

SEQUENCE LISTING

<110> MEDICAGO INC.
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<120> NEW INFLUENZA VIRUS IMMUNIZING EPITOPE

<130> 05014149-21PCT

<150> US 61/081,811

<151> 2008-07-18

<160> 36

<170> PatentIn version 3.5

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<211> 1556

<212> DNA

<213> Influenza A virus, subtype H1

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<212> DNA
<213> Influenza A virus, subtype H3

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<210> 4

<211> 1048

<212> DNA

<213> Influenza A virus, subtype H4

<400> 4

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<211> 1050

<212> DNA

<213> Influenza A virus, subtype H6

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<212> DNA

<213> Influenza A virus, subtype H7

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<211> 1363

<212> DNA

<213> Influenza A virus, subtype H9

<400> 9

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<212> DNA
<213> Influenza A virus, subtype H10

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cattgagcga gagaatgcc a ttgccactg ttatccaggg gcaaccataa atgaagaagc     360
attgaggcag aaaataatgg aaagtggagg aatcagcaag atgagcactg gcttcactta     420
tgggtcttcc atcacctcag ctgggaccac taaggcatgc atgagaaatg gaggagatag     480
tttctatgca gagctcaa at ggctagtgtc aaagacaaag ggacaaaatt tccctcagac     540
aaciaaacacc tatcggaata cggacacagc agaacatctc ataatatggg gaattcatca     600
cccttcagc acacaggaaa agaatgactt atacggaact cagtcactat ctatatcagt     660
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<210> 11

<211> 1698

<212> DNA

<213> Influenza A virus, subtype H11

<400> 11

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acggctacta	gctcagtgga	actggttgag	acagaacaca	ctggatcatt	ctgttcaatc	180
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cctatgtgtg	atgaactaat	tggaagact	tcatggtctt	acattgtgga	aaaaccaat	300
ccaacaaatg	gaatctgtta	cccaggaact	ttagagagtg	aagaagaact	aagactgaaa	360
ttcagtggtg	ttttagaatt	taacaaattc	gaagtattca	catcaaatgg	atggggtgct	420

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aacaacacca aaggagaga tgtactgatt gtttggggaa ttcattcatcc tgctacactg      600
acagaacata aagatctgta taaaaaggac agctcctatg tagcagtggg ttcagagacc      660
tacaacagaa gattcactcc agaaatcaac actaggccca gagtcaatgg acaggccgga      720
cggatgacat tctactggaa gatagtcaaa ccaggagaat caataacatt cgaatctaata      780
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gattctagtg ggaatgtgta taaaatactg tcaatttaca gctgcattgc aagcagtctt    1620
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<210> 12

<211> 1695

<212> DNA

<213> Influenza A virus, subtype H12

<400> 12

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gttccggtga cgcaggtgga agaacttgta catcgtggga ttgatccgat cctgtgtgga	180
acggaactag gatcaccact agtgcttgat gactgttcat tagagggctc aatcctaggc	240
aatcccaaat gtgatcttta tttgaatggc agggaaatggc catacatagt agagaggccc	300
aaagagatgg aaggagtttg ctatccaggg tcaattgaaa accaggaaga gctaagatct	360
ctgttttctt ccatcaaaaa atatgaaaga gtgaagatgt ttgatttcac caaatggaat	420
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gatgaacaag taaaattata caaaaatcct gatactctct cttcagtcac caccgtagaa	660
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agaatggatt actactgggc tgttcttaaa cctggacaaa cagtcaaat acaaccaat	780
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gaggagaatt ctacatataa aattctgagc atctacagca gtgttgctc aagcttagtt	1620
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<210> 13
<211> 1701
<212> DNA
<213> Influenza A virus, subtype H13

<400> 13
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120
gggtgccag tcaaccagctc cattgatctg attgagacaa accaacaagg aacatatctgt
180
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240
ggaaaccag cctgcaccag caactctggg atcagagagt ggtcatcact gattgagggac
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caactgttca gtggaatcag gtcatctcagt agaaaggaaat tgatcccaac taccctcctgg
420
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600
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<210> 14

<211> 1749

<212> DNA

<213> Influenza A virus, subtype H14

<400> 14

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cagtggaaaa cggcacatct gttaaaacac taacagacaa tcacgtagaa gttgtgtcag	180
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caacagggag agtaacagta tctaccgct cggaccaaact cagtattgtt cccaatatag	720
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1680 ggaattcctt ctcacatga tgccttgtct tcgtgycact gatctggga tttgttcata
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1749 tttctacac

<210> 15
<211> 1762
<212> DNA
<213> Influenza A virus, subtype H15

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<210> 16
<211> 1760
<212> DNA
<213> Influenza A virus, subtype H16
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<210> 17
<211> 1656
<212> DNA
<213> pcambia expression vector 660 containing the complete wild type HS

sequence

<400> 17

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aagggtcaact caatcattga caaaatgaac actcagtttg aggccgttg aagggaattt	1200
aataacttag aaaggagaat agagaattta aacaagaaga tggaagacgg gtttctagat	1260
gtctggactt ataatgccga acttctgggt ctcacggaaa atgagagAAC tctagacttt	1320
catgactcaa atgttaagaa cctctacgac aagggtccgac tacagcttag ggataatgca	1380
aaggagctgg gtaacggttg tttcgagttc tatcacaaat gtgataatga atgtatggaa	1440
agtataagaa acggaacgta caactatccg cagtattcag aagaagcaag attaaaaaga	1500
gaggaaataa gtggggtaaa attggaatca ataggaactt accaaatact gtcaatttat	1560
tcaacagtgg cgagttccct agcactggca atcatgatgg ctggtctatc tttatggatg	1620
tgctccaatg gatcggtaca atgcagaatt tgcatt	1656

<210> 18
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 18
gtattagtaa ttagaatttg gtgtc

25

<210> 19
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 19
ttgtagcttt tctttattgt tgggtatgca ctgttctttt tgataagcca

50

<210> 20
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 20
acccaacaat aaagaaaagc tacaataatg ccaaccaaga ggatcttttg

50

<210> 21
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 21
gtgagagggt gtatgttggtg gaatggcata gcagagttaa tcgcccccat

50

<210> 22
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer

<400> 22

atgggggcgga taaactctgc tatgccattc cacaacatac accctctcac 50

<210> 23

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 23

actttgagct cttaaagca aattctgcat tgtaacga 38

<210> 24

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 24

agttccccgg gctggtatat ttatatgttg tc 32

<210> 25

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 25

aatagagctc cattttctct caagatgatt aattaattaa ttagtc 46

<210> 26

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 26

aatagagctc gttaaaatgc ttcttctgtc cctatttata atatgg 46

<210> 27

<211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 27
 ttacgaattc tccttcctaa ttggtgtact atcatttatc aaagggga 48

<210> 28
 <211> 1719
 <212> DNA
 <213> Influenza A virus, subtype H5 from Indonesia/5/05 (H5N1)

<400> 28
 aagcttatgg agaaaatagt gcttcttctt gcaatagtca gtcttgtaa aagtgatcag 60
 atttgcatgg gttaccatgc aaacaattca acagagcagg ttgacacaat catggaaaag 120
 aacgttactg ttacacatgc ccaagacata ctggaaaaga cacacaacgg gaagctctgc 180
 gatctagatg gagtgaagcc tctaatttta agagattgta gtgtagctgg atggctctc 240
 gggaacccaa tgtgtgacga attcatcaat gtaccggaat ggtcttacat agtggagaag 300
 gccaatccaa ccaatgacct ctgttaccga gggagtttca acgactatga agaactgaaa 360
 cacctattga gcagaataaa ccattttgag aaaattcaaa tcatcccaa aagttcttgg 420
 tccgatcatg aagcctcatc aggagttagc tcagcatgtc catacctggg aagtcctcc 480
 ttttttagaa atgtggtatg gcttatcaaa aagaacagta catacccaac aataaagaaa 540
 agctacaata ataccaacca agaggatctt ttggtactgt ggggaattca ccatccta 600
 gatgggcag agcagacaag gctatatcaa aacccaacca cctatatttc cattgggaca 660
 tcaacactaa accagagatt ggtacaaaa atagctacta gatccaaagt aaacgggcaa 720
 agtgggaagga tggagtctt ctggacaatt ttaaaacct atgatgcaat caacttcgag 780
 agtaatggaa atttcattgc tccagaatat gcatacaaaa ttgtcaagaa aggggactca 840
 gcaattatga aaagtgaatt ggaatatggt aactgcaaca ccaagtgtca aactccaatg 900
 ggggcgataa actctagtat gccattccac aacatacacc ctctcaccat cggggaatgc 960
 cccaaatatg tgaaatcaaa cagattagtc cttgcaacag ggctcagaaa tagccctcaa 1020
 agagagagca gaagaaaaa gagaggacta tttggagcta tagcaggttt tatagagggga 1080
 ggatggcagg gaatggtaga tggttggtat ggggtaccacc atagcaatga gcaggggagt 1140

gggtacgctg cagacaaaga atccactcaa aaggaatag atggagtcaa caatlaagtc 1200
aactcaatca ttgacaaat gaacactcag tttagggcgg ttggaaggga atttaataac 1260
ttagaagaaga gaatatgagaa tttaaacaa aagatggag aagggttct agatgtctgg 1320
acttaatatg ccgaactct ggtctcatg gaaatgaga gaactctaga cttcctagac 1380
tcaatgtta agaactctc agacaaggtc cgaactcagc ttagggataa tgcagaagag 1440
ctgggttaacg gttgtttcga gtctctatcac aaatgtgata atgaatgtat ggaagtata 1500
agaaacggaa cgtacaaacta tccgagtat tcaagaaga caagattaaa aagagagaaa 1560
ataagtgggg taaaattgga atcaatagga acttaacaaa tactgtcaat ttattcaaca 1620
gtggcgagtt ccttagcact ggcaatcatg atggctgttc tacccttatg gatgtgtccc 1680
aatggatcgt tacaatgcag aatttgcatt taagagctc 1719

<210> 29
<211> 1656
<212> DNA
<213> pCAMBIA expression vector 680 containing the complete H5 sequence (Triple Mutant)

gatcagattt gcatgtgtta catgcaaac aattcaacag agcaggttga caaatcatg 60
gaaagaacg ttactgttac acatgcccaa gacatactgg aaaaagacaca caacgggaaag 120
ctctgcgata tagatggagt gaagcctcta attttaagag atgtagtgat agctggatgg 180
ctcctcggga acccaatgtg tgacgaattc atcaatgtac cggaatgttc ttacatagtg 240
gaggaaggcca atccaaccaa tgaacctctgt taccccaaggga gtttcaacga ctatgaaaga 300
ctgaaacacc tattagcag aataaaccat tttagaataa ttcaaatcat cccaataagt 360
tcttgttcgg atcatgaagc ctcatcagga gttagctcag catgtccata cctgggaagt 420
cctcctcttt ttagaaatgt gttatggctt atcaaaaaga acagtgcata cccaacata 480
aaagaaagct acaatattgc caaccaaagg gatcctcttg tactgtgggg aattcaacat 540
cctaatgtat cggcagagca gacaaggcta tatcaaaaac caacccaacta tatttccatt 600
gggacatcaa cactaaacca gagtatgtga ccaaaaatag ctactagatc caaagtataa 660
gggcaaatgt gaagtatgga gtctctcttg acaatttaa aacctaatga tgcatacaac 720
ttcggaggtta atggaaattt catctgtcca gaatatgcac acaaatgtc caagaaaggg 780
gaactcagcaa ttatgaaag ttgaatggaa tatgttgaa ctgcataaac gtgtcaaac 840

```

ccaatggggg cgataaaactc tgctatgcc a ttccacaaca tacacctct caccatcggg      900
gaatgcccc aatatgtgaa atcaaacaga ttagtccttg caacagggct cagaaatagc      960
cctcaaagag agagcagaag aaaaaagaga ggactatttg gagctatagc aggttttata     1020
gagggaggat ggcaggggaat ggtagatggg tggtaggggt accaccatag caatgagcag     1080
gggagtgggt acgctgcaga caaagaatcc actcaaaagg caatagatgg agtcaccaat     1140
aaggtcaact caatcattga caaaatgaac actcagtttg aggccgttgg aagggaatth     1200
aataacttag aaaggagaat agagaattta aacaagaaga tggaagacgg gtttctagat     1260
gtctggactt ataatgccga acttctgggt ctcatggaaa atgagagAAC tctagactth     1320
catgactcaa atgttaagaa cctctacgac aaggtccgac tacagcttag ggataatgca     1380
aaggagctgg gtaacgggtg tttcgagtgc tatcacaat gtgataatga atgtatggaa     1440
agtataagaa acggaacgta caactatccg cagtattcag aagaagcaag attaaaaaga     1500
gaggaaataa gtggggtaaa attggaatca ataggaactt accaaatact gtcaatttat     1560
tcaacagtgg cgagtccct agcactggca atcatgatgg ctgggtctatc tttatggatg     1620
tgctccaatg gatcggtaca atgcagaatt tgcatt                                1656

```

```

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> PCR primer

```

```

<400> 30
gtattagtaa ttagaatttg gtgtc                                25

```

```

<210> 31
<211> 44
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> PCR primer

```

```

<400> 31
gcaagaagaa gcaactattht ctccatttht tctcaagatg atta                                44

```

```

<210> 32

```

25/32

<211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 32
 ttaatcatct tgagagaaaa tggagaaaat agtgcttctt cttgc 45

<210> 33
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 33
 actttgagct cttaaatagca aattctgcat tgtaacga 38

<210> 34
 <211> 552
 <212> PRT
 <213> HA from Influenza, H5 from A/Vietnam/1194/04

<400> 34

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Gln Val
 1 5 10 15

Asp Thr Ile Met Glu Lys Asn Val Thr Val Thr His Ala Gln Asp Ile
 20 25 30

Leu Glu Lys Thr His Asn Gly Lys Leu Cys Asp Leu Asp Gly Val Lys
 35 40 45

Pro Leu Ile Leu Arg Asp Cys Ser Val Ala Gly Trp Leu Leu Gly Asn
 50 55 60

Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
 65 70 75 80

Glu Lys Ala Asn Pro Val Asn Asp Leu Cys Tyr Pro Gly Asp Phe Asn
 85 90 95

Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu

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

Leu Ala Ile Met Val Ala Gly Leu Ser Leu Trp Met Cys Ser Asn Gly
530 535 540

Ser Leu Gln Cys Arg Ile Cys Ile
545 550

<210> 35

<211> 1752

<212> DNA

<213> HA from Influenza, strain B/Florida/4/2006

<400> 35

atgaaggcaa taattgtact actcatggta gtaacatcca atgcagatcg aatctgcact	60
ggaataacat cttcaaactc acctcatgtg gtcaaaacag ccactcaagg ggaggtcaat	120
gtgactgggtg tgataccact aacaacaaca ccaacaaaat cttattttgc aaatctcaaa	180
ggaacaagga ccagagggaa actatgccca gactgtctca actgcacaga tctggatgtg	240
gctttgggca gaccaatgtg tgtggggacc acaccttcgg cgaaggcttc aatactccac	300
gaagtcaaac ctgttacatc cgggtgcttt cctataatgc acgacagaac aaaaatcagg	360
caactaccca atcttctcag aggatatgaa aatatcaggc tatcaaccca aaacgtcatc	420
gatgcggaaa aggcaccagg aggaccctac agacttgga cctcaggatc ttgccctaac	480
gtaccagta agagcggatt tttcgcaaca atggcttggg ctgtcccaa ggacaacaac	540
aaaaatgcaa cgaaccctact aacagtagaa gtaccataca tttgtacaga aggggaagac	600
caaatcactg tttgggggtt ccattcagat aacaaaacc aaatgaagaa cctctatgga	660
gactcaaate ctcaaaagtt cacctcatct gctaattggag taaccacaca ctatgtttct	720
cagattggca gcttccaga tcaaacagaa gacggaggac taccacaaag cggcaggatt	780
gttgttgatt acatgatgca aaaacctggg aaaacaggaa caattgtcta ccaagaggt	840
gttttgttgc ctcaaaaggt gtggtgcgcg agtggcagga gcaaagtaat aaaaggggcc	900
ttgcctttta ttggtgaagc agattgcctt catgaaaaat acggtggatt aaacaaaagc	960
aagccttact acacaggaga acatgcaaaa gccataggaa attgccaat atgggtgaaa	1020
acacctttga agctcgccaa tggaaccaa tatagacctc ctgcaaaact attaaaggaa	1080
aggggtttct tcggagctat tgctggtttc ctagaaggag gatgggaagg aatgattgca	1140
ggctggcacg gatacacatc tcacggagca catggagtgg cagtggcggc ggaccttaag	1200
agtacgcaag aagctataaa caagataaca aaaaatctca attctttgag tgagctagaa	1260
gtaaagaatc ttcaagact aagtgggtgc atggatgaac tccacaacga aatactcgag	1320

ctggatgaga aagtggatga tctcagagct gacactataa gctcgcaa at agaacttgca 1380
gtcttgcttt ccaacgaagg aataataaac agtgaagatg agcatctatt ggcacttgag 1440
agaaaactaa agaaaatgct gggtcctct gctgtagaga taggaaatgg atgcttcgaa 1500
accaaacaca agtgaacca gacctgctta gacaggatag ctgctggcac ctttaatgca 1560
ggagaatttt ctctcccccac ttttgattca ctgaacatta ctgctgcatc tttaaatgat 1620
gatggattgg ataaccatac tatactgctc tattactcaa ctgctgcttc tagtttggt 1680
gtaacattga tgctagctat ttttattgtt tatatggctc ccagagacaa cgtttcatgc 1740
tccatctgtc ta 1752

<210> 36

<211> 569

<212> PRT

<213> Mature HA from Influenza, strain B/Florida/4/2006

<400> 36

Asp Arg Ile Cys Thr Gly Ile Thr Ser Ser Asn Ser Pro His Val Val
1 5 10 15

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

Thr Thr Thr Pro Thr Lys Ser Tyr Phe Ala Asn Leu Lys Gly Thr Arg
35 40 45

Thr Arg Gly Lys Leu Cys Pro Asp Cys Leu Asn Cys Thr Asp Leu Asp
50 55 60

Val Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala Lys
65 70 75 80

Ala Ser Ile Leu His Glu Val Lys Pro Val Thr Ser Gly Cys Phe Pro
85 90 95

Ile Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg
100 105 110

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

Lys Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys Pro
 130 135 140

Asn Ala Thr Ser Lys Ser Gly Phe Phe Ala Thr Met Ala Trp Ala Val
 145 150 155 160

Pro Lys Asp Asn Asn Lys Asn Ala Thr Asn Pro Leu Thr Val Glu Val
 165 170 175

Pro Tyr Ile Cys Thr Glu Gly Glu Asp Gln Ile Thr Val Trp Gly Phe
 180 185 190

His Ser Asp Asn Lys Thr Gln Met Lys Asn Leu Tyr Gly Asp Ser Asn
 195 200 205

Pro Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val
 210 215 220

Ser Gln Ile Gly Ser Phe Pro Asp Gln Thr Glu Asp Gly Gly Leu Pro
 225 230 235 240

Gln Ser Gly Arg Ile Val Val Asp Tyr Met Met Gln Lys Pro Gly Lys
 245 250 255

Thr Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val
 260 265 270

Trp Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu
 275 280 285

Ile Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys
 290 295 300

Ser Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys
 305 310 315 320

Pro Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr
 325 330 335

Arg Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile
 340 345 350

Ala Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His
 355 360 365

Gly Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu
 370 375 380

Lys Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser
 385 390 395 400

Leu Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met
 405 410 415

Asp Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp
 420 425 430

Leu Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu
 435 440 445

Ser Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu
 450 455 460

Glu Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Glu Ile Gly
 465 470 475 480

Asn Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp
 485 490 495

Arg Ile Ala Ala Gly Thr Phe Asn Ala Gly Glu Phe Ser Leu Pro Thr
 500 505 510

Phe Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu
 515 520 525

Asp Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu
 530 535 540

Ala Val Thr Leu Met Leu Ala Ile Phe Ile Val Tyr Met Val Ser Arg
 545 550 555 560

Asp Asn Val Ser Cys Ser Ile Cys Leu

565