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<120> Increasing Virus Like Particle Yield in Plants

<130> V83991WO

<150> US 61/541,780
<151> 2011-09-30

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<213> Influenza virus

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65                  70                  75                  80

Pro Met Cys Asp Glu Phe Ile Asn Val Pro Glu Trp Ser Tyr Ile Val
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Glu Lys Ala Asn Pro Thr Asn Asp Leu Cys Tyr Pro Gly Ser Phe Asn
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Asp Tyr Glu Glu Leu Lys His Leu Leu Ser Arg Ile Asn His Phe Glu
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Lys Ile Gln Ile Ile Pro Lys Ser Ser Trp Ser Asp His Glu Ala Ser
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Ser Gly Val Ser Ser Ala Cys Pro Tyr Leu Gly Ser Pro Ser Phe Phe
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Arg Asn Val Val Trp Leu Ile Lys Lys Asn Ser Thr Tyr Pro Thr Ile
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Lys Lys Ser Tyr Asn Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp
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Gly Ile His His Pro Asn Asp Ala Ala Glu Gln Thr Arg Leu Tyr Gln
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Lys Cys Ile Tyr Arg Arg Phe Lys Tyr Gly Leu Lys Gly Gly Pro Ser
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            100                 105                 110

Thr Cys Tyr Pro Gly Asp Phe Ile Asp Tyr Glu Glu Leu Arg Glu Gln
        115                 120                 125

Leu Ser Ser Val Ser Ser Phe Glu Arg Phe Glu Ile Phe Pro Lys Thr
    130                 135                 140

Ser Ser Trp Pro Asn His Asp Ser Asn Lys Gly Val Thr Ala Ala Cys
145                 150                 155                 160

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

Lys Lys Gly Asn Ser Tyr Pro Lys Leu Ser Lys Ser Tyr Ile Asn Asp
            180                 185                 190

Lys Gly Lys Glu Val Leu Val Leu Trp Gly Ile His His Pro Ser Thr
        195                 200                 205

Ser Ala Asp Gln Gln Ser Leu Tyr Gln Asn Ala Asp Ala Tyr Val Phe
    210                 215                 220

Val Gly Ser Ser Arg Tyr Ser Lys Lys Phe Lys Pro Glu Ile Ala Ile
225                 230                 235                 240

Arg Pro Lys Val Arg Asp Gln Glu Gly Arg Met Asn Tyr Tyr Trp Thr
                245                 250                 255

Leu Val Glu Pro Gly Asp Lys Ile Thr Phe Glu Ala Thr Gly Asn Leu
            260                 265                 270

Val Val Pro Arg Tyr Ala Phe Ala Met Glu Arg Asn Ala Gly Ser Gly
        275                 280                 285

Ile Ile Ile Ser Asp Thr Pro Val His Asp Cys Asn Thr Thr Cys Gln
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    290                 295                 300

Thr Pro Lys Gly Ala Ile Asn Thr Ser Leu Pro Phe Gln Asn Ile His
305                 310                 315                 320

Pro Ile Thr Ile Gly Lys Cys Pro Lys Tyr Val Lys Ser Thr Lys Leu
                325                 330                 335

Arg Leu Ala Thr Gly Leu Arg Asn Ile Pro Ser Ile Gln Ser Arg Gly
            340                 345                 350

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

Val Asp Gly Trp Tyr Gly Tyr His His Gln Asn Glu Gln Gly Ser Gly
    370                 375                 380

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

Asn Lys Val Asn Ser Val Ile Glu Lys Met Asn Thr Gln Phe Thr Ala
                405                 410                 415

Val Gly Lys Glu Phe Asn His Leu Glu Lys Arg Ile Glu Asn Leu Asn
            420                 425                 430

Lys Lys Val Asp Asp Gly Phe Leu Asp Ile Trp Thr Tyr Asn Ala Glu
        435                 440                 445

Leu Leu Val Leu Leu Glu Asn Glu Arg Thr Leu Asp Tyr His Asp Ser
    450                 455                 460

Asn Val Lys Asn Leu Tyr Glu Lys Val Arg Ser Gln Leu Lys Asn Asn
465                 470                 475                 480

Ala Lys Glu Ile Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys Asp
                485                 490                 495

Asn Thr Cys Met Glu Ser Val Lys Asn Gly Thr Tyr Asp Tyr Pro Lys
            500                 505                 510
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Tyr Ser Glu Glu Ala Lys Leu Asn Arg Glu Glu Ile Asp Gly Val Lys
515 520 525

Leu Glu Ser Thr Arg Ile Tyr Gln Ile Leu Ala Ile Tyr Ser Thr Val
530 535 540

Ala Ser Ser Leu Val Leu Val Val Ser Leu Gly Ala Ile Ser Phe Trp
545 550 555 560

Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile
565 570

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<211> 40
<212> DNA
<213> Artificial Sequence

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<223> primer IF-S2+S4-H3 Per.c

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<210> 22
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> primer IF-S1a4-H3 Per.r

<400> 22
actaaagaaa ataggccttc aaatgcaaat gttgcaccta atgtt 45

<210> 23
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence of synthesized H3 gene

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atagtgaaaa caatcacgaa tgaccaaatt gaagttacta atgctactga gctggttcag 180

agttcctcaa caggtgaaat atgcgacagt cctcatcaga tccttgatgg aaaaaactgc 240

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gacctttttg ttgaacgcag caaagcctac agcaactgtt acccttatga tgtgccggat 360

tatgcctccc ttaggtcact agttgcctca tccggcacac tggagtttaa caatgaaagc 420

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aacagtttct ttagtagatt gaattggttg acccacttaa acttcaaata cccagcattg 540

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ccgggtacgg acaaagacca aatcttcctg tatgctcaag catcaggaag aatcacagtc 660

tctaccaaaa gaagccaaca aaccgtaagc ccgaatatcg gatctagacc cagagtaagg 720

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<211> 3465
<212> DNA
<213> Artificial Sequence

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acgtcttcaa agcaagtgga ttgatgtgat aacatggtgg agcacgacac acttgtctac 360

tccaaaaata tcaaagatac agtctcagaa gaccaaaggg caattgagac ttttcaacaa 420

agggtaatat ccggaaacct cctcggattc cattgcccag ctatctgtca ctttattgtg 480

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atcgttgaag atgcctctgc cgacagtggt cccaaagatg gacccccacc cacgaggagc 600

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tccactgacg taagggatga cgcacaatcc cactatcctt cgcaagaccc ttcctctata 720

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<212> PRT
<213> Influenza virus

<400> 25

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Ser Thr Ala Thr Leu Cys Leu Gly His His Ala Val Pro Asn Gly Thr
35 40 45

Ile Val Lys Thr Ile Thr Asn Asp Gln Ile Glu Val Thr Asn Ala Thr
50 55 60

Glu Leu Val Gln Ser Ser Ser Thr Gly Glu Ile Cys Asp Ser Pro His
65 70 75 80

Gln Ile Leu Asp Gly Lys Asn Cys Thr Leu Ile Asp Ala Leu Leu Gly
85 90 95

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Asp Pro Gln Cys Asp Gly Phe Gln Asn Lys Lys Trp Asp Leu Phe Val
            100                 105                 110

Glu Arg Ser Lys Ala Tyr Ser Asn Cys Tyr Pro Tyr Asp Val Pro Asp
        115                 120                 125

Tyr Ala Ser Leu Arg Ser Leu Val Ala Ser Ser Gly Thr Leu Glu Phe
    130                 135                 140

Asn Asn Glu Ser Phe Asn Trp Thr Gly Val Thr Gln Asn Gly Thr Ser
145                 150                 155                 160

Ser Ala Cys Ile Arg Arg Ser Lys Asn Ser Phe Phe Ser Arg Leu Asn
                165                 170                 175

Trp Leu Thr His Leu Asn Phe Lys Tyr Pro Ala Leu Asn Val Thr Met
            180                 185                 190

Pro Asn Asn Glu Gln Phe Asp Lys Leu Tyr Ile Trp Gly Val His His
        195                 200                 205

Pro Gly Thr Asp Lys Asp Gln Ile Phe Leu Tyr Ala Gln Ala Ser Gly
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Arg Ile Thr Val Ser Thr Lys Arg Ser Gln Gln Thr Val Ser Pro Asn
225                 230                 235                 240

Ile Gly Ser Arg Pro Arg Val Arg Asn Ile Pro Ser Arg Ile Ser Ile
                245                 250                 255

Tyr Trp Thr Ile Val Lys Pro Gly Asp Ile Leu Leu Ile Asn Ser Thr
            260                 265                 270

Gly Asn Leu Ile Ala Pro Arg Gly Tyr Phe Lys Ile Arg Ser Gly Lys
        275                 280                 285

Ser Ser Ile Met Arg Ser Asp Ala Pro Ile Gly Lys Cys Asn Ser Glu
    290                 295                 300
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Cys Ile Thr Pro Asn Gly Ser Ile Pro Asn Asp Lys Pro Phe Gln Asn
305                 310                 315                 320

Val Asn Arg Ile Thr Tyr Gly Ala Cys Pro Arg Tyr Val Lys Gln Asn
                325                 330                 335

Thr Leu Lys Leu Ala Thr Gly Met Arg Asn Val Pro Glu Lys Gln Thr
            340                 345                 350

Arg Gly Ile Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu
        355                 360                 365

Gly Met Val Asp Gly Trp Tyr Gly Phe Arg His Gln Asn Ser Glu Gly
    370                 375                 380

Arg Gly Gln Ala Ala Asp Leu Lys Ser Thr Gln Ala Ala Ile Asp Gln
385                 390                 395                 400

Ile Asn Gly Lys Leu Asn Arg Leu Ile Gly Lys Thr Asn Glu Lys Phe
                405                 410                 415

His Gln Ile Glu Lys Glu Phe Ser Glu Val Glu Gly Arg Ile Gln Asp
            420                 425                 430

Leu Glu Lys Tyr Val Glu Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn
        435                 440                 445

Ala Glu Leu Leu Val Ala Leu Glu Asn Gln His Thr Ile Asp Leu Thr
    450                 455                 460

Asp Ser Glu Met Asn Lys Leu Phe Glu Lys Thr Lys Lys Gln Leu Arg
465                 470                 475                 480

Glu Asn Ala Glu Asp Met Gly Asn Gly Cys Phe Lys Ile Tyr His Lys
                485                 490                 495

Cys Asp Asn Ala Cys Ile Gly Ser Ile Arg Asn Gly Thr Tyr Asp His
            500                 505                 510
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Asp Val Tyr Arg Asp Glu Ala Leu Asn Asn Arg Phe Gln Ile Lys Gly
515 520 525

Val Glu Leu Lys Ser Gly Tyr Lys Asp Trp Ile Leu Trp Ile Ser Phe
530 535 540

Ala Ile Ser Cys Phe Leu Leu Cys Val Ala Leu Leu Gly Phe Ile Met
545 550 555 560

Trp Ala Cys Gln Lys Gly Asn Ile Arg Cys Asn Ile Cys Ile
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<212> DNA
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<210> 27
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> primer IF-S1a4-B Bris.r

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<210> 28
<211> 1758
<212> DNA
<213> Artificial Sequence

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gccttgggca gaccaaaatg cacggggaaa ataccctcgg caagagtttc aatactccat 300

gaagtcagac ctgttacatc tgggtgcttt cctataatgc acgacagaac aaaaattaga 360

cagctgccta accttctccg aggatacgaa catatcaggt tatcaaccca taacgttatc 420

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<212> DNA
<213> Artificial Sequence

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Ser Ser Asn Ser Pro His Val Val Lys Thr Ala Thr Gln Gly Glu Val
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Asn Val Thr Gly Val Ile Pro Leu Thr Thr Thr Pro Thr Lys Ser His
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Cys Leu Asn Cys Thr Asp Leu Asp Val Ala Leu Gly Arg Pro Lys Cys
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Thr Gly Lys Ile Pro Ser Ala Arg Val Ser Ile Leu His Glu Val Arg
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Pro Val Thr Ser Gly Cys Phe Pro Ile Met His Asp Arg Thr Lys Ile
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Arg Gln Leu Pro Asn Leu Leu Arg Gly Tyr Glu His Ile Arg Leu Ser
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Thr His Asn Val Ile Asn Ala Glu Asn Ala Pro Gly Gly Pro Tyr Lys
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Asp Tyr Met Val Gln Lys Ser Gly Lys Thr Gly Thr Ile Thr Tyr Gln
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Arg Gly Ile Leu Leu Pro Gln Lys Val Trp Cys Ala Ser Gly Arg Ser
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Lys Val Ile Lys Gly Ser Leu Pro Leu Ile Gly Glu Ala Asp Cys Leu
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His Glu Lys Tyr Gly Gly Leu Asn Lys Ser Lys Pro Tyr Tyr Thr Gly
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Glu His Ala Lys Ala Ile Gly Asn Cys Pro Ile Trp Val Lys Thr Pro
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Asn Lys Ile Thr Lys Asn Leu Asn Ser Leu Ser Glu Leu Glu Val Lys
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Leu Glu Leu Asp Glu Lys Val Asp Asp Leu Arg Ala Asp Thr Ile Ser
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Ser Glu Asp Glu His Leu Leu Ala Leu Glu Arg Lys Leu Lys Lys Met
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Leu Gly Pro Ser Ala Val Glu Ile Gly Asn Gly Cys Phe Glu Thr Lys
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His Lys Cys Asn Gln Thr Cys Leu Asp Arg Ile Ala Ala Gly Thr Phe
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Asp Ala Gly Glu Phe Ser Leu Pro Thr Phe Asp Ser Leu Asn Ile Thr
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Ala Ala Ser Leu Asn Asp Asp Gly Leu Asp Asn Tyr Gln Ile Leu Ser
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Ile Tyr Ser Thr Val Ala Ser Ser Leu Ala Leu Ala Ile Met Met Ala
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caaacatttg gcaataaagt ttcttaagat tgaatcctgt tgccggtctt gcgatgatta 3660

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aagtcagttg gaaatcaata aaatgattat tttatgaata tatttcattg tgcaagtaga 3960

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caccccaaac aaaataacac tatatatatc ctcgtatgag gagaggcacg ttcagtgact 4080

cgacgattcc cgagcaaaaa aagtctcccc gtcacacata tagtgggtga cgcaattatc 4140

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<210> 41
<211> 577
<212> PRT
<213> Influenza virus

<400> 41

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Leu Val Pro Ser Gln Ile Phe Ala Asp Arg Ile Cys Thr Gly Ile Thr
20 25 30

Ser Ser Asn Ser Pro His Val Val Lys Thr Ala Thr Gln Gly Glu Val
35 40 45

Asn Val Thr Gly Val Ile Pro Leu Thr Thr Thr Pro Thr Lys Ser His
50 55 60

Phe Ala Asn Leu Lys Gly Thr Glu Thr Arg Gly Lys Leu Cys Pro Lys
65 70 75 80

Cys Leu Asn Cys Thr Asp Leu Asp Val Ala Leu Gly Arg Pro Lys Cys
85 90 95

Thr Gly Lys Ile Pro Ser Ala Arg Val Ser Ile Leu His Glu Val Arg
100 105 110

Pro Val Thr Ser Gly Cys Phe Pro Ile Met His Asp Arg Thr Lys Ile
115 120 125

Arg Gln Leu Pro Asn Leu Leu Arg Gly Tyr Glu His Ile Arg Leu Ser

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    130                 135                 140

Thr His Asn Val Ile Asn Ala Glu Asn Ala Pro Gly Gly Pro Tyr Lys
145                 150                 155                 160

Ile Gly Thr Ser Gly Ser Cys Pro Asn Ile Thr Asn Gly Asn Gly Phe
                165                 170                 175

Phe Ala Thr Met Ala Trp Ala Val Pro Lys Asn Asp Lys Asn Lys Thr
            180                 185                 190

Ala Thr Asn Pro Leu Thr Ile Glu Val Pro Tyr Ile Cys Thr Glu Gly
        195                 200                 205

Glu Asp Gln Ile Thr Val Trp Gly Phe His Ser Asp Asn Glu Thr Gln
    210                 215                 220

Met Ala Lys Leu Tyr Gly Asp Ser Lys Pro Gln Lys Phe Thr Ser Ser
225                 230                 235                 240

Ala Asn Gly Val Thr Thr His Tyr Val Ser Gln Ile Gly Gly Phe Pro
                245                 250                 255

Asn Gln Thr Glu Asp Gly Gly Leu Pro Gln Ser Gly Arg Ile Val Val
            260                 265                 270

Asp Tyr Met Val Gln Lys Ser Gly Lys Thr Gly Thr Ile Thr Tyr Gln
        275                 280                 285

Arg Gly Ile Leu Leu Pro Gln Lys Val Trp Cys Ala Ser Gly Arg Ser
    290                 295                 300

Lys Val Ile Lys Gly Ser Leu Pro Leu Ile Gly Glu Ala Asp Cys Leu
305                 310                 315                 320

His Glu Lys Tyr Gly Gly Leu Asn Lys Ser Lys Pro Tyr Tyr Thr Gly
                325                 330                 335

Glu His Ala Lys Ala Ile Gly Asn Cys Pro Ile Trp Val Lys Thr Pro
            340                 345                 350
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Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg Pro Pro Gly Gly Gly Trp
        355                 360                 365

Glu Gly Met Ile Ala Gly Trp His Gly Tyr Thr Ser His Gly Ala His
    370                 375                 380

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

Lys Ile Thr Lys Asn Leu Asn Ser Leu Ser Glu Leu Glu Val Lys Asn
                405                 410                 415

Leu Gln Arg Leu Ser Gly Ala Met Asp Glu Leu His Asn Glu Ile Leu
            420                 425                 430

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

Gln Ile Glu Leu Ala Val Leu Leu Ser Asn Glu Gly Ile Ile Asn Ser
    450                 455                 460

Glu Asp Glu His Leu Leu Ala Leu Glu Arg Lys Leu Lys Lys Met Leu
465                 470                 475                 480

Gly Pro Ser Ala Val Glu Ile Gly Asn Gly Cys Phe Glu Thr Lys His
                485                 490                 495

Lys Cys Asn Gln Thr Cys Leu Asp Arg Ile Ala Ala Gly Thr Phe Asp
            500                 505                 510

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

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

Tyr Ser Thr Ala Ala Ser Ser Leu Ala Val Thr Leu Met Ile Ala Ile
545                 550                 555                 560
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Phe Val Val Tyr Met Val Ser Arg Asp Asn Val Ser Cys Ser Ile Cys
565 570 575

Leu

<210> 42
<211> 1707
<212> DNA
<213> Influenza virus

<400> 42
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attggttacc atgcaaacaa ttcaacagag caggttgaca caatcatgga aaagaacgtt 120

actgttacac atgcccaaga catactggaa aagacacaca acgggaagct ctgcgatcta 180

gatggagtga agcctctaat tttaagagat tgtagtgtag ctggatggct cctcgggaac 240

ccaatgtgtg acgaattcat caatgtaccg gaatggtctt acatagtgga gaaggccaat 300

ccaaccaatg acctctgtta cccagggagt ttcaacgact atgaagaact gaaacaccta 360

ttgagcagaa taaaccattt tgagaaaatt caaatcatcc ccaaaagttc ttggtccgat 420

catgaagcct catcaggagt tagctcagca tgtccatacc tgggaagtcc ctccttttt 480

agaaatgtgg tatggcttat caaaaagaac agtacatacc caacaataaa gaaaagctac 540

aataatacca accaagagga tcttttggta ctgtggggaa ttcaccatcc taatgatgcg 600

gcagagcaga caaggctata tcaaaaccca accacctata tttccattgg gacatcaaca 660

ctaaaccaga gattggtacc aaaaatagct actagatcca aagtaaacgg gcaaagtgga 720

aggatggagt tcttctggac aattttaaaa cctaatgatg caatcaactt cgagagtaat 780

ggaaatttca ttgctccaga atatgcatac aaaattgtca agaaagggga ctcagcaatt 840

atgaaaagtg aattggaata tggtaactgc aacaccaagt gtcaaactcc aatgggggcg 900

ataaactcta gtatgccatt ccacaacata caccctctca ccatcgggga atgccccaaa 960

tatgtgaaat caaacagatt agtccttgca acagggctca gaaatagccc tcaaagagag 1020

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cagggaatgg tagatggttg gtatgggtac caccatagca atgagcaggg gagtgggtac 1140

gctgcagaca aagaatccac tcaaaaggca atagatggag tcaccaataa ggtcaactca 1200

atcattgaca aaatgaacac tcagtttgag gccgttggaa gggaatttaa taacttagaa 1260

aggagaatag agaatttaaa caagaagatg gaagacgggt ttctagatgt ctggacttat 1320

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gttaagaacc tctacgacaa ggtccgacta cagcttaggg ataatgcaaa ggagctgggt 1440

aacggttgtt tcgagttcta tcacaaatgt gataatgaat gtatggaaag tataagaaac 1500

ggaacgtaca actatccgca gtattcagaa gaagcaagat taaaaagaga ggaaataagt 1560

ggggtaaaat tggaatcaat aggaacttac caaatactgt caatttattc aacagtggcg 1620

agttccctag cactggcaat catgatggct ggtctatctt tatggatgtg ctccaatgga 1680

tcgttacaat gcagaatttg catttaa 1707

<210> 43
<211> 1734
<212> DNA
<213> Influenza virus

<400> 43
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cagatcttcg ccgatcgaat ctgcactgga ataacatcgt caaactcacc acatgtcgtc 120

aaaactgcta ctcaagggga ggtcaatgtg actggtgtaa taccactgac aacaacaccc 180

accaaatctc attttgcaaa tctcaaagga acagaaacca gggggaaact atgcccaaaa 240

tgcctcaact gcacagatct ggacgtagcc ttgggcagac caaaatgcac ggggaaaata 300

ccctcggcaa gagtttcaat actccatgaa gtcagacctg ttacatctgg gtgctttcct 360

ataatgcacg acagaacaaa aattagacag ctgcctaacc ttctccgagg atacgaacat 420

atcaggttat caacccataa cgttatcaat gcagaaaatg caccaggagg accctacaaa 480

attggaacct cagggtcttg ccctaacatt accaatggaa acggattttt cgcaacaatg 540

gcttgggccg tcccaaaaaa cgacaaaaac aaaacagcaa caaatccatt aacaatagaa 600

gtaccataca tttgtacaga aggagaagac caaattaccg tttgggggtt ccactctgac 660

aacgagaccc aaatggcaaa gctctatggg gactcaaagc cccagaagtt cacctcatct 720

gccaacggag tgaccacaca ttacgtttca cagattggtg gcttcccaaa tcaaacagaa 780

gacggaggac taccacaaag tggtagaatt gttgttgatt acatggtgca aaaatctggg 840

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tatagacctc ctggtggagg atgggaagga atgattgcag gttggcacgg atacacatcc 1140

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atactgcttt actactcaac tgctgcctcc agtttggctg taacactgat gatagctatc 1680

tttgttgttt atatggtctc cagagacaat gtttcttgct ccatctgtct ataa 1734

<210> 44
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> primer IF-H3V36111.S2+4c

<400> 44
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<210> 45
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> primer IF-H3V36111.s1-4r

<400> 45
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<210> 46
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence of synthesized H3 gene

<400> 46
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atagtgaaaa caatcacgaa tgaccaaatt gaagttacta atgctactga gctggttcag 180

aattcctcaa taggtgaaat atgcgacagt cctcatcaga tccttgatgg agaaaactgc 240

acactaatag atgctctatt gggagaccct cagtgtgatg gcttccaaaa taagaaatgg 300

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aacgtgacta tgccaaacaa tgaacaattt gacaaattgt acatttgggg ggttcaccac 600

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tctaccaaaa gaagccaaca agctgtaatc ccgaatatcg gatctagacc cagaataagg 720

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aggtgcaaca tttgcatttg a 1701

<210> 47
<211> 3465
<212> DNA
<213> Artificial Sequence

<220>
<223> expression cassette number 1391

<400> 47
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agggtaatat ccggaaacct cctcggattc cattgcccag ctatctgtca ctttattgtg 480

aagatagtgg aaaaggaagg tggctcctac aaatgccatc attgcgataa aggaaaggcc 540

atcgttgaag atgcctctgc cgacagtggt cccaaagatg gacccccacc cacgaggagc 600

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tccactgacg taagggatga cgcacaatcc cactatcctt cgcaagaccc ttcctctata 720

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gcgggtgcaa tatctctact tctgcttgac gaggtattgt tgcctgtact tctttcttct 1140

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aactaggata aattatcgcg cgcggtgtca tctatgttac tagat 3465

<210> 48
<211> 574
<212> PRT
<213> Influenza virus

<400> 48

Met Ala Lys Asn Val Ala Ile Phe Gly Leu Leu Phe Ser Leu Leu Val
1 5 10 15

Leu Val Pro Ser Gln Ile Phe Ala Gln Lys Leu Pro Gly Asn Asp Asn
20 25 30

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Ser Thr Ala Thr Leu Cys Leu Gly His His Ala Val Pro Asn Gly Thr
        35                  40                  45

Ile Val Lys Thr Ile Thr Asn Asp Gln Ile Glu Val Thr Asn Ala Thr
    50                  55                  60

Glu Leu Val Gln Asn Ser Ser Ile Gly Glu Ile Cys Asp Ser Pro His
65                  70                  75                  80

Gln Ile Leu Asp Gly Glu Asn Cys Thr Leu Ile Asp Ala Leu Leu Gly
                85                  90                  95

Asp Pro Gln Cys Asp Gly Phe Gln Asn Lys Lys Trp Asp Leu Phe Val
            100                 105                 110

Glu Arg Ser Lys Ala Tyr Ser Asn Cys Tyr Pro Tyr Asp Val Pro Asp
        115                 120                 125

Tyr Ala Ser Leu Arg Ser Leu Val Ala Ser Ser Gly Thr Leu Glu Phe
    130                 135                 140

Asn Asn Glu Ser Phe Asn Trp Thr Gly Val Thr Gln Asn Gly Thr Ser
145                 150                 155                 160

Ser Ala Cys Ile Arg Arg Ser Asn Asn Ser Phe Phe Ser Arg Leu Asn
                165                 170                 175

Trp Leu Thr His Leu Asn Phe Lys Tyr Pro Ala Leu Asn Val Thr Met
            180                 185                 190

Pro Asn Asn Glu Gln Phe Asp Lys Leu Tyr Ile Trp Gly Val His His
        195                 200                 205

Pro Gly Thr Asp Lys Asp Gln Ile Phe Leu Tyr Ala Gln Ser Ser Gly
    210                 215                 220

Arg Ile Thr Val Ser Thr Lys Arg Ser Gln Gln Ala Val Ile Pro Asn
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Arg Gly Lys Leu Cys Pro Asp Cys Leu Asn Cys Thr Asp Leu Asp Val
65 70 75 80

Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala Lys Ala
85 90 95

Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe Pro Ile
100 105 110

Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly
115 120 125

Tyr Glu Asn Ile Arg Leu Ser Thr Gln Asn Val Ile Asp Ala Glu Lys
130 135 140

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Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys Pro Asn
145                 150                 155                 160

Ala Thr Ser Lys Ile Gly Phe Phe Ala Thr Met Ala Trp Ala Val Pro
                165                 170                 175

Lys Asp Asn Tyr Lys Asn Ala Thr Asn Pro Leu Thr Val Glu Val Pro
            180                 185                 190

Tyr Ile Cys Thr Glu Gly Glu Asp Gln Ile Thr Val Trp Gly Phe His
        195                 200                 205

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

Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val Ser
225                 230                 235                 240

Gln Ile Gly Asp Phe Pro Asp Gln Thr Glu Asp Gly Gly Leu Pro Gln
                245                 250                 255

Ser Gly Arg Ile Val Val Asp Tyr Met Met Gln Lys Pro Gly Lys Thr
            260                 265                 270

Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val Trp
        275                 280                 285

Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu Ile
    290                 295                 300

Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys Ser
305                 310                 315                 320

Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys Pro
                325                 330                 335

Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg
            340                 345                 350
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Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile Ala
        355                 360                 365

Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His Gly
    370                 375                 380

Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu Lys
385                 390                 395                 400

Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser Leu
                405                 410                 415

Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met Asp
            420                 425                 430

Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp Leu
        435                 440                 445

Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu Ser
    450                 455                 460

Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu Glu
465                 470                 475                 480

Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Asp Ile Gly Asn
                485                 490                 495

Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp Arg
            500                 505                 510

Ile Ala Ala Gly Thr Phe Asn Ala Gly Glu Phe Ser Leu Pro Thr Phe
        515                 520                 525

Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu Asp
    530                 535                 540

Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu Ala
545                 550                 555                 560
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Val Thr Leu Met Leu Ala Ile Phe Ile Val Tyr Met Val Ser Arg Asp
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Asn Val Ser Cys Ser Ile Cys Leu
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<213> Artificial Sequence

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<223> primer HAB110(PrL-).r

<400> 55
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<210> 56
<211> 52
<212> DNA
<213> Artificial Sequence

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<223> primer HAB110(PrL-).c

<400> 56
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<212> DNA
<213> Artificial Sequence

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<223> Expression cassette number 1467

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tacaaatgcc atcattgcga taaaggaaag gccatcgttg aagatgcctc tgccgacagt 240

ggtcccaaag atggaccccc acccacgagg agcatcgtgg aaaaagaaga cgttccaacc 300

acgtcttcaa agcaagtgga ttgatgtgat aacatggtgg agcacgacac acttgtctac 360

tccaaaaata tcaaagatac agtctcagaa gaccaaaggg caattgagac ttttcaacaa 420

agggtaatat ccggaaacct cctcggattc cattgcccag ctatctgtca ctttattgtg 480

aagatagtgg aaaaggaagg tggctcctac aaatgccatc attgcgataa aggaaaggcc 540

atcgttgaag atgcctctgc cgacagtggt cccaaagatg gacccccacc cacgaggagc 600

atcgtggaaa aagaagacgt tccaaccacg tcttcaaagc aagtggattg atgtgatatc 660

tccactgacg taagggatga cgcacaatcc cactatcctt cgcaagaccc ttcctctata 720

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<211> 567
<212> PRT
<213> Influenza virus

<400> 58

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Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
        35                  40                  45


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


Arg Gly Lys Leu Cys Pro Asp Cys Leu Asn Cys Thr Asp Leu Asp Val
65                  70                  75                  80


Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala Lys Ala
                85                  90                  95


Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe Pro Ile
            100                 105                 110


Met His Asp Arg Thr Lys Ile Arg Gln Leu Pro Asn Leu Leu Arg Gly
        115                 120                 125


Tyr Glu Asn Ile Arg Leu Ser Thr Gln Asn Val Ile Asp Ala Glu Lys
    130                 135                 140


Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys Pro Asn
145                 150                 155                 160


Ala Thr Ser Lys Ile Gly Phe Phe Ala Thr Met Ala Trp Ala Val Pro
                165                 170                 175


Lys Asp Asn Tyr Lys Asn Ala Thr Asn Pro Leu Thr Val Glu Val Pro
            180                 185                 190
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Tyr Ile Cys Thr Glu Gly Glu Asp Gln Ile Thr Val Trp Gly Phe His
        195                 200                 205

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

Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val Ser
225                 230                 235                 240

Gln Ile Gly Asp Phe Pro Asp Gln Thr Glu Asp Gly Gly Leu Pro Gln
                245                 250                 255

Ser Gly Arg Ile Val Val Asp Tyr Met Met Gln Lys Pro Gly Lys Thr
            260                 265                 270

Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val Trp
        275                 280                 285

Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu Ile
    290                 295                 300

Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys Ser
305                 310                 315                 320

Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys Pro
                325                 330                 335

Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg
            340                 345                 350

Pro Pro Gly Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His Gly Tyr
        355                 360                 365

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

Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser Leu Ser
385                 390                 395                 400
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Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met Asp Glu
                405                 410                 415

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

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

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

Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Asp Ile Gly Asn Gly
465                 470                 475                 480

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

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

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

His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu Ala Val
    530                 535                 540

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

Val Ser Cys Ser Ile Cys Leu
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tttgcaaatc tcaaaggaac agaaaccaga gggaaactat gcccaaaatg cctcaactgc 180

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gtttcaatac tccatgaagt cagacctgtt acatctgggt gctttcctat aatgcacgac 300

agaacaaaaa ttagacagct gcctaaactt ctcagaggat acgaacatat caggttatca 360

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