His Asn Thr Arg Glu Gly Tyr Arg Thr Gln Ala Lys
1040 1045 1050

Gly	Pro	Trp	His	Ser	Glu	Glu	Leu	Glu	Ile	Arg	Phe	Glu	Glu	Cys
1055						1060					1065			
Pro	Gly	Thr	Lys	Val	His	Val	Glu	Glu	Thr	Cys	Gly	Thr	Arg	Gly
1070						1075					1080			
Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser	Gly	Arg	Val	Ile	Glu	Glu
1085						1090					1095			
Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro	Pro	Leu	Ser	Phe	Arg	Ala
1100						1105					1110			
Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu	Ile	Arg	Pro	Arg	Lys	Glu
1115						1120					1125			
Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met	Val	Thr	Ala	Gly	Ser	Thr
1130						1135					1140			
Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly	Val	Leu	Val	Ile	Leu	Leu
1145						1150					1155			
Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg	Met	Thr	Thr	Lys	Ile	Ile
1160						1165					1170			
Met	Ser	Thr	Ser	Met	Ala	Val	Leu	Val	Ala	Met	Ile	Leu	Gly	Gly
1175						1180					1185			
Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu	Val	Ile	Leu	Met	Gly	Ala
1190						1195					1200			
Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly	Asp	Val	Ala	His	Leu	Ala
1205						1210					1215			
Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro	Ala	Leu	Leu	Val	Ser	Phe
1220						1225					1230			
Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg	Glu	Ser	Met	Leu	Leu	Ala
1235						1240					1245			
Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala	Ile	Ser	Ala	Leu	Glu	Gly
1250						1255					1260			
Asp	Leu	Met	Val	Leu	Val	Asn	Gly	Phe	Ala	Leu	Ala	Trp	Leu	Ala
1265						1270					1275			

Ile	Arg	Ala	Met	Ala	Val	Pro	Arg	Thr	Asp	Asn	Ile	Ala	Leu	Ala
1280						1285					1290			
Val	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala	Arg	Gly	Thr	Leu	Leu	Val
1295						1300					1305			
Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys	Gly	Gly	Phe	Met	Leu	Leu
1310						1315					1320			
Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys	Lys	Asn	Leu	Pro	Phe	Val
1325						1330					1335			
Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg	Ile	Val	Asp	Pro	Ile	Asn
1340						1345					1350			
Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg	Ser	Gly	Lys	Arg	Ser	Trp
1355						1360					1365			
Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val	Gly	Leu	Ile	Cys	Ala	Leu
1370						1375					1380			
Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile	Glu	Met	Ala	Gly	Pro	Met
1385						1390					1395			
Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser	Tyr	Val	Val	Ser	Gly	Lys
1400						1405					1410			
Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala	Gly	Asp	Ile	Thr	Trp	Glu
1415						1420					1425			
Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser	Pro	Arg	Leu	Asp	Val	Ala
1430						1435					1440			
Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu	Val	Glu	Glu	Asp	Gly	Pro
1445						1450					1455			
Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val	Val	Leu	Met	Ala	Ile	Cys
1460						1465					1470			
Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe	Ala	Ala	Gly	Ala	Trp	Tyr
1475						1480					1485			

Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser	Gly	Ala	Leu	Trp	Asp	Val
1490						1495					1500			
Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly	Glu	Thr	Thr	Asp	Gly	Val
1505						1510					1515			
Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu	Gly	Ser	Thr	Gln	Val	Gly
1520						1525					1530			
Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe	His	Thr	Met	Trp	His	Val
1535						1540					1545			
Thr	Lys	Gly	Ala	Ala	Leu	Arg	Ser	Gly	Glu	Gly	Arg	Leu	Asp	Pro
1550						1555					1560			
Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu	Val	Ser	Tyr	Cys	Gly	Pro
1565						1570					1575			
Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly	Leu	Ser	Glu	Val	Gln	Leu
1580						1585					1590			
Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala	Arg	Asn	Ile	Gln	Thr	Leu
1595						1600					1605			
Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly	Asp	Ile	Gly	Ala	Val	Ala
1610						1615					1620			
Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly	Ser	Pro	Ile	Leu	Asp	Lys
1625						1630					1635			
Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly	Asn	Gly	Val	Val	Ile	Lys
1640						1645					1650			
Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr	Gln	Gly	Lys	Arg	Glu	Glu
1655						1660					1665			
Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro	Ser	Met	Leu	Lys	Lys	Lys
1670						1675					1680			
Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro	Gly	Ala	Gly	Lys	Thr	Arg
1685						1690					1695			
Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu	Ala	Ile	Lys	Lys	Arg	Leu
1700						1705					1710			

Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg	Val	Val	Ala	Ala	Glu	Met
1715						1720					1725			
Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val	Arg	Tyr	Met	Thr	Thr	Ala
1730						1735					1740			
Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu	Ile	Val	Asp	Leu	Met	Cys
1745						1750					1755			
His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu	Gln	Pro	Ile	Arg	Val	Pro
1760						1765					1770			
Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu	Ala	His	Phe	Thr	Asp	Pro
1775						1780					1785			
Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	Ser	Thr	Arg	Val	Glu	Met
1790						1795					1800			
Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	Ala	Thr	Pro	Pro	Gly	Thr
1805						1810					1815			
Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser	Pro	Ile	Met	Asp	Thr	Glu
1820						1825					1830			
Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser	Ser	Gly	Phe	Asp	Trp	Val
1835						1840					1845			
Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp	Phe	Val	Pro	Ser	Val	Arg
1850						1855					1860			
Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu	Thr	Lys	Ala	Gly	Lys	Arg
1865						1870					1875			
Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	Glu	Thr	Glu	Phe	Gln	Lys
1880						1885					1890			
Thr	Lys	Asn	Gln	Glu	Trp	Asp	Phe	Val	Ile	Thr	Thr	Asp	Ile	Ser
1895						1900					1905			
Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp	Arg	Val	Ile	Asp	Ser	Arg
1910						1915					1920			

Arg 1925	Cys	Leu	Lys	Pro	Val	Ile 1930	Leu	Asp	Gly	Glu	Arg 1935	Val	Ile	Leu
Ala 1940	Gly	Pro	Met	Pro	Val	Thr 1945	His	Ala	Ser	Ala	Ala 1950	Gln	Arg	Arg
Gly 1955	Arg	Ile	Gly	Arg	Asn	Pro 1960	Asn	Lys	Pro	Gly	Asp 1965	Glu	Tyr	Met
Tyr 1970	Gly	Gly	Gly	Cys	Ala	Glu 1975	Thr	Asp	Glu	Asp	His 1980	Ala	His	Trp
Leu 1985	Glu	Ala	Arg	Met	Leu	Leu 1990	Asp	Asn	Ile	Tyr	Leu 1995	Gln	Asp	Gly
Leu 2000	Ile	Ala	Ser	Leu	Tyr	Arg 2005	Pro	Glu	Ala	Asp	Lys 2010	Val	Ala	Ala
Ile 2015	Glu	Gly	Glu	Phe	Lys	Leu 2020	Arg	Thr	Glu	Gln	Arg 2025	Lys	Thr	Phe
Val 2030	Glu	Leu	Met	Lys	Arg	Gly 2035	Asp	Leu	Pro	Val	Trp 2040	Leu	Ala	Tyr
Gln 2045	Val	Ala	Ser	Ala	Gly	Ile 2050	Thr	Tyr	Thr	Asp	Arg 2055	Arg	Trp	Cys
Phe 2060	Asp	Gly	Thr	Thr	Asn	Asn 2065	Thr	Ile	Met	Glu	Asp 2070	Ser	Val	Pro
Ala 2075	Glu	Val	Trp	Thr	Lys	Tyr 2080	Gly	Glu	Lys	Arg	Val 2085	Leu	Lys	Pro
Arg 2090	Trp	Met	Asp	Ala	Arg	Val 2095	Cys	Ser	Asp	His	Ala 2100	Ala	Leu	Lys
Ser 2105	Phe	Lys	Glu	Phe	Ala	Ala 2110	Gly	Lys	Arg	Gly	Ala 2115	Ala	Leu	Gly
Val 2120	Met	Glu	Ala	Leu	Gly	Thr 2125	Leu	Pro	Gly	His	Met 2130	Thr	Glu	Arg
Phe 2135	Gln	Glu	Ala	Ile	Asp	Asn 2140	Leu	Ala	Val	Leu	Met 2145	Arg	Ala	Glu

Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala	Ala	Ala	Gln	Leu	Pro	Glu
2150						2155					2160			
Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly	Leu	Leu	Gly	Thr	Val	Ser
2165						2170					2175			
Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg	Asn	Lys	Gly	Ile	Gly	Lys
2180						2185					2190			
Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly	Ala	Ser	Ala	Trp	Leu	Met
2195						2200					2205			
Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg	Ile	Ala	Cys	Val	Leu	Ile
2210						2215					2220			
Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu	Ile	Pro	Glu	Pro	Glu	Lys
2225						2230					2235			
Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met	Ala	Ile	Ile	Ile	Met	Val
2240						2245					2250			
Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr	Ala	Asn	Glu	Leu	Gly	Trp
2255						2260					2265			
Leu	Glu	Arg	Thr	Lys	Asn	Asp	Ile	Ala	His	Leu	Met	Gly	Arg	Arg
2270						2275					2280			
Glu	Glu	Gly	Val	Thr	Met	Gly	Phe	Ser	Met	Asp	Ile	Asp	Leu	Arg
2285						2290					2295			
Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala	Ala	Leu	Thr	Thr	Leu	Ile
2300						2305					2310			
Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr	Thr	Ser	Tyr	Asn	Asn	Tyr
2315						2320					2325			
Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala	Gly	Val	Leu	Phe	Gly	Met
2330						2335					2340			
Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp	Asp	Phe	Gly	Val	Pro	Leu
2345						2350					2355			

Leu	Met	Val	Gly	Cys	Tyr	Ser	Gln	Leu	Thr	Pro	Leu	Thr	Leu	Ile
2360						2365					2370			
Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His	Tyr	Met	Tyr	Leu	Ile	Pro
2375						2380					2385			
Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala	Ala	Gln	Lys	Arg	Thr	Ala
2390						2395					2400			
Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val	Asp	Gly	Ile	Val	Val	Thr
2405						2410					2415			
Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro	Gln	Val	Glu	Lys	Lys	Met
2420						2425					2430			
Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala	Ile	Ser	Ser	Ala	Val	Leu
2435						2440					2445			
Leu	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu	Ala	Gly	Ala	Leu	Ile	Thr
2450						2455					2460			
Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly	Ser	Pro	Asn	Lys	Tyr	Trp
2465						2470					2475			
Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys	Asn	Ile	Phe	Arg	Gly	Ser
2480						2485					2490			
Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr	Thr	Val	Thr	Arg	Asn	Ala
2495						2500					2505			
Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly	Thr	Gly	Glu	Thr	Leu	Gly
2510						2515					2520			
Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln	Met	Ser	Ala	Leu	Glu	Phe
2525						2530					2535			
Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr	Glu	Val	Cys	Arg	Glu	Glu
2540						2545					2550			
Ala	Arg	Arg	Ala	Leu	Lys	Asn	Gly	Val	Ala	Thr	Gly	Gly	His	Ala
2555						2560					2565			
Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg	Trp	Leu	Val	Glu	Arg	Gly
2570						2575					2580			

Tyr	Leu	Gln	Pro	His	Gly	Lys	Val	Val	Asp	Leu	Gly	Cys	Gly	Arg
2585						2590					2595			
Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr	Ile	Arg	Lys	Val	Gln	Glu
2600						2605					2610			
Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro	Gly	His	Glu	Glu	Pro	Met
2615						2620					2625			
Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile	Val	Arg	Leu	Lys	Ser	Gly
2630						2635					2640			
Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu	Pro	Cys	Asp	Thr	Leu	Leu
2645						2650					2655			
Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser	Pro	Glu	Val	Glu	Glu	Thr
2660						2665					2670			
Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val	Gly	Asp	Trp	Leu	Glu	Lys
2675						2680					2685			
Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val	Leu	Cys	Pro	Tyr	Thr	Ser
2690						2695					2700			
Thr	Met	Met	Glu	Thr	Met	Glu	Arg	Leu	Gln	Arg	Arg	Tyr	Gly	Gly
2705						2710					2715			
Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg	Asn	Ser	Thr	His	Glu	Met
2720						2725					2730			
Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn	Ile	Ile	Lys	Ser	Val	Ser
2735						2740					2745			
Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg	Met	Asp	Gly	Pro	Arg	Arg
2750						2755					2760			
Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn	Leu	Gly	Ser	Gly	Thr	Arg
2765						2770					2775			
Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro	Asn	Met	Lys	Ile	Ile	Gly
2780						2785					2790			

Lys	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu	His	Ala	Glu	Thr	Trp	Phe
2795						2800					2805			
Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr	Trp	Ala	Tyr	His	Gly	Ser
2810						2815					2820			
Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala	Ser	Ser	Leu	Val	Asn	Gly
2825						2830					2835			
Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp	Asp	Val	Val	Thr	Gly	Val
2840						2845					2850			
Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr	Pro	Tyr	Gly	Gln	Gln	Arg
2855						2860					2865			
Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg	Val	Pro	Asp	Pro	Gln	Glu
2870						2875					2880			
Gly	Thr	Arg	Gln	Thr	Met	Asn	Met	Val	Ser	Ser	Trp	Leu	Trp	Lys
2885						2890					2895			
Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg	Val	Cys	Thr	Lys	Glu	Glu
2900						2905					2910			
Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala	Ala	Leu	Gly	Ala	Ile	Phe
2915						2920					2925			
Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	Val	Glu	Ala	Val	Asn	Asp
2930						2935					2940			
Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys	Glu	Arg	Glu	His	His	Leu
2945						2950					2955			
Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr	Asn	Met	Met	Gly	Lys	Arg
2960						2965					2970			
Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys	Ala	Lys	Gly	Ser	Arg	Ala
2975						2980					2985			
Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg	Phe	Leu	Glu	Phe	Glu	Ala
2990						2995					3000			
Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp	Met	Gly	Arg	Glu	Asn	Ser
3005						3010					3015			

Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu	Gln	Arg	Leu	Gly	Tyr	Ile
3020						3025					3030			
Leu	Glu	Glu	Met	Asn	Arg	Ala	Pro	Gly	Gly	Lys	Met	Tyr	Ala	Asp
3035						3040					3045			
Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile	Ser	Lys	Phe	Asp	Leu	Glu
3050						3055					3060			
Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met	Glu	Glu	Gly	His	Arg	Ala
3065						3070					3075			
Leu	Ala	Leu	Ala	Val	Ile	Lys	Tyr	Thr	Tyr	Gln	Asn	Lys	Val	Val
3080						3085					3090			
Lys	Val	Leu	Arg	Pro	Ala	Glu	Gly	Gly	Lys	Thr	Val	Met	Asp	Ile
3095						3100					3105			
Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser	Gly	Gln	Val	Val	Thr	Tyr
3110						3115					3120			
Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val	Val	Gln	Leu	Ile	Arg	Asn
3125						3130					3135			
Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met	Gln	Asp	Leu	Trp	Leu	Leu
3140						3145					3150			
Arg	Lys	Pro	Glu	Lys	Val	Thr	Arg	Trp	Leu	Gln	Cys	Asn	Gly	Trp
3155						3160					3165			
Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser	Gly	Asp	Asp	Cys	Val	Val
3170						3175					3180			
Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His	Ala	Leu	Arg	Phe	Leu	Asn
3185						3190					3195			
Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr	Gln	Glu	Trp	Lys	Pro	Ser
3200						3205					3210			
Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val	Pro	Phe	Cys	Ser	His	His
3215						3220					3225			

Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly	Arg	Ser	Ile	Val	Val	Pro
	3230					3235					3240			
Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly	Arg	Ala	Arg	Val	Ser	Pro
	3245					3250					3255			
Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr	Ala	Cys	Leu	Ala	Lys	Ser
	3260					3265					3270			
Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr	Phe	His	Arg	Arg	Asp	Leu
	3275					3280					3285			
Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser	Ala	Val	Pro	Val	Asp	Trp
	3290					3295					3300			
Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser	Ile	His	Gly	Lys	Gly	Glu
	3305					3310					3315			
Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Met	Val	Trp	Asn	Arg	Val	Trp
	3320					3325					3330			
Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp	Lys	Thr	Pro	Val	Thr	Lys
	3335					3340					3345			
Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys	Arg	Glu	Asp	Leu	Trp	Cys
	3350					3355					3360			
Gly	Ser	Leu	Ile	Gly	His	Arg	Pro	Arg	Thr	Thr	Trp	Ala	Glu	Asn
	3365					3370					3375			
Ile	Lys	Asp	Thr	Val	Asn	Met	Val	Arg	Arg	Ile	Ile	Gly	Asp	Glu
	3380					3385					3390			
Glu	Lys	Tyr	Met	Asp	Tyr	Leu	Ser	Thr	Gln	Val	Arg	Tyr	Leu	Gly
	3395					3400					3405			
Glu	Glu	Gly	Ser	Thr	Pro	Gly	Val	Leu						
	3410					3415								

<210> 104
 <211> 3422
 <212> PRT
 <213> Zika virus isolate ARB13565 polyprotein
 <400> 104

225		230		235		240									
Thr	Lys	His	Leu	Ile	Lys	Val	Glu	Asn	Trp	Ile	Phe	Arg	Asn	Pro	Gly
			245						250					255	
Phe	Ala	Leu	Ala	Ala	Val	Ala	Ile	Ala	Trp	Leu	Leu	Gly	Ser	Ser	Thr
		260						265					270		
Ser	Gln	Lys	Val	Ile	Tyr	Leu	Val	Met	Ile	Leu	Leu	Ile	Ala	Pro	Ala
		275					280					285			
Tyr	Ser	Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly
	290					295					300				
Met	Ser	Gly	Gly	Thr	Trp	Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys
305					310					315					320
Val	Thr	Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val
			325						330					335	
Thr	Thr	Thr	Val	Ser	Asn	Met	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Glu
			340					345					350		
Ala	Ser	Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	Gly
		355					360					365			
Glu	Ala	Tyr	Leu	Asp	Lys	Gln	Ser	Asp	Thr	Gln	Tyr	Val	Cys	Lys	Arg
	370					375					380				
Thr	Leu	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys
385					390					395					400
Gly	Ser	Leu	Val	Thr	Cys	Ala	Lys	Phe	Thr	Cys	Ser	Lys	Lys	Met	Thr
			405						410					415	
Gly	Lys	Ser	Ile	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu	Ser
			420				425						430		
Val	His	Gly	Ser	Gln	His	Ser	Gly	Met	Ile	Val	Asn	Asp	Ile	Gly	His
		435					440					445			
Glu	Thr	Asp	Glu	Asn	Arg	Ala	Lys	Val	Glu	Val	Thr	Pro	Asn	Ser	Pro
	450					455					460				

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
 465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
 485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
 500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
 515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
 530 535 540

Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala
 545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser
 565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
 580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro
 595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
 610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
 625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
 645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe
 660 665 670

Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His
 675 680 685

His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr

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

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
 930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
 945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
 965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Ala His Ser Asp Leu
 980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
 995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
 1010 1015 1020

Thr Leu Trp Thr Asp Gly Val Glu Glu Ser Asp Leu Ile Ile Pro
 1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
 1040 1045 1050

Tyr Arg Thr Gln Ala Lys Gly Pro Trp His Ser Glu Glu Leu Glu
 1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
 1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
 1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
 1100 1105 1110

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu
 1115 1120 1125

Ile Arg Pro Arg Lys Glu Pro Glu Ser Asn Leu Val Arg Ser Met
 1130 1135 1140

Val Thr Ala Gly Ser Thr Asp His Met Asp His Phe Ser Leu Gly

1145		1150		1155
Val Leu 1160	Val Ile Leu Leu	Met 1165	Val Gln Glu Gly	Leu 1170 Lys Lys Arg
Met 1175	Thr Thr Lys Ile Ile	Met 1180	Ser Thr Ser Met	Ala 1185 Val Leu Val
Ala 1190	Met Ile Leu Gly Gly	Phe 1195	Leu Met Ser Asp	Leu 1200 Ala Lys Leu
Val 1205	Ile Leu Met Gly Ala	Thr 1210	Phe Ala Glu Met	Asn 1215 Thr Gly Gly
Asp 1220	Val Ala His Leu Ala	Leu 1225	Val Ala Ala Phe	Lys 1230 Val Arg Pro
Ala 1235	Leu Leu Val Ser Phe	Ile 1240	Phe Arg Ala Asn	Trp 1245 Thr Pro Arg
Glu 1250	Ser Met Leu Leu Ala	Leu 1255	Ala Ser Cys Leu	Leu 1260 Gln Thr Ala
Ile 1265	Ser Ala Leu Glu Gly	Asp 1270	Leu Met Val Leu	Val 1275 Asn Gly Phe
Ala 1280	Leu Ala Trp Leu Ala	Ile 1285	Arg Ala Met Ala	Val 1290 Pro Arg Thr
Asp 1295	Asn Ile Ala Leu Ala	Ile 1300	Leu Ala Ala Leu	Thr 1305 Pro Leu Ala
Arg 1310	Gly Thr Leu Leu Val	Ala 1315	Trp Arg Ala Gly	Leu 1320 Ala Thr Cys
Gly 1325	Gly Phe Met Leu Leu	Ser 1330	Leu Lys Gly Lys	Gly 1335 Ser Val Lys
Lys 1340	Asn Leu Pro Phe Val	Met 1345	Ala Leu Gly Leu	Thr 1350 Ala Val Arg
Ile 1355	Val Asp Pro Ile Asn	Val 1360	Val Gly Leu Leu	Leu 1365 Leu Thr Arg

Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Val	Glu	Glu	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
1460						1465					1470			
Val	Leu	Met	Ala	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ala	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly

1580						1585						1590			
Leu	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala	
1595						1600					1605				
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly	
1610						1615					1620				
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly	
1625						1630					1635				
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly	
1640						1645					1650				
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr	
1655						1660					1665				
Gln	Gly	Lys	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro	
1670						1675					1680				
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro	
1685						1690					1695				
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu	
1700						1705					1710				
Ala	Ile	Lys	Lys	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg	
1715						1720					1725				
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val	
1730						1735					1740				
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu	
1745						1750					1755				
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu	
1760						1765					1770				
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu	
1775						1780					1785				
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	
1790						1795					1800				

Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	Asn	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Ile	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Met	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn
1985						1990					1995			
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu
2000						2005					2010			
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr

2015						2020						2025					
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu			
2030						2035						2040					
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr			
2045						2050						2055					
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile			
2060						2065						2070					
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Lys	Tyr	Gly	Glu			
2075						2080						2085					
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser			
2090						2095						2100					
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys			
2105						2110						2115					
Arg	Gly	Val	Ala	Leu	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro			
2120						2125						2130					
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala			
2135						2140						2145					
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala			
2150						2155						2160					
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly			
2165						2170						2175					
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg			
2180						2185						2190					
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly			
2195						2200						2205					
Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg			
2210						2215						2220					
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu			
2225						2230						2235					

Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
	2240					2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
	2255					2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Asn	Asp	Ile	Ala
	2270					2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Val	Thr	Met	Gly	Phe	Ser
	2285					2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
	2300					2305					2310			
Ala	Leu	Thr	Thr	Leu	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
	2315					2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
	2330					2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
	2345					2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu
	2360					2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
	2375					2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
	2390					2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
	2405					2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro
	2420					2425					2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala
	2435					2440					2445			
Ile	Ser	Ser	Ala	Val	Leu	Leu	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu

2450		2455		2460
Ala Gly	Ala Leu Ile Thr	Ala Ala Thr Ser Thr	Leu Trp Glu Gly	
2465		2470	2475	
Ser Pro	Asn Lys Tyr Trp	Asn Ser Ser Thr Ala	Thr Ser Leu Cys	
2480		2485	2490	
Asn Ile	Phe Arg Gly Ser	Tyr Leu Ala Gly Ala	Ser Leu Ile Tyr	
2495		2500	2505	
Thr Val	Thr Arg Asn Ala	Gly Leu Val Lys Arg	Arg Gly Gly Gly	
2510		2515	2520	
Thr Gly	Glu Thr Leu Gly	Glu Lys Trp Lys Ala	Arg Leu Asn Gln	
2525		2530	2535	
Met Ser	Ala Leu Glu Phe	Tyr Ser Tyr Lys Lys	Ser Gly Ile Thr	
2540		2545	2550	
Glu Val	Cys Arg Glu Glu	Ala Arg Arg Ala Leu	Lys Asp Gly Val	
2555		2560	2565	
Ala Thr	Gly Gly His Ala	Val Ser Arg Gly Ser	Ala Lys Leu Arg	
2570		2575	2580	
Trp Leu	Val Glu Arg Gly	Tyr Leu Gln Pro His	Gly Lys Val Val	
2585		2590	2595	
Asp Leu	Gly Cys Gly Arg	Gly Gly Trp Ser Tyr	Tyr Ala Ala Thr	
2600		2605	2610	
Ile Arg	Lys Val Gln Glu	Val Lys Gly Tyr Thr	Lys Gly Gly Pro	
2615		2620	2625	
Gly His	Glu Glu Pro Met	Leu Val Gln Ser Tyr	Gly Trp Asn Ile	
2630		2635	2640	
Val Arg	Leu Lys Ser Gly	Val Asp Val Phe His	Met Ala Ala Glu	
2645		2650	2655	
Pro Cys	Asp Thr Leu Leu	Cys Asp Ile Gly Glu	Ser Ser Ser Ser	
2660		2665	2670	

Pro	Glu	Val	Glu	Glu	Thr	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
	2675					2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
	2690					2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Met	Glu	Arg	Leu
	2705					2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
	2720					2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
	2735					2740					2745			
Val	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
	2750					2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
	2765					2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro
	2780					2785					2790			
Asn	Met	Lys	Val	Ile	Gly	Lys	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
	2795					2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
	2810					2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala
	2825					2830					2835			
Ser	Ser	Leu	Val	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
	2840					2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr
	2855					2860					2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg
	2870					2875					2880			
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Ala	Met	Asn	Met	Val

2885						2890						2895			
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg	
2900						2905					2910				
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala	
2915						2920					2925				
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	
2930						2935					2940				
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys	
2945						2950					2955				
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr	
2960						2965					2970				
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys	
2975						2980					2985				
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg	
2990						2995					3000				
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp	
3005						3010					3015				
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu	
3020						3025					3030				
Gln	Arg	Leu	Gly	Tyr	Ile	Leu	Glu	Glu	Met	Asn	Arg	Ala	Pro	Gly	
3035						3040					3045				
Gly	Lys	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile	
3050						3055					3060				
Ser	Lys	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met	
3065						3070					3075				
Glu	Glu	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Val	Ile	Lys	Tyr	Thr	
3080						3085					3090				
Lys	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Gly	Gly	Lys	
3095						3100					3105				

Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser	Gly
3110						3115					3120			
Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val	Val
3125						3130					3135			
Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met	Gln
3140						3145					3150			
Asp	Leu	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Lys	Val	Thr	Arg	Trp	Leu
3155						3160					3165			
Gln	Cys	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser	Gly
3170						3175					3180			
Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His	Ala
3185						3190					3195			
Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr	Gln
3200						3205					3210			
Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val	Pro
3215						3220					3225			
Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly	Arg
3230						3235					3240			
Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly	Arg
3245						3250					3255			
Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr	Ala
3260						3265					3270			
Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr	Phe
3275						3280					3285			
His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser	Ala
3290						3295					3300			
Val	Pro	Val	Asp	Trp	Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser	Ile
3305						3310					3315			
His	Gly	Lys	Gly	Glu	Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Met	Val

3320		3325		3330
Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp Lys				
3335		3340		3345
Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys Arg				
3350		3355		3360
Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg Thr				
3365		3370		3375
Thr Trp Ala Glu Asn Ile Lys Asp Thr Val Asn Met Val Arg Arg				
3380		3385		3390
Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr Gln				
3395		3400		3405
Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu				
3410		3415		3420
<210> 105				
<211> 3417				
<212> PRT				
<213> Zika virus strain MR 766 polyprotein				
<400> 105				
Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met				
1	5	10	15	
Leu Lys Arg Gly Val Ala Arg Val Asn Pro Leu Gly Gly Leu Lys Arg				
	20	25	30	
Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu				
	35	40	45	
Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly				
	50	55	60	
Leu Ile Asn Arg Trp Gly Thr Val Gly Lys Lys Glu Ala Met Glu Ile				
65	70	75	80	
Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn				
	85	90	95	

Ala	Arg	Lys	Glu	Arg	Lys	Arg	Arg	Gly	Ala	Asp	Thr	Ser	Ile	Gly	Ile	
			100					105					110			
Val	Gly	Leu	Leu	Leu	Thr	Thr	Ala	Met	Ala	Ala	Glu	Ile	Thr	Arg	Arg	
		115					120					125				
Gly	Ser	Ala	Tyr	Tyr	Met	Tyr	Leu	Asp	Arg	Ser	Asp	Ala	Gly	Lys	Ala	
	130					135					140					
Ile	Ser	Phe	Ala	Thr	Thr	Leu	Gly	Val	Asn	Lys	Cys	His	Val	Gln	Ile	
145					150					155					160	
Met	Asp	Leu	Gly	His	Met	Cys	Asp	Ala	Thr	Met	Ser	Tyr	Glu	Cys	Pro	
				165					170					175		
Met	Leu	Asp	Glu	Gly	Val	Glu	Pro	Asp	Asp	Val	Asp	Cys	Trp	Cys	Asn	
			180					185					190			
Thr	Thr	Ser	Thr	Trp	Val	Val	Tyr	Gly	Thr	Cys	His	His	Lys	Lys	Gly	
		195					200					205				
Glu	Ala	Arg	Arg	Ser	Arg	Arg	Ala	Val	Thr	Leu	Pro	Ser	His	Ser	Thr	
	210					215					220					
Arg	Lys	Leu	Gln	Thr	Arg	Ser	Gln	Thr	Trp	Leu	Glu	Ser	Arg	Glu	Tyr	
225					230					235					240	
Thr	Lys	His	Leu	Ile	Lys	Val	Glu	Asn	Trp	Ile	Phe	Arg	Asn	Pro	Gly	
				245					250					255		
Phe	Thr	Leu	Val	Ala	Val	Ala	Ile	Ala	Trp	Leu	Leu	Gly	Ser	Ser	Thr	
			260					265					270			
Ser	Gln	Lys	Val	Ile	Tyr	Leu	Val	Met	Ile	Leu	Leu	Ile	Ala	Pro	Ala	
		275					280					285				
Tyr	Ser	Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	
	290					295					300					
Met	Ser	Gly	Gly	Thr	Trp	Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys	
305					310					315					320	
Val	Thr	Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val	
				325					330					335		

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

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

Thr Arg Cys Gly Thr Gly Val Phe Val Tyr Asn Asp Val Glu Ala Trp
805 810 815

Arg Asp Arg Tyr Lys Tyr His Pro Asp Ser Pro Arg Arg Leu Ala Ala
820 825 830

Ala Val Lys Gln Ala Trp Glu Glu Gly Ile Cys Gly Ile Ser Ser Val
835 840 845

Ser Arg Met Glu Asn Ile Met Trp Lys Ser Val Glu Gly Glu Leu Asn
850 855 860

Ala Ile Leu Glu Glu Asn Gly Val Gln Leu Thr Val Val Val Gly Ser
865 870 875 880

Val Lys Asn Pro Met Trp Arg Gly Pro Gln Arg Leu Pro Val Pro Val
885 890 895

Asn Glu Leu Pro His Gly Trp Lys Ala Trp Gly Lys Ser Tyr Phe Val
900 905 910

Arg Ala Ala Lys Thr Asn Asn Ser Phe Val Val Asp Gly Asp Thr Leu
915 920 925

Lys Glu Cys Pro Leu Lys His Arg Ala Trp Asn Ser Phe Leu Val Glu
930 935 940

Asp His Gly Phe Gly Val Phe His Thr Ser Val Trp Leu Lys Val Arg
945 950 955 960

Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala Val Ile Gly Thr Ala Val
965 970 975

Lys Gly Lys Glu Ala Ala His Ser Asp Leu Gly Tyr Trp Ile Glu Ser
980 985 990

Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg Ala His Leu Ile Glu Met
995 1000 1005

Lys Thr Cys Glu Trp Pro Lys Ser His Thr Leu Trp Thr Asp Gly
1010 1015 1020

Val	Glu	Glu	Ser	Asp	Leu	Ile	Ile	Pro	Lys	Ser	Leu	Ala	Gly	Pro
1025						1030					1035			
Leu	Ser	His	His	Asn	Thr	Arg	Glu	Gly	Tyr	Arg	Thr	Gln	Val	Lys
1040						1045					1050			
Gly	Pro	Trp	His	Ser	Glu	Glu	Leu	Glu	Ile	Arg	Phe	Glu	Glu	Cys
1055						1060					1065			
Pro	Gly	Thr	Lys	Val	His	Val	Glu	Glu	Thr	Cys	Gly	Thr	Arg	Gly
1070						1075					1080			
Pro	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ser	Gly	Arg	Val	Ile	Glu	Glu
1085						1090					1095			
Trp	Cys	Cys	Arg	Glu	Cys	Thr	Met	Pro	Pro	Leu	Ser	Phe	Arg	Ala
1100						1105					1110			
Lys	Asp	Gly	Cys	Trp	Tyr	Gly	Met	Glu	Ile	Arg	Pro	Arg	Lys	Glu
1115						1120					1125			
Pro	Glu	Ser	Asn	Leu	Val	Arg	Ser	Met	Val	Thr	Ala	Gly	Ser	Thr
1130						1135					1140			
Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly	Val	Leu	Val	Ile	Leu	Leu
1145						1150					1155			
Met	Val	Gln	Glu	Gly	Leu	Lys	Lys	Arg	Met	Thr	Thr	Lys	Ile	Ile
1160						1165					1170			
Met	Ser	Thr	Ser	Met	Ala	Val	Leu	Val	Ala	Met	Ile	Leu	Gly	Gly
1175						1180					1185			
Phe	Ser	Met	Ser	Asp	Leu	Ala	Lys	Leu	Val	Ile	Leu	Met	Gly	Ala
1190						1195					1200			
Thr	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly	Asp	Val	Ala	His	Leu	Ala
1205						1210					1215			
Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro	Ala	Leu	Leu	Val	Ser	Phe
1220						1225					1230			
Ile	Phe	Arg	Ala	Asn	Trp	Thr	Pro	Arg	Glu	Ser	Met	Leu	Leu	Ala
1235						1240					1245			

Leu	Ala	Ser	Cys	Leu	Leu	Gln	Thr	Ala	Ile	Ser	Ala	Leu	Glu	Gly
1250						1255					1260			
Asp	Leu	Met	Val	Leu	Val	Asn	Gly	Phe	Ala	Leu	Ala	Trp	Leu	Ala
1265						1270					1275			
Ile	Arg	Ala	Met	Ala	Val	Pro	Arg	Thr	Asp	Asn	Ile	Ala	Leu	Ala
1280						1285					1290			
Ile	Leu	Ala	Ala	Leu	Thr	Pro	Leu	Ala	Arg	Gly	Thr	Leu	Leu	Val
1295						1300					1305			
Ala	Trp	Arg	Ala	Gly	Leu	Ala	Thr	Cys	Gly	Gly	Phe	Met	Leu	Leu
1310						1315					1320			
Ser	Leu	Lys	Gly	Lys	Gly	Ser	Val	Lys	Lys	Asn	Leu	Pro	Phe	Val
1325						1330					1335			
Ala	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg	Ile	Val	Asp	Pro	Ile	Asn
1340						1345					1350			
Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg	Ser	Gly	Lys	Arg	Ser	Trp
1355						1360					1365			
Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val	Gly	Leu	Ile	Cys	Ala	Leu
1370						1375					1380			
Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile	Glu	Met	Ala	Gly	Pro	Met
1385						1390					1395			
Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser	Tyr	Val	Val	Ser	Gly	Lys
1400						1405					1410			
Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala	Gly	Asp	Ile	Thr	Trp	Glu
1415						1420					1425			
Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser	Pro	Arg	Leu	Asp	Val	Ala
1430						1435					1440			
Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu	Val	Glu	Glu	Asp	Gly	Pro
1445						1450					1455			

Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val	Val	Leu	Met	Ala	Ile	Cys
	1460					1465					1470			
Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe	Ala	Ala	Gly	Ala	Trp	Tyr
	1475					1480					1485			
Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser	Gly	Ala	Leu	Trp	Asp	Val
	1490					1495					1500			
Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly	Glu	Thr	Thr	Asp	Gly	Val
	1505					1510					1515			
Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu	Gly	Ser	Thr	Gln	Val	Gly
	1520					1525					1530			
Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe	His	Thr	Met	Trp	His	Val
	1535					1540					1545			
Thr	Lys	Gly	Ala	Ala	Leu	Arg	Ser	Gly	Glu	Gly	Arg	Leu	Asp	Pro
	1550					1555					1560			
Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu	Val	Ser	Tyr	Cys	Gly	Pro
	1565					1570					1575			
Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly	Val	Ser	Glu	Val	Gln	Leu
	1580					1585					1590			
Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala	Arg	Asn	Ile	Gln	Thr	Leu
	1595					1600					1605			
Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly	Asp	Ile	Gly	Ala	Val	Ala
	1610					1615					1620			
Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly	Ser	Pro	Ile	Leu	Asp	Lys
	1625					1630					1635			
Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly	Asn	Gly	Val	Val	Ile	Lys
	1640					1645					1650			
Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr	Gln	Gly	Lys	Arg	Glu	Glu
	1655					1660					1665			
Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro	Ser	Met	Leu	Lys	Lys	Lys
	1670					1675					1680			

Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro	Gly	Ala	Gly	Lys	Thr	Arg
1685						1690					1695			
Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu	Ala	Ile	Lys	Lys	Arg	Leu
1700						1705					1710			
Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg	Val	Val	Ala	Ala	Glu	Met
1715						1720					1725			
Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val	Arg	Tyr	Met	Thr	Thr	Ala
1730						1735					1740			
Val	Lys	Val	Thr	His	Ser	Gly	Thr	Glu	Ile	Val	Asp	Leu	Met	Cys
1745						1750					1755			
His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu	Gln	Pro	Ile	Arg	Val	Pro
1760						1765					1770			
Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu	Ala	His	Phe	Thr	Asp	Pro
1775						1780					1785			
Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile	Ser	Thr	Arg	Val	Glu	Met
1790						1795					1800			
Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr	Ala	Thr	Pro	Pro	Gly	Thr
1805						1810					1815			
Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser	Pro	Ile	Met	Asp	Thr	Glu
1820						1825					1830			
Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser	Ser	Gly	Phe	Asp	Trp	Val
1835						1840					1845			
Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp	Phe	Val	Pro	Ser	Val	Arg
1850						1855					1860			
Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu	Thr	Lys	Ala	Gly	Lys	Arg
1865						1870					1875			
Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe	Glu	Thr	Glu	Phe	Gln	Lys
1880						1885					1890			

Thr	Lys	Asn	Gln	Glu	Trp	Asp	Phe	Val	Ile	Thr	Thr	Asp	Ile	Ser
	1895					1900					1905			
Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp	Arg	Val	Ile	Asp	Ser	Arg
	1910					1915					1920			
Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp	Gly	Glu	Arg	Val	Ile	Leu
	1925					1930					1935			
Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala	Ser	Ala	Ala	Gln	Arg	Arg
	1940					1945					1950			
Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys	Pro	Gly	Asp	Glu	Tyr	Met
	1955					1960					1965			
Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp	Glu	Asp	His	Ala	His	Trp
	1970					1975					1980			
Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn	Ile	Tyr	Leu	Gln	Asp	Gly
	1985					1990					1995			
Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu	Ala	Asp	Lys	Val	Ala	Ala
	2000					2005					2010			
Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr	Glu	Gln	Arg	Lys	Thr	Phe
	2015					2020					2025			
Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu	Pro	Val	Trp	Leu	Ala	Tyr
	2030					2035					2040			
Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr	Thr	Asp	Arg	Arg	Trp	Cys
	2045					2050					2055			
Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile	Met	Glu	Asp	Ser	Val	Pro
	2060					2065					2070			
Ala	Glu	Val	Trp	Thr	Lys	Tyr	Gly	Glu	Lys	Arg	Val	Leu	Lys	Pro
	2075					2080					2085			
Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser	Asp	His	Ala	Ala	Leu	Lys
	2090					2095					2100			
Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys	Arg	Gly	Ala	Ala	Leu	Gly
	2105					2110					2115			

Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro	Gly	His	Met	Thr	Glu	Arg
2120						2125					2130			
Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala	Val	Leu	Met	Arg	Ala	Glu
2135						2140					2145			
Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala	Ala	Ala	Gln	Leu	Pro	Glu
2150						2155					2160			
Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly	Leu	Leu	Gly	Thr	Val	Ser
2165						2170					2175			
Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg	Asn	Lys	Gly	Ile	Gly	Lys
2180						2185					2190			
Met	Gly	Phe	Glu	Met	Val	Thr	Leu	Gly	Ala	Ser	Ala	Trp	Leu	Met
2195						2200					2205			
Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg	Ile	Ala	Cys	Val	Leu	Ile
2210						2215					2220			
Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu	Ile	Pro	Glu	Pro	Glu	Lys
2225						2230					2235			
Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met	Ala	Ile	Ile	Ile	Met	Val
2240						2245					2250			
Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr	Ala	Asn	Glu	Leu	Gly	Trp
2255						2260					2265			
Leu	Glu	Arg	Thr	Lys	Asn	Asp	Ile	Ala	His	Leu	Met	Gly	Lys	Arg
2270						2275					2280			
Glu	Glu	Gly	Thr	Thr	Val	Gly	Phe	Ser	Met	Asp	Ile	Asp	Leu	Arg
2285						2290					2295			
Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala	Ala	Leu	Thr	Thr	Leu	Ile
2300						2305					2310			
Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr	Thr	Ser	Tyr	Asn	Asn	Tyr
2315						2320					2325			

Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala	Gly	Val	Leu	Phe	Gly	Met
2330						2335					2340			
Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp	Asp	Leu	Gly	Val	Pro	Leu
2345						2350					2355			
Leu	Met	Met	Gly	Cys	Tyr	Ser	Gln	Leu	Thr	Pro	Leu	Thr	Leu	Ile
2360						2365					2370			
Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His	Tyr	Met	Tyr	Leu	Ile	Pro
2375						2380					2385			
Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala	Ala	Gln	Lys	Arg	Thr	Ala
2390						2395					2400			
Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val	Asp	Gly	Ile	Val	Val	Thr
2405						2410					2415			
Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro	Gln	Val	Glu	Lys	Lys	Met
2420						2425					2430			
Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala	Val	Ser	Ser	Ala	Val	Leu
2435						2440					2445			
Leu	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu	Ala	Gly	Ala	Leu	Ile	Thr
2450						2455					2460			
Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly	Ser	Pro	Asn	Lys	Tyr	Trp
2465						2470					2475			
Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys	Asn	Ile	Phe	Arg	Gly	Ser
2480						2485					2490			
Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr	Thr	Val	Thr	Arg	Asn	Ala
2495						2500					2505			
Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly	Thr	Gly	Glu	Thr	Leu	Gly
2510						2515					2520			
Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln	Met	Ser	Ala	Leu	Glu	Phe
2525						2530					2535			
Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr	Glu	Val	Cys	Arg	Glu	Glu
2540						2545					2550			

Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val	Ala	Thr	Gly	Gly	His	Ala
2555						2560					2565			
Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg	Trp	Leu	Val	Glu	Arg	Gly
2570						2575					2580			
Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Val	Asp	Leu	Gly	Cys	Gly	Arg
2585						2590					2595			
Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr	Ile	Arg	Lys	Val	Gln	Glu
2600						2605					2610			
Val	Arg	Gly	Tyr	Thr	Lys	Gly	Gly	Pro	Gly	His	Glu	Glu	Pro	Met
2615						2620					2625			
Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile	Ile	Arg	Leu	Lys	Ser	Gly
2630						2635					2640			
Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu	Ser	Cys	Asp	Thr	Leu	Leu
2645						2650					2655			
Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser	Pro	Glu	Val	Glu	Glu	Thr
2660						2665					2670			
Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val	Gly	Asp	Trp	Leu	Glu	Lys
2675						2680					2685			
Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val	Leu	Cys	Pro	Tyr	Thr	Ser
2690						2695					2700			
Thr	Met	Met	Glu	Thr	Met	Glu	Arg	Leu	Gln	Arg	Arg	Tyr	Gly	Gly
2705						2710					2715			
Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg	Asn	Ser	Thr	His	Glu	Met
2720						2725					2730			
Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn	Ile	Ile	Lys	Ser	Val	Ser
2735						2740					2745			
Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg	Met	Asp	Gly	Pro	Arg	Arg
2750						2755					2760			

Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn	Leu	Gly	Ser	Gly	Thr	Arg
2765						2770					2775			
Ala	Val	Ala	Ser	Cys	Ala	Glu	Ala	Pro	Asn	Met	Lys	Val	Ile	Gly
2780						2785					2790			
Arg	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu	His	Ala	Glu	Thr	Trp	Phe
2795						2800					2805			
Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr	Trp	Ala	Tyr	His	Gly	Ser
2810						2815					2820			
Tyr	Glu	Ala	Pro	Thr	Gln	Gly	Ser	Ala	Ser	Ser	Leu	Val	Asn	Gly
2825						2830					2835			
Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp	Asp	Val	Val	Thr	Gly	Val
2840						2845					2850			
Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr	Pro	Tyr	Gly	Gln	Gln	Arg
2855						2860					2865			
Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg	Val	Pro	Asp	Pro	Gln	Glu
2870						2875					2880			
Gly	Thr	Arg	Gln	Val	Met	Asn	Met	Val	Ala	Ser	Trp	Leu	Trp	Lys
2885						2890					2895			
Glu	Leu	Gly	Lys	Arg	Lys	Arg	Pro	Arg	Val	Cys	Thr	Lys	Glu	Glu
2900						2905					2910			
Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala	Ala	Leu	Gly	Ala	Ile	Phe
2915						2920					2925			
Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	Val	Glu	Ala	Val	Asn	Asp
2930						2935					2940			
Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys	Glu	Arg	Glu	His	His	Leu
2945						2950					2955			
Arg	Gly	Glu	Cys	His	Ser	Cys	Val	Tyr	Asn	Met	Met	Gly	Lys	Arg
2960						2965					2970			
Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys	Ala	Lys	Gly	Ser	Arg	Ala
2975						2980					2985			

Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg	Phe	Leu	Glu	Phe	Glu	Ala
2990						2995					3000			
Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp	Met	Gly	Arg	Glu	Asn	Ser
3005						3010					3015			
Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu	Gln	Arg	Leu	Gly	Tyr	Val
3020						3025					3030			
Leu	Glu	Glu	Met	Ser	Arg	Ala	Pro	Gly	Gly	Lys	Met	Tyr	Ala	Asp
3035						3040					3045			
Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile	Ser	Lys	Phe	Asp	Leu	Glu
3050						3055					3060			
Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met	Asp	Glu	Gly	His	Arg	Thr
3065						3070					3075			
Leu	Ala	Leu	Ala	Val	Ile	Lys	Tyr	Thr	Tyr	Gln	Asn	Lys	Val	Val
3080						3085					3090			
Lys	Val	Leu	Arg	Pro	Ala	Glu	Gly	Gly	Lys	Thr	Val	Met	Asp	Ile
3095						3100					3105			
Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser	Gly	Gln	Val	Val	Thr	Tyr
3110						3115					3120			
Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val	Val	Gln	Leu	Ile	Arg	Asn
3125						3130					3135			
Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met	Gln	Asp	Leu	Trp	Leu	Leu
3140						3145					3150			
Arg	Lys	Pro	Glu	Lys	Val	Thr	Arg	Trp	Leu	Gln	Ser	Ser	Gly	Trp
3155						3160					3165			
Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser	Gly	Asp	Asp	Cys	Val	Val
3170						3175					3180			
Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His	Ala	Leu	Arg	Phe	Leu	Asn
3185						3190					3195			

Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr	Gln	Glu	Trp	Lys	Pro	Ser
3200						3205					3210			
Thr	Gly	Trp	Ser	Asn	Trp	Glu	Glu	Val	Pro	Phe	Cys	Ser	His	His
3215						3220					3225			
Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly	Arg	Ser	Ile	Val	Val	Pro
3230						3235					3240			
Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly	Arg	Ala	Arg	Val	Ser	Pro
3245						3250					3255			
Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr	Ala	Cys	Leu	Ala	Lys	Ser
3260						3265					3270			
Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr	Phe	His	Arg	Arg	Asp	Leu
3275						3280					3285			
Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser	Ala	Val	Pro	Val	Asp	Trp
3290						3295					3300			
Val	Pro	Thr	Gly	Arg	Thr	Thr	Trp	Ser	Ile	His	Gly	Lys	Gly	Glu
3305						3310					3315			
Trp	Met	Thr	Thr	Glu	Asp	Met	Leu	Met	Val	Trp	Asn	Arg	Val	Trp
3320						3325					3330			
Ile	Glu	Glu	Asn	Asp	His	Met	Glu	Asp	Lys	Thr	Pro	Val	Thr	Lys
3335						3340					3345			
Trp	Thr	Asp	Ile	Pro	Tyr	Leu	Gly	Lys	Arg	Glu	Asp	Leu	Trp	Cys
3350						3355					3360			
Gly	Ser	Leu	Ile	Gly	His	Arg	Pro	Arg	Thr	Thr	Trp	Ala	Glu	Asn
3365						3370					3375			
Ile	Lys	Asp	Thr	Val	Ser	Met	Val	Arg	Arg	Ile	Ile	Gly	Asp	Glu
3380						3385					3390			
Glu	Lys	Tyr	Met	Asp	Tyr	Leu	Ser	Thr	Gln	Val	Arg	Tyr	Leu	Gly
3395						3400					3405			
Glu	Glu	Gly	Ser	Thr	Pro	Gly	Val	Leu						
3410						3415								

<210> 106
 <211> 3423
 <212> PRT
 <213> Zika virus isolate Brazil-ZKV2015

<400> 106

Met Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn Met
 1 5 10 15

Leu Lys Arg Gly Val Ala Arg Val Ser Pro Phe Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met Val Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Leu Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met Glu Ile
 65 70 75 80

Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile Ile Asn
 85 90 95

Ala Arg Lys Glu Lys Lys Arg Arg Gly Ala Asp Thr Ser Val Gly Ile
 100 105 110

Val Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Val Thr Arg Arg
 115 120 125

Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala
 130 135 140

Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile
 145 150 155 160

Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro
 165 170 175

Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp Cys Trp Cys Asn
 180 185 190

Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His His Lys Lys Gly

195																
Glu	Ala	Arg	Arg	Ser	Arg	Arg	Ala	Val	Thr	Leu	Pro	Ser	His	Ser	Thr	
210						215					220					
Arg	Lys	Leu	Gln	Thr	Arg	Ser	Gln	Thr	Trp	Leu	Glu	Ser	Arg	Glu	Tyr	
225					230					235					240	
Thr	Lys	His	Leu	Ile	Arg	Val	Glu	Asn	Trp	Ile	Phe	Arg	Asn	Pro	Gly	
				245					250					255		
Phe	Ala	Leu	Ala	Ala	Ala	Ala	Ile	Ala	Trp	Leu	Leu	Gly	Ser	Ser	Thr	
			260					265					270			
Ser	Gln	Lys	Val	Ile	Tyr	Leu	Val	Met	Ile	Leu	Leu	Ile	Ala	Pro	Ala	
		275					280					285				
Tyr	Ser	Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	
290						295					300					
Met	Ser	Gly	Gly	Thr	Trp	Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys	
305					310					315					320	
Val	Thr	Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val	
				325					330					335		
Thr	Thr	Thr	Val	Ser	Asn	Met	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Glu	
			340					345					350			
Ala	Ser	Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	Gly	
		355					360					365				
Glu	Ala	Tyr	Leu	Asp	Lys	Gln	Ser	Asp	Thr	Gln	Tyr	Val	Cys	Lys	Arg	
370						375					380					
Thr	Leu	Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	
385					390					395					400	
Gly	Ser	Leu	Val	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Lys	Lys	Met	Thr	
				405					410					415		
Gly	Lys	Ser	Ile	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu	Ser	
			420					425					430			

Val His Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His
435 440 445

Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro
450 455 460

Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys
465 470 475 480

Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met
485 490 495

Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro
500 505 510

Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn
515 520 525

Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr
530 535 540

Val Val Val Leu Gly Thr Gln Glu Gly Ala Val His Thr Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly
580 585 590

Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro
595 600 605

Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly
610 615 620

Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln
625 630 635 640

Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr
645 650 655

Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe

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

Arg Leu Pro Val Pro Val Asn Glu Leu Pro His Gly Trp Lys Ala Trp
900 905 910

Gly Lys Ser Tyr Phe Val Arg Ala Ala Lys Thr Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Leu Lys Glu Cys Pro Leu Lys His Arg Ala Trp
930 935 940

Asn Ser Phe Leu Val Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Val Trp Leu Lys Val Arg Glu Asp Tyr Ser Leu Glu Cys Asp Pro Ala
965 970 975

Val Ile Gly Thr Ala Val Lys Gly Lys Glu Ala Val His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Lys Asn Asp Thr Trp Arg Leu Lys Arg
995 1000 1005

Ala His Leu Ile Glu Met Lys Thr Cys Glu Trp Pro Lys Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Ile Glu Glu Ser Asp Leu Ile Ile Pro
1025 1030 1035

Lys Ser Leu Ala Gly Pro Leu Ser His His Asn Thr Arg Glu Gly
1040 1045 1050

Tyr Arg Thr Gln Met Lys Gly Pro Trp His Ser Glu Glu Leu Glu
1055 1060 1065

Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val Glu Glu
1070 1075 1080

Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala Ser
1085 1090 1095

Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
1100 1105 1110

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu

1115						1120						1125			
Ile Arg Pro Arg Lys Glu	Pro Glu Ser Asn Leu	Val Arg Ser Met													
1130						1135						1140			
Val Thr Ala Gly Ser Thr	Asp His Met Asp His	Phe Ser Leu Gly													
1145						1150						1155			
Val Leu Val Ile Leu Leu	Met Val Gln Glu Gly	Leu Lys Lys Arg													
1160						1165						1170			
Met Thr Thr Lys Ile Ile	Ile Ser Thr Ser Met	Ala Val Leu Val													
1175						1180						1185			
Ala Met Ile Leu Gly Gly	Phe Ser Met Ser Asp	Leu Ala Lys Leu													
1190						1195						1200			
Ala Ile Leu Met Gly Ala	Thr Phe Ala Glu Met	Asn Thr Gly Gly													
1205						1210						1215			
Asp Val Ala His Leu Ala	Leu Ile Ala Ala Phe	Lys Val Arg Pro													
1220						1225						1230			
Ala Leu Leu Val Ser Phe	Ile Phe Arg Ala Asn	Trp Thr Pro Arg													
1235						1240						1245			
Glu Ser Met Leu Leu Ala	Leu Ala Ser Cys Phe	Leu Gln Thr Ala													
1250						1255						1260			
Ile Ser Ala Leu Glu Gly	Asp Leu Met Val Leu	Ile Asn Gly Phe													
1265						1270						1275			
Ala Leu Ala Trp Leu Ala	Ile Arg Ala Met Val	Val Pro Arg Thr													
1280						1285						1290			
Asp Asn Ile Thr Leu Ala	Ile Leu Ala Ala Leu	Thr Pro Leu Ala													
1295						1300						1305			
Arg Gly Thr Leu Leu Val	Ala Trp Arg Ala Gly	Leu Ala Thr Cys													
1310						1315						1320			
Gly Gly Phe Met Leu Leu	Ser Leu Lys Gly Lys	Gly Ser Val Lys													
1325						1330						1335			

Lys	Asn	Leu	Pro	Phe	Val	Met	Ala	Leu	Gly	Leu	Thr	Ala	Val	Arg
1340						1345					1350			
Leu	Val	Asp	Pro	Ile	Asn	Val	Val	Gly	Leu	Leu	Leu	Leu	Thr	Arg
1355						1360					1365			
Ser	Gly	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Leu	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Leu	Ala	Gly	Gly	Phe	Ala	Lys	Ala	Asp	Ile
1385						1390					1395			
Glu	Met	Ala	Gly	Pro	Met	Ala	Ala	Val	Gly	Leu	Leu	Ile	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Arg	Ala
1415						1420					1425			
Gly	Asp	Ile	Thr	Trp	Glu	Lys	Asp	Ala	Glu	Val	Thr	Gly	Asn	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Glu	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Val	Glu	Asp	Asp	Gly	Pro	Pro	Met	Arg	Glu	Ile	Ile	Leu	Lys	Val
1460						1465					1470			
Val	Leu	Met	Thr	Ile	Cys	Gly	Met	Asn	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Gly	Ala	Trp	Tyr	Val	Tyr	Val	Lys	Thr	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Leu	Trp	Asp	Val	Pro	Ala	Pro	Lys	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Asp	Gly	Val	Tyr	Arg	Val	Met	Thr	Arg	Arg	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Val	Gly	Val	Met	Gln	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly

1550						1555						1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asp	Val	Lys	Gln	Asp	Leu	
1565						1570					1575				
Val	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Ala	Ala	Trp	Asp	Gly	
1580						1585					1590				
His	Ser	Glu	Val	Gln	Leu	Leu	Ala	Val	Pro	Pro	Gly	Glu	Arg	Ala	
1595						1600					1605				
Arg	Asn	Ile	Gln	Thr	Leu	Pro	Gly	Ile	Phe	Lys	Thr	Lys	Asp	Gly	
1610						1615					1620				
Asp	Ile	Gly	Ala	Val	Ala	Leu	Asp	Tyr	Pro	Ala	Gly	Thr	Ser	Gly	
1625						1630					1635				
Ser	Pro	Ile	Leu	Asp	Lys	Cys	Gly	Arg	Val	Ile	Gly	Leu	Tyr	Gly	
1640						1645					1650				
Asn	Gly	Val	Val	Ile	Lys	Asn	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Thr	
1655						1660					1665				
Gln	Gly	Arg	Arg	Glu	Glu	Glu	Thr	Pro	Val	Glu	Cys	Phe	Glu	Pro	
1670						1675					1680				
Ser	Met	Leu	Lys	Lys	Lys	Gln	Leu	Thr	Val	Leu	Asp	Leu	His	Pro	
1685						1690					1695				
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Glu	Ile	Val	Arg	Glu	
1700						1705					1710				
Ala	Ile	Lys	Thr	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg	
1715						1720					1725				
Val	Val	Ala	Ala	Glu	Met	Glu	Glu	Ala	Leu	Arg	Gly	Leu	Pro	Val	
1730						1735					1740				
Arg	Tyr	Met	Thr	Thr	Ala	Val	Asn	Val	Thr	His	Ser	Gly	Thr	Glu	
1745						1750					1755				
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Leu	
1760						1765					1770				

Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ser	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ser	Thr	Arg	Val	Glu	Met	Gly	Glu	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Thr	Arg	Asp	Ala	Phe	Pro	Asp	Ser	Asn	Ser
1820						1825					1830			
Pro	Ile	Met	Asp	Thr	Glu	Val	Glu	Val	Pro	Glu	Arg	Ala	Trp	Ser
1835						1840					1845			
Ser	Gly	Phe	Asp	Trp	Val	Thr	Asp	His	Ser	Gly	Lys	Thr	Val	Trp
1850						1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Asn	Gly	Asn	Glu	Ile	Ala	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Arg	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Phe	Gln	Lys	Thr	Lys	His	Gln	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Arg	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Gly	Glu	Arg	Val	Ile	Leu	Ala	Gly	Pro	Met	Pro	Val	Thr	His	Ala
1940						1945					1950			
Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	Asn	Lys
1955						1960					1965			
Pro	Gly	Asp	Glu	Tyr	Leu	Tyr	Gly	Gly	Gly	Cys	Ala	Glu	Thr	Asp
1970						1975					1980			
Glu	Asp	His	Ala	His	Trp	Leu	Glu	Ala	Arg	Met	Leu	Leu	Asp	Asn

1985						1990						1995					
Ile	Tyr	Leu	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Pro	Glu			
2000						2005					2010						
Ala	Asp	Lys	Val	Ala	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	Arg	Thr			
2015						2020					2025						
Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	Asp	Leu			
2030						2035					2040						
Pro	Val	Trp	Leu	Ala	Tyr	Gln	Val	Ala	Ser	Ala	Gly	Ile	Thr	Tyr			
2045						2050					2055						
Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Thr	Thr	Asn	Asn	Thr	Ile			
2060						2065					2070						
Met	Glu	Asp	Ser	Val	Pro	Ala	Glu	Val	Trp	Thr	Arg	His	Gly	Glu			
2075						2080					2085						
Lys	Arg	Val	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Val	Cys	Ser			
2090						2095					2100						
Asp	His	Ala	Ala	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	Gly	Lys			
2105						2110					2115						
Arg	Gly	Ala	Ala	Phe	Gly	Val	Met	Glu	Ala	Leu	Gly	Thr	Leu	Pro			
2120						2125					2130						
Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Ile	Asp	Asn	Leu	Ala			
2135						2140					2145						
Val	Leu	Met	Arg	Ala	Glu	Thr	Gly	Ser	Arg	Pro	Tyr	Lys	Ala	Ala			
2150						2155					2160						
Ala	Ala	Gln	Leu	Pro	Glu	Thr	Leu	Glu	Thr	Ile	Met	Leu	Leu	Gly			
2165						2170					2175						
Leu	Leu	Gly	Thr	Val	Ser	Leu	Gly	Ile	Phe	Phe	Val	Leu	Met	Arg			
2180						2185					2190						
Asn	Lys	Gly	Ile	Gly	Lys	Met	Gly	Phe	Gly	Met	Val	Thr	Leu	Gly			
2195						2200					2205						

Ala	Ser	Ala	Trp	Leu	Met	Trp	Leu	Ser	Glu	Ile	Glu	Pro	Ala	Arg
2210						2215					2220			
Ile	Ala	Cys	Val	Leu	Ile	Val	Val	Phe	Leu	Leu	Leu	Val	Val	Leu
2225						2230					2235			
Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn	Gln	Met
2240						2245					2250			
Ala	Ile	Ile	Ile	Met	Val	Ala	Val	Gly	Leu	Leu	Gly	Leu	Ile	Thr
2255						2260					2265			
Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp	Leu	Ser
2270						2275					2280			
His	Leu	Met	Gly	Arg	Arg	Glu	Glu	Gly	Ala	Thr	Ile	Gly	Phe	Ser
2285						2290					2295			
Met	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser	Ala	Trp	Ala	Ile	Tyr	Ala
2300						2305					2310			
Ala	Leu	Thr	Thr	Phe	Ile	Thr	Pro	Ala	Val	Gln	His	Ala	Val	Thr
2315						2320					2325			
Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met	Ala	Met	Ala	Thr	Gln	Ala
2330						2335					2340			
Gly	Val	Leu	Phe	Gly	Met	Gly	Lys	Gly	Met	Pro	Phe	Tyr	Ala	Trp
2345						2350					2355			
Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Ile	Gly	Cys	Tyr	Ser	Gln	Leu
2360						2365					2370			
Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Ile	Ile	Leu	Leu	Val	Ala	His
2375						2380					2385			
Tyr	Met	Tyr	Leu	Ile	Pro	Gly	Leu	Gln	Ala	Ala	Ala	Ala	Arg	Ala
2390						2395					2400			
Ala	Gln	Lys	Arg	Thr	Ala	Ala	Gly	Ile	Met	Lys	Asn	Pro	Val	Val
2405						2410					2415			
Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp	Thr	Met	Thr	Ile	Asp	Pro

2420						2425						2430			
Gln	Val	Glu	Lys	Lys	Met	Gly	Gln	Val	Leu	Leu	Ile	Ala	Val	Ala	
2435						2440					2445				
Val	Ser	Ser	Ala	Ile	Leu	Ser	Arg	Thr	Ala	Trp	Gly	Trp	Gly	Glu	
2450						2455					2460				
Ala	Gly	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Ser	Thr	Leu	Trp	Glu	Gly	
2465						2470					2475				
Ser	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser	Thr	Ala	Thr	Ser	Leu	Cys	
2480						2485					2490				
Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala	Gly	Ala	Ser	Leu	Ile	Tyr	
2495						2500					2505				
Thr	Val	Thr	Arg	Asn	Ala	Gly	Leu	Val	Lys	Arg	Arg	Gly	Gly	Gly	
2510						2515					2520				
Thr	Gly	Glu	Thr	Leu	Gly	Glu	Lys	Trp	Lys	Ala	Arg	Leu	Asn	Gln	
2525						2530					2535				
Met	Ser	Ala	Leu	Glu	Phe	Tyr	Ser	Tyr	Lys	Lys	Ser	Gly	Ile	Thr	
2540						2545					2550				
Glu	Val	Cys	Arg	Glu	Glu	Ala	Arg	Arg	Ala	Leu	Lys	Asp	Gly	Val	
2555						2560					2565				
Ala	Thr	Gly	Gly	His	Ala	Val	Ser	Arg	Gly	Ser	Ala	Lys	Leu	Arg	
2570						2575					2580				
Trp	Leu	Val	Glu	Arg	Gly	Tyr	Leu	Gln	Pro	Tyr	Gly	Lys	Val	Ile	
2585						2590					2595				
Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Ser	Tyr	Tyr	Ala	Ala	Thr	
2600						2605					2610				
Ile	Arg	Lys	Val	Gln	Glu	Val	Lys	Gly	Tyr	Thr	Lys	Gly	Gly	Pro	
2615						2620					2625				
Gly	His	Glu	Glu	Pro	Val	Leu	Val	Gln	Ser	Tyr	Gly	Trp	Asn	Ile	
2630						2635					2640				

Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val	Phe	His	Met	Ala	Ala	Glu
2645						2650					2655			
Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser	Ser	Ser	Ser
2660						2665					2670			
Pro	Glu	Val	Glu	Glu	Ala	Arg	Thr	Leu	Arg	Val	Leu	Ser	Met	Val
2675						2680					2685			
Gly	Asp	Trp	Leu	Glu	Lys	Arg	Pro	Gly	Ala	Phe	Cys	Ile	Lys	Val
2690						2695					2700			
Leu	Cys	Pro	Tyr	Thr	Ser	Thr	Met	Met	Glu	Thr	Leu	Glu	Arg	Leu
2705						2710					2715			
Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Val	Pro	Leu	Ser	Arg
2720						2725					2730			
Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Gly	Ala	Lys	Ser	Asn
2735						2740					2745			
Thr	Ile	Lys	Ser	Val	Ser	Thr	Thr	Ser	Gln	Leu	Leu	Leu	Gly	Arg
2750						2755					2760			
Met	Asp	Gly	Pro	Arg	Arg	Pro	Val	Lys	Tyr	Glu	Glu	Asp	Val	Asn
2765						2770					2775			
Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Val	Ser	Cys	Ala	Glu	Ala	Pro
2780						2785					2790			
Asn	Met	Lys	Ile	Ile	Gly	Asn	Arg	Ile	Glu	Arg	Ile	Arg	Ser	Glu
2795						2800					2805			
His	Ala	Glu	Thr	Trp	Phe	Phe	Asp	Glu	Asn	His	Pro	Tyr	Arg	Thr
2810						2815					2820			
Trp	Ala	Tyr	His	Gly	Ser	Tyr	Val	Ala	Pro	Thr	Gln	Gly	Ser	Ala
2825						2830					2835			
Ser	Ser	Leu	Ile	Asn	Gly	Val	Val	Arg	Leu	Leu	Ser	Lys	Pro	Trp
2840						2845					2850			
Asp	Val	Val	Thr	Gly	Val	Thr	Gly	Ile	Ala	Met	Thr	Asp	Thr	Thr

2855						2860						2865			
Pro	Tyr	Gly	Gln	Gln	Arg	Val	Phe	Lys	Glu	Lys	Val	Asp	Thr	Arg	
2870						2875					2880				
Val	Pro	Asp	Pro	Gln	Glu	Gly	Thr	Arg	Gln	Val	Met	Ser	Met	Val	
2885						2890					2895				
Ser	Ser	Trp	Leu	Trp	Lys	Glu	Leu	Gly	Lys	His	Lys	Arg	Pro	Arg	
2900						2905					2910				
Val	Cys	Thr	Lys	Glu	Glu	Phe	Ile	Asn	Lys	Val	Arg	Ser	Asn	Ala	
2915						2920					2925				
Ala	Leu	Gly	Ala	Ile	Phe	Glu	Glu	Glu	Lys	Glu	Trp	Lys	Thr	Ala	
2930						2935					2940				
Val	Glu	Ala	Val	Asn	Asp	Pro	Arg	Phe	Trp	Ala	Leu	Val	Asp	Lys	
2945						2950					2955				
Glu	Arg	Glu	His	His	Leu	Arg	Gly	Glu	Cys	Gln	Ser	Cys	Val	Tyr	
2960						2965					2970				
Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	Gln	Gly	Glu	Phe	Gly	Lys	
2975						2980					2985				
Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	Met	Trp	Leu	Gly	Ala	Arg	
2990						2995					3000				
Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	Leu	Asn	Glu	Asp	His	Trp	
3005						3010					3015				
Met	Gly	Arg	Glu	Asn	Ser	Gly	Gly	Gly	Val	Glu	Gly	Leu	Gly	Leu	
3020						3025					3030				
Gln	Arg	Leu	Gly	Tyr	Val	Leu	Glu	Glu	Met	Ser	Arg	Ile	Pro	Gly	
3035						3040					3045				
Gly	Arg	Met	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp	Asp	Thr	Arg	Ile	
3050						3055					3060				
Ser	Arg	Phe	Asp	Leu	Glu	Asn	Glu	Ala	Leu	Ile	Thr	Asn	Gln	Met	
3065						3070					3075				

Glu	Lys	Gly	His	Arg	Ala	Leu	Ala	Leu	Ala	Ile	Ile	Lys	Tyr	Thr
3080						3085					3090			
Tyr	Gln	Asn	Lys	Val	Val	Lys	Val	Leu	Arg	Pro	Ala	Glu	Lys	Gly
3095						3100					3105			
Lys	Thr	Val	Met	Asp	Ile	Ile	Ser	Arg	Gln	Asp	Gln	Arg	Gly	Ser
3110						3115					3120			
Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe	Thr	Asn	Leu	Val
3125						3130					3135			
Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala	Glu	Glu	Val	Leu	Glu	Met
3140						3145					3150			
Gln	Asp	Leu	Trp	Leu	Leu	Arg	Arg	Ser	Glu	Lys	Val	Thr	Asn	Trp
3155						3160					3165			
Leu	Gln	Ser	Asn	Gly	Trp	Asp	Arg	Leu	Lys	Arg	Met	Ala	Val	Ser
3170						3175					3180			
Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Ile	Asp	Asp	Arg	Phe	Ala	His
3185						3190					3195			
Ala	Leu	Arg	Phe	Leu	Asn	Asp	Met	Gly	Lys	Val	Arg	Lys	Asp	Thr
3200						3205					3210			
Gln	Glu	Trp	Lys	Pro	Ser	Thr	Gly	Trp	Asp	Asn	Trp	Glu	Glu	Val
3215						3220					3225			
Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys	Leu	His	Leu	Lys	Asp	Gly
3230						3235					3240			
Arg	Ser	Ile	Val	Val	Pro	Cys	Arg	His	Gln	Asp	Glu	Leu	Ile	Gly
3245						3250					3255			
Arg	Ala	Arg	Val	Ser	Pro	Gly	Ala	Gly	Trp	Ser	Ile	Arg	Glu	Thr
3260						3265					3270			
Ala	Cys	Leu	Ala	Lys	Ser	Tyr	Ala	Gln	Met	Trp	Gln	Leu	Leu	Tyr
3275						3280					3285			
Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met	Ala	Asn	Ala	Ile	Cys	Ser

3290		3295		3300
Ser Val Pro Val Asp Trp Val Pro Thr Gly Arg Thr Thr Trp Ser				
3305		3310		3315
Ile His Gly Lys Gly Glu Trp Met Thr Thr Glu Asp Met Leu Val				
3320		3325		3330
Val Trp Asn Arg Val Trp Ile Glu Glu Asn Asp His Met Glu Asp				
3335		3340		3345
Lys Thr Pro Val Thr Lys Trp Thr Asp Ile Pro Tyr Leu Gly Lys				
3350		3355		3360
Arg Glu Asp Leu Trp Cys Gly Ser Leu Ile Gly His Arg Pro Arg				
3365		3370		3375
Thr Thr Trp Ala Glu Asn Ile Lys Asn Thr Val Asn Met Val Arg				
3380		3385		3390
Arg Ile Ile Gly Asp Glu Glu Lys Tyr Met Asp Tyr Leu Ser Thr				
3395		3400		3405
Gln Val Arg Tyr Leu Gly Glu Glu Gly Ser Thr Pro Gly Val Leu				
3410		3415		3420

<210> 107
 <211> 3429
 <212> PRT
 <213> Spondweni virus strain SM-6 V-1 polyprotein

<400> 107

Met Lys Asn Pro Lys Arg Ala Gly Ser Ser Arg Leu Val Asn Met Leu
1 5 10 15
Arg Arg Gly Ala Ala Arg Val Ile Pro Pro Gly Gly Gly Leu Lys Arg
20 25 30
Leu Pro Val Gly Leu Leu Leu Gly Arg Gly Pro Ile Lys Met Ile Leu
35 40 45
Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Thr Gly
50 55 60

Leu Ile Asn Arg Trp Gly Lys Val Gly Lys Lys Glu Ala Ile Lys Ile
65 70 75 80

Leu Thr Lys Phe Lys Ala Asp Val Gly Thr Met Leu Arg Ile Ile Asn
85 90 95

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

Ala Leu Leu Val Ser Ile Val Ala Val Glu Val Thr Lys Lys Gly Asp
115 120 125

Thr Tyr Tyr Met Phe Ala Asp Lys Lys Asp Ala Gly Lys Val Val Thr
130 135 140

Phe Glu Thr Glu Ser Gly Pro Asn Arg Cys Ser Ile Gln Ala Met Asp
145 150 155 160

Ile Gly His Met Cys Pro Ala Thr Met Ser Tyr Glu Cys Pro Val Leu
165 170 175

Glu Pro Gln Tyr Glu Pro Glu Asp Val Asp Cys Trp Cys Asn Ser Thr
180 185 190

Ala Ala Trp Ile Val Tyr Gly Thr Cys Thr His Lys Thr Thr Gly Glu
195 200 205

Thr Arg Arg Ser Arg Arg Ser Ile Thr Leu Pro Ser His Ala Ser Gln
210 215 220

Lys Leu Glu Thr Arg Ser Ser Thr Trp Leu Glu Ser Arg Glu Tyr Ser
225 230 235 240

Lys Tyr Leu Ile Lys Val Glu Asn Trp Ile Leu Arg Asn Pro Gly Tyr
245 250 255

Ala Leu Val Ala Ala Val Ile Gly Trp Thr Leu Gly Ser Ser Arg Ser
260 265 270

Gln Lys Ile Ile Phe Val Thr Leu Leu Met Leu Val Ala Pro Ala Tyr
275 280 285

Ser Ile Arg Cys Ile Gly Ile Gly Asn Arg Asp Phe Ile Glu Gly Met
290 295 300

Ser Gly Gly Thr Trp Val Asp Ile Val Leu Glu His Gly Gly Cys Val
 305 310 315 320

Thr Val Met Ser Asn Asp Lys Pro Thr Leu Asp Phe Glu Leu Val Thr
 325 330 335

Thr Thr Ala Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala
 340 345 350

Asn Ile Ser Glu Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu
 355 360 365

Ala Tyr Leu Asp Lys Met Ala Asp Ser Gln Phe Val Cys Lys Arg Gly
 370 375 380

Tyr Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly
 385 390 395 400

Ser Ile Val Thr Cys Ala Lys Phe Thr Cys Val Lys Lys Leu Thr Gly
 405 410 415

Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Val Leu Val Ser Val
 420 425 430

His Ala Ser Gln His Gly Gly Met Ile Asn Asn Asp Thr Asn His Gln
 435 440 445

His Asp Lys Glu Asn Arg Ala Arg Ile Asp Ile Thr Ala Ser Ala Pro
 450 455 460

Arg Val Glu Val Glu Leu Gly Ser Phe Gly Ser Phe Ser Met Glu Cys
 465 470 475 480

Glu Pro Arg Ser Gly Leu Asn Phe Gly Asp Leu Tyr Tyr Leu Thr Met
 485 490 495

Asn Asn Lys His Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Ser
 500 505 510

Leu Pro Trp His Thr Gly Ala Thr Ser Asn Asn His His Trp Asn Asn
 515 520 525

Lys Glu Ala Leu Val Glu Phe Arg Glu Ala His Ala Lys Lys Gln Thr
530 535 540

Ala Val Val Leu Gly Ser Gln Glu Gly Ala Val His Ala Ala Leu Ala
545 550 555 560

Gly Ala Leu Glu Ala Glu Ser Asp Gly His Lys Ala Thr Ile Tyr Ser
565 570 575

Gly His Leu Lys Cys Arg Leu Lys Leu Asp Lys Leu Arg Leu Lys Gly
580 585 590

Met Ser Tyr Ala Leu Cys Thr Gly Ala Phe Thr Phe Ala Arg Thr Pro
595 600 605

Ser Glu Thr Ile His Gly Thr Ala Thr Val Glu Leu Gln Tyr Ala Gly
610 615 620

Glu Asp Gly Pro Cys Lys Val Pro Ile Val Ile Thr Ser Asp Thr Asn
625 630 635 640

Ser Met Ala Ser Thr Gly Arg Leu Ile Thr Ala Asn Pro Val Val Thr
645 650 655

Glu Ser Gly Ala Asn Ser Lys Met Met Val Glu Ile Asp Pro Pro Phe
660 665 670

Gly Asp Ser Tyr Ile Ile Val Gly Thr Gly Thr Thr Lys Ile Thr His
675 680 685

His Trp His Arg Ala Gly Ser Ser Ile Gly Arg Ala Phe Glu Ala Thr
690 695 700

Met Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp
705 710 715 720

Phe Gly Ser Val Gly Gly Met Phe Asn Ser Val Gly Lys Phe Val His
725 730 735

Gln Val Phe Gly Ser Ala Phe Lys Ala Leu Phe Gly Gly Met Ser Trp
740 745 750

Phe Thr Gln Leu Leu Ile Gly Phe Leu Leu Ile Trp Met Gly Leu Asn
755 760 765

Ala Arg Gly Gly Thr Val Ala Met Ser Phe Met Gly Ile Gly Ala Met
770 775 780

Leu Ile Phe Leu Ala Thr Ser Val Ser Gly Asp Thr Gly Cys Ser Val
785 790 795 800

Asp Ile Ser Arg Arg Glu Met Arg Cys Gly Ser Gly Ile Phe Val Tyr
805 810 815

Asn Asp Val Asp Ala Trp Arg Ser Arg Tyr Lys Tyr His Pro Glu Thr
820 825 830

Pro Arg Ala Leu Ala Ala Ala Val Lys Thr Ala Trp Glu Glu Gly Thr
835 840 845

Cys Gly Ile Thr Ser Val Ser Arg Met Glu Asn Leu Met Trp Ser Ser
850 855 860

Val Ala Gly Glu Leu Asn Ala Ile Leu Glu Asp Asn Ser Val Pro Leu
865 870 875 880

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

Arg Leu Lys Pro Pro Ala Ser Glu Leu Pro Gln Gly Trp Lys Ser Trp
900 905 910

Gly Lys Ser Tyr Phe Val Ser Ala Ala Lys Asn Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Met Lys Glu Cys Pro Arg Gln Lys Arg Ala Trp
930 935 940

Asn Ser Leu Arg Ile Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Ile Trp Leu Lys Phe His Glu Asp Asn Ser Thr Glu Cys Asp Thr Ala
965 970 975

Ile Ile Gly Thr Ala Val Arg Gly Lys Glu Ala Val His Ser Asp Leu
980 985 990

Gly	Tyr	Trp	Ile	Glu	Ser	Glu	Arg	Asn	Asp	Thr	Trp	Arg	Leu	Ser	Arg	995	1000	1005
Ala	His	Leu	Ile	Glu	Ala	Lys	Thr	Cys	Glu	Trp	Pro	Arg	Ser	His		1010	1015	1020
Thr	Leu	Trp	Thr	Asp	Gly	Val	Glu	Glu	Ser	Glu	Leu	Ile	Ile	Pro		1025	1030	1035
Arg	Gly	Leu	Ala	Gly	Pro	Phe	Ser	His	His	Asn	Thr	Arg	Ala	Gly		1040	1045	1050
Tyr	Lys	Thr	Gln	Asn	Lys	Gly	Pro	Trp	His	Leu	Gly	Asp	Val	Glu		1055	1060	1065
Ile	Gln	Phe	Ala	Thr	Cys	Pro	Gly	Thr	Thr	Val	Val	Gln	Asp	Gln		1070	1075	1080
Glu	Cys	Arg	Asp	Arg	Gly	Ala	Ser	Leu	Arg	Thr	Thr	Thr	Ala	Ser		1085	1090	1095
Gly	Arg	Val	Ile	Asn	Glu	Trp	Cys	Cys	Arg	Ser	Cys	Thr	Met	Pro		1100	1105	1110
Pro	Leu	Ser	Phe	Lys	Thr	Lys	Asp	Gly	Cys	Trp	Tyr	Ala	Met	Glu		1115	1120	1125
Ile	Arg	Pro	Val	Lys	Glu	Gln	Glu	Ser	Asn	Leu	Val	Arg	Ser	His		1130	1135	1140
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly		1145	1150	1155
Leu	Val	Val	Val	Met	Leu	Met	Val	Gln	Glu	Gly	Met	Lys	Lys	Arg		1160	1165	1170
Met	Thr	Ser	Lys	Ala	Ile	Ile	Thr	Ser	Ala	Ala	Phe	Leu	Leu	Ala		1175	1180	1185
Val	Met	Ile	Val	Gly	Gly	Phe	Thr	Tyr	Gln	Asp	Phe	Gly	Arg	Leu		1190	1195	1200
Val	Val	Leu	Val	Gly	Ala	Ala	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly		1205	1210	1215

Asp	Val	Ala	His	Leu	Ala	Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro
1220						1225					1230			
Ala	Met	Leu	Val	Ser	Phe	Met	Phe	Arg	Ala	Leu	Trp	Thr	Pro	Arg
1235						1240					1245			
Glu	Ser	Leu	Leu	Leu	Ala	Leu	Ala	Ala	Cys	Leu	Leu	Gln	Val	Ser
1250						1255					1260			
Val	Thr	Pro	Leu	Asp	His	Ser	Ile	Met	Ile	Val	Val	Asp	Gly	Ile
1265						1270					1275			
Ala	Leu	Ser	Trp	Leu	Cys	Leu	Lys	Ala	Ile	Leu	Val	Pro	Arg	Thr
1280						1285					1290			
Pro	Asn	Ile	Ala	Leu	Pro	Leu	Leu	Ala	Met	Leu	Ser	Pro	Met	Leu
1295						1300					1305			
Gln	Gly	Thr	Thr	Ile	Val	Ala	Trp	Arg	Ala	Met	Met	Ala	Ala	Leu
1310						1315					1320			
Ala	Val	Ile	Thr	Leu	Ala	Ser	Met	Lys	His	Gly	Arg	Gly	Val	Lys
1325						1330					1335			
Lys	Thr	Phe	Pro	Tyr	Thr	Ile	Gly	Cys	Ile	Leu	Gly	Ser	Met	Gly
1340						1345					1350			
Leu	Val	Glu	Asn	Leu	Gly	Leu	Val	Gly	Leu	Leu	Leu	Leu	Thr	Ala
1355						1360					1365			
Ser	Lys	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Met	Thr	Ala	Val
1370						1375					1380			
Gly	Leu	Ile	Cys	Ala	Ile	Val	Gly	Gly	Leu	Thr	Lys	Thr	Asp	Ile
1385						1390					1395			
Asp	Met	Ala	Gly	Pro	Met	Ala	Ala	Ile	Gly	Leu	Leu	Val	Val	Ser
1400						1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Lys	Val
1415						1420					1425			

Cys	Asp	Ile	Ser	Trp	Asp	Lys	Asp	Ala	Glu	Ile	Thr	Gly	Thr	Ser
1430						1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Asp	Ser	Gly	Asp	Phe	Ser	Leu
1445						1450					1455			
Ile	Gln	Asp	Asp	Gly	Pro	Pro	Thr	Arg	Glu	Ile	Val	Leu	Lys	Val
1460						1465					1470			
Phe	Leu	Met	Cys	Val	Cys	Gly	Val	Ser	Pro	Ile	Ala	Ile	Pro	Phe
1475						1480					1485			
Ala	Ala	Ala	Ala	Trp	Phe	Val	Tyr	Ile	Lys	Ser	Gly	Lys	Arg	Ser
1490						1495					1500			
Gly	Ala	Met	Trp	Asp	Ile	Pro	Ser	Pro	Arg	Glu	Val	Lys	Lys	Gly
1505						1510					1515			
Glu	Thr	Thr	Ala	Gly	Val	Tyr	Arg	Ile	Met	Thr	Arg	Lys	Leu	Leu
1520						1525					1530			
Gly	Ser	Thr	Gln	Val	Gly	Ala	Gly	Val	Met	His	Glu	Gly	Val	Phe
1535						1540					1545			
His	Thr	Met	Trp	His	Val	Thr	Lys	Gly	Ser	Ala	Leu	Arg	Ser	Gly
1550						1555					1560			
Glu	Gly	Arg	Leu	Asp	Pro	Tyr	Trp	Gly	Asn	Val	Lys	Gln	Asp	Leu
1565						1570					1575			
Ile	Ser	Tyr	Cys	Gly	Pro	Trp	Lys	Leu	Asp	Gly	Lys	Trp	Asp	Gly
1580						1585					1590			
Val	Ser	Glu	Val	Gln	Leu	Ile	Ala	Val	Ala	Pro	Gly	Glu	Arg	Ala
1595						1600					1605			
Arg	Asn	Val	Gln	Thr	Lys	Pro	Gly	Val	Phe	Lys	Thr	Thr	Asp	Gly
1610						1615					1620			
Glu	Ile	Gly	Ala	Leu	Ala	Leu	Asp	Phe	Pro	Gly	Gly	Ser	Ser	Gly
1625						1630					1635			
Ser	Pro	Ile	Ile	Asp	Lys	Asn	Gly	His	Val	Ile	Gly	Leu	Tyr	Gly
1640						1645					1650			

Asn	Gly	Val	Val	Val	Lys	Ser	Gly	Ser	Tyr	Val	Ser	Ala	Ile	Met
1655						1660					1665			
Gln	Thr	Glu	Lys	Met	Glu	Glu	Pro	Ala	Val	Asp	Cys	Phe	Glu	Glu
1670						1675					1680			
Asp	Met	Leu	Arg	Lys	Lys	Lys	Leu	Thr	Val	Leu	Asp	Leu	His	Pro
1685						1690					1695			
Gly	Ala	Gly	Lys	Thr	Arg	Arg	Val	Leu	Pro	Gln	Ile	Val	Lys	Ala
1700						1705					1710			
Ala	Ile	Lys	Lys	Arg	Leu	Arg	Thr	Val	Ile	Leu	Ala	Pro	Thr	Arg
1715						1720					1725			
Val	Val	Ala	Ala	Glu	Met	Ala	Glu	Ala	Leu	Lys	Asp	Leu	Pro	Ile
1730						1735					1740			
Arg	Tyr	Met	Thr	Pro	Ala	Val	Ser	Ala	Thr	His	Asp	Gly	Asn	Glu
1745						1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Met
1760						1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
1775						1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ala	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
1790						1795					1800			
Ala	Thr	Arg	Val	Asp	Met	Gly	Asp	Ala	Ala	Ala	Ile	Phe	Met	Thr
1805						1810					1815			
Ala	Thr	Pro	Pro	Gly	Ser	Thr	Glu	Ala	Phe	Pro	Asp	Ser	Asn	Ala
1820						1825					1830			
Pro	Ile	Thr	Asp	Val	Glu	Thr	Glu	Val	Pro	Asp	Lys	Ala	Trp	Asn
1835						1840					1845			
Ser	Gly	Phe	Glu	Trp	Ile	Thr	Asp	Tyr	Pro	Gly	Lys	Thr	Val	Trp
1850						1855					1860			

Phe	Val	Pro	Ser	Val	Arg	Met	Gly	Asn	Glu	Ile	Ser	Ala	Cys	Leu
1865						1870					1875			
Thr	Lys	Ala	Gly	Lys	Ser	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
1880						1885					1890			
Glu	Thr	Glu	Tyr	Gln	Lys	Thr	Lys	Asn	Gly	Glu	Trp	Asp	Phe	Val
1895						1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
1910						1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Lys	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
1925						1930					1935			
Asp	Met	Glu	Glu	Arg	Val	Val	Leu	Ala	Gly	Pro	Met	Ala	Val	Thr
1940						1945					1950			
Pro	Ser	Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro
1955						1960					1965			
Asn	Lys	Thr	Gly	Asp	Glu	Phe	Tyr	Tyr	Gly	Gly	Gly	Cys	Ala	Ala
1970						1975					1980			
Thr	Asp	Asp	Asp	His	Ala	His	Trp	Val	Glu	Ala	Arg	Met	Leu	Leu
1985						1990					1995			
Asp	Asn	Ile	Tyr	Leu	Gln	Asp	Asn	Leu	Val	Ala	Ser	Leu	Tyr	Lys
2000						2005					2010			
Pro	Glu	Gln	Gly	Lys	Val	Ser	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu
2015						2020					2025			
Arg	Gly	Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly
2030						2035					2040			
Asp	Leu	Pro	Val	Trp	Leu	Ser	Tyr	Gln	Val	Ala	Ala	Ser	Gly	Leu
2045						2050					2055			
Ser	Tyr	Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Lys	Asn	Asn	Asn
2060						2065					2070			
Thr	Ile	Leu	Glu	Asp	Cys	Val	Pro	Val	Glu	Val	Trp	Thr	Lys	Phe
2075						2080					2085			

Gly	Glu	Lys	Lys	Ile	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Ile
2090						2095					2100			
Cys	Ser	Asp	His	Ala	Ser	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala
2105						2110					2115			
Gly	Lys	Arg	Thr	Ile	Ala	Thr	Gly	Leu	Ile	Glu	Ala	Phe	Gly	Met
2120						2125					2130			
Leu	Pro	Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Val	Asp	Asn
2135						2140					2145			
Leu	Ala	Val	Leu	Met	Arg	Ala	Glu	Ala	Gly	Ser	Arg	Ala	His	Arg
2150						2155					2160			
Met	Ala	Ala	Ala	Gln	Leu	Pro	Glu	Thr	Met	Glu	Thr	Ile	Leu	Leu
2165						2170					2175			
Leu	Ser	Leu	Leu	Ala	Phe	Val	Ser	Leu	Gly	Val	Phe	Phe	Val	Leu
2180						2185					2190			
Met	Arg	Ala	Lys	Gly	Leu	Gly	Lys	Met	Gly	Ser	Gly	Met	Ile	Val
2195						2200					2205			
Leu	Ala	Gly	Ser	Gly	Trp	Leu	Met	Trp	Met	Ser	Glu	Val	Glu	Pro
2210						2215					2220			
Ala	Arg	Ile	Ala	Cys	Val	Val	Ile	Ile	Val	Phe	Leu	Leu	Met	Val
2225						2230					2235			
Val	Leu	Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn
2240						2245					2250			
Gln	Leu	Ala	Leu	Ile	Ile	Leu	Ile	Ala	Thr	Gly	Leu	Ile	Thr	Leu
2255						2260					2265			
Ile	Ala	Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp
2270						2275					2280			
Leu	Thr	Arg	Leu	Phe	Trp	Arg	Glu	His	Ala	Glu	Pro	Thr	Gly	Gly
2285						2290					2295			

Arg	Gly	Phe	Ser	Phe	Ser	Leu	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser
	2300					2305					2310			
Ala	Trp	Ala	Ile	Tyr	Ala	Ala	Met	Thr	Thr	Leu	Ile	Thr	Pro	Thr
	2315					2320					2325			
Val	Gln	His	Ala	Val	Thr	Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met
	2330					2335					2340			
Ala	Met	Ala	Thr	Gln	Ala	Gly	Val	Leu	Phe	Gly	Met	Gly	Arg	Gly
	2345					2350					2355			
Val	Pro	Phe	Tyr	Lys	Trp	Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Leu
	2360					2365					2370			
Gly	Cys	Tyr	Ser	Gln	Leu	Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Leu
	2375					2380					2385			
Val	Met	Leu	Ala	Ala	His	Tyr	Leu	Tyr	Leu	Ile	Pro	Gly	Leu	Gln
	2390					2395					2400			
Ala	Thr	Ala	Ala	Arg	Ala	Ala	Gln	Arg	Arg	Thr	Ala	Ala	Gly	Ile
	2405					2410					2415			
Met	Lys	Asn	Pro	Val	Val	Asp	Gly	Ile	Val	Val	Thr	Asp	Ile	Asp
	2420					2425					2430			
Pro	Ile	Gln	Ile	Asp	Pro	Asn	Val	Glu	Lys	Lys	Met	Gly	Gln	Val
	2435					2440					2445			
Met	Leu	Ile	Phe	Val	Ala	Leu	Ala	Ser	Ala	Val	Leu	Met	Arg	Thr
	2450					2455					2460			
Ala	Trp	Gly	Trp	Gly	Glu	Ala	Gly	Ala	Leu	Ala	Ser	Ala	Ala	Ala
	2465					2470					2475			
Ala	Thr	Leu	Trp	Glu	Gly	Ala	Pro	Asn	Lys	Tyr	Trp	Asn	Ser	Ser
	2480					2485					2490			
Thr	Ala	Thr	Ser	Leu	Cys	Asn	Ile	Phe	Arg	Gly	Ser	Tyr	Leu	Ala
	2495					2500					2505			
Gly	Pro	Ser	Leu	Ile	Tyr	Thr	Val	Thr	Arg	Asn	Ala	Gly	Ile	Met
	2510					2515					2520			

Lys	Lys	Arg	Gly	Gly	Gly	Asn	Gly	Glu	Thr	Val	Gly	Glu	Lys	Trp
2525						2530					2535			
Lys	Glu	Arg	Leu	Asn	Arg	Met	Thr	Ala	Leu	Glu	Phe	Tyr	Ala	Tyr
2540						2545					2550			
Lys	Arg	Ser	Gly	Ile	Thr	Glu	Val	Cys	Arg	Glu	Pro	Ala	Arg	Arg
2555						2560					2565			
Ala	Leu	Lys	Asp	Gly	Val	Val	Thr	Gly	Gly	His	Ala	Val	Ser	Arg
2570						2575					2580			
Gly	Ser	Ala	Lys	Leu	Arg	Trp	Met	Val	Glu	Arg	Gly	His	Val	Asn
2585						2590					2595			
Leu	Val	Gly	Arg	Val	Val	Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp
2600						2605					2610			
Ser	Tyr	Tyr	Ala	Ala	Ser	Gln	Lys	Gln	Val	Leu	Glu	Val	Arg	Gly
2615						2620					2625			
Tyr	Thr	Lys	Gly	Gly	Ala	Gly	His	Glu	Glu	Pro	Met	Asn	Val	Gln
2630						2635					2640			
Ser	Tyr	Gly	Trp	Asn	Ile	Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val
2645						2650					2655			
Phe	Tyr	Leu	Pro	Ser	Glu	Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile
2660						2665					2670			
Gly	Glu	Ser	Ser	Ser	Ser	Pro	Ala	Val	Glu	Glu	Ala	Arg	Thr	Leu
2675						2680					2685			
Arg	Val	Leu	Gly	Met	Val	Glu	Thr	Trp	Leu	Glu	Arg	Gly	Val	Lys
2690						2695					2700			
Asn	Phe	Cys	Ile	Lys	Val	Leu	Cys	Pro	Tyr	Thr	Ser	Ala	Met	Ile
2705						2710					2715			
Glu	Arg	Leu	Glu	Ala	Leu	Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val
2720						2725					2730			

Arg	Val	Pro	Leu	Ser	Arg	Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val
2735						2740					2745			
Ser	Gly	Ala	Lys	Ser	Asn	Ile	Ile	Arg	Ser	Val	Asn	Ala	Thr	Ser
2750						2755					2760			
Gln	Leu	Leu	Met	His	Arg	Met	Asp	Ile	Pro	Thr	Arg	Lys	Thr	Lys
2765						2770					2775			
Phe	Glu	Glu	Asp	Val	Asn	Leu	Gly	Thr	Gly	Thr	Arg	Ala	Val	Glu
2780						2785					2790			
Ser	Arg	Ala	Asp	Pro	Pro	Asp	Met	Lys	Lys	Leu	Gly	Ser	Arg	Ile
2795						2800					2805			
Glu	Arg	Leu	Arg	Lys	Glu	Tyr	Gly	Ser	Thr	Trp	His	Tyr	Asp	Glu
2810						2815					2820			
Asn	His	Pro	Tyr	Arg	Thr	Trp	His	Tyr	His	Gly	Ser	Tyr	Glu	Ala
2825						2830					2835			
Asp	Thr	Gln	Gly	Ser	Ala	Ser	Ser	Met	Val	Asn	Gly	Val	Val	Arg
2840						2845					2850			
Leu	Leu	Ser	Lys	Pro	Trp	Asp	Ala	Leu	Ser	Ser	Val	Thr	Asn	Ile
2855						2860					2865			
Ala	Met	Thr	Asp	Thr	Thr	Pro	Phe	Gly	Gln	Gln	Arg	Val	Phe	Lys
2870						2875					2880			
Glu	Lys	Val	Asp	Thr	Arg	Thr	Pro	Asp	Pro	Lys	Gln	Gly	Thr	Gln
2885						2890					2895			
Arg	Val	Met	Ala	Ile	Thr	Ser	Gln	Trp	Leu	Trp	Asp	Arg	Leu	Ala
2900						2905					2910			
Arg	Asn	Lys	Thr	Pro	Arg	Met	Cys	Thr	Arg	Gln	Glu	Phe	Ile	Asn
2915						2920					2925			
Lys	Val	Asn	Ser	His	Ala	Ala	Leu	Gly	Pro	Val	Phe	Arg	Glu	Gln
2930						2935					2940			
Gln	Gly	Trp	Gly	Ser	Ala	Ala	Glu	Ala	Val	Val	Asp	Pro	Arg	Phe
2945						2950					2955			

Trp	Glu	Leu	Val	Asp	Asn	Glu	Arg	Glu	Ala	His	Leu	Arg	Gly	Glu
2960						2965					2970			
Cys	Leu	Thr	Cys	Val	Tyr	Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys
2975						2980					2985			
Leu	Gly	Glu	Phe	Gly	Lys	Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr
2990						2995					3000			
Met	Trp	Leu	Gly	Ala	Arg	Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe
3005						3010					3015			
Leu	Asn	Glu	Asp	His	Trp	Leu	Ser	Arg	Glu	Asn	Ser	Gly	Gly	Gly
3020						3025					3030			
Val	Glu	Gly	Leu	Gly	Leu	Gln	Lys	Leu	Gly	Tyr	Ile	Leu	Glu	Glu
3035						3040					3045			
Ile	Ser	Arg	Arg	Pro	Gly	Gly	Lys	Met	Tyr	Ala	Asp	Asp	Thr	Ala
3050						3055					3060			
Gly	Trp	Asp	Thr	Arg	Ile	Thr	Lys	Cys	Asp	Leu	Glu	Asn	Glu	Ala
3065						3070					3075			
Arg	Ile	Leu	Glu	Lys	Met	Asp	Gly	Ile	His	Lys	Lys	Leu	Ala	Arg
3080						3085					3090			
Ala	Val	Ile	Glu	Leu	Thr	Tyr	Lys	His	Lys	Val	Val	Arg	Val	Leu
3095						3100					3105			
Arg	Pro	Ala	Pro	Gln	Gly	Lys	Val	Val	Met	Asp	Ile	Ile	Ser	Arg
3110						3115					3120			
Pro	Asp	Gln	Arg	Gly	Ser	Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn
3125						3130					3135			
Thr	Tyr	Thr	Asn	Leu	Val	Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala
3140						3145					3150			
Glu	Ala	Val	Ile	Asn	Glu	Arg	Asp	Met	Glu	Glu	Leu	Gln	Asn	Pro
3155						3160					3165			

Trp	Lys	Val	Ile	Asn	Trp	Leu	Glu	Gly	Asn	Gly	Trp	Asp	Arg	Leu
3170						3175					3180			
Arg	Ser	Met	Ala	Val	Ser	Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Met
3185						3190					3195			
Asp	Asp	Arg	Phe	Ala	Tyr	Ala	Leu	Asn	Phe	Leu	Asn	Asp	Met	Gly
3200						3205					3210			
Lys	Val	Arg	Lys	Asp	Val	Gln	Glu	Trp	Lys	Pro	Ser	Pro	Gly	Trp
3215						3220					3225			
Thr	Asn	Trp	Glu	Glu	Val	Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys
3230						3235					3240			
Leu	Pro	Met	Lys	Asp	Gly	Arg	Thr	Ile	Ile	Val	Pro	Cys	Arg	His
3245						3250					3255			
Gln	Asp	Glu	Leu	Ile	Gly	Arg	Ala	Arg	Val	Ser	Pro	Gly	Lys	Gly
3260						3265					3270			
Trp	Ser	Leu	Ser	Glu	Thr	Ala	Cys	Leu	Gly	Lys	Ser	Tyr	Ala	Gln
3275						3280					3285			
Met	Trp	Leu	Leu	Leu	Tyr	Phe	His	Arg	Arg	Asp	Leu	Arg	Leu	Met
3290						3295					3300			
Ala	Asn	Ala	Ile	Cys	Ser	Ala	Val	Pro	Val	Ser	Trp	Val	Pro	Thr
3305						3310					3315			
Gly	Arg	Thr	Thr	Trp	Ser	Ile	His	Gly	Arg	Gly	Glu	Trp	Met	Thr
3320						3325					3330			
Thr	Glu	Asp	Met	Leu	Glu	Val	Trp	Asn	Arg	Val	Trp	Ile	Ile	Glu
3335						3340					3345			
Asn	Glu	Tyr	Met	Glu	Asp	Lys	Thr	Pro	Val	Thr	Glu	Trp	Thr	Asp
3350						3355					3360			
Val	Pro	Tyr	Leu	Gly	Lys	Arg	Glu	Asp	Leu	Trp	Cys	Gly	Ser	Leu
3365						3370					3375			
Ile	Gly	His	Arg	Pro	Arg	Ser	Thr	Trp	Ala	Glu	Asn	Ile	Trp	Ala
3380						3385					3390			

Ala Ile Tyr Gln Val Arg Arg Ala Ile Gly Glu Thr Glu Glu Tyr
 3395 3400 3405

Arg Asp Tyr Met Ser Thr Gln Val Arg Tyr Gly Ser Glu Glu Gly
 3410 3415 3420

Pro Ser Ala Gly Val Leu
 3425

<210> 108

<211> 3429

<212> PRT

<213> Spondweni virus, NCBI Reference Sequence: NC_029055.1

<400> 108

Met Lys Asn Pro Lys Arg Ala Gly Ser Ser Arg Leu Val Asn Met Leu
 1 5 10 15

Arg Arg Gly Ala Ala Arg Val Ile Pro Pro Gly Gly Gly Leu Lys Arg
 20 25 30

Leu Pro Val Gly Leu Leu Leu Gly Arg Gly Pro Ile Lys Met Ile Leu
 35 40 45

Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser Thr Gly
 50 55 60

Leu Ile Asn Arg Trp Gly Lys Val Gly Lys Lys Glu Ala Ile Lys Ile
 65 70 75 80

Leu Thr Lys Phe Lys Ala Asp Val Gly Thr Met Leu Arg Ile Ile Asn
 85 90 95

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

Ala Leu Leu Val Ser Ile Val Ala Val Glu Val Thr Lys Lys Gly Asp
 115 120 125

Thr Tyr Tyr Met Phe Ala Asp Lys Lys Asp Ala Gly Lys Val Val Thr
 130 135 140

Phe Glu Thr Glu Ser Gly Pro Asn Arg Cys Ser Ile Gln Ala Met Asp

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

Tyr Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly
 385 390 395 400

Ser Ile Val Thr Cys Ala Lys Phe Thr Cys Val Lys Lys Leu Thr Gly
 405 410 415

Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Val Leu Val Ser Val
 420 425 430

His Ala Ser Gln His Gly Gly Met Ile Asn Asn Asp Thr Asn His Gln
 435 440 445

His Asp Lys Glu Asn Arg Ala Arg Ile Asp Ile Thr Ala Ser Ala Pro
 450 455 460

Arg Val Glu Val Glu Leu Gly Ser Phe Gly Ser Phe Ser Met Glu Cys
 465 470 475 480

Glu Pro Arg Ser Gly Leu Asn Phe Gly Asp Leu Tyr Tyr Leu Thr Met
 485 490 495

Asn Asn Lys His Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Ser
 500 505 510

Leu Pro Trp His Thr Gly Ala Thr Ser Asn Asn His His Trp Asn Asn
 515 520 525

Lys Glu Ala Leu Val Glu Phe Arg Glu Ala His Ala Lys Lys Gln Thr
 530 535 540

Ala Val Val Leu Gly Ser Gln Glu Gly Ala Val His Ala Ala Leu Ala
 545 550 555 560

Gly Ala Leu Glu Ala Glu Ser Asp Gly His Lys Ala Thr Ile Tyr Ser
 565 570 575

Gly His Leu Lys Cys Arg Leu Lys Leu Asp Lys Leu Arg Leu Lys Gly
 580 585 590

Met Ser Tyr Ala Leu Cys Thr Gly Ala Phe Thr Phe Ala Arg Thr Pro
 595 600 605

Ser Glu Thr Ile His Gly Thr Ala Thr Val Glu Leu Gln Tyr Ala Gly

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

Cys Gly Ile Thr Ser Val Ser Arg Met Glu Asn Leu Met Trp Ser Ser
850 855 860

Val Ala Gly Glu Leu Asn Ala Ile Leu Glu Asp Asn Ser Val Pro Leu
865 870 875 880

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

Arg Leu Lys Pro Pro Ala Ser Glu Leu Pro Gln Gly Trp Lys Ser Trp
900 905 910

Gly Lys Ser Tyr Phe Val Ser Ala Ala Lys Asn Asn Asn Ser Phe Val
915 920 925

Val Asp Gly Asp Thr Met Lys Glu Cys Pro Arg Gln Lys Arg Ala Trp
930 935 940

Asn Ser Leu Arg Ile Glu Asp His Gly Phe Gly Val Phe His Thr Ser
945 950 955 960

Ile Trp Leu Lys Phe His Glu Asp Asn Ser Thr Glu Cys Asp Thr Ala
965 970 975

Ile Ile Gly Thr Ala Val Arg Gly Lys Glu Ala Val His Ser Asp Leu
980 985 990

Gly Tyr Trp Ile Glu Ser Glu Arg Asn Asp Thr Trp Arg Leu Ser Arg
995 1000 1005

Ala His Leu Ile Glu Ala Lys Thr Cys Glu Trp Pro Arg Ser His
1010 1015 1020

Thr Leu Trp Thr Asp Gly Val Glu Glu Ser Glu Leu Ile Ile Pro
1025 1030 1035

Arg Gly Leu Ala Gly Pro Phe Ser His His Asn Thr Arg Ala Gly
1040 1045 1050

Tyr Lys Thr Gln Asn Lys Gly Pro Trp His Leu Gly Asp Val Glu
1055 1060 1065

Ile Gln Phe Ala Thr Cys Pro Gly Thr Thr Val Val Gln Asp Gln

1070						1075						1080			
Glu	Cys	Arg	Asp	Arg	Gly	Ala	Ser	Leu	Arg	Thr	Thr	Thr	Ala	Ser	
1085						1090					1095				
Gly	Arg	Val	Ile	Asn	Glu	Trp	Cys	Cys	Arg	Ser	Cys	Thr	Met	Pro	
1100						1105					1110				
Pro	Leu	Ser	Phe	Lys	Thr	Lys	Asp	Gly	Cys	Trp	Tyr	Ala	Met	Glu	
1115						1120					1125				
Ile	Arg	Pro	Val	Lys	Glu	Gln	Glu	Ser	Asn	Leu	Val	Arg	Ser	His	
1130						1135					1140				
Val	Thr	Ala	Gly	Ser	Thr	Asp	His	Met	Asp	His	Phe	Ser	Leu	Gly	
1145						1150					1155				
Leu	Val	Val	Val	Met	Leu	Met	Val	Gln	Glu	Gly	Met	Lys	Lys	Arg	
1160						1165					1170				
Met	Thr	Ser	Lys	Ala	Ile	Ile	Thr	Ser	Ala	Ala	Phe	Leu	Leu	Ala	
1175						1180					1185				
Val	Met	Ile	Val	Gly	Gly	Phe	Thr	Tyr	Gln	Asp	Phe	Gly	Arg	Leu	
1190						1195					1200				
Val	Val	Leu	Val	Gly	Ala	Ala	Phe	Ala	Glu	Met	Asn	Thr	Gly	Gly	
1205						1210					1215				
Asp	Val	Ala	His	Leu	Ala	Leu	Val	Ala	Ala	Phe	Lys	Val	Arg	Pro	
1220						1225					1230				
Ala	Met	Leu	Val	Ser	Phe	Met	Phe	Arg	Ala	Leu	Trp	Thr	Pro	Arg	
1235						1240					1245				
Glu	Ser	Leu	Leu	Leu	Ala	Leu	Ala	Ala	Cys	Leu	Leu	Gln	Val	Ser	
1250						1255					1260				
Val	Thr	Pro	Leu	Asp	His	Ser	Ile	Met	Ile	Val	Val	Asp	Gly	Ile	
1265						1270					1275				
Ala	Leu	Ser	Trp	Leu	Cys	Leu	Lys	Ala	Ile	Leu	Val	Pro	Arg	Thr	
1280						1285					1290				

Pro	Asn	Ile	Ala	Leu	Pro	Leu	Leu	Ala	Met	Leu	Ser	Pro	Met	Leu
	1295					1300					1305			
Gln	Gly	Thr	Thr	Ile	Val	Ala	Trp	Arg	Ala	Met	Met	Ala	Ala	Leu
	1310					1315					1320			
Ala	Val	Ile	Thr	Leu	Ala	Ser	Met	Lys	His	Gly	Arg	Gly	Val	Lys
	1325					1330					1335			
Lys	Thr	Phe	Pro	Tyr	Thr	Ile	Gly	Cys	Ile	Leu	Gly	Ser	Met	Gly
	1340					1345					1350			
Leu	Val	Glu	Asn	Leu	Gly	Leu	Val	Gly	Leu	Leu	Leu	Leu	Thr	Ala
	1355					1360					1365			
Ser	Lys	Lys	Arg	Ser	Trp	Pro	Pro	Ser	Glu	Val	Met	Thr	Ala	Val
	1370					1375					1380			
Gly	Leu	Ile	Cys	Ala	Ile	Val	Gly	Gly	Leu	Thr	Lys	Thr	Asp	Ile
	1385					1390					1395			
Asp	Met	Ala	Gly	Pro	Met	Ala	Ala	Ile	Gly	Leu	Leu	Val	Val	Ser
	1400					1405					1410			
Tyr	Val	Val	Ser	Gly	Lys	Ser	Val	Asp	Met	Tyr	Ile	Glu	Lys	Val
	1415					1420					1425			
Cys	Asp	Ile	Ser	Trp	Asp	Lys	Asp	Ala	Glu	Ile	Thr	Gly	Thr	Ser
	1430					1435					1440			
Pro	Arg	Leu	Asp	Val	Ala	Leu	Asp	Asp	Ser	Gly	Asp	Phe	Ser	Leu
	1445					1450					1455			
Ile	Gln	Asp	Asp	Gly	Pro	Pro	Thr	Arg	Glu	Ile	Val	Leu	Lys	Val
	1460					1465					1470			
Phe	Leu	Met	Cys	Val	Cys	Gly	Val	Ser	Pro	Ile	Ala	Ile	Pro	Phe
	1475					1480					1485			
Ala	Ala	Ala	Ala	Trp	Phe	Val	Tyr	Ile	Lys	Ser	Gly	Lys	Arg	Ser
	1490					1495					1500			
Gly	Ala	Met	Trp	Asp	Ile	Pro	Ser	Pro	Arg	Glu	Val	Lys	Lys	Gly

1505						1510						1515			
Glu Thr Thr Ala Gly Val Tyr Arg Ile Met Thr Arg Lys Leu Leu	1520					1525						1530			
Gly Ser Thr Gln Val Gly Ala Gly Val Met His Glu Gly Val Phe	1535					1540						1545			
His Thr Met Trp His Val Thr Lys Gly Ser Ala Leu Arg Ser Gly	1550					1555						1560			
Glu Gly Arg Leu Asp Pro Tyr Trp Gly Asn Val Lys Gln Asp Leu	1565					1570						1575			
Ile Ser Tyr Cys Gly Pro Trp Lys Leu Asp Gly Lys Trp Asp Gly	1580					1585						1590			
Val Ser Glu Val Gln Leu Ile Ala Val Ala Pro Gly Glu Arg Ala	1595					1600						1605			
Arg Asn Val Gln Thr Lys Pro Gly Val Phe Lys Thr Thr Asp Gly	1610					1615						1620			
Glu Ile Gly Ala Leu Ala Leu Asp Phe Pro Gly Gly Ser Ser Gly	1625					1630						1635			
Ser Pro Ile Ile Asp Lys Asn Gly His Val Ile Gly Leu Tyr Gly	1640					1645						1650			
Asn Gly Val Val Val Lys Ser Gly Ser Tyr Val Ser Ala Ile Met	1655					1660						1665			
Gln Thr Glu Lys Met Glu Glu Pro Ala Val Asp Cys Phe Glu Glu	1670					1675						1680			
Asp Met Leu Arg Lys Lys Lys Leu Thr Val Leu Asp Leu His Pro	1685					1690						1695			
Gly Ala Gly Lys Thr Arg Arg Val Leu Pro Gln Ile Val Lys Ala	1700					1705						1710			
Ala Ile Lys Lys Arg Leu Arg Thr Val Ile Leu Ala Pro Thr Arg	1715					1720						1725			

Val	Val	Ala	Ala	Glu	Met	Ala	Glu	Ala	Leu	Lys	Asp	Leu	Pro	Ile
	1730					1735					1740			
Arg	Tyr	Met	Thr	Pro	Ala	Val	Ser	Ala	Thr	His	Asp	Gly	Asn	Glu
	1745					1750					1755			
Ile	Val	Asp	Leu	Met	Cys	His	Ala	Thr	Phe	Thr	Ser	Arg	Leu	Met
	1760					1765					1770			
Gln	Pro	Ile	Arg	Val	Pro	Asn	Tyr	Asn	Leu	Tyr	Ile	Met	Asp	Glu
	1775					1780					1785			
Ala	His	Phe	Thr	Asp	Pro	Ala	Ser	Ile	Ala	Ala	Arg	Gly	Tyr	Ile
	1790					1795					1800			
Ala	Thr	Arg	Val	Asp	Met	Gly	Asp	Ala	Ala	Ala	Ile	Phe	Met	Thr
	1805					1810					1815			
Ala	Thr	Pro	Pro	Gly	Ser	Thr	Glu	Ala	Phe	Pro	Asp	Ser	Asn	Ala
	1820					1825					1830			
Pro	Ile	Thr	Asp	Val	Glu	Thr	Glu	Val	Pro	Asp	Lys	Ala	Trp	Asn
	1835					1840					1845			
Ser	Gly	Phe	Glu	Trp	Ile	Thr	Asp	Tyr	Pro	Gly	Lys	Thr	Val	Trp
	1850					1855					1860			
Phe	Val	Pro	Ser	Val	Arg	Met	Gly	Asn	Glu	Ile	Ser	Ala	Cys	Leu
	1865					1870					1875			
Thr	Lys	Ala	Gly	Lys	Ser	Val	Ile	Gln	Leu	Ser	Arg	Lys	Thr	Phe
	1880					1885					1890			
Glu	Thr	Glu	Tyr	Gln	Lys	Thr	Lys	Asn	Gly	Glu	Trp	Asp	Phe	Val
	1895					1900					1905			
Val	Thr	Thr	Asp	Ile	Ser	Glu	Met	Gly	Ala	Asn	Phe	Lys	Ala	Asp
	1910					1915					1920			
Arg	Val	Ile	Asp	Ser	Arg	Lys	Cys	Leu	Lys	Pro	Val	Ile	Leu	Asp
	1925					1930					1935			
Asp	Met	Glu	Glu	Arg	Val	Val	Leu	Ala	Gly	Pro	Met	Ala	Val	Thr

1940						1945						1950			
Pro	Ser	Ser	Ala	Ala	Gln	Arg	Arg	Gly	Arg	Ile	Gly	Arg	Asn	Pro	
1955						1960					1965				
Asn	Lys	Thr	Gly	Asp	Glu	Phe	Tyr	Tyr	Gly	Gly	Gly	Cys	Ala	Ala	
1970						1975					1980				
Thr	Asp	Asp	Asp	His	Ala	His	Trp	Val	Glu	Ala	Arg	Met	Leu	Leu	
1985						1990					1995				
Asp	Asn	Ile	Tyr	Leu	Gln	Asp	Asn	Leu	Val	Ala	Ser	Leu	Tyr	Lys	
2000						2005					2010				
Pro	Glu	Gln	Gly	Lys	Val	Ser	Ala	Ile	Glu	Gly	Glu	Phe	Lys	Leu	
2015						2020					2025				
Arg	Gly	Glu	Gln	Arg	Lys	Thr	Phe	Val	Glu	Leu	Met	Lys	Arg	Gly	
2030						2035					2040				
Asp	Leu	Pro	Val	Trp	Leu	Ser	Tyr	Gln	Val	Ala	Ala	Ser	Gly	Leu	
2045						2050					2055				
Ser	Tyr	Thr	Asp	Arg	Arg	Trp	Cys	Phe	Asp	Gly	Lys	Asn	Asn	Asn	
2060						2065					2070				
Thr	Ile	Leu	Glu	Asp	Cys	Val	Pro	Val	Glu	Val	Trp	Thr	Lys	Phe	
2075						2080					2085				
Gly	Glu	Lys	Lys	Ile	Leu	Lys	Pro	Arg	Trp	Met	Asp	Ala	Arg	Ile	
2090						2095					2100				
Cys	Ser	Asp	His	Ala	Ser	Leu	Lys	Ser	Phe	Lys	Glu	Phe	Ala	Ala	
2105						2110					2115				
Gly	Lys	Arg	Thr	Ile	Ala	Thr	Gly	Leu	Ile	Glu	Ala	Phe	Gly	Met	
2120						2125					2130				
Leu	Pro	Gly	His	Met	Thr	Glu	Arg	Phe	Gln	Glu	Ala	Val	Asp	Asn	
2135						2140					2145				
Leu	Ala	Val	Leu	Met	Arg	Ala	Glu	Ala	Gly	Ser	Arg	Ala	His	Arg	
2150						2155					2160				

Met	Ala	Ala	Ala	Gln	Leu	Pro	Glu	Thr	Met	Glu	Thr	Ile	Leu	Leu
2165						2170					2175			
Leu	Ser	Leu	Leu	Ala	Phe	Val	Ser	Leu	Gly	Val	Phe	Phe	Val	Leu
2180						2185					2190			
Met	Arg	Ala	Lys	Gly	Leu	Gly	Lys	Met	Gly	Ser	Gly	Met	Ile	Val
2195						2200					2205			
Leu	Ala	Gly	Ser	Gly	Trp	Leu	Met	Trp	Met	Ser	Glu	Val	Glu	Pro
2210						2215					2220			
Ala	Arg	Ile	Ala	Cys	Val	Val	Ile	Ile	Val	Phe	Leu	Leu	Met	Val
2225						2230					2235			
Val	Leu	Ile	Pro	Glu	Pro	Glu	Lys	Gln	Arg	Ser	Pro	Gln	Asp	Asn
2240						2245					2250			
Gln	Leu	Ala	Leu	Ile	Ile	Leu	Ile	Ala	Thr	Gly	Leu	Ile	Thr	Leu
2255						2260					2265			
Ile	Ala	Ala	Asn	Glu	Leu	Gly	Trp	Leu	Glu	Arg	Thr	Lys	Ser	Asp
2270						2275					2280			
Leu	Thr	Arg	Leu	Phe	Trp	Arg	Glu	His	Ala	Glu	Pro	Thr	Gly	Gly
2285						2290					2295			
Arg	Gly	Phe	Ser	Phe	Ser	Leu	Asp	Ile	Asp	Leu	Arg	Pro	Ala	Ser
2300						2305					2310			
Ala	Trp	Ala	Ile	Tyr	Ala	Ala	Met	Thr	Thr	Leu	Ile	Thr	Pro	Thr
2315						2320					2325			
Val	Gln	His	Ala	Val	Thr	Thr	Ser	Tyr	Asn	Asn	Tyr	Ser	Leu	Met
2330						2335					2340			
Ala	Met	Ala	Thr	Gln	Ala	Gly	Val	Leu	Phe	Gly	Met	Gly	Arg	Gly
2345						2350					2355			
Val	Pro	Phe	Tyr	Lys	Trp	Asp	Phe	Gly	Val	Pro	Leu	Leu	Met	Leu
2360						2365					2370			
Gly	Cys	Tyr	Ser	Gln	Leu	Thr	Pro	Leu	Thr	Leu	Ile	Val	Ala	Leu

2375		2380		2385
Val Met 2390	Leu Ala Ala His	Tyr 2395	Leu Tyr Leu Ile	Pro Gly Leu Gln 2400
Ala Thr 2405	Ala Ala Arg Ala	Ala 2410	Gln Arg Arg Thr	Ala Ala Gly Ile 2415
Met Lys 2420	Asn Pro Val Val	Asp 2425	Gly Ile Val Val	Thr Asp Ile Asp 2430
Pro Ile 2435	Gln Ile Asp Pro	Asn 2440	Val Glu Lys Lys	Met Gly Gln Val 2445
Met Leu 2450	Ile Phe Val Ala	Leu 2455	Ala Ser Ala Val	Leu Met Arg Thr 2460
Ala Trp 2465	Gly Trp Gly Glu	Ala 2470	Gly Ala Leu Ala	Ser Ala Ala Ala 2475
Ala Thr 2480	Leu Trp Glu Gly	Ala 2485	Pro Asn Lys Tyr	Trp Asn Ser Ser 2490
Thr Ala 2495	Thr Ser Leu Cys	Asn 2500	Ile Phe Arg Gly	Ser Tyr Leu Ala 2505
Gly Pro 2510	Ser Leu Ile Tyr	Thr 2515	Val Thr Arg Asn	Ala Gly Ile Met 2520
Lys Lys 2525	Arg Gly Gly Gly	Asn 2530	Gly Glu Thr Val	Gly Glu Lys Trp 2535
Lys Glu 2540	Arg Leu Asn Arg	Met 2545	Thr Ala Leu Glu	Phe Tyr Ala Tyr 2550
Lys Arg 2555	Ser Gly Ile Thr	Glu 2560	Val Cys Arg Glu	Pro Ala Arg Arg 2565
Ala Leu 2570	Lys Asp Gly Val	Val 2575	Thr Gly Gly His	Ala Val Ser Arg 2580
Gly Ser 2585	Ala Lys Leu Arg	Trp 2590	Met Val Glu Arg	Gly His Val Asn 2595

Leu	Val	Gly	Arg	Val	Val	Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp
2600						2605					2610			
Ser	Tyr	Tyr	Ala	Ala	Ser	Gln	Lys	Gln	Val	Leu	Glu	Val	Arg	Gly
2615						2620					2625			
Tyr	Thr	Lys	Gly	Gly	Ala	Gly	His	Glu	Glu	Pro	Met	Asn	Val	Gln
2630						2635					2640			
Ser	Tyr	Gly	Trp	Asn	Ile	Val	Arg	Leu	Lys	Ser	Gly	Val	Asp	Val
2645						2650					2655			
Phe	Tyr	Leu	Pro	Ser	Glu	Pro	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile
2660						2665					2670			
Gly	Glu	Ser	Ser	Ser	Ser	Pro	Ala	Val	Glu	Glu	Ala	Arg	Thr	Leu
2675						2680					2685			
Arg	Val	Leu	Gly	Met	Val	Glu	Thr	Trp	Leu	Glu	Arg	Gly	Val	Lys
2690						2695					2700			
Asn	Phe	Cys	Ile	Lys	Val	Leu	Cys	Pro	Tyr	Thr	Ser	Ala	Met	Ile
2705						2710					2715			
Glu	Arg	Leu	Glu	Ala	Leu	Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val
2720						2725					2730			
Arg	Val	Pro	Leu	Ser	Arg	Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val
2735						2740					2745			
Ser	Gly	Ala	Lys	Ser	Asn	Ile	Ile	Arg	Ser	Val	Asn	Ala	Thr	Ser
2750						2755					2760			
Gln	Leu	Leu	Met	His	Arg	Met	Asp	Ile	Pro	Thr	Arg	Lys	Thr	Lys
2765						2770					2775			
Phe	Glu	Glu	Asp	Val	Asn	Leu	Gly	Thr	Gly	Thr	Arg	Ala	Val	Glu
2780						2785					2790			
Ser	Arg	Ala	Asp	Pro	Pro	Asp	Met	Lys	Lys	Leu	Gly	Ser	Arg	Ile
2795						2800					2805			
Glu	Arg	Leu	Arg	Lys	Glu	Tyr	Gly	Ser	Thr	Trp	His	Tyr	Asp	Glu

2810						2815						2820			
Asn	His	Pro	Tyr	Arg	Thr	Trp	His	Tyr	His	Gly	Ser	Tyr	Glu	Ala	
2825						2830					2835				
Asp	Thr	Gln	Gly	Ser	Ala	Ser	Ser	Met	Val	Asn	Gly	Val	Val	Arg	
2840						2845					2850				
Leu	Leu	Ser	Lys	Pro	Trp	Asp	Ala	Leu	Ser	Ser	Val	Thr	Asn	Ile	
2855						2860					2865				
Ala	Met	Thr	Asp	Thr	Thr	Pro	Phe	Gly	Gln	Gln	Arg	Val	Phe	Lys	
2870						2875					2880				
Glu	Lys	Val	Asp	Thr	Arg	Thr	Pro	Asp	Pro	Lys	Gln	Gly	Thr	Gln	
2885						2890					2895				
Arg	Val	Met	Ala	Ile	Thr	Ser	Gln	Trp	Leu	Trp	Asp	Arg	Leu	Ala	
2900						2905					2910				
Arg	Asn	Lys	Thr	Pro	Arg	Met	Cys	Thr	Arg	Gln	Glu	Phe	Ile	Asn	
2915						2920					2925				
Lys	Val	Asn	Ser	His	Ala	Ala	Leu	Gly	Pro	Val	Phe	Arg	Glu	Gln	
2930						2935					2940				
Gln	Gly	Trp	Gly	Ser	Ala	Ala	Glu	Ala	Val	Val	Asp	Pro	Arg	Phe	
2945						2950					2955				
Trp	Glu	Leu	Val	Asp	Asn	Glu	Arg	Glu	Ala	His	Leu	Arg	Gly	Glu	
2960						2965					2970				
Cys	Leu	Thr	Cys	Val	Tyr	Asn	Met	Met	Gly	Lys	Arg	Glu	Lys	Lys	
2975						2980					2985				
Leu	Gly	Glu	Phe	Gly	Lys	Ala	Lys	Gly	Ser	Arg	Ala	Ile	Trp	Tyr	
2990						2995					3000				
Met	Trp	Leu	Gly	Ala	Arg	Phe	Leu	Glu	Phe	Glu	Ala	Leu	Gly	Phe	
3005						3010					3015				
Leu	Asn	Glu	Asp	His	Trp	Leu	Ser	Arg	Glu	Asn	Ser	Gly	Gly	Gly	
3020						3025					3030				

Val	Glu	Gly	Leu	Gly	Leu	Gln	Lys	Leu	Gly	Tyr	Ile	Leu	Glu	Glu
	3035					3040					3045			
Ile	Ser	Arg	Arg	Pro	Gly	Gly	Lys	Met	Tyr	Ala	Asp	Asp	Thr	Ala
	3050					3055					3060			
Gly	Trp	Asp	Thr	Arg	Ile	Thr	Lys	Cys	Asp	Leu	Glu	Asn	Glu	Ala
	3065					3070					3075			
Arg	Ile	Leu	Glu	Lys	Met	Asp	Gly	Ile	His	Lys	Lys	Leu	Ala	Arg
	3080					3085					3090			
Ala	Val	Ile	Glu	Leu	Thr	Tyr	Lys	His	Lys	Val	Val	Arg	Val	Leu
	3095					3100					3105			
Arg	Pro	Ala	Pro	Gln	Gly	Lys	Val	Val	Met	Asp	Ile	Ile	Ser	Arg
	3110					3115					3120			
Pro	Asp	Gln	Arg	Gly	Ser	Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn
	3125					3130					3135			
Thr	Tyr	Thr	Asn	Leu	Val	Val	Gln	Leu	Ile	Arg	Asn	Met	Glu	Ala
	3140					3145					3150			
Glu	Ala	Val	Ile	Asn	Glu	Arg	Asp	Met	Glu	Glu	Leu	Gln	Asn	Pro
	3155					3160					3165			
Trp	Lys	Val	Ile	Asn	Trp	Leu	Glu	Gly	Asn	Gly	Trp	Asp	Arg	Leu
	3170					3175					3180			
Arg	Ser	Met	Ala	Val	Ser	Gly	Asp	Asp	Cys	Val	Val	Lys	Pro	Met
	3185					3190					3195			
Asp	Asp	Arg	Phe	Ala	Tyr	Ala	Leu	Asn	Phe	Leu	Asn	Asp	Met	Gly
	3200					3205					3210			
Lys	Val	Arg	Lys	Asp	Val	Gln	Glu	Trp	Lys	Pro	Ser	Pro	Gly	Trp
	3215					3220					3225			
Thr	Asn	Trp	Glu	Glu	Val	Pro	Phe	Cys	Ser	His	His	Phe	Asn	Lys
	3230					3235					3240			
Leu	Pro	Met	Lys	Asp	Gly	Arg	Thr	Ile	Ile	Val	Pro	Cys	Arg	His

3245		3250		3255
Gln Asp	Glu Leu Ile Gly	Arg Ala Arg Val Ser	Pro Gly Lys Gly	
3260		3265	3270	
Trp Ser	Leu Ser Glu Thr	Ala Cys Leu Gly Lys	Ser Tyr Ala Gln	
3275		3280	3285	
Met Trp	Leu Leu Leu Tyr	Phe His Arg Arg Asp	Leu Arg Leu Met	
3290		3295	3300	
Ala Asn	Ala Ile Cys Ser	Ala Val Pro Val Ser	Trp Val Pro Thr	
3305		3310	3315	
Gly Arg	Thr Thr Trp Ser	Ile His Gly Arg Gly	Glu Trp Met Thr	
3320		3325	3330	
Thr Glu	Asp Met Leu Glu	Val Trp Asn Arg Val	Trp Ile Ile Glu	
3335		3340	3345	
Asn Glu	Tyr Met Glu Asp	Lys Thr Pro Val Thr	Glu Trp Thr Asp	
3350		3355	3360	
Val Pro	Tyr Leu Gly Lys	Arg Glu Asp Leu Trp	Cys Gly Ser Leu	
3365		3370	3375	
Ile Gly	His Arg Pro Arg	Ser Thr Trp Ala Glu	Asn Ile Trp Ala	
3380		3385	3390	
Ala Ile	Tyr Gln Val Arg	Arg Ala Ile Gly Glu	Thr Glu Glu Tyr	
3395		3400	3405	
Arg Asp	Tyr Met Ser Thr	Gln Val Arg Tyr Gly	Ser Glu Glu Gly	
3410		3415	3420	
Pro Ser	Ala Gly Val Leu			
3425				

<210> 109
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:88

 <400> 109

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

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser

<210> 110

<211> 403

<212> PRT

<213> sE of SEQ ID NO:89

<400> 110

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr

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

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser

<210> 111
<211> 403
<212> PRT
<213> sE of SEQ ID NO:90

<400> 111

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

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

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser

<210> 112
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:91

<400> 112

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly Tyr Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Lys Leu Phe Ser Gly His
275 280 285

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

290		295		300											
Tyr	Ser	Leu	Cys	Thr	Ala	Ala	Phe	Thr	Phe	Thr	Lys	Val	Pro	Ala	Glu
305					310					315					320
Thr	Leu	His	Gly	Thr	Val	Thr	Val	Glu	Val	Gln	Tyr	Ala	Gly	Thr	Asp
				325					330					335	
Gly	Pro	Cys	Lys	Ile	Pro	Val	Gln	Met	Ala	Val	Asp	Met	Gln	Thr	Leu
			340					345					350		
Thr	Pro	Val	Gly	Arg	Leu	Ile	Thr	Ala	Asn	Pro	Val	Ile	Thr	Glu	Ser
		355					360					365			
Thr	Glu	Asn	Ser	Lys	Met	Met	Leu	Glu	Leu	Asp	Pro	Pro	Phe	Gly	Asp
	370					375					380				
Ser	Tyr	Ile	Val	Ile	Gly	Val	Gly	Asp	Lys	Lys	Ile	Thr	His	His	Trp
385					390					395					400

His Arg Ser

<210> 113
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:92

<400> 113

Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Met	Ser
1			5					10						15	
Gly	Gly	Thr	Trp	Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys	Val	Thr
			20					25					30		
Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val	Thr	Thr
		35					40					45			
Thr	Val	Ser	Asn	Met	Ala	Glu	Ile	Arg	Ser	Tyr	Cys	Tyr	Glu	Ala	Ser
	50					55					60				
Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Ala
65					70					75					80

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

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser

<210> 114

<211> 403

<212> PRT

<213> sE of SEQ ID NO:93

<400> 114

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Ile Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser

				100						105						110
Leu	Val	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Lys	Lys	Met	Thr	Gly	Lys	
		115					120					125				
Ser	Ile	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu	Ser	Val	His	
	130					135					140					
Gly	Ser	Gln	His	Ser	Gly	Met	Ile	Val	Asn	Asp	Thr	Gly	His	Glu	Thr	
145					150					155					160	
Asp	Glu	Asn	Arg	Ala	Lys	Val	Glu	Ile	Thr	Pro	Asn	Ser	Pro	Arg	Ala	
				165					170					175		
Glu	Ala	Thr	Leu	Gly	Gly	Phe	Gly	Ser	Leu	Gly	Leu	Asp	Cys	Glu	Pro	
			180					185					190			
Arg	Thr	Gly	Leu	Asp	Phe	Ser	Asp	Leu	Tyr	Tyr	Leu	Thr	Met	Asn	Asn	
		195					200					205				
Lys	His	Trp	Leu	Val	His	Lys	Glu	Trp	Phe	His	Asp	Ile	Pro	Leu	Pro	
	210					215					220					
Trp	His	Ala	Gly	Ala	Asp	Thr	Gly	Thr	Pro	His	Trp	Asn	Asn	Lys	Glu	
225					230					235					240	
Ala	Leu	Val	Glu	Phe	Lys	Asp	Ala	His	Ala	Lys	Arg	Gln	Thr	Val	Val	
				245					250					255		
Val	Leu	Gly	Ser	Gln	Glu	Gly	Ala	Val	His	Thr	Ala	Leu	Ala	Gly	Ala	
			260					265					270			
Leu	Glu	Ala	Glu	Met	Asp	Gly	Ala	Lys	Gly	Arg	Leu	Ser	Ser	Gly	His	
		275					280					285				
Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Arg	Leu	Lys	Gly	Val	Ser	
	290					295					300					
Tyr	Ser	Leu	Cys	Thr	Ala	Ala	Phe	Thr	Phe	Thr	Lys	Ile	Pro	Ala	Glu	
305					310					315					320	
Thr	Leu	His	Gly	Thr	Val	Thr	Val	Glu	Val	Gln	Tyr	Ala	Gly	Thr	Asp	
				325					330					335		

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser

<210> 115
<211> 403
<212> PRT
<213> sE of SEQ ID NO:94

<400> 115

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Ile Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser

<210> 116
<211> 403
<212> PRT
<213> sE of SEQ ID NO:95

<400> 116

Ile Ser Cys Ile Gly Val Ser Asn Arg Asp Leu Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Glu Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Met
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Leu Ser Asp Met Ala Ser Ala Ser Arg Cys Pro Thr Gln Gly Glu Pro
65 70 75 80

Ser Leu Asp Lys Gln Ser Asp Thr Gln Ser Val Cys Lys Arg Thr Leu
85 90 95

Gly Asp Arg Gly Trp Gly Asn Gly Cys Gly Ile Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ser Lys Phe Thr Cys Cys Lys Lys Met Pro Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Pro Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Ile Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
 180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
 195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
 210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
 225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
 245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Ser Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp

370 375 380
 Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp
 385 390 395 400

 His Arg Ser

 <210> 117
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:96

 <220>
 <221> misc_feature
 <222> (152)..(156)
 <223> Xaa can be any naturally occurring amino acid

 <400> 117

 Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

 Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

 Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

 Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

 Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

 Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

 Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

 Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

 Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Xaa Xaa Xaa Xaa Xaa Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
 180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
 195 200 205

Lys His Arg Leu Val Arg Lys Glu Trp Phe His Asp Ile Pro Leu Pro
 210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
 225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
 245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp
 385 390 395 400

Leu Lys Lys

<210> 118
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:97

<400> 118

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Ile Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Val Cys Thr Ala Ala Lys Val Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp

400

<400> 119

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Xaa Xaa Xaa Xaa Xaa
145 150 155 160

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

Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser

<210> 120
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:99

<400> 120

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Ala Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser

<210> 121
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:100

<400> 121

Ile	Arg	Cys	Ile	Gly	Val	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Met	Ser
1				5					10					15	

Gly	Gly	Thr	Trp	Val	Asp	Val	Val	Leu	Glu	His	Gly	Gly	Cys	Val	Thr
			20					25					30		

Val	Met	Ala	Gln	Asp	Lys	Pro	Thr	Val	Asp	Ile	Glu	Leu	Val	Thr	Thr
		35					40					45			

Thr	Val	Ser	Asn	Met	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Glu	Ala	Ser
	50					55					60				

Ile	Ser	Asp	Met	Ala	Ser	Asp	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Ala
65					70				75						80

Tyr	Leu	Asp	Lys	Gln	Ser	Asp	Thr	Gln	Tyr	Val	Cys	Lys	Arg	Thr	Leu
			85						90					95	

Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser
			100					105					110		

Leu	Val	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Lys	Lys	Met	Thr	Gly	Lys
		115					120					125			

Ser	Ile	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu	Ser	Val	His
	130					135					140				

Gly	Ser	Gln	His	Ser	Gly	Met	Ile	Val	Asn	Asp	Thr	Gly	His	Glu	Thr
145					150					155					160

Asp	Glu	Asn	Arg	Ala	Lys	Val	Glu	Ile	Thr	Pro	Asn	Ser	Pro	Arg	Ala
				165					170					175	

Glu	Ala	Thr	Leu	Gly	Gly	Phe	Gly	Ser	Leu	Gly	Leu	Asp	Cys	Glu	Pro
			180					185					190		

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser

<210> 122

<211> 403

<212> PRT

<213> sE of SEQ ID NO:101

<400> 122

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro

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

<210> 123
 <211> 403
 <212> PRT
 <213> sE of SEQ ID NO:102
 <400> 123

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

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser

<210> 124
<211> 397
<212> PRT
<213> sE of SEQ ID NO:103

<400> 124

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr

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

Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp
260 265 270

Gly Ala Lys Gly Arg Leu Phe Ser Gly His Leu Lys Cys Arg Leu Lys
275 280 285

Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala
290 295 300

Ala Phe Thr Phe Thr Lys Val Pro Ala Glu Thr Leu His Gly Thr Val
305 310 315 320

Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro
325 330 335

Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu
340 345 350

Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met
355 360 365

Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly
370 375 380

Val Gly Asp Lys Lys Ile Thr His His Trp His Arg Ser
385 390 395

<210> 125

<211> 403

<212> PRT

<213> sE of SEQ ID NO:104

<400> 125

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Ile Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser

<210> 126
 <211> 397
 <212> PRT
 <213> sE of SEQ ID NO:105

<400> 126

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Glu Asn Arg Ala Lys
145 150 155 160

Val Glu Val Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly
165 170 175

Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe
180 185 190

Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His
195 200 205

Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp
210 215 220

Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys
225 230 235 240

Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu
245 250 255

Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp
260 265 270

Gly Ala Lys Gly Arg Leu Phe Ser Gly His Leu Lys Cys Arg Leu Lys
275 280 285

Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala
290 295 300

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

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
 180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
 195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
 210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
 225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
 245 250 255

Val Leu Gly Thr Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser

<210> 128
 <211> 404
 <212> PRT
 <213> sE of SEQ ID NO:107

<400> 128

Ile Arg Cys Ile Gly Ile Gly Asn Arg Asp Phe Ile Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Ile Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ser Asn Asp Lys Pro Thr Leu Asp Phe Glu Leu Val Thr Thr
 35 40 45

Thr Ala Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Asn
 50 55 60

Ile Ser Glu Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Met Ala Asp Ser Gln Phe Val Cys Lys Arg Gly Tyr
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Ile Val Thr Cys Ala Lys Phe Thr Cys Val Lys Lys Leu Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Val Leu Val Ser Val His

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

Ser Gly Ala Asn Ser Lys Met Met Val Glu Ile Asp Pro Pro Phe Gly
 370 375 380

Asp Ser Tyr Ile Ile Val Gly Thr Gly Thr Thr Lys Ile Thr His His
 385 390 395 400

Trp His Arg Ala

<210> 129
 <211> 404
 <212> PRT
 <213> sE of SEQ ID NO:108

<400> 129

Ile Arg Cys Ile Gly Ile Gly Asn Arg Asp Phe Ile Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Ile Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ser Asn Asp Lys Pro Thr Leu Asp Phe Glu Leu Val Thr Thr
 35 40 45

Thr Ala Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Asn
 50 55 60

Ile Ser Glu Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Met Ala Asp Ser Gln Phe Val Cys Lys Arg Gly Tyr
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Ile Val Thr Cys Ala Lys Phe Thr Cys Val Lys Lys Leu Thr Gly Lys
 115 120 125

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

Ala Ser Gln His Gly Gly Met Ile Asn Asn Asp Thr Asn His Gln His
 145 150 155 160

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

Asp Ser Tyr Ile Ile Val Gly Thr Gly Thr Thr Lys Ile Thr His His
 385 390 395 400

Trp His Arg Ala

<210> 130

<211> 504

<212> PRT

<213> E-protein of SEQ ID NO:88 + stem anchor

<400> 130

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Gly Thr Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 132

<211> 504

<212> PRT

<213> E-protein of SEQ ID NO:90 + stem anchor

<400> 132

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr

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

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
 435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
 450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
 465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile

485

490

495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 133

<211> 504

<212> PRT

<213> E-protein of SEQ ID NO:91 + stem anchor

<400> 133

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly Tyr Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Lys Leu Phe Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Ile Pro Val Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
420 425 430

Ser Val Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Ile His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 134

<211> 504

<212> PRT

<213> E-protein of SEQ ID NO:92 + stem anchor

<400> 134

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Ile Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser

				100						105						110
Leu	Val	Thr	Cys	Ala	Lys	Phe	Ala	Cys	Ser	Lys	Lys	Met	Thr	Gly	Lys	
		115					120					125				
Ser	Ile	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Arg	Ile	Met	Leu	Ser	Val	His	
	130					135					140					
Gly	Ser	Gln	His	Ser	Gly	Met	Ile	Val	Asn	Asp	Thr	Gly	His	Glu	Thr	
145					150					155					160	
Asp	Glu	Asn	Arg	Ala	Lys	Val	Glu	Ile	Thr	Pro	Asn	Ser	Pro	Arg	Ala	
				165					170					175		
Glu	Ala	Thr	Leu	Gly	Gly	Phe	Gly	Ser	Leu	Gly	Leu	Asp	Cys	Glu	Pro	
			180					185					190			
Arg	Thr	Gly	Leu	Asp	Phe	Ser	Asp	Leu	Tyr	Tyr	Leu	Thr	Met	Asn	Asn	
		195					200					205				
Lys	His	Trp	Leu	Val	His	Lys	Glu	Trp	Phe	His	Asp	Ile	Pro	Leu	Pro	
	210					215					220					
Trp	His	Ala	Gly	Ala	Asp	Thr	Gly	Thr	Pro	His	Trp	Asn	Asn	Lys	Glu	
225					230					235					240	
Ala	Leu	Val	Glu	Phe	Lys	Asp	Ala	His	Ala	Lys	Arg	Gln	Thr	Val	Val	
				245					250					255		
Val	Leu	Gly	Ser	Gln	Glu	Gly	Ala	Val	His	Thr	Ala	Leu	Ala	Gly	Ala	
			260					265					270			
Leu	Glu	Ala	Glu	Met	Asp	Gly	Ala	Lys	Gly	Arg	Leu	Ser	Ser	Gly	His	
		275					280					285				
Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Arg	Leu	Lys	Gly	Val	Ser	
	290					295					300					
Tyr	Ser	Leu	Cys	Thr	Ala	Ala	Phe	Thr	Phe	Thr	Lys	Ile	Pro	Ala	Glu	
305					310					315					320	
Thr	Leu	His	Gly	Thr	Val	Thr	Val	Glu	Val	Gln	Tyr	Ala	Gly	Thr	Asp	
				325					330					335		

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 135

<211> 504

<212> PRT

<213> E-protein of SEQ ID NO:93 + stem anchor

<400> 135

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

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

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
 435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
 450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
 465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
 485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 136

<211> 504

<212> PRT

<213> E-protein of SEQ ID NO:94 + stem anchor

<400> 136

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Ile Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro

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

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
420 425 430

Ser Val Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Ile His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 137

<211> 504

<212> PRT

<213> E-protein of SEQ ID NO:95 + stem anchor

<400> 137

Ile Ser Cys Ile Gly Val Ser Asn Arg Asp Leu Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Glu Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Met
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Leu Ser Asp Met Ala Ser Ala Ser Arg Cys Pro Thr Gln Gly Glu Pro
65 70 75 80

Ser Leu Asp Lys Gln Ser Asp Thr Gln Ser Val Cys Lys Arg Thr Leu
85 90 95

Gly Asp Arg Gly Trp Gly Asn Gly Cys Gly Ile Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ser Lys Phe Thr Cys Cys Lys Lys Met Pro Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Pro Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Ile Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Ser Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Ile His Gln Ile
 435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
 450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys
 465 470 475 480

Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile
 485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
 500

<210> 138
 <211> 504
 <212> PRT
 <213> E-protein of SEQ ID NO:96 + stem anchor

<220>
 <221> misc_feature
 <222> (152)..(156)
 <223> Xaa can be any naturally occurring amino acid

<400> 138

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser

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

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp
385 390 395 400

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

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
420 425 430

Ser Val Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Val His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys

Asp	Glu	Asn	Arg	Ala	Lys	Val	Glu	Val	Thr	Pro	Asn	Ser	Pro	Arg	Ala	
				165					170					175		
Glu	Ala	Thr	Leu	Gly	Gly	Phe	Gly	Ser	Leu	Gly	Leu	Asp	Cys	Glu	Pro	
			180					185					190			
Arg	Thr	Gly	Leu	Asp	Phe	Ser	Asp	Leu	Tyr	Tyr	Leu	Thr	Met	Asn	Asn	
		195					200					205				
Lys	His	Trp	Leu	Val	His	Lys	Glu	Trp	Phe	His	Asp	Ile	Pro	Leu	Pro	
	210					215					220					
Trp	His	Ala	Gly	Ala	Asp	Thr	Gly	Thr	Pro	His	Trp	Asn	Asn	Lys	Glu	
225					230					235					240	
Ala	Leu	Val	Glu	Phe	Lys	Asp	Ala	His	Ala	Lys	Arg	Gln	Thr	Val	Val	
				245					250					255		
Val	Leu	Gly	Ser	Gln	Glu	Gly	Ala	Val	His	Thr	Ala	Leu	Ala	Gly	Ala	
			260					265					270			
Leu	Glu	Ala	Glu	Met	Asp	Gly	Ala	Lys	Gly	Arg	Leu	Phe	Ser	Gly	His	
		275					280					285				
Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Arg	Leu	Lys	Gly	Val	Ser	
	290					295					300					
Tyr	Ser	Leu	Cys	Thr	Ala	Val	Cys	Thr	Ala	Ala	Lys	Val	Pro	Ala	Glu	
305					310					315					320	
Thr	Leu	His	Gly	Thr	Val	Thr	Val	Glu	Val	Gln	Tyr	Ala	Gly	Thr	Asp	
				325					330					335		
Gly	Pro	Cys	Lys	Val	Pro	Ala	Gln	Met	Ala	Val	Asp	Met	Gln	Thr	Leu	
			340					345					350			
Thr	Pro	Val	Gly	Arg	Leu	Ile	Thr	Ala	Asn	Pro	Val	Ile	Thr	Glu	Ser	
		355					360					365				
Thr	Glu	Asn	Ser	Lys	Met	Met	Leu	Glu	Leu	Asp	Pro	Pro	Phe	Gly	Asp	
	370					375					380					
Ser	Tyr	Ile	Val	Ile	Gly	Val	Gly	Asp	Lys	Lys	Ile	Thr	His	His	Trp	
385					390					395					400	

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
420 425 430

Ser Val Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Ile His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 140

<211> 504

<212> PRT

<213> E-protein of SEQ ID NO:98 + stem anchor

<220>

<221> misc_feature

<222> (156)..(162)

<223> Xaa can be any naturally occurring amino acid

<400> 140

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Xaa Xaa Xaa Xaa Xaa
145 150 155 160

Xaa Xaa Asn Arg Ala Glu Val Glu Val Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His
275 280 285

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

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

<210> 141
 <211> 504
 <212> PRT

<213> E-protein of SEQ ID NO:99 + stem anchor

<400> 141

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Ala Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
 225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
 245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
 435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Leu Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 142

<211> 504

<212> PRT

<213> E-protein of SEQ ID NO:100 + stem anchor

<400> 142

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
 145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
 165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
 180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
 195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
 210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
 225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
 245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp

370 375 380
 Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400
 His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415
 Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430
 Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
 435 440 445
 Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
 450 455 460
 Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys
 465 470 475 480
 Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Leu Ile
 485 490 495
 Phe Leu Ser Thr Ala Val Ser Ala
 500

 <210> 143
 <211> 504
 <212> PRT
 <213> E-protein of SEQ ID NO:101 + stem anchor

 <400> 143

 Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

 Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

 Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

 Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Thr Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His
275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Gly
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
420 425 430

Ser Val Gly Gly Val Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 144

<211> 504

<212> PRT

<213> E-protein of SEQ ID NO:102 + stem anchor

<400> 144

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Ile Gly His Glu Thr
145 150 155 160

Asp Glu Asn Arg Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala
165 170 175

Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro
180 185 190

Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn
195 200 205

Lys His Trp Leu Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro
210 215 220

Trp His Ala Gly Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu
 225 230 235 240

Ala Leu Val Glu Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val
 245 250 255

Val Leu Gly Ser Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala
 260 265 270

Leu Glu Ala Glu Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His
 275 280 285

Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser
 290 295 300

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu
 305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
 325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
 340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
 355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
 370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Val His Gln Ile
 435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser

450 455 460
 Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys
 465 470 475 480
 Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile
 485 490 495
 Phe Leu Ser Thr Ala Val Ser Ala
 500

 <210> 145
 <211> 498
 <212> PRT
 <213> E-protein of SEQ ID NO:103 + stem anchor

 <400> 145
 Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15
 Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30
 Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45
 Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60
 Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80
 Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95
 Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110
 Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125
 Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

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

Val Gly Asp Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr
 385 390 395 400

Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala
 405 410 415

Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Val Phe
 420 425 430

Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys
 435 440 445

Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile Gly Thr
 450 455 460

Leu Leu Val Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile Ser Leu
 465 470 475 480

Thr Cys Leu Ala Leu Gly Gly Val Met Ile Phe Leu Ser Thr Ala Val
 485 490 495

Ser Ala

<210> 146
 <211> 504
 <212> PRT
 <213> E-protein of SEQ ID NO:104 + stem anchor

<400> 146

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala

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

Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu
305 310 315 320

Thr Leu His Gly Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp
325 330 335

Gly Pro Cys Lys Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu
340 345 350

Thr Pro Val Gly Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser
355 360 365

Thr Glu Asn Ser Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp
370 375 380

Ser Tyr Ile Val Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp
385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
420 425 430

Ser Val Gly Gly Val Phe Asn Ser Leu Gly Lys Gly Val His Gln Ile
435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys
465 470 475 480

Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile
485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
500

<210> 147

<211> 498

<212> PRT

<213> E-protein of SEQ ID NO:105 + stem anchor

<400> 147

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Glu Asn Arg Ala Lys
145 150 155 160

Val Glu Val Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly
165 170 175

Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe
180 185 190

Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His
195 200 205

Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp
210 215 220

Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys
 225 230 235 240

Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu
 245 250 255

Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp
 260 265 270

Gly Ala Lys Gly Arg Leu Phe Ser Gly His Leu Lys Cys Arg Leu Lys
 275 280 285

Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala
 290 295 300

Ala Phe Thr Phe Thr Lys Val Pro Ala Glu Thr Leu His Gly Thr Val
 305 310 315 320

Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro
 325 330 335

Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu
 340 345 350

Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met
 355 360 365

Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly
 370 375 380

Val Gly Asp Lys Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr
 385 390 395 400

Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala
 405 410 415

Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Val Phe
 420 425 430

Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys
 435 440 445

Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile Gly Thr
 450 455 460

Leu Leu Val Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile Ser Leu
 465 470 475 480

Thr Cys Leu Ala Leu Gly Gly Val Met Ile Phe Leu Ser Thr Ala Val
 485 490 495

Ser Ala

<210> 148

<211> 504

<212> PRT

<213> E-protein of SEQ ID NO:106 + stem anchor

<400> 148

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
 35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
 50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Leu Val Thr Cys Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys
 115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
 130 135 140

Gly Ser Gln His Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr

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

Ser Tyr Ile Val Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp
 385 390 395 400

His Arg Ser Gly Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg
 405 410 415

Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly
 420 425 430

Ser Val Gly Gly Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile
 435 440 445

Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser
 450 455 460

Gln Ile Leu Ile Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys
 465 470 475 480

Asn Gly Ser Ile Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile
 485 490 495

Phe Leu Ser Thr Ala Val Ser Ala
 500

<210> 149
 <211> 505
 <212> PRT
 <213> E-protein of SEQ ID NO:107 + stem anchor

<400> 149

Ile Arg Cys Ile Gly Ile Gly Asn Arg Asp Phe Ile Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Ile Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ser Asn Asp Lys Pro Thr Leu Asp Phe Glu Leu Val Thr Thr
 35 40 45

Thr Ala Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Asn
 50 55 60

Ile Ser Glu Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Met Ala Asp Ser Gln Phe Val Cys Lys Arg Gly Tyr
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Ile Val Thr Cys Ala Lys Phe Thr Cys Val Lys Lys Leu Thr Gly Lys
115 120 125

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

Ala Ser Gln His Gly Gly Met Ile Asn Asn Asp Thr Asn His Gln His
145 150 155 160

Asp Lys Glu Asn Arg Ala Arg Ile Asp Ile Thr Ala Ser Ala Pro Arg
165 170 175

Val Glu Val Glu Leu Gly Ser Phe Gly Ser Phe Ser Met Glu Cys Glu
180 185 190

Pro Arg Ser Gly Leu Asn Phe Gly Asp Leu Tyr Tyr Leu Thr Met Asn
195 200 205

Asn Lys His Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Ser Leu
210 215 220

Pro Trp His Thr Gly Ala Thr Ser Asn Asn His His Trp Asn Asn Lys
225 230 235 240

Glu Ala Leu Val Glu Phe Arg Glu Ala His Ala Lys Lys Gln Thr Ala
245 250 255

Val Val Leu Gly Ser Gln Glu Gly Ala Val His Ala Ala Leu Ala Gly
260 265 270

Ala Leu Glu Ala Glu Ser Asp Gly His Lys Ala Thr Ile Tyr Ser Gly
275 280 285

His Leu Lys Cys Arg Leu Lys Leu Asp Lys Leu Arg Leu Lys Gly Met
290 295 300

Ser Tyr Ala Leu Cys Thr Gly Ala Phe Thr Phe Ala Arg Thr Pro Ser
 305 310 315 320

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

Asp Gly Pro Cys Lys Val Pro Ile Val Ile Thr Ser Asp Thr Asn Ser
 340 345 350

Met Ala Ser Thr Gly Arg Leu Ile Thr Ala Asn Pro Val Val Thr Glu
 355 360 365

Ser Gly Ala Asn Ser Lys Met Met Val Glu Ile Asp Pro Pro Phe Gly
 370 375 380

Asp Ser Tyr Ile Ile Val Gly Thr Gly Thr Thr Lys Ile Thr His His
 385 390 395 400

Trp His Arg Ala Gly Ser Ser Ile Gly Arg Ala Phe Glu Ala Thr Met
 405 410 415

Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe
 420 425 430

Gly Ser Val Gly Gly Met Phe Asn Ser Val Gly Lys Phe Val His Gln
 435 440 445

Val Phe Gly Ser Ala Phe Lys Ala Leu Phe Gly Gly Met Ser Trp Phe
 450 455 460

Thr Gln Leu Leu Ile Gly Phe Leu Leu Ile Trp Met Gly Leu Asn Ala
 465 470 475 480

Arg Gly Gly Thr Val Ala Met Ser Phe Met Gly Ile Gly Ala Met Leu
 485 490 495

Ile Phe Leu Ala Thr Ser Val Ser Gly
 500 505

<210> 150

<211> 505

<212> PRT

<213> E-protein of SEQ ID NO:108 + stem anchor

<400> 150

Ile Arg Cys Ile Gly Ile Gly Asn Arg Asp Phe Ile Glu Gly Met Ser
 1 5 10 15

Gly Gly Thr Trp Val Asp Ile Val Leu Glu His Gly Gly Cys Val Thr
 20 25 30

Val Met Ser Asn Asp Lys Pro Thr Leu Asp Phe Glu Leu Val Thr Thr
 35 40 45

Thr Ala Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Asn
 50 55 60

Ile Ser Glu Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
 65 70 75 80

Tyr Leu Asp Lys Met Ala Asp Ser Gln Phe Val Cys Lys Arg Gly Tyr
 85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110

Ile Val Thr Cys Ala Lys Phe Thr Cys Val Lys Lys Leu Thr Gly Lys
 115 120 125

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

Ala Ser Gln His Gly Gly Met Ile Asn Asn Asp Thr Asn His Gln His
 145 150 155 160

Asp Lys Glu Asn Arg Ala Arg Ile Asp Ile Thr Ala Ser Ala Pro Arg
 165 170 175

Val Glu Val Glu Leu Gly Ser Phe Gly Ser Phe Ser Met Glu Cys Glu
 180 185 190

Pro Arg Ser Gly Leu Asn Phe Gly Asp Leu Tyr Tyr Leu Thr Met Asn
 195 200 205

Asn Lys His Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Ser Leu
 210 215 220

Pro Trp His Thr Gly Ala Thr Ser Asn Asn His His Trp Asn Asn Lys

225					230						235				240
Glu	Ala	Leu	Val	Glu	Phe	Arg	Glu	Ala	His	Ala	Lys	Lys	Gln	Thr	Ala
				245					250					255	
Val	Val	Leu	Gly	Ser	Gln	Glu	Gly	Ala	Val	His	Ala	Ala	Leu	Ala	Gly
			260					265					270		
Ala	Leu	Glu	Ala	Glu	Ser	Asp	Gly	His	Lys	Ala	Thr	Ile	Tyr	Ser	Gly
		275					280					285			
His	Leu	Lys	Cys	Arg	Leu	Lys	Leu	Asp	Lys	Leu	Arg	Leu	Lys	Gly	Met
	290					295					300				
Ser	Tyr	Ala	Leu	Cys	Thr	Gly	Ala	Phe	Thr	Phe	Ala	Arg	Thr	Pro	Ser
305					310					315					320
Glu	Thr	Ile	His	Gly	Thr	Ala	Thr	Val	Glu	Leu	Gln	Tyr	Ala	Gly	Glu
				325					330					335	
Asp	Gly	Pro	Cys	Lys	Val	Pro	Ile	Val	Ile	Thr	Ser	Asp	Thr	Asn	Ser
			340					345					350		
Met	Ala	Ser	Thr	Gly	Arg	Leu	Ile	Thr	Ala	Asn	Pro	Val	Val	Thr	Glu
		355					360					365			
Ser	Gly	Ala	Asn	Ser	Lys	Met	Met	Val	Glu	Ile	Asp	Pro	Pro	Phe	Gly
	370					375					380				
Asp	Ser	Tyr	Ile	Ile	Val	Gly	Thr	Gly	Thr	Thr	Lys	Ile	Thr	His	His
385					390					395					400
Trp	His	Arg	Ala	Gly	Ser	Ser	Ile	Gly	Arg	Ala	Phe	Glu	Ala	Thr	Met
				405					410					415	
Arg	Gly	Ala	Lys	Arg	Met	Ala	Val	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe
			420					425					430		
Gly	Ser	Val	Gly	Gly	Met	Phe	Asn	Ser	Val	Gly	Lys	Phe	Val	His	Gln
		435					440					445			
Val	Phe	Gly	Ser	Ala	Phe	Lys	Ala	Leu	Phe	Gly	Gly	Met	Ser	Trp	Phe
	450					455					460				

Thr Gln Leu Leu Ile Gly Phe Leu Leu Ile Trp Met Gly Leu Asn Ala
 465 470 475 480

Arg Gly Gly Thr Val Ala Met Ser Phe Met Gly Ile Gly Ala Met Leu
 485 490 495

Ile Phe Leu Ala Thr Ser Val Ser Gly
 500 505

<210> 151
 <211> 589
 <212> PRT
 <213> Artificial sequence

<220>
 <223> SEQ ID NO 61 without N-terminal RR

<400> 151

Gly Ala Asp Thr Ser Val Gly Ile Val Gly Leu Leu Leu Thr Thr Ala
 1 5 10 15

Met Ala Ala Glu Val Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu
 20 25 30

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

Met Asn Lys Cys Tyr Ile Gln Ile Met Asp Leu Gly His Met Cys Asp
 50 55 60

Ala Thr Met Ser Tyr Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro
 65 70 75 80

Asp Asp Val Asp Cys Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr
 85 90 95

Gly Thr Cys His His Lys Lys Gly Glu Ala Arg Arg Ser Arg Arg Ala
 100 105 110

Val Thr Leu Pro Ser His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln
 115 120 125

Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu
 130 135 140

Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile
 145 150 155 160

Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val
 165 170 175

Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val
 180 185 190

Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp
 195 200 205

Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys
 210 215 220

Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala
 225 230 235 240

Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser
 245 250 255

Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser
 260 265 270

Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly
 275 280 285

Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys
 290 295 300

Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn
 305 310 315 320

Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly
 325 330 335

Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys
 340 345 350

Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly
 355 360 365

Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe

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

<210> 152
 <211> 690
 <212> PRT

<213> Artificial sequence

<220>

<223> SEQ ID NO 62 without N-terminal RR

<400> 152

Gly Ala Asp Thr Ser Val Gly Ile Val Gly Leu Leu Leu Thr Thr Ala
1 5 10 15

Met Ala Ala Glu Val Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu
20 25 30

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

Met Asn Lys Cys Tyr Ile Gln Ile Met Asp Leu Gly His Met Cys Asp
50 55 60

Ala Thr Met Ser Tyr Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro
65 70 75 80

Asp Asp Val Asp Cys Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr
85 90 95

Gly Thr Cys His His Lys Lys Gly Glu Ala Arg Arg Ser Arg Arg Ala
100 105 110

Val Thr Leu Pro Ser His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln
115 120 125

Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu
130 135 140

Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile
145 150 155 160

Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val
165 170 175

Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val
180 185 190

Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp
195 200 205

Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys
 210 215 220

Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala
 225 230 235 240

Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser
 245 250 255

Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser
 260 265 270

Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly
 275 280 285

Asn Gly Cys Gly Asp Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys
 290 295 300

Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn
 305 310 315 320

Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly
 325 330 335

Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg Ala Lys
 340 345 350

Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly
 355 360 365

Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe
 370 375 380

Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His
 385 390 395 400

Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp
 405 410 415

Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys
 420 425 430

Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu

435																
Gly	Ala	Val	His	Thr	Ala	Leu	Ala	Gly	Ala	Leu	Glu	Ala	Glu	Met	Asp	
450						455					460					
Gly	Ala	Lys	Gly	Arg	Leu	Ser	Ser	Gly	His	Leu	Lys	Cys	Arg	Leu	Lys	
465					470					475					480	
Met	Asp	Lys	Leu	Arg	Leu	Lys	Gly	Val	Ser	Tyr	Ser	Leu	Cys	Thr	Ala	
				485					490					495		
Ala	Phe	Thr	Phe	Thr	Lys	Ile	Pro	Ala	Glu	Thr	Leu	His	Gly	Thr	Val	
				500				505					510			
Thr	Val	Glu	Val	Gln	Tyr	Ala	Gly	Thr	Asp	Gly	Pro	Cys	Lys	Val	Pro	
		515					520					525				
Ala	Gln	Met	Ala	Val	Asp	Met	Gln	Thr	Leu	Thr	Pro	Val	Gly	Arg	Leu	
		530				535					540					
Ile	Thr	Ala	Asn	Pro	Val	Ile	Thr	Glu	Ser	Thr	Glu	Asn	Ser	Lys	Met	
545					550					555					560	
Met	Leu	Glu	Leu	Asp	Pro	Pro	Phe	Gly	Asp	Ser	Tyr	Ile	Val	Ile	Gly	
				565					570					575		
Val	Gly	Glu	Lys	Lys	Ile	Thr	His	His	Trp	His	Arg	Ser	Gly	Ser	Thr	
			580					585					590			
Ile	Gly	Lys	Ala	Phe	Glu	Ala	Thr	Val	Arg	Gly	Ala	Lys	Arg	Met	Ala	
		595					600					605				
Val	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Val	Gly	Gly	Ala	Leu	
	610					615					620					
Asn	Ser	Leu	Gly	Lys	Gly	Ile	His	Gln	Ile	Phe	Gly	Ala	Ala	Phe	Lys	
625					630					635					640	
Ser	Leu	Phe	Gly	Gly	Met	Ser	Trp	Phe	Ser	Gln	Ile	Leu	Ile	Gly	Thr	
				645					650					655		
Leu	Leu	Met	Trp	Leu	Gly	Leu	Asn	Thr	Lys	Asn	Gly	Ser	Ile	Ser	Leu	
			660					665					670			

Met Cys Leu Ala Leu Gly Gly Val Leu Ile Phe Leu Ser Thr Ala Val
675 680 685

Ser Ala
690

<210> 153
<211> 19800
<212> DNA
<213> Artificial sequence

<220>
<223> pTM3 ATU3-GFP MV Schwarz sequence + GFP within ATU3

<400> 153
tataagcggc cgctaatacg actcactata gggccaactt tgtttggtct gatgagtccg 60
tgaggacgaa acccgagatc ccgggtcacc aaacaaagtt gggtaaggat agttcaatca 120
atgatcatct tctagtgcac ttaggattca agatcctatt atcagggaca agagcaggat 180
tagggatata cgagatggcc acacttttaa ggagcttagc attgttcaaa agaaacaagg 240
acaaaccacc cattacatca ggatccggtg gagccatcag aggaatcaaa cacattatta 300
tagtaccaat ccctggagat tcctcaatta ccactcgatc cagacttctg gaccggttgg 360
tgaggttaat tggaaacccg gatgtgagcg ggcccaaact aacaggggca ctaataggta 420
tattatcctt atttgtggag tctccaggtc aattgattca gaggatcacc gatgaccctg 480
acgttagcat aaggctgtta gaggttgtcc agagtgacca gtcacaatct ggccttacct 540
tcgcatcaag aggtaccaac atggaggatg aggcggacca atacttttca catgatgatc 600
caattagtag tgatcaatcc aggttcggat ggttcgggaa caaggaaatc tcagatattg 660
aagtgcaaga ccctgaggga ttcaacatga ttctgggtac catcctagcc caaatttggg 720
tcttgctcgc aaaggcgggt acggccccag acacggcagc tgattcggag ctaagaaggt 780
ggataaagta caccacaaca agaagggtag ttggtgaatt tagattggag agaaaatggt 840
tggatgtggt gaggaacagg attgccgagg acctctcctt acgccgattc atggtcgtc 900
taatcctgga tatcaagaga acacccggaa acaaaccag gattgctgaa atgatatgtg 960
acattgatac atatatcgta gaggcaggat tagccagttt tctcctgact attaagtttg 1020
ggatagaaac tatgtatcct gctcttgac tgcatagaatt tgctggtgag ttatccacac 1080
ttgagtcctt gatgaacctt taccagcaaa tgggggaaac tgcaccctac atggtaatcc 1140
tggagaactc aattcagaac aagttcagtg caggatcata ccctctgctc tggagctatg 1200

ccatgggagt	aggagtggaa	cttgaaaact	ccatgggagg	tttgaacttt	ggccgatctt	1260
actttgatcc	agcatatttt	agattagggc	aagagatggt	aaggaggtca	gctggaaagg	1320
tcagttccac	attggcatct	gaactcggta	tactgcccga	ggatgcaagg	cttgtttcag	1380
agattgcaat	gcatactact	gaggacaaga	tcagtagagc	ggttggaccc	agacaagccc	1440
aagtatcatt	tctacacggt	gatcaaagtg	agaatgagct	accgagattg	gggggcaagg	1500
aagataggag	ggtcaaacag	agtcgaggag	aagccaggga	gagctacaga	gaaaccgggc	1560
ccagcagagc	aagtgatgcg	agagctgccc	atcttccaac	cggcacaccc	ctagacattg	1620
acactgcaac	ggagtccagc	caagatccgc	aggacagtcg	aaggtcagct	gacgccctgc	1680
ttaggctgca	agccatggca	ggaatctcgg	aagaacaagg	ctcagacacg	gacacccta	1740
tagtgtacaa	tgacagaaat	cttctagact	aggtgcgaga	ggccgagggc	cagaacaaca	1800
tccgcctacc	atccatcatt	gttataaaaa	acttaggaac	caggtccaca	cagccgccag	1860
cccatcaacc	atccactccc	acgattggag	ccaatggcag	aagagcaggc	acgccatgtc	1920
aaaaacggac	tggaatgcat	ccgggctctc	aaggccgagc	ccatcggctc	actggccatc	1980
gaggaagcta	tggcagcatg	gtcagaaata	tcagacaacc	caggacagga	gcgagccacc	2040
tgcagggaag	agaaggcagg	cagttcgggt	ctcagcaaac	catgcctctc	agcaattgga	2100
tcaactgaag	gcggtgcacc	tcgcatccgc	ggtcagggac	ctggagagag	cgatgacgac	2160
gctgaaaactt	tgggaatccc	ccaagaaat	ctccaggcat	caagcactgg	gttacagtgt	2220
tattacgttt	atgatcacag	cggatgaagc	gttaagggaa	tccaagatgc	tgactctatc	2280
atggttcaat	caggccttga	tggatgagc	accctctcag	gaggagacaa	tgaatctgaa	2340
aacagcgatg	tggatattgg	cgaacctgat	accgagggat	atgctatcac	tgaccgggga	2400
tctgctccca	tctctatggg	gttcagggct	tctgatgttg	aaactgcaga	aggaggggag	2460
atccacgagc	tcttgagact	ccaatccaga	ggcaacaact	ttccgaagct	tgggaaaact	2520
ctcaatgttc	ctccgcccc	ggaccccggt	agggccagca	cttccgggac	acccattaaa	2580
aagggcacag	acgcgagatt	agcctcattt	ggaacggaga	tcgcgtcttt	attgacaggt	2640
ggtgcaaccc	aatgtgctcg	aaagtcaccc	tcggaaccat	cagggccagg	tgcacctgcg	2700
gggaatgtcc	ccgagtgtgt	gagcaatgcc	gcactgatac	aggagtggac	acccgaatct	2760
ggtaccacaa	tctccccgag	atcccagaat	aatgaagaag	ggggagacta	ttatgatgat	2820
gagctgttct	ctgatgtcca	agatattaaa	acagccttgg	ccaaaataca	cgaggataat	2880
cagaagataa	tctccaagct	agaatcactg	ctgttattga	agggagaagt	tgagtcaatt	2940

aagaagcaga tcaacaggca aaatatcagc atatccaccc tggaaggaca cctctcaagc	3000
atcatgatcg ccattcctgg acttggaag gatcccaacg acccactgc agatgtcgaa	3060
atcaatccccg acttgaaacc catcataggc agagattcag gccgagcact ggccgaagtt	3120
ctcaagaaac ccgttgccag ccgacaactc caaggaatga caaatggacg gaccagttcc	3180
agaggacagc tgctgaagga atttcagcta aagccgatcg ggaaaaagat gagctcagcc	3240
gtcgggtttg ttcttgacac cggccctgca tcacgcagtg taatccgctc cattataaaa	3300
tccagccggc tagaggagga tcggaagcgt tacctgatga ctctccttga tgatatcaaa	3360
ggagccaatg atcttgccaa gttccaccag atgctgatga agataataat gaagtagcta	3420
cagctcaact tacctgccaa ccccatgcc a gtcgaccaa ctagtacaac ctaaatccat	3480
tataaaaaac ttaggagcaa agtgattgcc tccaaggtc cacaatgaca gagacctacg	3540
acttcgacaa gtcggcatgg gacatcaaag ggtcgatcgc tccgatacaa ccaccacct	3600
acagtgatgg caggctggtg cccaggtca gagtcataga tcctggtcta ggcgacagga	3660
aggatgaatg ctttatgtac atgtttctgc tgggggttgt tgaggacagc gattccctag	3720
ggcctccaat cgggagagca tttgggttcc tgcccttagg tgttggcaga tccacagcaa	3780
agcccgaaaa actcctcaaa gaggccactg agcttgacat agttgttaga cgtacagcag	3840
ggctcaatga aaaactggtg ttctacaaca acacccact aactctctc acaccttga	3900
gaaaggtcct aacaacaggg agtgtcttca acgcaaacca agtgtgcaat gcggttaatc	3960
tgataccgct cgataccccg cagaggttcc gtgttgttta tatgagcatc acccgtcttt	4020
cggataacgg gtattacacc gttcctagaa gaatgctgga attcagatcg gtcaatgcag	4080
tggccttcaa cctgctggtg acccttagga ttgacaaggc gataggccct gggaagatca	4140
tcgacaatac agagcaactt cctgaggcaa catttatggt ccacatcggg aacttcagga	4200
gaaagaagag tgaagtctac tctgccgatt attgcaaaat gaaaatcgaa aagatgggcc	4260
tggtttttgc acttggtggg atagggggca ccagtcttca cattagaagc acaggcaaaa	4320
tgagcaagac tctccatgca caactcgggt tcaagaagac cttatgttac ccgctgatgg	4380
atatcaatga agaccttaat cgattactct ggaggagcag atgcaagata gtaagaatcc	4440
aggcagtttt gcagccatca gttcctcaag aattccgcat ttacgacgac gtgatcataa	4500
atgatgacca aggactattc aaagttctgt agaccgtagt gccagcaat gcccgaaaac	4560
gacccccctc acaatgacag ccagaaggcc cggacaaaaa agccccctcc gaaagactcc	4620
acggaccaag cgagaggcca gccagcagcc gacggcaagc gcgaacacca ggcggcccca	4680

gcacagaaca gccctgacac aaggccacca ccagccaccc caatctgcat cctcctcgtg	4740
ggacccccga ggaccaaccc ccaaggctgc ccccgatcca aaccaccaac cgcaccccca	4800
ccacccccgg gaaagaaacc cccagcaatt ggaaggcccc tccccctctt cctcaacaca	4860
agaactccac aaccgaaccg cacaagcgac cgaggtgacc caaccgcagg catccgactc	4920
cctagacaga tcctctctcc ccggcaaact aaacaaaact tagggccaag gaacatacac	4980
acccaacaga acccagaccc cggtccacgg cgccgcgccc ccaacccccg acaaccagag	5040
ggagccccca accaatcccc cggtctcccc cggtgcccac aggcagggac accaaccccc	5100
gaacagaccc agcacccaac catcgacaat ccaagacggg ggggcccccc caaaaaaagg	5160
ccccagggg ccgacagcca gcaccgcgag gaagcccacc cccccacac acgaccacgg	5220
caaccaaacc agaaccaga ccaccctggg ccaccagctc ccagactcgg ccatcacccc	5280
gcagaaagga aaggccacaa cccgcgcacc ccagccccga tccggcgggg agccacccaa	5340
cccgaaccag caccgaagag cgatccccga aggacccccg aaccgcaaag gacatcagta	5400
tcccacagcc tctccaagtc ccccggtctc ctctcttctt cgaagggacc aaaagatcaa	5460
tccaccacac ccgacgacac tcaactcccc acccctaaag gagacaccgg gaatcccaga	5520
atcaagactc atccaatgtc catcatgggt ctcaaggtga acgtctctgc catattcatg	5580
gcagtactgt taactctcca aacaccacc ggtcaaattc attggggcaa tctctctaag	5640
ataggggtgg taggaatagg aagtgcgaag taaaaagtta tgactcgttc cagccatcaa	5700
tcattagtca taaaattaat gcccaatata actctcctca ataactgcac gagggtagag	5760
attgcagaat acaggagact actgagaaca gttttggaac caattagaga tgcacttaat	5820
gcaatgaccc agaataataag accggttcag agtgtagctt caagtaggag acacaagaga	5880
tttgcgggag tagtcctggc aggtgcggcc ctaggcgttg ccacagctgc tcagataaca	5940
gccggcattg cacttcacca gtccatgctg aactctcaag ccatcgacaa tctgagagcg	6000
agcctggaaa ctactaatca ggcaattgag acaatcagac aagcagggca ggagatgata	6060
ttggctgttc aggggtgtcca agactacatc aataatgagc tgataccgtc tatgaaccaa	6120
ctatcttgtg atttaatcgg ccagaagctc gggctcaaatt tgctcagata ctatacagaa	6180
atcctgtcat tatttggtccc cagtttacgg gaccccatat ctgcggagat atctatccag	6240
gctttgagct atgcgcttgg aggagacatc aataaggtgt tagaaaagct cggatacagt	6300
ggaggtgatt tactgggcat cttagagagc ggaggaataa aggcccggat aactcacgtc	6360
gacacagagt cctacttcat tgtcctcagt atagcctatc cgacgctgtc cgagattaag	6420

ggggtgattg tccaccggct agaggggggtc tcgtacaaca taggctctca agagtgggtat	6480
accactgtgc ccaagtatgt tgcaacccaa ggggtacctta tctcgaattt tgatgagtca	6540
tcgtgtactt tcatgccaga ggggactgtg tgcagccaaa atgccttgta cccgatgagt	6600
cctctgctcc aagaatgcct ccgggggtac accaagtcct gtgctcgtac actcgtatcc	6660
gggtcttttg ggaaccgggtt cattttatca caagggaacc taatagccaa ttgtgcatca	6720
atcctttgca agtgttacac aacaggaacg atcattaatc aagaccctga caagatccta	6780
acatacattg ctgccgatca ctgcccggta gtcgaggtga acggcgtgac catccaagtc	6840
gggagcagga ggtatccaga cgctgtgtac ttgcacagaa ttgacctcgg tcctcccata	6900
tcattggaga ggttggacgt agggacaaat ctggggaatg caattgctaa gttggaggat	6960
gccaaggaat tgttggagtc atcggaccag atattgagga gtatgaaagg tttatcgagc	7020
actagcatag tctacatcct gattgcagtg tgtcttgag ggttgatagg gatccccgct	7080
ttaatatgtt gctgcagggg gcgttgtaac aaaaaggag aacaagttgg tatgtcaaga	7140
ccaggcctaa agcctgatct tacgggaaca tcaaaatcct atgtaaggtc gctctgatcc	7200
tctacaactc ttgaaacaca aatgtccac aagtctcctc ttcgtcatca agcaaccacc	7260
gcaccagca tcaagccac ctgaaattat ctccggcttc cctctggccg aacaatatcg	7320
gtagttaatc aaaacttagg gtgcaagatc atccacaatg tcaccacaac gagaccgat	7380
aaatgccttc taaaagata acccccatcc caagggaagt aggatagtca ttaacagaga	7440
acatcttatg attgatagac cttatgtttt gctggctgtt ctgtttgtca tgtttctgag	7500
cttgatcggg ttgctagcca ttgcaggcat tagacttcat cgggcagcca tctacaccgc	7560
agagatccat aaaagcctca gcaccaatct agatgtaact aactcaatcg agcatcaggt	7620
caaggacgtg ctgacaccac tcttcaaat catcgggtgat gaagtgggcc tgaggacacc	7680
tcagagattc actgacctag tgaaattaat ctctgacaag attaaattcc ttaatccgga	7740
tagggagtac gacttcagag atctcacttg gtgtatcaac ccgccagaga gaatcaaatt	7800
ggattatgat caatactgtg cagatgtggc tgctgaagag ctcatgaatg cattggtgaa	7860
ctcaactcta ctggagacca gaacaaccaa tcagttccta gctgtctcaa agggaaactg	7920
ctcagggcc actacaatca gaggtcaatt ctcaaacatg tcgctgtccc tgtagactt	7980
gtatttaggt cgaggttaca atgtgtcatc tatagtcact atgacatccc agggaatgta	8040
tgggggaact tacctagtgg aaaagcctaa tctgagcagc aaaaggtcag agttgtcaca	8100
actgagcatg taccgagtgt ttgaagtagg tgttatcaga aatccgggtt tgggggctcc	8160

ggtgttccat	atgacaaact	atcttgagca	accagtcagt	aatgatctca	gcaactgtat	8220
ggtggctttg	ggggagctca	aactcgcagc	cctttgtcac	ggggaagatt	ctatcacaat	8280
tccctatcag	ggatcagggg	aaggtgtcag	cttcagctc	gtcaagctag	gtgtctggaa	8340
atccccaacc	gacatgcaat	cctgggtccc	cttatcaacg	gatgatccag	tgatagacag	8400
gctttacctc	tcattctcaca	gaggtgttat	cgctgacaat	caagcaaaat	gggctgtccc	8460
gacaacacga	acagatgaca	agttgcgaat	ggagacatgc	ttccaacagg	cgtgtaaggg	8520
taaaatccaa	gcactctgcg	agaatcccga	gtgggcacca	ttgaaggata	acaggattcc	8580
ttcatacggg	gtcttgtctg	ttgatctgag	tctgacagtt	gagcttaaaa	tcaaaattgc	8640
ttcgggattc	gggccattga	tcacacacgg	ttcagggatg	gacctataca	aatccaacca	8700
caacaatgtg	tattggctga	ctatcccgcc	aatgaagaac	ctagccttag	gtgtaatcaa	8760
cacattggag	tggtatccga	gattcaaggt	tagtccctac	ctcttactg	tccaatttaa	8820
ggaagcaggc	gaagactgcc	atgcccacac	atacctacct	gcggagggtg	atggtgatgt	8880
caaactcagt	tccaatctgg	tgattctacc	tggtcaagat	ctccaatatg	ttttggcaac	8940
ctacgatact	tccaggggtg	aacatgctgt	ggtttattac	gtttacagcc	caagccgctc	9000
atthttcttac	ttttatcctt	ttagggttgc	tataaagggg	gtccccatcg	aattacaagt	9060
ggaatgcttc	acatgggacc	aaaaactctg	gtgccgtcac	ttctgtgtgc	ttgcggactc	9120
agaatctggt	ggacatatca	ctcactctgg	gatggtgggc	atgggagtca	gctgcacagt	9180
cacccgggaa	gatggaacca	atcgcagata	gggctgctag	tgaaccaatc	acatgatgtc	9240
accagacat	caggcatacc	cactagtcta	ccctccatca	ttgttataaa	aaacttagga	9300
accaggtcca	cacagccgcc	agcccatcaa	cgcgtacgat	ggtgagcaag	ggcgaggagc	9360
tggtcaccgg	ggtggtgccc	atcctggtcg	agctggacgg	cgacgtaaac	ggccacaagt	9420
tcagcgtgtc	cggcgagggc	gagggcgatg	ccacctacgg	caagctgacc	ctgaagttca	9480
tctgcaccac	cggcaagctg	cccgtgccct	ggcccaccct	cgtgaccacc	ctgacctacg	9540
gcgtgcagtg	cttcagccgc	taccccgacc	acatgaagca	gcacgacttc	ttcaagtccg	9600
ccatgcccga	aggctacgtc	caggagcgca	ccatcttctt	caaggacgac	ggcaactaca	9660
agacccgcgc	cgaggtgaag	ttcaggggcg	acaccctggt	gaaccgcatc	gagctgaagg	9720
gcatcgactt	caaggaggac	ggcaacatcc	tggggcacia	gctggagtac	aactacaaca	9780
gccacaacgt	ctatatcatg	gccgacaagc	agaagaacgg	catcaaggtg	aacttcaaga	9840
tccgccacia	catcgaggac	ggcagcgtgc	agctcgccga	ccactaccag	cagaacaccc	9900

ccatcggcga	cggccccgtg	ctgctgcccg	acaaccacta	cctgagcacc	cagtccgccc	9960
tgagcaaaga	ccccaacgag	aagcgcgac	acatggtcct	gctggagttc	gtgaccgccc	10020
ccgggatcac	tctcggcatg	gacgagctgt	acaagtaggc	gcgcagcgct	tagacgtctc	10080
gcgatcgatg	ctagtgtgaa	atagacatca	gaattaagaa	aaacgtaggg	tccaagtggc	10140
tccccgttat	ggactcgcta	tctgtcaacc	agatcttata	ccctgaagtt	cacctagata	10200
gcccgatagt	taccaataag	atagtagcca	tcctggagta	tgctcgagtc	cctcacgctt	10260
acagcctgga	ggaccctaca	ctgtgtcaga	acatcaagca	ccgcctaaaa	aacggatttt	10320
ccaaccaa	gattataaac	aatgtggaag	ttgggaatgt	catcaagtcc	aagcttagga	10380
gttatccggc	ccactctcat	attccatata	caaattgtaa	tcaggattta	tttaacatag	10440
aagacaaaga	gtcaacgagg	aagatccgtg	aactcctcaa	aaaggggaat	tcgctgtact	10500
caaagtcag	tgataagggt	ttccaatgct	taaggacac	taactcacgg	cttggcctag	10560
gctccgaatt	gagggaggac	atcaaggaga	aagttattaa	cttgggagtt	tacatgcaca	10620
gctcccagtg	gtttgagccc	tttctgtttt	ggtttacagt	caagactgag	atgaggtcag	10680
tgattaaatc	acaaacccat	acttgccata	ggaggagaca	cacacctgta	ttcttcactg	10740
gtagttcagt	tgagttgcta	atctctcgtg	accttggtgc	tataatcagt	aaagagtctc	10800
aacatgtata	ttacctgaca	tttgaactgg	ttttgatgta	ttgtgatgtc	atagagggga	10860
ggttaatgac	agagaccgct	atgactattg	atgctaggta	tacagagctt	ctaggaagag	10920
tcagatacat	gtggaaaactg	atagatgggt	tcttccctgc	actcgggaat	ccaacttata	10980
aaattgtagc	catgctggag	cctctttcac	ttgcttacct	gcagctgagg	gatataacag	11040
tagaactcag	aggtgctttc	cttaaccact	gctttactga	aatacatgat	gttcttgacc	11100
aaaacgggtt	ttctgatgaa	ggtacttata	atgagttaac	tgaagctcta	gattacattt	11160
tcataactga	tgacatacat	ctgacagggg	agattttctc	atttttcaga	agtttcggcc	11220
accccagact	tgaagcagta	acggctgctg	aaaatgtag	gaaatacatg	aatcagccta	11280
aagtcattgt	gtatgagact	ctgatgaaag	gtcatgccat	attttgtgga	atcataatca	11340
acggctatcg	tgacaggcac	ggaggcagtt	ggccaccgct	gaccctcccc	ctgcatgctg	11400
cagacacaat	ccggaatgct	caagcttcag	gtgaagggtt	aacacatgag	cagtgcgttg	11460
ataactggaa	atcttttgct	ggagtgaaat	ttggctgctt	tatgcctctt	agcctggata	11520
gtgatctgac	aatgtacct	aaggacaagg	cacttgctgc	tctccaaagg	gaatgggatt	11580
cagtttacc	gaaagagttc	ctgcgttacg	accctcccaa	gggaaccggg	tcacggaggc	11640

ttgtagatgt	tttccttaat	gattcgagct	ttgacccata	tgatgtgata	atgtatgttg	11700
taagtggagc	ttacctccat	gacctgagct	tcaacctgtc	ttacagcctg	aaagaaaagg	11760
agatcaagga	aacaggtaga	ctttttgcta	aaatgactta	caaaatgagg	gcatgccaaag	11820
tgattgctga	aaatctaata	tcaaacggga	ttggcaaata	ttttaaggac	aatgggatgg	11880
ccaaggatga	gcacgatttg	actaaggcac	tccacactct	agctgtctca	ggagtcccca	11940
aagatctcaa	agaaagtcac	aggggggggc	cagtcttaaa	aacctactcc	cgaagcccag	12000
tccacacaag	taccaggaac	gtgagagcag	caaaagggtt	tatagggttc	cctcaagtaa	12060
ttcggcagga	ccaagacact	gatcatccgg	agaatatgga	agcttacgag	acagtcagtg	12120
catttatcac	gactgatctc	aagaagtact	gccttaattg	gagatatgag	accatcagct	12180
tgtttgcaca	gaggctaaat	gagatttacg	gattgccctc	atttttccag	tggctgcata	12240
agaggcttga	gacctctgtc	ctgtatgtaa	gtgaccctca	ttgccccccc	gaccttgacg	12300
cccatatccc	gttatataaa	gtccccaatg	atcaaatctt	cattaagtac	cctatgggag	12360
gtatagaagg	gtattgtcag	aagctgtgga	ccatcagcac	cattccctat	ctataacctg	12420
ctgcttatga	gagcggagta	aggattgctt	cgttagtgca	aggggacaat	cagaccatag	12480
ccgtaacaaa	aagggtaccc	agcacatggc	cctacaacct	taagaaacgg	gaagctgcta	12540
gagtaactag	agattacttt	gtaattctta	ggcaaaggct	acatgatatt	ggccatcacc	12600
tcaaggcaaa	tgagacaatt	gtttcatcac	atttttttgt	ctattcaaaa	ggaatatatt	12660
atgatgggct	acttgtgtcc	caatcactca	agagcatcgc	aagatgtgta	ttctggtcag	12720
agactatagt	tgatgaaaca	agggcagcat	gcagtaatat	tgctacaaca	atggctaaaa	12780
gcatcgagag	aggttatgac	cgttaccttg	catattccct	gaacgtccta	aaagtgatac	12840
agcaaattct	gatctctctt	ggcttcacaa	tcaattcaac	catgaccggg	gatgtagtca	12900
taccctcct	cacaaacaac	gacctcttaa	taaggatggc	actgttgccc	gctcctattg	12960
gggggatgaa	ttatctgaat	atgagcaggc	tgtttgtcag	aaacatcggt	gatccagtaa	13020
catcatcaat	tgctgatctc	aagagaatga	ttctcgcctc	actaatgcct	gaagagaccc	13080
tccatcaagt	aatgacacaa	caaccggggg	actcttcatt	cctagactgg	gctagcgacc	13140
cttactcagc	aaatcttgta	tgtgtccaga	gcatcactag	actcctcaag	aacataactg	13200
caaggtttgt	cctgatccat	agtccaaacc	caatgttaaa	aggattattc	catgatgaca	13260
gtaaagaaga	ggacgaggga	ctggcggcat	tcctcatgga	caggcatatt	atagtaccta	13320
gggcagctca	tgaaatcctg	gatcatagt	tcacaggggc	aagagagtct	attgcaggca	13380

tgctggatac	cacaaaaggc	ttgattcgag	ccagcatgag	gaaggggggg	ttaacctctc	13440
gagtgataac	cagattgtcc	aattatgact	atgaacaatt	cagagcaggg	atggtgctat	13500
tgacaggaag	aaagagaaat	gtcctcattg	acaaagagtc	atgttcagtg	cagctggcga	13560
gagctctaag	aagccatatg	tgggcgaggc	tagctcgagg	acggcctatt	tacggccttg	13620
aggtccctga	tgtactagaa	tctatgcgag	gccaccttat	tcggcgtcac	gagacatgtg	13680
tcatctgcga	gtgtggatca	gtcaactacg	gatgggtttt	tgtcccctcg	ggttgccaac	13740
tggatgatat	tgacaaggaa	acatcatcct	tgagagtccc	atatattggt	tctaccactg	13800
atgagagAAC	agacatgaag	cttgccttcg	taagagcccc	aagtcgatcc	ttgcgatctg	13860
ctgttagaat	agcaacagtg	tactcatggg	cttacggtga	tgatgatagc	tcttggaacg	13920
aagcctgggt	gttggctagg	caaagggcca	atgtgagcct	ggaggagcta	agggtgatca	13980
ctcccatctc	aacttcgact	aatttagcgc	ataggttgag	ggatcgtagc	actcaagtga	14040
aatactcagg	tacatccctt	gtccgagtgg	cgagggtatac	cacaatctcc	aacgacaatc	14100
tctcatttgt	catatcagat	aagaaggttg	atactaactt	tatataccaa	caaggaatgc	14160
ttctaggggt	gggtgtttta	gaaacattgt	ttcgactcga	gaaagatacc	ggatcatcta	14220
acacggtatt	acatcttcac	gtcgaaacag	attgttgCGT	gatcccgatg	atagatcatc	14280
ccaggatacc	cagctccccg	aagctagagc	tgagggcaga	gctatgtacc	aaccattga	14340
tatatgataa	tgcaccttta	attgacagag	atgcaacaag	gctatacacc	cagagccata	14400
ggaggcacct	tgtggaattt	gttacatggg	ccacacccca	actatatcac	attttagcta	14460
agtccacagc	actatctatg	attgacctgg	taacaaaatt	tgagaaggac	catatgaatg	14520
aaatttcagc	tctcataggg	gatgacgata	tcaatagttt	cataactgag	tttctgctca	14580
tagagccaag	attattcact	atctacttgg	gccagtgtgc	ggccatcaat	tgggcatttg	14640
atgtacatta	tcatagacca	tcagggaat	atcagatggg	tgagctgttg	tcatcgttcc	14700
tttctagaat	gagcaaagga	gtgtttaagg	tgcttgTcaa	tgctctaagc	cacccaaaga	14760
tctacaagaa	attctggcat	tgtggtatta	tagagcctat	ccatggtcct	tacttgatg	14820
ctcaaaaact	gcacacaact	gtgtgcaaca	tggtttacac	atgctatatg	acctacctcg	14880
acctgttggt	gaatgaagag	ttagaagagt	tcacatttct	cttgtgtgaa	agcgacgagg	14940
atgtagtacc	ggacagattc	gacaacatcc	aggcaaaaca	cttatgtggt	ctggcagatt	15000
tgtactgtca	accagggacc	tgcccaccaa	ttcgaggctc	aagaccggta	gagaaatgtg	15060
cagttctaac	cgaccatatc	aaggcagagg	ctatgttatc	tccagcagga	tcttcgtgga	15120

acataaatcc aattattgta gaccattact catgctctct gacttatctc cggcgaggat	15180
cgatcaaaca gataagattg agagttgata caggattcat ttctgacgcc ctgctgagg	15240
taaatgtcag tcagccaaag atcggcagca acaacatctc aaatatgagc atcaaggctt	15300
tcagaccccc acacgatgat gttgcaaaat tgctcaaaga tatcaacaca agcaagcaca	15360
atcttcccat ttcagggggc aatctcgcca attatgaaat ccatgctttc cgcagaatcg	15420
ggttgaactc atctgcttgc taaaaagctg ttgagatata aacattaatt aggagatgcc	15480
ttgagccagg ggaggacggc ttgttcttgg gtgagggata gggttctatg ttgatcactt	15540
ataaagagat acttaaaacta aacaagtgtc tctataatag tggggtttcc gccaattcta	15600
gatctgggtc aaggggaatta gcaccctatc cctccgaagt tggccttgtc gaacacagaa	15660
tgggagtagg taatattgtc aaagtgtctt ttaacgggag gcccgagtc acgtgggtag	15720
gcagtgtaga ttgcttcaat ttcatagtta gtaatatccc tacctctagt gtgggggtta	15780
tccattcaga tatagagacc ttgcctgaca aagatactat agagaagcta gaggaattgg	15840
cagccatctt atcgatggct ctgctcctgg gcaaaatagg atcaatactg gtgattaagc	15900
ttatgccttt cagcggggat tttgttcagg gatttataag ttatgtaggg tctcattata	15960
gagaagtga ccttgtatac cctagatata gcaacttcat ctctactgaa tcttatttgg	16020
ttatgacaga tctcaaggct aaccggctaa tgaatcctga aaagattaag cagcagataa	16080
ttgaatcatc tgtgaggact tcacctggac ttataggtca catcctatcc attaagcaac	16140
taagctgcat acaagcaatt gtgggagacg cagttagtag aggtgatata aatcctactc	16200
tgaaaaaact tacacctata gagcaggtgc tgatcaattg cgggttggca attaacggac	16260
ctaagctgtg caaagaattg atccaccatg atgttgctc agggcaagat ggattgctta	16320
attctatact catcctctac agggagttgg caagattcaa agacaacca agaagtcaac	16380
aagggatgtt ccacgcttac cccgtattgg taagtagcag gcaacgagaa cttatatcta	16440
ggatcacccg caaattctgg gggcacattc ttctttactc cgggaacaaa aagttgataa	16500
ataagtttat ccagaatctc aagtccggct atctgatact agacttacac cagaatatct	16560
tcgttaagaa tctatccaag tcagagaaac agattattat gacggggggg ttgaaacgtg	16620
agtgggtttt taaggtaaca gtcaaggaga ccaaagaatg gtataagtta gtcggatata	16680
gtgccctgat taaggactaa ttggttgaac tccggaaccc taatcctgcc ctaggtggtt	16740
aggcattatt tgcaatatat taaagaaaac tttgaaaata cgaagtttct attcccagct	16800
ttgtctggtg gccggcatgg tcccagcctc ctgctggcg ccggctgggc aacattccga	16860

ggggaccgtc	ccctcggtaa	tggcgaatgg	gacgcggccg	atccggctgc	taacaaagcc	16920
cgaaaggaag	ctgagttggc	tgctgccacc	gctgagcaat	aactagcata	accccttggg	16980
gcctctaaac	gggtcttgag	gggttttttg	ctgaaaggag	gaactatatc	cggatgcggc	17040
cgcgggccct	atggtaccca	gcttttgttc	ccttttagtga	gggttaattc	cgagcttggc	17100
gtaatcatgg	tcatagctgt	ttcctgtgtg	aaattgttat	ccgctcacia	ttccacacia	17160
cataggagcc	ggaagcataa	agtgtaaagc	ctgggggtgcc	taatgagtga	ggtaactcac	17220
attaattgcg	ttgcgctcac	tgcccgtttt	ccagtcggga	aacctgtcgt	gccagctgca	17280
ttaatgaatc	ggccaacgcg	cggggagagg	cggtttgctg	attgggcgct	cttccgcttc	17340
ctcgctcact	gactcgctgc	gctcggtcgt	tcggctgcgg	cgagcgggat	cagctcactc	17400
aaaggcggtg	atacggttat	ccacagaatc	aggggataac	gcaggaaaga	acatgtgagc	17460
aaaaggccag	caaaaggcca	ggaaccgtaa	aaaggccgcg	ttgctggcgt	ttttccatag	17520
gctcggtccc	cctgacgagc	atcacaaaaa	tcgacgctca	agtcagagggt	ggcgaaaccc	17580
gacaggacta	taaagatacc	aggcgttccc	ccctggaagc	tccctcgtgc	gctctcctgt	17640
tccgaccctg	ccgcttaccg	gatacctgtc	cgcctttctc	ccttcgggaa	gcgtggcgct	17700
ttctcaatgc	tcacgctgta	ggtatctcag	ttcgggtgtg	gtcgttcgct	ccaagctggg	17760
ctgtgtgcac	gaaccccccg	ttcagccga	ccgctgcgcc	ttatccggta	actatcgtct	17820
tgagtccaac	ccggtaaagc	acgacttata	gccactggca	gcagccactg	gtaacaggat	17880
tagcagagcg	aggatatgtg	gcggtgctac	agagttcttg	aagtgggtggc	ctaactacgg	17940
ctacactaga	aggacagtat	ttggtatctg	cgctctgctg	aagccagtta	ccttcggaaa	18000
aagagttggg	agctcttgat	ccggcaaaca	aaccaccgct	ggtagcgggtg	gtttttttgt	18060
ttgcaagcag	cagattacgc	gcagaaaaaa	aggatctcaa	gaagatcctt	tgatcttttc	18120
tacggggtct	gacgctcagt	ggaacgaaaa	ctcacgttaa	gggatttttg	tcatgagatt	18180
atcaaaaagg	atcttcacct	agatcctttt	aaattaaaaa	tgaagtttta	aatcaatcta	18240
aagtatatat	gagtaaactt	ggtctgacag	ttaccaatgc	ttaatcagtg	aggcacctat	18300
ctcagcgatc	tgtctatttc	gttcatccat	agttgcctga	ctgcccgctg	tgtagataac	18360
tacgatacgg	gagggcttac	catctggccc	cagtgcctga	atgataccgc	gagaccacg	18420
ctcaccggct	ccagatttat	cagcaataaa	ccagccagcc	ggaagggccg	agcgcagaag	18480
tggtcctgca	actttatccg	cctccatcca	gtctattaat	tgttgccggg	aagctagagt	18540
aagtagttcg	ccagttaata	gtttgcgcaa	cgttggtgcc	attgctacag	gcatcggtgt	18600

gtcacgctcg	tcgtttggta	tggcttcatt	cagctccggt	tcccaacgat	caaggcgagt	18660
tacatgatcc	cccatgttgt	gaaaaaaagc	ggtagctcc	ttcggtcctc	cgatcgttgt	18720
cagaagtaag	ttggccgcag	tgttatcact	catgcttatg	gcagcactgc	ataattctct	18780
tactgtcatg	ccatccgtaa	gatgcttttc	tgtgactggt	gagtactcaa	ccaagtcatt	18840
ctgagaatag	tgtatgcggc	gaccgagttg	ctcttgcccg	gcgtcaatac	gggataatac	18900
cgcgccacat	agcagaactt	taaaagtgt	catcattgga	aaacgttctt	cggggcgaaa	18960
actctcaagg	atcttaccgc	tgtagagatc	cagttcgatg	taaccactc	gtgcacccaa	19020
ctgatcttca	gcattcttta	ctttcaccag	cgtttctggg	tgagcaaaaa	caggaaggca	19080
aatgccgca	aaaaagggaa	taagggcgac	acggaaatgt	tgaatactca	tactcttcct	19140
ttttcaatat	tattgaagca	tttatcaggg	ttattgtctc	atgagcggat	acatatattga	19200
atgtatttag	aaaaataaac	aaataggggt	tccgcgcaca	tttccccgaa	aagtgccacc	19260
tgaaattgta	aacgttaata	ttttgttaaa	attcgcgtta	aatttttggt	aatcagctc	19320
attttttaac	caataggccg	aatcggcaa	aatcccttat	aatcaaaaag	aatagaccga	19380
gataggggtg	agtgttggtc	cagtttgga	caagagtcca	ctattaaaga	acgtggactc	19440
caacgtcaaa	gggcgaaaaa	ccgtctatca	gggcgatggc	ccactacgtg	aaccatcacc	19500
ctaatcaagt	tttttggggg	cgaggtgccg	taaagcacta	aatcggaacc	ctaaaggag	19560
cccccgattt	agagcttgac	ggggaaagcc	ggcgaaacgtg	gcgagaaagg	aagggaagaa	19620
agcgaaagga	gcgggcgcta	gggcgctggc	aagtgtagcg	gtcacgctgc	gcgtaaccac	19680
cacacccgcc	gcgcttaatg	cgccgctaca	gggcgcgtcc	cattcgccat	tcaggctgcg	19740
caactgttgg	gaagggcgat	cggtgcgggc	ctcttcgcta	ttacgccagc	caccgcggtg	19800

<210> 154
 <211> 10
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Kozak sequence

<400> 154
 gccaccatgg

10

<210> 155
 <211> 12
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Kozak sequence + alanine after start codon
 <400> 155
 gccaccatgg ca 12

<210> 156
 <211> 63
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Enhanced honeybee melittin signal peptide
 <400> 156
 atgaaattct tagtcaacgt tgcccttggt tttatgggtcg tatacatttc ttacatctat 60
 gcg 63

<210> 157
 <211> 19
 <212> PRT
 <213> Homo sapiens azurocidin signal peptide

<400> 157
 Met Thr Arg Leu Thr Val Leu Ala Leu Leu Ala Gly Leu Leu Ala Ser
 1 5 10 15

Ser Arg Ala

<210> 158
 <211> 18
 <212> PRT
 <213> Homo sapiens serum albumin signal peptide

<400> 158
 Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
 1 5 10 15

Tyr Ser

<210> 159
 <211> 23
 <212> PRT
 <213> Homo sapiens Leukocyte immunoglobulin-like receptor subfamily B member 1 signal peptide

<400> 159

Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
 1 5 10 15

Pro Arg Thr His Val Gln Ala
 20

<210> 160
 <211> 30
 <212> PRT
 <213> Bos taurus prolactin signal peptide

<400> 160

Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
 1 5 10 15

Leu Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser
 20 25 30

<210> 161
 <211> 58
 <212> PRT
 <213> Lymphocytic choriomeningitis virus (strain Armstrong), pre-glycoprotein polyprotein GP complex signal peptide

<400> 161

Met Gly Gln Ile Val Thr Met Phe Glu Ala Leu Pro His Ile Ile Asp
 1 5 10 15

Glu Val Ile Asn Ile Val Ile Ile Val Leu Ile Val Ile Thr Gly Ile
 20 25 30

Lys Ala Val Tyr Asn Phe Ala Thr Cys Gly Ile Phe Ala Leu Ile Ser
 35 40 45

Phe Leu Leu Leu Ala Gly Arg Ser Cys Gly
 50 55

<210> 162
 <211> 27
 <212> PRT
 <213> Homo sapiens insulin receptor signal peptide

<400> 162

Met Ala Thr Gly Gly Arg Arg Gly Ala Ala Ala Ala Pro Leu Leu Val
 1 5 10 15

Ala Val Ala Ala Leu Leu Leu Gly Ala Ala Gly
20 25

<210> 163
<211> 20
<212> PRT
<213> Drosophila melanogaster BM-40 signal peptide

<400> 163

Met Arg Ser Leu Trp Leu Leu Leu Gly Leu Gly Leu Leu Ala Val Ser
1 5 10 15

His Val Gln Ala
20

<210> 164
<211> 16
<212> PRT
<213> Vesicular stomatitis virus Glycoprotein protein signal peptide

<400> 164

Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1 5 10 15

<210> 165
<211> 18
<212> PRT
<213> Homo sapiens Chymotrypsinogen B signal peptide

<400> 165

Met Ala Ser Leu Trp Leu Leu Ser Cys Phe Ser Leu Val Gly Ala Ala
1 5 10 15

Phe Gly

<210> 166
<211> 20
<212> PRT
<213> Homo sapiens Interleukin-2 signal peptide

<400> 166

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser

<210> 167
 <211> 17
 <212> PRT
 <213> Gaussia princeps Luciferase signal peptide

<400> 167

Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
 1 5 10 15

Ala

<210> 168
 <211> 19
 <212> PRT
 <213> Gaussia princeps Gluc Luciferase signal peptide

<400> 168

Met Gly Val Lys Val Leu Phe Ala Leu Ile Cys Ile Ala Val Ala Glu
 1 5 10 15

Val Thr Gly

<210> 169
 <211> 17
 <212> PRT
 <213> Influenza A virus (strain A/Puerto Rico/8/1934 H1N1) Hemagglutinin (HA) signal peptide

<400> 169

Met Lys Ala Asn Leu Leu Val Leu Leu Cys Ala Leu Ala Ala Asp
 1 5 10 15

Ala

<210> 170
 <211> 15
 <212> PRT
 <213> Influenza A virus (strain A/Japan/305/1957 H2N2) Hemagglutinin (HA) signal peptide

<400> 170

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly

1	5	10	15
---	---	----	----

<210> 171
 <211> 16
 <212> PRT
 <213> Influenza A virus (strain A/Hong Kong/156/1997 H5N1 genotype Gs/Gd)
 Hemagglutinin signal peptide

<400> 171

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

<210> 172
 <211> 21
 <212> PRT
 <213> Hepatitis C Virus (HCV) 1b E1 signal peptide

<400> 172

Met	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu
1				5						10				15	

Thr Thr Pro Ala Ser
 20

<210> 173
 <211> 20
 <212> PRT
 <213> Hepatitis C Virus 1b E2 signal peptide

<400> 173

Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala
1				5						10				15	

Gly Val Asp Gly
 20

<210> 174
 <211> 19
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Signal peptide based on HCV 1b

<400> 174

Met	Asp	Ala	Met	Lys	Val	Leu	Leu	Leu	Val	Phe	Val	Ser	Pro	Ser	Gln
1				5					10					15	

Val Thr Gly

<210> 175

<211> 22

<212> PRT

<213> Homo sapiens Tissue-type plasminogen activator signal peptide 1

<400> 175

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
20

<210> 176

<211> 25

<212> PRT

<213> Homo sapiens Tissue-type plasminogen activator signal peptide 2

<400> 176

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

Ala Val Phe Val Asp Ser Val Thr Gly
20 25

<210> 177

<211> 26

<212> PRT

<213> Murray Valley encephalitis (MVE) virus prM signal peptide

<400> 177

Lys Lys Arg Gly Gly Ser Glu Thr Ser Val Leu Met Leu Ile Phe Met
1 5 10 15

Leu Ile Gly Phe Ala Ala Ala Leu Lys Leu
20 25

<210> 178

<211> 26

<212> PRT

<213> Yellow fever virus signal peptide

<400> 178

Lys Arg Arg Ser His Asp Val Leu Thr Val Gln Phe Leu Ile Leu Gly

1 5 10 15

Met Leu Leu Met Thr Gly Gly Val Thr Leu
20 25

<210> 179
<211> 24
<212> PRT
<213> Kunjin virus signal peptide

<400> 179

Lys Lys Arg Gly Gly Lys Thr Gly Ile Ala Phe Met Ile Gly Leu Ile
1 5 10 15

Ala Gly Val Gly Ala Val Thr Leu
20

<210> 180
<211> 26
<212> PRT
<213> Tick-borne encephalitis virus signal peptide

<400> 180

Lys Arg Arg Ser Ala Thr Asp Trp Met Ser Trp Leu Leu Val Ile Thr
1 5 10 15

Leu Leu Gly Met Thr Leu Ala Ala Thr Val
20 25

<210> 181
<211> 20
<212> PRT
<213> Dengue virus signal peptide

<400> 181

Arg Arg Arg Thr Ala Gly Met Ile Ile Met Leu Ile Pro Thr Val Met
1 5 10 15

Ala Phe His Leu
20

<210> 182
<211> 24
<212> PRT
<213> West Nile virus signal peptide

<400> 182

Lys Lys Arg Gly Gly Thr Ala Gly Phe Thr Ile Leu Leu Gly Leu Ile
1 5 10 15

Ala Cys Ala Gly Ala Val Thr Leu
20

<210> 183
<211> 28
<212> PRT
<213> Japanese encephalitis signal peptide 1

<400> 183

Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met Trp Leu Ala Ser Leu
1 5 10 15

Ala Val Val Ile Ala Tyr Ala Gly Ala Met Lys Leu
20 25

<210> 184
<211> 24
<212> PRT
<213> Japanese encephalitis SA-14 JE isolate (GenBank accession # M55506)
signal peptide 2

<400> 184

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala
20

<210> 185
<211> 56
<212> PRT
<213> Tick-borne encephalitis virus stem anchor sequence

<400> 185

Lys Gly Ser Ser Ile Gly Arg Val Phe Gln Lys Thr Lys Lys Gly Ile
1 5 10 15

Glu Arg Leu Thr Val Ile Gly Glu His Ala Trp Asp Phe Gly Ser Ala
20 25 30

Gly Gly Phe Leu Ser Ser Ile Gly Lys Ala Val His Thr Val Leu Gly
35 40 45

Gly Ala Phe Asn Ser Ile Phe Gly
50 55

<210> 186
<211> 56
<212> PRT
<213> Dengue virus stem anchor sequence 1

<400> 186

Lys Gly Ser Ser Ile Gly Lys Met Phe Glu Ala Thr Ala Arg Gly Ala
1 5 10 15

Arg Arg Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile
20 25 30

Gly Gly Val Phe Thr Ser Val Gly Lys Leu Val His Gln Ile Phe Gly
35 40 45

Thr Ala Tyr Gly Val Leu Phe Ser
50 55

<210> 187
<211> 56
<212> PRT
<213> Dengue virus stem anchor sequence 2

<400> 187

Lys Gly Ser Ser Ile Gly Gln Met Phe Glu Thr Thr Met Arg Gly Ala
1 5 10 15

Lys Arg Met Ala Ile Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Leu
20 25 30

Gly Gly Val Phe Thr Ser Ile Gly Lys Ala Leu His Gln Val Phe Gly
35 40 45

Ala Ile Tyr Gly Ala Ala Phe Ser
50 55

<210> 188
<211> 56
<212> PRT
<213> Japanese encephalitis stem anchor sequence

<400> 188

Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu Lys Gly Ala
 1 5 10 15

Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile
 20 25 30

Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly
 35 40 45

Gly Ala Phe Arg Thr Leu Phe Gly
 50 55

<210> 189

<211> 56

<212> PRT

<213> St. Louis encephalitis virus stem anchor sequence

<400> 189

Glu Gly Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala
 1 5 10 15

Gln Arg Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile
 20 25 30

Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly
 35 40 45

Gly Ala Phe Arg Thr Leu Phe Gly
 50 55

<210> 190

<211> 56

<212> PRT

<213> West Nile virus stem anchor sequence

<400> 190

Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala
 1 5 10 15

Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val
 20 25 30

Gly Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly
 35 40 45

Gly Ala Phe Arg Ser Leu Phe Gly
50 55

<210> 191
<211> 56
<212> PRT
<213> Yellow fever virus encephalitis sequence

<400> 191

Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met Lys Gly Ala
1 5 10 15

Glu Arg Leu Ala Val Met Gly Asp Ala Ala Trp Asp Phe Ser Ser Ala
20 25 30

Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr Val Phe Gly
35 40 45

Ser Ala Phe Gln Gly Leu Phe Gly
50 55

<210> 192
<211> 19075
<212> DNA
<213> Artificial sequence

<220>
<223> pTM 2ATU MV Schw short

<400> 192
gcggccgcta atacgactca ctatagggcc aactttgttt ggtctgatga gtccgtgagg 60
acgaaacccg gagtcccggg tcaccaaaca aagttgggta aggatagttc aatcaatgat 120
catcttctag tgcacttagg attcaagatc ctattatcag ggacaagagc aggattaggg 180
atatccgaga tggccacact ttttaaggagc ttagcattgt tcaaaagaaa caaggacaaa 240
ccaccatta catcaggatc cgggtggagcc atcagaggaa tcaaacacat tattatagta 300
ccaatccctg gagattcctc aattaccact cgatccagac ttctggaccg gttggtgagg 360
ttaattggaa acccggatgt gagcggggcc aaactaacag gggcactaat aggtatatta 420
tccttatttg tggagtctcc aggtcaattg attcagagga tcaccgatga ccctgacgtt 480
agcataaggc tgttagaggt tgtccagagt gaccagtcac aatctggcct taccttcgca 540
tcaagaggta ccaacatgga ggatgaggcg gaccaatact tttcacatga tgatccaatt 600
agtagtgatc aatccagggt cggatggttc ggaacaagg aaatctcaga tattgaagtg 660

caagaccctg agggattcaa catgattctg ggtaccatcc tagcccaaat ttgggtcttg	720
ctcgcaaagg cggttacggc cccagacacg gcagctgatt cggagctaag aaggtggata	780
aagtacaccc aacaaagaag ggtagttggg gaatttagat tggagagaaa atggttgat	840
gtggtgagga acaggattgc cgaggacctc tccttacgcc gattcatggt cgctctaate	900
ctggatatca agagaacacc cggaacaaa cccaggattg ctgaaatgat atgtgacatt	960
gatacatata tcgtagaggc aggattagcc agttttatcc tgactattaa gtttgggata	1020
gaaactatgt atcctgctct tggactgcat gaatttgctg gtgagttatc cacacttgag	1080
tccttgatga acctttacca gcaaatgggg gaaactgcac cctacatggt aatcctggag	1140
aactcaattc agaacaagtt cagtgcagga tcataccctc tgctctggag ctatgccatg	1200
ggagtaggag tggaacttga aaactccatg ggaggtttga actttggccg atcttacttt	1260
gatccagcat attttagatt agggcaagag atggtaagga ggtcagctgg aaaggtcagt	1320
tccacattgg catctgaact cggtatcact gccgaggatg caaggcttgt ttcagagatt	1380
gcaatgcata ctactgagga caagatcagt agagcggttg gaccagaca agcccaagta	1440
tcatttctac acggtgatca aagtgagaat gagctaccga gattgggggg caaggaagat	1500
aggaggggtca aacagagtcg aggagaagcc agggagagct acagagaaac cgggccagc	1560
agagcaagtg atgagagagc tgcccatctt ccaaccggca caccctaga cattgacact	1620
gcaacggagt ccagccaaga tccgcaggac agtcgaaggt cagctgacgc cctgcttagg	1680
ctgcaagcca tggcaggaat ctcggaagaa caaggctcag acacggacac ccctatagtg	1740
tacaatgaca gaaatcttct agactaggtg cgagaggccg agggccagaa caacatccgc	1800
ctaccatcca tcattgttat aaaaaactta ggaaccaggt ccacacagcc gccagcccat	1860
caaccatcca ctcccacgat tggagccaat ggcagaagag caggcacgcc atgtcaaaaa	1920
cggactggaa tgcattccggg ctctcaaggc cgagcccatc ggctcactgg ccatcgagga	1980
agctatggca gcatgggtcag aaatatcaga caaccagga caggagcgag ccacctgcag	2040
ggaagagaag gcaggcagtt cgggtctcag caaacatgc ctctcagcaa ttggatcaac	2100
tgaaggcggg gcacctcgca tccgcgggtc gggacctgga gagagcgatg acgacgtga	2160
aactttggga atcccccaa gaaatctcca ggcataagc actgggttac agtggtatta	2220
cgtttatgat cacagcgggtg aagcgggttaa gggaaatcaa gatgctgact ctatcatggt	2280
tcaatcaggc cttgatgggtg atagcacctc ctgaggagga gacaatgaat ctgaaaacag	2340
cgatgtggat attggcgaac ctgataccga gggatatgct atcactgacc ggggatctgc	2400

tcccatctct	atgggggttca	gggcttctga	tgttgaaact	gcagaaggag	gggagatcca	2460
cgagctcctg	agactccaat	ccagaggcaa	caactttccg	aagcttggga	aaactctcaa	2520
tgttcctccg	ccccggacc	ccggtagggc	cagcacttcc	gggacacca	ttaaaaagg	2580
cacagacgcg	agattagcct	catttggaa	ggagatcgcg	tctttattga	caggtggtgc	2640
aaccaatgt	gctcgaaagt	caccctcgga	accatcagg	ccaggtgcac	ctgcggggaa	2700
tgtccccgag	tgtgtgagca	atgccgcact	gatacaggag	tggacacccg	aatctggtac	2760
cacaatctcc	ccgagatccc	agaataatga	agaaggggga	gactattatg	atgatgagct	2820
gttctctgat	gtccaagata	ttaaaacagc	cttggccaaa	atacacgagg	ataatcagaa	2880
gataatctcc	aagctagaat	cactgctggt	attgaaggga	gaagttgagt	caattaagaa	2940
gcagatcaac	aggcaaaata	tcagcatatc	caccctggaa	ggacacctct	caagcatcat	3000
gatcgccatt	cctggacttg	ggaaggatcc	caacgacccc	actgcagatg	tcgaaatcaa	3060
tcccgacttg	aaacccatca	taggcagaga	ttcaggccga	gcactggccg	aagttctcaa	3120
gaaacccgtt	gccagccgac	aactccaagg	aatgacaaat	ggacggacca	gttccagagg	3180
acagctgctg	aaggaatttc	agctaaagcc	gatcgggaaa	aagatgagct	cagccgtcgg	3240
gtttgttcct	gacaccggcc	ctgcatcacg	cagtgtaatc	cgctccatta	taaaatccag	3300
ccggctagag	gaggatcgga	agcgttacct	gatgactctc	cttgatgata	tcaaaggagc	3360
caatgatctt	gccaaagtcc	accagatgct	gatgaagata	ataatgaagt	agctacagct	3420
caacttacct	gccaaaccca	tgccagtcga	cccaactagc	ctaccctcca	tcattgttat	3480
aaaaaactta	ggaaccagg	ccacacagcc	gccagcccat	caacgcgtac	ggcgcgcagc	3540
gcttagacgt	ctcgcgatcg	atactagtag	aacctaaatc	cattataaaa	aacttaggag	3600
caaagtgatt	gcctcccaag	gtccacaatg	acagagacct	acgacttcga	caagtcggca	3660
tgggacatca	aagggtcgat	cgctccgata	caaccaccca	cctacagtga	tggcaggctg	3720
gtgccccagg	tcagagtcac	agatcctggt	ctaggcgaca	ggaaggatga	atgctttatg	3780
tacatgtttc	tgctgggggt	tgttgaggac	agcgattccc	tagggcctcc	aatcgggcga	3840
gcatttgggt	tcctgccctt	aggtgttggc	agatccacag	caaagcccga	aaaactcctc	3900
aaagaggcca	ctgagcttga	catagttggt	agacgtacag	cagggtcaa	tgaaaaactg	3960
gtgttctaca	acaacacccc	actaactctc	ctcacacctt	ggagaaaggt	cctaacaaca	4020
gggagtgtct	tcaacgcaaa	ccaagtgtgc	aatgcggtta	atctgatacc	gctcgatacc	4080
ccgcagaggt	tccgtgttgt	ttatatgagc	atcacccgtc	tttcggataa	cgggtattac	4140

accgttccta	gaagaatgct	ggaattcaga	tcggtcaatg	cagtggcctt	caacctgctg	4200
gtgaccctta	ggattgacaa	ggcgataggc	cctgggaaga	tcacgacaa	tacagagcaa	4260
cttcctgagg	caacatttat	gtccacatc	gggaacttca	ggagaaagaa	gagtgaagtc	4320
tactctgccg	attattgcaa	aatgaaaatc	gaaaagatgg	gcctgggtttt	tgcacttggt	4380
gggatagggg	gcaccagtct	tcacattaga	agcacaggca	aatgagcaa	gactctccat	4440
gcacaactcg	ggttcaagaa	gaccttatgt	tacccgctga	tggatatcaa	tgaagacctt	4500
aatcgattac	tctggaggag	cagatgcaag	atagtaagaa	tccaggcagt	tttgacgcca	4560
tcagttcctc	aagaattccg	catttacgac	gacgtgatca	taaatgatga	ccaaggacta	4620
ttcaaagttc	tgtagaccgt	agtgcccgac	aatgcccga	aacgaccccc	ctcacaatga	4680
cagccagaag	gcccggacaa	aaaagcccc	tccgaaagac	tccacggacc	aagcgagagg	4740
ccagccagca	gccgacggca	agcgcgaa	ccaggcggcc	ccagcacaga	acagccctga	4800
cacaaggcca	ccaccagcca	cccaatctg	catcctcctc	gtgggacccc	cgaggaccaa	4860
cccccaaggc	tgcccccgat	caaaccacc	aaccgcatcc	ccaccacccc	cgggaaagaa	4920
acccccagca	attggaaggc	ccctccccct	cttcctcaac	acaagaactc	cacaaccgaa	4980
ccgcacaagc	gaccgaggtg	acccaaccgc	aggcatccga	ctccctagac	agatcctctc	5040
tccccggcaa	actaaacaaa	acttagggcc	aaggaaacata	cacacccaac	agaaccagaa	5100
ccccggccca	cggcgccgcg	cccccaacc	ccgacaacca	gagggagccc	ccaaccaatc	5160
ccgccggctc	ccccggtgcc	cacaggcagg	gacaccaacc	cccgaacaga	cccagcaccc	5220
aaccatcgac	aatccaagac	ggggggggccc	ccccaaaaaa	aggccccccag	gggccgacag	5280
ccagcacccg	gaggaagccc	acccacccca	cacacgacca	cggcaaccaa	accagaaccc	5340
agaccaccct	gggccaccag	ctcccagact	cggccatcac	cccgcagaaa	ggaaaggcca	5400
caaccgcgc	acccagccc	cgatccggcg	gggagccacc	caaccgaac	cagcacccaa	5460
gagcgatccc	cgaaggaccc	ccgaaccgca	aaggacatca	gtatcccaca	gcctctccaa	5520
gtcccccggt	ctcctcctct	tctcgaagg	acaaaagat	caatccacca	cacccgacga	5580
cactcaactc	cccacccta	aaggagacac	cgggaatccc	agaatcaaga	ctcatccaat	5640
gtccatcatg	ggtctcaagg	tgaacgtctc	tgccatattc	atggcagtac	tgtaactct	5700
ccaaacaccc	accggtcaaa	tccattgggg	caatctctct	aagatagggg	tggtaggaat	5760
aggaagtgca	agctacaaag	ttatgactcg	ttccagccat	caatcattag	tcataaaatt	5820
aatgcccaat	ataactctcc	tcaataactg	cacgagggta	gagattgcag	aatacaggag	5880

actactgaga	acagtttttg	aaccaattag	agatgcactt	aatgcaatga	cccagaatat	5940
aagaccggtt	cagagtgtag	cttcaagtag	gagacacaag	agatttgcg	gagtagtcct	6000
ggcaggtg	gccctaggcg	ttgccacagc	tgctcagata	acagccggca	ttgcacttca	6060
ccagtccatg	ctgaactctc	aagccatcga	caatctgaga	gcgagcctgg	aaactactaa	6120
tcaggcaatt	gagacaatca	gacaagcagg	gcaggagatg	atattggctg	ttcagggtgt	6180
ccaagactac	atcaataatg	agctgatacc	gtctatgaac	caactatctt	gtgatttaat	6240
cggccagaag	ctcgggctca	aattgctcag	atactataca	gaaatcctgt	cattatttgg	6300
ccccagttta	cgggacccca	tatctgcgga	gatatctatc	caggctttga	gctatgcgct	6360
tggaggagac	atcaataagg	tgtagaaaa	gtcgcgatac	agtggagggtg	atttactggg	6420
catcttagag	agcggaggaa	taaaggcccg	gataactcac	gtcgacacag	agtcctactt	6480
cattgtcctc	agtatagcct	atccgacgct	gtccgagatt	aaggggggtga	ttgtccaccg	6540
gctagagggg	gtctcgtaca	acataggctc	tcaagagtgg	tataccactg	tgcccaagta	6600
tggtgcaacc	caaggggtacc	ttatctcgaa	ttttgatgag	tcatcgtgta	ctttcatgcc	6660
agaggggact	gtgtgcagcc	aaaatgcctt	gtacccgatg	agtcctctgc	tccaagaatg	6720
cctccggggg	tacaccaagt	cctgtgctcg	tacactcgta	tccgggtctt	ttgggaaccg	6780
gttcatttta	tcacaaggga	acctaatagc	caattgtgca	tcaatccttt	gcaagtgtta	6840
cacaacagga	acgatcatta	atcaagacce	tgacaagatc	ctaacataca	ttgctgccga	6900
tcactgcccc	gtagtcgagg	tgaacggcgt	gaccatccaa	gtcgggagca	ggaggatatcc	6960
agacgctgtg	tacttgcaca	gaattgacct	cggtcctccc	atatcattgg	agaggttgga	7020
cgtagggaca	aatctgggga	atgcaattgc	taagttggag	gatgccaaagg	aattgttgga	7080
gtcatcggac	cagatattga	ggagtatgaa	aggtttatcg	agcactagca	tagtctacat	7140
cctgattgca	gtgtgtcttg	gagggttgat	agggatcccc	gctttaatat	gttgctgcag	7200
ggggcgttgt	aacaaaaagg	gagaacaagt	tggtatgtca	agaccaggcc	taaagcctga	7260
tcttacggga	acatcaaaat	cctatgtaag	gtcgctctga	tcctctacaa	ctcttgaaac	7320
acaaatgtcc	cacaagtctc	ctcttcgtca	tcaagcaacc	accgcaccca	gcatcaagcc	7380
cacctgaaat	tatctccggc	ttccctctgg	ccgaacaata	tcggtagtta	atcaaaaactt	7440
agggtgcaag	atcatccaca	atgtcaccac	aacgagaccg	gataaatgcc	ttctacaaag	7500
ataaccccc	tcccaaggga	agtaggatag	tcattaacag	agaacatctt	atgattgata	7560
gaccttatgt	tttgctggct	gttctgtttg	tcatgtttct	gagcttgatc	gggttgctag	7620

ccattgcagg cattagactt catcgggcag ccatctacac cgcagagatc cataaaagcc	7680
tcagcaccaa tctagatgta actaactcaa tcgagcatca ggtcaaggac gtgctgacac	7740
cactcttcaa aatcatcggg gatgaagtgg gcctgaggac acctcagaga ttcactgacc	7800
tagtgaaatt aatctctgac aagattaaat tccttaatcc ggatagggag tacgacttca	7860
gagatctcac ttggtgtatc aaccgccag agagaatcaa attggattat gatcaatact	7920
gtgcagatgt ggctgctgaa gagctcatga atgcattggg gaactcaact ctactggaga	7980
ccagaacaac caatcagttc ctagctgtct caaagggaaa ctgctcaggg ccactacaa	8040
tcagagggtca attctcaaac atgtcgtgtt ccctgttaga cttgtattta ggtcgagggt	8100
acaatgtgtc atctatagtc actatgacat ccaggggaat gtatggggga acttacctag	8160
tggaaaagcc taatctgagc agcaaaagggt cagagttgtc acaactgagc atgtaccgag	8220
tgtttgaagt aggtgttatc agaaatccgg gtttgggggc tccggtgttc catatgacaa	8280
actatcttga gcaaccagtc agtaatgac tcagcaactg tatggtggct ttgggggagc	8340
tcaaactcgc agccctttgt cacggggaag attctatcac aattccctat cagggatcag	8400
ggaaagggtgt cagcttccag ctctcaagc taggtgtctg gaaatcccca accgacatgc	8460
aatcctgggt ccccttatca acggatgac cagtgataga caggctttac ctctcatctc	8520
acagagggtgt tatcgctgac aatcaagcaa aatgggctgt cccgacaaca cgaacagatg	8580
acaagttgcg aatggagaca tgcttccaac aggcgtgtaa gggtaaaatc caagcactct	8640
gcgagaatcc cgagtgggca ccattgaagg ataacaggat tccttcatac ggggtcttgt	8700
ctgttgatct gagtctgaca gttgagctta aaatcaaaat tgcttcggga ttcgggccat	8760
tgatcacaca cggttcaggg atggacctat acaaatccaa ccacaacaat gtgtattggc	8820
tgactatccc gccaatgaag aacctagcct taggtgtaat caacacattg gagtggatac	8880
cgagattcaa ggttagtccc tacctcttca ctgtcccaat taaggaagca ggcgaagact	8940
gccatgcccc aacataccta cctgcggagg tggatggtga tgtcaaactc agttccaatc	9000
tggtgattct acctggtcaa gatctccaat atgttttggc aacctacgat acttccaggg	9060
ttgaacatgc tgtggtttat tacgtttaca gcccaagccg ctcatTTTTct tacttttatc	9120
cttttaggtt gcctataaag ggggtcccca tcgaattaca agtggaatgc ttcacatggg	9180
acaaaaaact ctggtgccgt cacttctgtg tgcttgcgga ctcagaatct ggtggacata	9240
tcactcactc tgggatggtg ggcatgggag tcagctgcac agtcacccgg gaagatggaa	9300
ccaatcgag atagggtgc tagtgaacca atcacatgat gtcaccaga catcaggcat	9360

accactagt	gtgaaataga	catcagaatt	aagaaaaacg	taggggtccaa	gtggttcccc	9420
gttatggact	cgctatctgt	caaccagatc	ttataccctg	aagttcacct	agatagcccg	9480
atagttacca	ataagatagt	agccatcctg	gagtatgctc	gagtcacctca	cgcttacagc	9540
ctggaggacc	ctacactgtg	tcagaacatc	aagcaccgcc	taaaaaacgg	attttccaac	9600
caaatgatta	taaacaatgt	ggaagttggg	aatgtcatca	agtcceaagct	taggagttat	9660
ccggcccact	ctcatattcc	atatccaaat	tgtaatcagg	atttatttaa	catagaagac	9720
aaagagtcaa	cgaggaagat	ccgtgaactc	ctcaaaaagg	ggaattcgct	gtactccaaa	9780
gtcagtgata	aggttttcca	atgcttaagg	gacactaact	cacggcttgg	cctaggctcc	9840
gaattgaggg	aggacatcaa	ggagaaagtt	attaacttgg	gagtttacat	gcacagctcc	9900
cagtggtttg	agccctttct	gttttggttt	acagtcaaga	ctgagatgag	gtcagtgatt	9960
aaatcacaaa	cccatacttg	ccataggagg	agacacacac	ctgtattctt	cactggtagt	10020
tcagttgagt	tgctaattctc	tcgtgacctt	gttgctataa	tcagtaaaga	gtctcaacat	10080
gtatattacc	tgacatttga	actggttttg	atgtattgtg	atgtcataga	ggggaggtta	10140
atgacagaga	ccgctatgac	tattgatgct	aggatatacag	agcttctagg	aagagtcaga	10200
tacatgtgga	aactgataga	tggtttcttc	cctgcactcg	ggaatccaac	ttatcaaatt	10260
gtagccatgc	tggagcctct	ttcacttgct	tacctgcagc	tgagggatat	aacagtagaa	10320
ctcagaggtg	ctttccttaa	ccactgcttt	actgaaatac	atgatgttct	tgacaaaaac	10380
gggttttctg	atgaaggtac	ttatcatgag	ttactgaag	ctctagatta	cattttcata	10440
actgatgaca	tacatctgac	aggggagatt	ttctcatttt	tcagaagttt	cggccacccc	10500
agacttgaag	cagtaacggc	tgctgaaaat	gttaggaaat	acatgaatca	gcctaaagtc	10560
attgtgtatg	agactctgat	gaaaggatcat	gccatatttt	gtggaatcat	aatcaacggc	10620
tatcgtgaca	ggcacggagg	cagttggcca	ccgctgaccc	tccccctgca	tgctgcagac	10680
acaatccgga	atgctcaagc	ttcaggtgaa	gggttaacac	atgagcagtg	cgttgataac	10740
tggaaatctt	ttgctggagt	gaaatttggc	tgctttatgc	ctcttagcct	ggatagtgat	10800
ctgacaatgt	acctaaagga	caaggcactt	gctgctctcc	aaagggaatg	ggattcagtt	10860
tacccgaaag	agttcctgcg	ttacgaccct	cccaaggga	ccgggtcacg	gaggcttgta	10920
gatgttttcc	ttaatgattc	gagctttgac	ccatatgatg	tgataatgta	tgttgtaagt	10980
ggagcttacc	tccatgaccc	tgagttcaac	ctgtcttaca	gcctgaaaga	aaaggagatc	11040
aaggaaacag	gtagactttt	tgctaaaatg	acttacaaaa	tgagggcacg	ccaagtgatt	11100

gctgaaaatc	taatctcaaa	cgggattggc	aaatatTTtTa	aggacaatgg	gatggccaag	11160
gatgagcacg	atttgactaa	ggcactccac	actctagctg	tctcaggagt	ccccaagat	11220
ctcaaagaaa	gtcacagggg	ggggccagtc	ttaaaaacct	actcccgaag	cccagtccac	11280
acaagtacca	ggaacgtgag	agcagcaaaa	gggtttatag	ggttccctca	agtaattcgg	11340
caggaccaag	acactgatca	tccggagaat	atggaagctt	acgagacagt	cagtgcattt	11400
atcacgactg	atctcaagaa	gtactgcctt	aattggagat	atgagaccat	cagcttgttt	11460
gcacagaggc	taaatgagat	ttacggattg	ccctcatttt	tccagtggct	gcataagagg	11520
cttgagacct	ctgtcctgta	tgtaagtga	cctcattgcc	cccccgacct	tgacgccccat	11580
atcccgttat	ataaagtccc	caatgatcaa	atcttcatta	agtaccctat	gggaggtata	11640
gaagggtatt	gtcagaagct	gtggaccatc	agcaccattc	cctatctata	cctggctgct	11700
tatgagagcg	gagtaaggat	tgcttcgtta	gtgcaagggg	acaatcagac	catagccgta	11760
acaaaaaggg	taccagcac	atggccctac	aaccttaaga	aacgggaagc	tgctagagta	11820
actagagatt	actttgtaat	tcttaggcaa	aggctacatg	atattggcca	tcacctcaag	11880
gcaaatgaga	caattgtttc	atcacatttt	tttgtctatt	caaaaggaat	atattatgat	11940
gggctacttg	tgtccaatc	actcaagagc	atcgcaagat	gtgtattctg	gtcagagact	12000
atagttgatg	aaacaagggc	agcatgcagt	aatattgcta	caacaatggc	taaaagcatc	12060
gagagagggt	atgaccgtta	ccttgcatat	tccctgaacg	tcctaaaagt	gatacagcaa	12120
attctgatct	ctcttggtt	cacaatcaat	tcaaccatga	cccgggatgt	agtcataccc	12180
ctcctcacia	acaacgacct	cttaataagg	atggcactgt	tgcccgtctc	tattgggggg	12240
atgaattatc	tgaatatgag	caggctgttt	gtcagaaaca	tcggtgatcc	agtaacatca	12300
tcaattgctg	atctcaagag	aatgattctc	gcctcactaa	tgctgaaga	gacctccat	12360
caagtaatga	cacaacaacc	gggggactct	tcattcctag	actgggctag	cgacccttac	12420
tcagcaaadc	ttgtatgtgt	ccagagcatc	actagactcc	tcaagaacat	aactgcaagg	12480
tttgtcctga	tccatagtcc	aaaccaatg	ttaaaaggat	tattccatga	tgacagtaaa	12540
gaagaggacg	agggactggc	ggcattcctc	atggacaggc	atattatagt	acctagggca	12600
gctcatgaaa	tcctggatca	tagtgtcaca	ggggcaagag	agtctattgc	aggcatgctg	12660
gataccacia	aaggcttgat	tcgagccagc	atgaggaagg	gggggttaac	ctctcgagtg	12720
ataaccagat	tgtccaatta	tgactatgaa	caattcagag	cagggatggg	gctattgaca	12780
ggaagaaaga	gaaatgtcct	cattgacaaa	gagtcatgtt	cagtgcagct	ggcgagagct	12840

ctaagaagcc	atatgtgggc	gaggctagct	cgaggacggc	ctattttacgg	ccttgaggtc	12900
cctgatgtac	tagaatctat	gcgaggccac	cttattcggc	gtcatgagac	atgtgtcatc	12960
tgcgagtgtg	gatcagtcaa	ctacggatgg	ttttttgtcc	cctcggggtg	ccaactggat	13020
gatattgaca	aggaaacatc	atccttgaga	gtcccatata	ttggttctac	cactgatgag	13080
agaacagaca	tgaagcttgc	cttcgtaaga	gccccaaagtc	gatccttgcg	atctgctgtt	13140
agaatagcaa	cagtgtactc	atgggcttac	ggtgatgatg	atagctcttg	gaacgaagcc	13200
tggttggttg	ctaggcaaag	ggccaatgtg	agcctggagg	agctaagggt	gatcactccc	13260
atctcaactt	cgactaattt	agcgcatagg	ttgagggatc	gtagcactca	agtgaatac	13320
tcaggtacat	cccttgtccg	agtggcgagg	tataccacaa	tctccaacga	caatctctca	13380
tttgtcatat	cagataagaa	ggttgatact	aactttatat	accaacaagg	aatgcttcta	13440
gggttggttg	ttttagaaac	attgtttcga	ctcgagaaag	ataccggatc	atctaacacg	13500
gtattacatc	ttcacgtcga	aacagattgt	tgcgtgatcc	cgatgataga	tcatcccagg	13560
ataccagct	cccgaagct	agagctgagg	gcagagctat	gtaccaaccc	attgatatat	13620
gataatgcac	ctttaattga	cagagatgca	acaaggctat	acaccagag	ccataggagg	13680
caccttgtgg	aatttggttac	atgggtccaca	ccccaaactat	atcacatttt	agctaagtcc	13740
acagcactat	ctatgattga	cctggtaaca	aaatttgaga	aggaccatat	gaatgaaatt	13800
tcagctctca	taggggatga	cgatatcaat	agtttcataa	ctgagtttct	gctcatagag	13860
ccaagattat	tcactatcta	cttgggccag	tgtgcggcca	tcaattgggc	atttgatgta	13920
cattatcata	gaccatcagg	gaaatatcag	atgggtgagc	tgttgatcatc	gttcctttct	13980
agaatgagca	aaggagtgtt	taaggtgctt	gtcaatgctc	taagccaccc	aaagatctac	14040
aagaaattct	ggcattgtgg	tattatagag	cctatccatg	gtccttctact	tgatgctcaa	14100
aacttgcaca	caactgtgtg	caacatgggt	tacacatgct	atatgaccta	cctcgacctg	14160
ttgttgaatg	aagagttaga	agagttcaca	tttctcttgt	gtgaaagcga	cgaggatgta	14220
gtaccggaca	gattcgacaa	catccaggca	aaacacttat	gtgttctggc	agatttgtac	14280
tgtcaaccag	ggacctgccc	accaattcga	ggtctaagac	cggtagagaa	atgtgcagtt	14340
ctaaccgacc	atatcaaggc	agaggctatg	ttatctccag	caggatcttc	gtggaacata	14400
aatccaatta	ttgtagacca	ttactcatgc	tctctgactt	atctccggcg	aggatcgatc	14460
aaacagataa	gattgagagt	tgatccagga	ttcatthttcg	acgccctcgc	tgaggtaaatt	14520
gtcagtcagc	caaagatcgg	cagcaacaac	atctcaaata	tgagcatcaa	ggctttcaga	14580

ccccacacg atgatgttgc aaaattgctc aaagatatca acacaagcaa gcacaatctt	14640
cccatttcag ggggcaatct cgccaattat gaaatccatg ctttccgcag aatcggggtg	14700
aactcatctg cttgctacaa agctgttgag atatcaacat taattaggag atgccttgag	14760
ccaggggagg acggcttggt cttgggtgag ggatcgggtt ctatgttgat cacttataaa	14820
gagatactta aactaaacaa gtgcttctat aatagtgggg tttccgcaa ttctagatct	14880
ggtcaaaggg aattagcacc ctatccctcc gaagtggcc ttgtcgaaca cagaatggga	14940
gtaggtaata ttgtcaaagt gctctttaac gggaggcccg aagtcacgtg gtaggcagt	15000
gtagattgct tcaatttcac agttagtaat atccctacct ctagtgtggg gtttatccat	15060
tcagatatag agaccttgcc tgacaaagat actatagaga agctagagga attggcagcc	15120
atcttatcga tggctctgct cctgggcaaa ataggatcaa tactggtgat taagcttatg	15180
cctttcagcg gggattttgt tcagggattt ataagttatg tagggctctca ttatagagaa	15240
gtgaaccttg tataccctag atacagcaac ttcactctta ctgaatctta tttggttatg	15300
acagatctca aggctaaccg gctaataaat cctgaaaaga ttaagcagca gataattgaa	15360
tcactctgtga ggacttcacc tggacttata ggtcacatcc tatccattaa gcaactaagc	15420
tgcatacaag caattgtggg agacgcagtt agtagagggtg atatcaatcc tactctgaaa	15480
aaacttacac ctatagagca ggtgctgac aattgcgggt tggcaattaa cggacctaa	15540
ctgtgcaaag aattgatcca ccatgatgtt gcctcagggc aagatggatt gcttaattct	15600
atactcatcc tctacaggga gttggcaaga ttcaaagaca accaaagaag tcaacaagg	15660
atgttccacg cttaccccg attggtaagt agcaggcaac gagaacttat atctaggatc	15720
acccgcaaat tctgggggca cattcttctt tactccggga acaaaaagtt gataaataag	15780
tttatccaga atctcaagtc cggctatctg atactagact tacaccagaa tatcttcggt	15840
aagaatctat ccaagtcaga gaaacagatt attatgacgg ggggtttgaa acgtgagtgg	15900
gtttttaagg taacagtcaa ggagaccaa gaatggtata agttagtcgg atacagtgcc	15960
ctgattaagg actaattggt tgaactccg aaccctaata ctgccctagg tggtaggca	16020
ttatttgcaa tatattaaag aaaactttga aaatacgaag tttctattcc cagctttgtc	16080
tgggtggccg catggtccca gcctcctcgc tggcgccggc tgggcaacat tccgagggga	16140
ccgtcccctc ggtaatggcg aatgggacgc ggccgatccg gctgctaaca aagcccga	16200
ggaagctgag ttggctgctg ccaccgctga gcaataacta gcataacccc ttggggcctc	16260
taaacgggtc ttgaggggtt ttttgctgaa aggaggaact atatccgat gcggccgcg	16320

gccctatggg	accagcttt	tggtcccttt	agtgagggtt	aattccgagc	ttggcgtaat	16380
catggtcata	gctgttttct	gtgtgaaatt	gttatccgct	cacaattcca	cacaacatag	16440
gagccggaag	cataaagtgt	aaagcctggg	gtgcctaata	agtgaggtaa	ctcacattaa	16500
ttgcgttgcg	ctcactgccc	gctttccagt	cgggaaacct	gtcgtgccag	ctgcattaat	16560
gaatcggcca	acgcgcgggg	agaggcggtt	tgcgtattgg	gcgctcttcc	gcttcctcgc	16620
tcactgactc	gctgcgctcg	gtcgttcggc	tgcggcgagc	ggtatcagct	cactcaaagg	16680
cggtaatacg	gttatccaca	gaatcagggg	ataacgcagg	aaagaacatg	tgagcaaaag	16740
gccagcaaaa	ggccaggaac	cgtaaaaagg	ccgcgttgct	ggcgtttttc	cataggctcg	16800
gccccctga	cgagcatcac	aaaaatcgac	gctcaagtca	gaggtggcga	aacccgacag	16860
gactataaag	ataccaggcg	ttccccctg	gaagctccct	cgtgcgctct	cctgttccga	16920
ccctgccgct	taccggatac	ctgtccgcct	ttctcccttc	gggaagcggt	gcgctttctc	16980
aatgctcacg	ctgtaggtat	ctcagttcgg	tgtagggtcg	tcgctccaag	ctgggctgtg	17040
tgcacgaacc	ccccgttcag	cccgaccgct	gcgccttata	cggtaactat	cgtcttgagt	17100
ccaacccggt	aagacacgac	ttatcgccac	tggcagcagc	cactggtaac	aggattagca	17160
gagcgaggta	tgtaggcggt	gctacagagt	tcttgaagtg	gtggcctaac	tacggctaca	17220
ctagaaggac	agtatttggg	atctgcgctc	tgctgaagcc	agttaccttc	gaaaaaagag	17280
ttggtagctc	ttgatccggc	aaacaaacca	ccgctggtag	cgggtggtttt	tttgtttgca	17340
agcagcagat	tacgcgcaga	aaaaaaggat	ctcaagaaga	tcctttgatc	ttttctacgg	17400
ggctctgacg	tcagtggaac	gaaaactcac	gttaagggat	tttggtcata	agattatcaa	17460
aaaggatctt	cacctagatc	cttttaaatt	aaaaatgaag	ttttaaatca	atctaaagta	17520
tatatgagta	aacttgggtc	gacagttacc	aatgcttaat	cagtgaggca	cctatctcag	17580
cgatctgtct	atttcgttca	tccatagttg	cctgactgcc	cgtcgtgtag	ataactacga	17640
tacgggaggg	cttaccatct	ggccccagtg	ctgcaatgat	accgcgagac	ccacgctcac	17700
cggctccaga	tttatcagca	ataaaccagc	cagccggaag	ggccgagcgc	agaagtggtc	17760
ctgcaacttt	atccgcctcc	atccagtcta	ttaattgttg	ccgggaagct	agagtaagta	17820
gttcgccagt	taatagtttg	cgcaacgttg	ttgccattgc	tacaggcatc	gtggtgtcac	17880
gctcgtcggt	tggtatggct	tcattcagct	ccggttccca	acgatcaagg	cgagttacat	17940
gatccccat	gttgtgaaaa	aaagcggtta	gctccttcgg	tcctccgata	gttgtcagaa	18000
gtaagtggc	cgcagtggtta	tcactcatgc	ttatggcagc	actgcataat	tctcttactg	18060

tcatgccatc cgtaagatgc ttttctgtga ctggtgagta ctcaaccaag tcattctgag	18120
aatagtgtat gcggcgaccg agttgctctt gcccggcgtc aatacgggat aataccgcgc	18180
cacatagcag aacttttaaaa gtgctcatca ttggaaaacg ttcttcgggg cgaaaactct	18240
caaggatctt accgctgttg agatccagtt cgatgtaacc cactcgtgca cccaactgat	18300
cttcagcatc ttttactttc accagcgttt ctgggtgagc aaaaacagga aggcaaatg	18360
ccgcaaaaaa gggaataagg gcgacacgga aatgttgaat actcatactc ttcctttttc	18420
aatattattg aagcatttat cagggttatt gtctcatgag cggatacata tttgaatgta	18480
tttagaaaaa taaacaaata ggggttccgc gcacatttcc ccgaaaagtg ccacctgaaa	18540
ttgtaaacgt taatatTTTTg ttaaaattcg cgttaaattt ttgttaaadc agctcatttt	18600
ttaaccaata ggccgaaatc ggcaaaatcc cttataaatc aaaagaatag accgagatag	18660
ggttgagtgt tgttccagtt tggaacaaga gtccactatt aaagaacgtg gactccaacg	18720
tcaaagggcg aaaaaccgtc tatcagggcg atggcccact acgtgaacca tcaccctaata	18780
caagtTTTTT ggggtcgagg tgccgtaaag cactaaatcg gaaccctaaa gggagcccc	18840
gatttagagc ttgacgggga aagccggcga acgtggcgag aaaggaaggg aagaaagcga	18900
aaggagcggg cgctagggcg ctggcaagt tagcggtcac gctgcgcgta accaccacac	18960
ccgccgcgct taatgcgccg ctacagggcg cgtcccatc gccattcagg ctgcgcaact	19020
gttggggaagg gcgatcggtg cgggcctctt cgctattacg ccagccaccg cgggtg	19075