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<213> ORGANISM: Hepatitis C virus

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 <213> ORGANISM: Hepatitis C virus

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 <211> LENGTH: 7987
 <212> TYPE: DNA
 <213> ORGANISM: Hepatitis C virus

<400> SEQUENCE: 13

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<210> SEQ ID NO 14
<211> LENGTH: 400
<212> TYPE: PRT
<213> ORGANISM: Hepatitis C virus
    
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<400> SEQUENCE: 14

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Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro Arg Leu Pro
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Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg
  35          40          45
Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala Gln Ile Thr
  50          55          60
Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro Arg Thr Cys
  65          70          75          80
Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr Thr Thr Gly
  85          90          95
Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr Ser Arg Ala Leu Trp Arg
  100         105         110
Val Ala Ala Glu Glu Tyr Val Glu Val Thr Arg Val Gly Asp Phe His
  115         120         125
Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro Cys Gln Val
  130         135         140
Pro Ala Pro Glu Phe Phe Thr Glu Val Asp Gly Val Arg Leu His Arg
  145         150         155         160
Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Glu Glu Val Thr Phe Leu
  165         170         175
Val Gly Leu Asn Gln Tyr Leu Val Gly Ser Gln Leu Pro Cys Glu Pro
  180         185         190
Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp Pro Ser His
  195         200         205
Ile Thr Ala Glu Thr Ala Lys Arg Arg Leu Ala Arg Gly Ser Pro Pro
  210         215         220
Ser Leu Ala Ser Ser Ser Ala Ser Gln Leu Tyr Ser Phe Glu Pro Leu
  225         230         235         240
Gln Ala Glu Glu Asp Glu Arg Glu Val Ser Val Pro Ala Glu Ile Leu
  245         250         255
    
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Arg Arg Ser Arg Lys Phe Pro Arg Ala Met Pro Ile Trp Ala Arg Pro
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 Asp Tyr Asn Pro Pro Leu Leu Glu Ser Trp Lys Asp Pro Asp Tyr Val
 275 280 285
 Pro Pro Val Val His Gly Cys Pro Leu Pro Pro Ala Lys Ala Pro Pro
 290 295 300
 Ile Pro Pro Pro Arg Arg Lys Arg Thr Val Val Leu Ser Glu Ser Thr
 305 310 315
 Val Ser Ser Ala Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly Ser Ser
 325 330 335
 Glu Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala Ser Pro Asp Gln
 340 345 350
 Pro Ser Asp Asp Gly Asp Ala Gly Ser Asp Val Glu Ser Tyr Ser Ser
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<210> SEQ ID NO 15
 <211> LENGTH: 1985
 <212> TYPE: PRT
 <213> ORGANISM: Hepatitis C virus
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 Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys
 35 40 45
 Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr
 50 55 60
 Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp
 65 70 75 80
 Gln Asp Leu Val Gly Trp Arg Ala Pro Pro Gly Ala Arg Ser Leu Thr
 85 90 95
 Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
 100 105 110
 Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
 115 120 125
 Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
 130 135 140
 Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys
 145 150 155 160
 Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met
 165 170 175
 Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro
 180 185 190
 Ala Val Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly
 195 200 205
 Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr
 210 215 220
 Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly

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Val Arg Thr Ile Thr Thr 260	Gly Ala Pro Ile Thr Tyr Ser Thr Tyr Gly 265		
Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile 275		280	285
Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile 290		295	300
Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val 305		310	315
Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn 325		330	335
Ile Glu Glu Val Ala Leu Ser Ser Thr Gly Glu Ile Pro Phe Tyr Gly 340		345	350
Lys Ala Ile Pro Ile Glu Thr Ile Lys Gly Gly Arg His Leu Ile Phe 355		360	365
Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly 370		375	380
Leu Gly Leu Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val 385		390	395
Ile Pro Thr Ser Gly Asp Val Ile Val Val Ala Thr Asp Ala Leu Met 405		410	415
Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys 420		425	430
Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu 435		440	445
Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly 450		455	460
Arg Thr Gly Arg Gly Arg Met Gly Ile Tyr Arg Phe Val Thr Pro Gly 465		470	475
Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr 485		490	495
Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val 500		505	510
Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp 515		520	525
His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp 530		535	540
Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr 545		550	555
Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro 565		570	575
Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr 580		585	590
Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn 595		600	605
Glu Val Thr Thr Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met 610		615	620
Ser Ala Asp Leu Glu Val Val Thr Ser Thr Trp Val Leu Val Gly Gly 625		630	635
Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Thr Thr Gly Ser Val Val 645		650	655

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 660 665 670

Arg Glu Val Leu Tyr Arg Glu Phe Asp Glu Met Glu Glu Cys Ala Ser
 675 680 685

His Leu Pro Tyr Ile Glu Gln Gly Met Gln Leu Ala Glu Gln Phe Lys
 690 695 700

Gln Lys Ala Ile Gly Leu Leu Gln Thr Ala Thr Lys Gln Ala Glu Ala
 705 710 715 720

Ala Ala Pro Val Val Glu Ser Lys Trp Arg Thr Leu Glu Ala Phe Trp
 725 730 735

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

Leu Ser Thr Leu Pro Gly Asn Pro Ala Ile Ala Ser Leu Met Ala Phe
 755 760 765

Thr Ala Ser Ile Thr Ser Pro Leu Thr Thr Gln His Thr Leu Leu Phe
 770 775 780

Asn Ile Leu Gly Gly Trp Val Ala Ala Gln Leu Ala Pro Pro Ser Ala
 785 790 795 800

Ala Ser Ala Phe Val Gly Ala Gly Ile Ala Gly Ala Ala Val Gly Ser
 805 810 815

Ile Gly Leu Gly Lys Val Leu Val Asp Ile Leu Ala Gly Tyr Gly Ala
 820 825 830

Gly Val Ala Gly Ala Leu Val Ala Phe Lys Val Met Ser Gly Glu Met
 835 840 845

Pro Ser Thr Glu Asp Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro
 850 855 860

Gly Ala Leu Val Val Gly Val Val Cys Ala Ala Ile Leu Arg Arg His
 865 870 875 880

Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala
 885 890 895

Phe Ala Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val Pro Glu
 900 905 910

Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu Thr Ile
 915 920 925

Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu Asp Cys Ser
 930 935 940

Thr Pro Cys Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys
 945 950 955 960

Thr Val Leu Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro
 965 970 975

Arg Leu Pro Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly
 980 985 990

Val Trp Arg Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala
 995 1000 1005

Gln Ile Thr Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro
 1010 1015 1020

Arg Thr Cys Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr
 1025 1030 1035 1040

Thr Thr Gly Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr Ser Arg Ala
 1045 1050 1055

Leu Trp Arg Val Ala Ala Glu Glu Tyr Val Glu Val Thr Arg Val Gly
 1060 1065 1070

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Asp Phe His Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro
 1075 1080 1085
 Cys Gln Val Pro Ala Pro Glu Phe Phe Thr Glu Val Asp Gly Val Arg
 1090 1095 1100
 Leu His Arg Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Glu Glu Val
 1105 1110 1115 1120
 Thr Phe Leu Val Gly Leu Asn Gln Tyr Leu Val Gly Ser Gln Leu Pro
 1125 1130 1135
 Cys Glu Pro Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp
 1140 1145 1150
 Pro Ser His Ile Thr Ala Glu Thr Ala Lys Arg Arg Leu Ala Arg Gly
 1155 1160 1165
 Ser Pro Pro Ser Leu Ala Ser Ser Ser Ala Ile Gln Leu Ser Ala Pro
 1170 1175 1180
 Ser Leu Lys Ala Thr Cys Thr Thr Arg His Asp Ser Pro Asp Ala Asp
 1185 1190 1195 1200
 Leu Ile Glu Ala Asn Leu Leu Trp Arg Gln Glu Met Gly Gly Asn Ile
 1205 1210 1215
 Thr Arg Val Glu Ser Glu Asn Lys Val Val Ile Leu Asp Ser Phe Glu
 1220 1225 1230
 Pro Leu Gln Ala Glu Glu Asp Glu Arg Glu Val Ser Val Pro Ala Glu
 1235 1240 1245
 Ile Leu Arg Arg Ser Arg Lys Phe Pro Arg Ala Met Pro Ile Trp Ala
 1250 1255 1260
 Arg Pro Asp Tyr Asn Pro Pro Leu Leu Glu Ser Trp Lys Asp Pro Asp
 1265 1270 1275 1280
 Tyr Val Pro Pro Val Val His Gly Cys Pro Leu Pro Pro Ala Lys Ala
 1285 1290 1295
 Pro Pro Ile Pro Pro Pro Arg Arg Lys Arg Thr Val Val Leu Ser Glu
 1300 1305 1310
 Ser Thr Val Ser Ser Ala Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly
 1315 1320 1325
 Ser Ser Glu Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala Ser Pro
 1330 1335 1340
 Asp Gln Pro Ser Asp Asp Gly Asp Ala Gly Ser Asp Val Glu Ser Tyr
 1345 1350 1355 1360
 Ser Ser Met Pro Pro Leu Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser
 1365 1370 1375
 Asp Gly Ser Trp Ser Thr Val Ser Glu Glu Ala Ser Glu Asp Val Val
 1380 1385 1390
 Cys Cys Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys
 1395 1400 1405
 Ala Ala Glu Glu Thr Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu
 1410 1415 1420
 Leu Arg His His Asn Leu Val Tyr Ala Thr Thr Ser Arg Ser Ala Ser
 1425 1430 1435 1440
 Leu Arg Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp
 1445 1450 1455
 His Tyr Arg Asp Val Leu Lys Glu Met Lys Ala Lys Ala Ser Thr Val
 1460 1465 1470
 Lys Ala Lys Leu Leu Ser Val Glu Glu Ala Cys Lys Leu Thr Pro Pro
 1475 1480 1485
 His Ser Ala Arg Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn

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1490	1495	1500
Leu Ser Ser Lys Ala Val Asn His Ile Arg Ser Val Trp Lys Asp Leu 1505 1510 1515 1520		
Leu Glu Asp Thr Glu Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn 1525 1530 1535		
Glu Val Phe Cys Val Gln Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg 1540 1545 1550		
Leu Ile Val Phe Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala 1555 1560 1565		
Leu Tyr Asp Val Val Ser Thr Leu Pro Gln Ala Val Met Gly Ser Ser 1570 1575 1580		
Tyr Gly Phe Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn 1585 1590 1595 1600		
Ala Trp Lys Ala Lys Lys Cys Pro Met Gly Phe Ala Tyr Asp Thr Arg 1605 1610 1615		
Cys Phe Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser 1620 1625 1630		
Ile Tyr Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Arg 1635 1640 1645		
Ser Leu Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys 1650 1655 1660		
Gly Gln Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr 1665 1670 1675 1680		
Thr Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ala Ala Ala 1685 1690 1695		
Cys Arg Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp 1700 1705 1710		
Asp Leu Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Glu Ala 1715 1720 1725		
Ser Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro 1730 1735 1740		
Gly Asp Pro Pro Lys Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys 1745 1750 1755 1760		
Ser Ser Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr 1765 1770 1775		
Tyr Leu Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu 1780 1785 1790		
Thr Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met 1795 1800 1805		
Tyr Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe 1810 1815 1820		
Ser Ile Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln 1825 1830 1835 1840		
Ile Tyr Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile 1845 1850 1855		
Ile Gln Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser 1860 1865 1870		
Pro Gly Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val 1875 1880 1885		
Pro Pro Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg 1890 1895 1900		
Leu Leu Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe 1905 1910 1915 1920		

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Asn Trp Ala Val Arg Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala
 1925 1930 1935

Ser Gln Leu Asp Leu Ser Ser Trp Phe Val Ala Gly Tyr Ser Gly Gly
 1940 1945 1950

Asp Ile Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Trp Phe Met Trp
 1955 1960 1965

Cys Leu Leu Leu Ser Val Gly Val Gly Ile Tyr Leu Leu Pro Asn
 1970 1975 1980

Arg
 1985

<210> SEQ ID NO 16
 <211> LENGTH: 447
 <212> TYPE: PRT
 <213> ORGANISM: Hepatitis C virus

<400> SEQUENCE: 16

Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys Thr Val Leu
 1 5 10 15

Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro Arg Leu Pro
 20 25 30

Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg
 35 40 45

Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala Gln Ile Thr
 50 55 60

Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro Arg Thr Cys
 65 70 75 80

Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr Thr Thr Gly
 85 90 95

Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr Ser Arg Ala Leu Trp Arg
 100 105 110

Val Ala Ala Glu Glu Tyr Val Glu Val Thr Arg Val Gly Asp Phe His
 115 120 125

Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro Cys Gln Val
 130 135 140

Pro Ala Pro Glu Phe Phe Thr Glu Val Asp Gly Val Arg Leu His Arg
 145 150 155 160

Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Glu Glu Val Thr Phe Leu
 165 170 175

Val Gly Leu Asn Gln Tyr Leu Val Gly Ser Gln Leu Pro Cys Glu Pro
 180 185 190

Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp Pro Ser His
 195 200 205

Ile Thr Ala Glu Thr Ala Lys Arg Arg Leu Ala Arg Gly Ser Pro Pro
 210 215 220

Ser Leu Ala Ser Ser Ser Ala Ile Gln Leu Ser Ala Pro Ser Leu Lys
 225 230 235 240

Ala Thr Cys Thr Thr Arg His Asp Ser Pro Asp Ala Asp Leu Ile Glu
 245 250 255

Ala Asn Leu Leu Trp Arg Gln Glu Met Gly Gly Asn Ile Thr Arg Val
 260 265 270

Glu Ser Glu Asn Lys Val Val Ile Leu Asp Ser Phe Glu Pro Leu Gln
 275 280 285

Ala Glu Glu Asp Glu Arg Glu Val Ser Val Pro Ala Glu Ile Leu Arg

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290	295	300
Arg Ser Arg Lys Phe Pro Arg Ala Met Pro Ile Trp Ala Arg Pro Asp 305 310 315 320		
Tyr Asn Pro Pro Leu Leu Glu Ser Trp Lys Asp Pro Asp Tyr Val Pro 325 330 335		
Pro Val Val His Gly Cys Pro Leu Pro Pro Ala Lys Ala Pro Pro Ile 340 345 350		
Pro Pro Pro Arg Arg Lys Arg Thr Val Val Leu Ser Glu Ser Thr Val 355 360 365		
Ser Ser Ala Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly Ser Ser Glu 370 375 380		
Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala Ser Pro Asp Gln Pro 385 390 395 400		
Ser Asp Asp Gly Asp Ala Gly Ser Asp Val Glu Ser Tyr Ser Ser Met 405 410 415		
Pro Pro Leu Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly Ser 420 425 430		
Trp Ser Thr Val Ser Glu Glu Ala Ser Glu Asp Val Val Cys Cys 435 440 445		

<210> SEQ ID NO 17
 <211> LENGTH: 1985
 <212> TYPE: PRT
 <213> ORGANISM: Hepatitis C virus

<400> SEQUENCE: 17

Met Ala Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly 1 5 10 15
Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Arg Asn Gln Val Glu Gly 20 25 30
Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys 35 40 45
Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr 50 55 60
Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp 65 70 75 80
Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr 85 90 95
Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala 100 105 110
Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu 115 120 125
Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu 130 135 140
Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys 145 150 155 160
Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met 165 170 175
Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro 180 185 190
Ala Val Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly 195 200 205
Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr 210 215 220

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Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly
 225 230 235 240

Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly
 245 250 255

Val Arg Thr Ile Thr Thr Gly Ala Pro Ile Thr Tyr Ser Thr Tyr Gly
 260 265 270

Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile
 275 280 285

Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile
 290 295 300

Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val
 305 310 315 320

Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn
 325 330 335

Ile Glu Glu Val Ala Leu Ser Ser Thr Gly Glu Ile Pro Phe Tyr Gly
 340 345 350

Lys Ala Ile Pro Ile Glu Thr Ile Lys Gly Gly Arg His Leu Ile Phe
 355 360 365

Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly
 370 375 380

Leu Gly Leu Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val
 385 390 395 400

Ile Pro Thr Ser Gly Asp Val Ile Val Val Ala Thr Asp Ala Leu Met
 405 410 415

Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys
 420 425 430

Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu
 435 440 445

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

Arg Thr Gly Arg Gly Arg Met Gly Ile Tyr Arg Phe Val Thr Pro Gly
 465 470 475 480

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

Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val
 500 505 510

Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp
 515 520 525

His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp
 530 535 540

Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr
 545 550 555 560

Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro
 565 570 575

Pro Ser Trp Asp Gln Met Trp Glu Cys Leu Ile Arg Leu Lys Pro Thr
 580 585 590

Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn
 595 600 605

Glu Val Thr Thr Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met
 610 615 620

Ser Ala Asp Leu Glu Val Val Thr Ser Thr Trp Val Leu Val Gly Gly
 625 630 635 640

Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Thr Thr Gly Ser Val Val

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645				650				655							
Ile	Val	Gly	Arg	Ile	Ile	Leu	Ser	Gly	Lys	Pro	Ala	Ile	Ile	Pro	Asp
			660					665				670			
Arg	Glu	Val	Leu	Tyr	Arg	Glu	Phe	Asp	Glu	Met	Glu	Glu	Cys	Ala	Ser
		675					680					685			
His	Leu	Pro	Tyr	Ile	Glu	Gln	Gly	Met	Gln	Leu	Ala	Glu	Gln	Phe	Lys
	690					695					700				
Gln	Lys	Ala	Ile	Gly	Leu	Leu	Gln	Thr	Ala	Thr	Lys	Gln	Ala	Glu	Ala
	705				710					715				720	
Ala	Ala	Pro	Val	Val	Glu	Ser	Lys	Trp	Arg	Thr	Leu	Glu	Ala	Phe	Trp
			725						730					735	
Ala	Lys	His	Met	Trp	Asn	Phe	Ile	Ser	Gly	Ile	Gln	Tyr	Leu	Ala	Gly
			740						745				750		
Leu	Ser	Thr	Leu	Pro	Gly	Asn	Pro	Ala	Ile	Ala	Ser	Leu	Met	Ala	Phe
		755				760						765			
Thr	Ala	Ser	Ile	Thr	Ser	Pro	Leu	Thr	Thr	Gln	His	Thr	Leu	Leu	Phe
		770				775					780				
Asn	Ile	Leu	Gly	Gly	Trp	Val	Ala	Ala	Gln	Leu	Ala	Pro	Pro	Ser	Ala
	785				790					795					800
Ala	Ser	Ala	Phe	Val	Gly	Ala	Gly	Ile	Ala	Gly	Ala	Ala	Val	Gly	Ser
			805						810					815	
Ile	Gly	Leu	Gly	Lys	Val	Leu	Val	Asp	Ile	Leu	Ala	Gly	Tyr	Gly	Ala
		820						825				830			
Gly	Val	Ala	Gly	Ala	Leu	Val	Ala	Phe	Lys	Val	Met	Ser	Gly	Glu	Met
		835				840						845			
Pro	Ser	Thr	Glu	Asp	Leu	Val	Asn	Leu	Leu	Pro	Ala	Ile	Leu	Ser	Pro
		850				855					860				
Gly	Ala	Leu	Val	Val	Gly	Val	Val	Cys	Ala	Ala	Ile	Leu	Arg	Arg	His
	865				870					875					880
Val	Gly	Pro	Gly	Glu	Gly	Ala	Val	Gln	Trp	Met	Asn	Arg	Leu	Ile	Ala
			885						890					895	
Phe	Ala	Ser	Arg	Gly	Asn	His	Val	Ser	Pro	Thr	His	Tyr	Val	Pro	Glu
			900						905				910		
Ser	Asp	Ala	Ala	Ala	Arg	Val	Thr	Gln	Ile	Leu	Ser	Gly	Leu	Thr	Ile
		915					920					925			
Thr	Gln	Leu	Leu	Lys	Arg	Leu	His	Gln	Trp	Ile	Asn	Glu	Asp	Cys	Ser
		930				935					940				
Thr	Pro	Cys	Ser	Gly	Ser	Trp	Leu	Arg	Asp	Val	Trp	Asp	Trp	Ile	Cys
		945			950					955				960	
Thr	Val	Leu	Thr	Asp	Phe	Lys	Thr	Trp	Leu	Gln	Ser	Lys	Leu	Leu	Pro
			965						970					975	
Arg	Leu	Pro	Gly	Val	Pro	Phe	Phe	Ser	Cys	Gln	Arg	Gly	Tyr	Lys	Gly
			980						985				990		
Val	Trp	Arg	Gly	Asp	Gly	Ile	Met	Gln	Thr	Thr	Cys	Pro	Cys	Gly	Ala
		995					1000					1005			
Gln	Ile	Thr	Gly	His	Val	Lys	Asn	Gly	Ser	Met	Arg	Ile	Val	Gly	Pro
	1010					1015					1020				
Arg	Thr	Cys	Ser	Asn	Thr	Trp	His	Gly	Thr	Phe	Pro	Ile	Asn	Ala	Tyr
	1025				1030					1035				1040	
Thr	Thr	Gly	Pro	Cys	Thr	Pro	Ser	Pro	Ala	Pro	Asn	Tyr	Ser	Arg	Ala
			1045						1050					1055	
Leu	Trp	Arg	Val	Ala	Ala	Glu	Glu	Tyr	Val	Glu	Val	Thr	Arg	Val	Gly
			1060						1065					1070	

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Asp Phe His Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro
 1075 1080 1085
 Cys Gln Val Pro Ala Pro Glu Phe Phe Thr Glu Val Asp Gly Val Arg
 1090 1095 1100
 Leu His Arg Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Glu Glu Val
 1105 1110 1115 1120
 Thr Phe Leu Val Gly Leu Asn Gln Tyr Leu Val Gly Ser Gln Leu Pro
 1125 1130 1135
 Cys Glu Pro Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp
 1140 1145 1150
 Pro Ser His Ile Thr Ala Glu Thr Ala Lys Arg Gly Leu Ala Arg Gly
 1155 1160 1165
 Ser Pro Pro Ser Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro
 1170 1175 1180
 Ser Leu Lys Ala Thr Cys Thr Thr Arg His Asp Ser Pro Asp Ala Asp
 1185 1190 1195 1200
 Leu Ile Glu Ala Asn Leu Leu Trp Arg Gln Glu Met Gly Gly Asn Ile
 1205 1210 1215
 Thr Arg Val Glu Ser Glu Asn Lys Val Val Ile Leu Asp Ser Phe Glu
 1220 1225 1230
 Pro Leu Gln Ala Glu Glu Asp Glu Arg Glu Val Ser Val Pro Ala Glu
 1235 1240 1245
 Ile Leu Arg Arg Ser Arg Lys Phe Pro Arg Ala Met Pro Ile Trp Ala
 1250 1255 1260
 Arg Pro Asp Tyr Asn Pro Pro Leu Leu Glu Ser Trp Lys Asp Pro Asp
 1265 1270 1275 1280
 Tyr Val Pro Pro Val Val His Gly Cys Pro Leu Pro Pro Ala Lys Ala
 1285 1290 1295
 Pro Pro Ile Pro Pro Pro Arg Arg Lys Arg Thr Val Val Leu Ser Glu
 1300 1305 1310
 Ser Thr Val Ser Ser Ala Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly
 1315 1320 1325
 Ser Ser Glu Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala Ser Pro
 1330 1335 1340
 Asp Gln Pro Ser Asp Asp Gly Asp Ala Gly Ser Asp Val Glu Ser Tyr
 1345 1350 1355 1360
 Ser Ser Met Pro Pro Leu Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser
 1365 1370 1375
 Asp Gly Ser Trp Ser Thr Val Ser Glu Glu Ala Ser Glu Asp Val Val
 1380 1385 1390
 Cys Cys Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys
 1395 1400 1405
 Ala Ala Glu Glu Thr Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu
 1410 1415 1420
 Leu Arg His His Asn Leu Val Tyr Ala Thr Thr Ser Arg Ser Ala Ser
 1425 1430 1435 1440
 Leu Arg Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp
 1445 1450 1455
 His Tyr Arg Asp Val Leu Lys Glu Met Lys Ala Lys Ala Ser Thr Val
 1460 1465 1470
 Lys Ala Lys Leu Leu Ser Val Glu Glu Ala Cys Lys Leu Thr Pro Pro
 1475 1480 1485

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His Ser Ala Arg Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn
 1490 1495 1500

Leu Ser Ser Lys Ala Val Asn His Ile Arg Ser Val Trp Lys Asp Leu
 1505 1510 1515 1520

Leu Glu Asp Thr Glu Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn
 1525 1530 1535

Glu Val Phe Cys Val Gln Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg
 1540 1545 1550

Leu Ile Val Phe Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala
 1555 1560 1565

Leu Tyr Asp Val Val Ser Thr Leu Pro Gln Ala Val Met Gly Ser Ser
 1570 1575 1580

Tyr Gly Phe Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn
 1585 1590 1595 1600

Ala Trp Lys Ala Lys Lys Cys Pro Met Gly Phe Ala Tyr Asp Thr Arg
 1605 1610 1615

Cys Phe Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser
 1620 1625 1630

Ile Tyr Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Arg
 1635 1640 1645

Ser Leu Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys
 1650 1655 1660

Gly Gln Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr
 1665 1670 1675 1680

Thr Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ala Ala Ala
 1685 1690 1695

Cys Arg Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp
 1700 1705 1710

Asp Leu Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Glu Ala
 1715 1720 1725

Ser Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro
 1730 1735 1740

Gly Asp Pro Pro Lys Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys
 1745 1750 1755 1760

Ser Ser Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr
 1765 1770 1775

Tyr Leu Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu
 1780 1785 1790

Thr Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met
 1795 1800 1805

Tyr Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe
 1810 1815 1820

Ser Ile Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln
 1825 1830 1835 1840

Ile Tyr Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile
 1845 1850 1855

Ile Gln Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser
 1860 1865 1870

Pro Gly Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val
 1875 1880 1885

Pro Pro Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg
 1890 1895 1900

Leu Leu Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe

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1905		1910		1915		1920
Asn Trp Ala Val Arg Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala						
		1925		1930		1935
Ser Gln Leu Asp Leu Ser Ser Trp Phe Val Ala Gly Tyr Ser Gly Gly		1940		1945		1950
Asp Ile Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Trp Phe Met Trp		1955		1960		1965
Cys Leu Leu Leu Leu Ser Val Gly Val Gly Ile Tyr Leu Leu Pro Asn		1970		1975		1980
Arg						
1985						
<210> SEQ ID NO 18						
<211> LENGTH: 447						
<212> TYPE: PRT						
<213> ORGANISM: Hepatitis C virus						
<400> SEQUENCE: 18						
Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys Thr Val Leu						
1		5		10		15
Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro Arg Leu Pro		20		25		30
Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg		35		40		45
Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala Gln Ile Thr		50		55		60
Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro Arg Thr Cys		65		70		75
75						80
Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr Thr Thr Gly		85		90		95
Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr Ser Arg Ala Leu Trp Arg		100		105		110
Val Ala Ala Glu Glu Tyr Val Glu Val Thr Arg Val Gly Asp Phe His		115		120		125
Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro Cys Gln Val		130		135		140
Pro Ala Pro Glu Phe Phe Thr Glu Val Asp Gly Val Arg Leu His Arg		145		150		155
155						160
Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Glu Glu Val Thr Phe Leu		165		170		175
Val Gly Leu Asn Gln Tyr Leu Val Gly Ser Gln Leu Pro Cys Glu Pro		180		185		190
Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp Pro Ser His		195		200		205
Ile Thr Ala Glu Thr Ala Lys Arg Gly Leu Ala Arg Gly Ser Pro Pro		210		215		220
220						225
Ser Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Lys		230		235		240
240						245
Ala Thr Cys Thr Thr Arg His Asp Ser Pro Asp Ala Asp Leu Ile Glu		245		250		255
Ala Asn Leu Leu Trp Arg Gln Glu Met Gly Gly Asn Ile Thr Arg Val		260		265		270
270						275
Glu Ser Glu Asn Lys Val Val Ile Leu Asp Ser Phe Glu Pro Leu Gln		275		280		285
285						

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Ala Glu Glu Asp Glu Arg Glu Val Ser Val Pro Ala Glu Ile Leu Arg
 290 295 300

Arg Ser Arg Lys Phe Pro Arg Ala Met Pro Ile Trp Ala Arg Pro Asp
 305 310 315 320

Tyr Asn Pro Pro Leu Leu Glu Ser Trp Lys Asp Pro Asp Tyr Val Pro
 325 330 335

Pro Val Val His Gly Cys Pro Leu Pro Pro Ala Lys Ala Pro Pro Ile
 340 345 350

Pro Pro Pro Arg Arg Lys Arg Thr Val Val Leu Ser Glu Ser Thr Val
 355 360 365

Ser Ser Ala Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly Ser Ser Glu
 370 375 380

Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala Ser Pro Asp Gln Pro
 385 390 395 400

Ser Asp Asp Gly Asp Ala Gly Ser Asp Val Glu Ser Tyr Ser Ser Met
 405 410 415

Pro Pro Leu Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly Ser
 420 425 430

Trp Ser Thr Val Ser Glu Glu Ala Ser Glu Asp Val Val Cys Cys
 435 440 445

<210> SEQ ID NO 19
 <211> LENGTH: 447
 <212> TYPE: PRT
 <213> ORGANISM: Hepatitis C virus
 <400> SEQUENCE: 19

Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys Thr Val Leu
 1 5 10 15

Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro Arg Leu Pro
 20 25 30

Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg
 35 40 45

Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala Gln Ile Thr
 50 55 60

Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro Arg Thr Cys
 65 70 75 80

Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr Thr Thr Gly
 85 90 95

Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr Ser Arg Ala Leu Trp Arg
 100 105 110

Val Ala Ala Glu Glu Tyr Val Glu Val Thr Arg Val Gly Asp Phe His
 115 120 125

Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro Cys Gln Val
 130 135 140

Pro Ala Pro Glu Phe Phe Thr Glu Val Asp Gly Val Arg Leu His Arg
 145 150 155 160

Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Glu Glu Val Thr Phe Leu
 165 170 175

Val Gly Leu Asn Gln Tyr Leu Val Gly Ser Gln Leu Pro Cys Glu Pro
 180 185 190

Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp Pro Ser His
 195 200 205

Ile Thr Ala Glu Thr Ala Lys Arg Arg Leu Ala Arg Gly Ser Pro Pro
 210 215 220

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Ser Leu Ser Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Lys
 225 230 235 240

Ala Thr Cys Thr Thr Arg His Asp Ser Pro Asp Ala Asp Leu Ile Glu
 245 250 255

Ala Asn Leu Leu Trp Arg Gln Glu Met Gly Gly Asn Ile Thr Arg Val
 260 265 270

Glu Ser Glu Asn Lys Val Val Ile Leu Asp Ser Phe Glu Pro Leu Gln
 275 280 285

Ala Glu Glu Asp Glu Arg Glu Val Ser Val Pro Ala Glu Ile Leu Arg
 290 295 300

Arg Ser Arg Lys Phe Pro Arg Ala Met Pro Ile Trp Ala Arg Pro Asp
 305 310 315 320

Tyr Asn Pro Pro Leu Leu Glu Ser Trp Lys Asp Pro Asp Tyr Val Pro
 325 330 335

Pro Val Val His Gly Cys Pro Leu Pro Pro Ala Lys Ala Pro Pro Ile
 340 345 350

Pro Pro Pro Arg Arg Lys Arg Thr Val Val Leu Ser Glu Ser Thr Val
 355 360 365

Ser Ser Ala Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly Ser Ser Glu
 370 375 380

Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala Ser Pro Asp Gln Pro
 385 390 395 400

Ser Asp Asp Gly Asp Ala Gly Ser Asp Val Glu Ser Tyr Ser Ser Met
 405 410 415

Pro Pro Leu Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly Ser
 420 425 430

Trp Ser Thr Val Ser Glu Glu Ala Ser Glu Asp Val Val Cys Cys
 435 440 445

<210> SEQ ID NO 20
 <211> LENGTH: 447
 <212> TYPE: PRT
 <213> ORGANISM: Hepatitis C virus

<400> SEQUENCE: 20

Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys Thr Val Leu
 1 5 10 15

Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro Arg Leu Pro
 20 25 30

Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg
 35 40 45

Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala Gln Ile Thr
 50 55 60

Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro Arg Thr Cys
 65 70 75 80

Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr Thr Thr Gly
 85 90 95

Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr Ser Arg Ala Leu Trp Arg
 100 105 110

Val Ala Ala Glu Glu Tyr Val Glu Val Thr Arg Val Gly Asp Phe His
 115 120 125

Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro Cys Gln Val
 130 135 140

Pro Ala Pro Glu Phe Phe Thr Glu Val Asp Gly Val Arg Leu His Arg

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145	150	155	160
Tyr Ala Pro Ala Cys Lys Pro Leu Leu Arg Glu Glu Val Thr Phe Leu	165	170	175
Val Gly Leu Asn Gln Tyr Leu Val Gly Ser Gln Leu Pro Cys Glu Pro	180	185	190
Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp Pro Ser His	195	200	205
Ile Thr Ala Glu Thr Ala Lys Arg Arg Leu Ala Arg Gly Ser Pro Pro	210	215	220
Cys Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Lys	225	230	235
Ala Thr Cys Thr Thr Arg His Asp Ser Pro Asp Ala Asp Leu Ile Glu	245	250	255
Ala Asn Leu Leu Trp Arg Gln Glu Met Gly Gly Asn Ile Thr Arg Val	260	265	270
Glu Ser Glu Asn Lys Val Val Ile Leu Asp Ser Phe Glu Pro Leu Gln	275	280	285
Ala Glu Glu Asp Glu Arg Glu Val Ser Val Pro Ala Glu Ile Leu Arg	290	295	300
Arg Ser Arg Lys Phe Pro Arg Ala Met Pro Ile Trp Ala Arg Pro Asp	305	310	315
Tyr Asn Pro Pro Leu Leu Glu Ser Trp Lys Asp Pro Asp Tyr Val Pro	325	330	335
Pro Val Val His Gly Cys Pro Leu Pro Pro Ala Lys Ala Pro Pro Ile	340	345	350
Pro Pro Pro Arg Arg Lys Arg Thr Val Val Leu Ser Glu Ser Thr Val	355	360	365
Ser Ser Ala Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly Ser Ser Glu	370	375	380
Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala Ser Pro Asp Gln Pro	385	390	395
Ser Asp Asp Gly Asp Ala Gly Ser Asp Val Glu Ser Tyr Ser Ser Met	405	410	415
Pro Pro Leu Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly Ser	420	425	430
Trp Ser Thr Val Ser Glu Glu Ala Ser Glu Asp Val Val Cys Cys	435	440	445

<210> SEQ ID NO 21
 <211> LENGTH: 447
 <212> TYPE: PRT
 <213> ORGANISM: Hepatitis C virus

<400> SEQUENCE: 21

Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys Thr Val Leu	1	5	10	15
Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro Arg Leu Pro	20	25	30	
Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg	35	40	45	
Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala Gln Ile Thr	50	55	60	
Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro Arg Thr Cys	65	70	75	80

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Ser	Asn	Thr	Trp	His	Gly	Thr	Phe	Pro	Ile	Asn	Ala	Tyr	Thr	Thr	Gly	85	90	95	
Pro	Cys	Thr	Pro	Ser	Pro	Ala	Pro	Asn	Tyr	Ser	Arg	Ala	Leu	Trp	Arg	100	105	110	
Val	Ala	Ala	Glu	Glu	Tyr	Val	Glu	Val	Thr	Arg	Val	Gly	Asp	Phe	His	115	120	125	
Tyr	Val	Thr	Gly	Met	Thr	Thr	Asp	Asn	Val	Lys	Cys	Pro	Cys	Gln	Val	130	135	140	
Pro	Ala	Pro	Glu	Phe	Phe	Thr	Glu	Val	Asp	Gly	Val	Arg	Leu	His	Arg	145	150	155	160
Tyr	Ala	Pro	Ala	Cys	Lys	Pro	Leu	Leu	Arg	Glu	Glu	Val	Thr	Phe	Leu	165	170	175	
Val	Gly	Leu	Asn	Gln	Tyr	Leu	Val	Gly	Ser	Gln	Leu	Pro	Cys	Glu	Pro	180	185	190	
Glu	Pro	Asp	Val	Ala	Val	Leu	Thr	Ser	Met	Leu	Thr	Asp	Pro	Ser	His	195	200	205	
Ile	Thr	Ala	Glu	Thr	Ala	Lys	Arg	Arg	Leu	Ala	Arg	Gly	Ser	Pro	Pro	210	215	220	
Pro	Leu	Ala	Ser	Ser	Ser	Ala	Ser	Gln	Leu	Ser	Ala	Pro	Ser	Leu	Lys	225	230	235	240
Ala	Thr	Cys	Thr	Thr	Arg	His	Asp	Ser	Pro	Asp	Ala	Asp	Leu	Ile	Glu	245	250	255	
Ala	Asn	Leu	Leu	Trp	Arg	Gln	Glu	Met	Gly	Gly	Asn	Ile	Thr	Arg	Val	260	265	270	
Glu	Ser	Glu	Asn	Lys	Val	Val	Ile	Leu	Asp	Ser	Phe	Glu	Pro	Leu	Gln	275	280	285	
Ala	Glu	Glu	Asp	Glu	Arg	Glu	Val	Ser	Val	Pro	Ala	Glu	Ile	Leu	Arg	290	295	300	
Arg	Ser	Arg	Lys	Phe	Pro	Arg	Ala	Met	Pro	Ile	Trp	Ala	Arg	Pro	Asp	305	310	315	320
Tyr	Asn	Pro	Pro	Leu	Leu	Glu	Ser	Trp	Lys	Asp	Pro	Asp	Tyr	Val	Pro	325	330	335	
Pro	Val	Val	His	Gly	Cys	Pro	Leu	Pro	Pro	Ala	Lys	Ala	Pro	Pro	Ile	340	345	350	
Pro	Pro	Pro	Arg	Arg	Lys	Arg	Thr	Val	Val	Leu	Ser	Glu	Ser	Thr	Val	355	360	365	
Ser	Ser	Ala	Leu	Ala	Glu	Leu	Ala	Thr	Lys	Thr	Phe	Gly	Ser	Ser	Glu	370	375	380	
Ser	Ser	Ala	Val	Asp	Ser	Gly	Thr	Ala	Thr	Ala	Ser	Pro	Asp	Gln	Pro	385	390	395	400
Ser	Asp	Asp	Gly	Asp	Ala	Gly	Ser	Asp	Val	Glu	Ser	Tyr	Ser	Ser	Met	405	410	415	
Pro	Pro	Leu	Glu	Gly	Glu	Pro	Gly	Asp	Pro	Asp	Leu	Ser	Asp	Gly	Ser	420	425	430	
Trp	Ser	Thr	Val	Ser	Glu	Glu	Ala	Ser	Glu	Asp	Val	Val	Cys	Cys	435	440	445		

What is claimed is:

1. A polynucleotide comprising a non-naturally occurring HCV subtype 1b sequence that is capable of productive replication in a host cell, or is capable of being transcribed into a non-naturally occurring HCV sequence that is capable of productive replication in a host cell, wherein the HCV sequence comprises, from 5' to 3' on the positive-sense

⁶⁰ nucleic acid, a functional 5' non-translated region (5' NTR); one or more protein coding regions, including at least one polyprotein coding region that is capable of replicating HCV RNA; and a functional HCV 3' non-translated region (3' ⁶⁵ NTR), wherein said polynucleotide further comprises an adaptive mutation in the NS5A coding region such that the adaptive mutation results in a change in the NS5A amino

acid sequence selected from the group consisting of Ser (1179) to Ile, Arg (1164) to Gly, Ala(1174) to Ser, Ser(1172) to Cys, and Ser(1172) to Pro of SEQ ID NO:3 that confers improved cell culture characteristics to said polynucleotide.

2. The polynucleotide of claim 1, having a transfection efficiency into mammalian cells of greater than 0.01%.

3. The polynucleotide of claim 2, wherein the transfection efficiency into mammalian cells is greater than 0.1%.

4. The polynucleotide of claim 2, wherein the transfection efficiency into mammalian cells is greater than 1%.

5. The polynucleotide of claim 2, wherein the transfection efficiency into mammalian cells is greater than 5%.

6. The polynucleotide of claim 1, wherein the HCV is impaired in its ability to cause disease, establish chronic infections, trigger autoimmune responses, and transform cells.

7. The polynucleotide of claim 1, wherein the transfection efficiency into mammalian cells is about 6%.

8. The polynucleotide of claim 1, wherein the polynucleotide is double-stranded DNA.

9. A vector comprising the polynucleotide of claim 8 operably associated with a promoter.

10. An isolated host cell or a non-human transgenic organism comprising the vector of claim 9.

11. An isolated host cell or an isolated host cell engrafted in a host organism comprising the polynucleotide of claim 1, wherein the isolated host cell is a mammalian cell.

12. The isolated host cell of claim 11 wherein the isolated host cell is a human cell.

13. The isolated host cell of claim 12 wherein the isolated host cell is a liver cell.

14. The polynucleotide of claim 1, further comprising a mutation in the NS3 or NS4B coding region.

15. The polynucleotide of claim 1, further comprising a mutation in the coding region of NS3 that results in a change in the NS3 amino acid sequence selected from the group consisting of Gin (87) to Arg and Lys (584) to Glu of SEQ ID NO:3.

16. The polynucleotide of claim 1, further comprising a mutation in the coding region of NS4B that results in a Ser(925) to Gly change in the NS4B amino acid sequence of SEQ ID NO:3.

17. The polynucleotide of claim 1, further comprising both a mutation in the coding region of NS3 that results in a Lys (584) to Glu change in the NS3 amino acid sequence of SEQ ID NO:3 and a mutation in the coding region of NS4B that results in a Ser(925) to Gly change in the NS4B amino acid sequence of SEQ ID NO:3.

18. A polynucleotide comprising a non-naturally occurring HCV subtype 1 b sequence that is capable of productive replication in a host cell, or is capable of being transcribed into a non-naturally occurring HCV sequence that is capable of productive replication in a host cell, wherein the HCV sequence comprises, from 5' to 3' on the positive-sense nucleic acid, a functional 5' non-translated region (5' NTR); one or more protein coding regions, including at least one

polyprotein coding region that is capable of replicating HCV RNA; and a functional HCV 3' non-translated region (3' NTR), wherein said polynucleotide further comprises an adaptive mutation in the NS5A coding region comprising a deletion of the ISDR encoding region corresponding to nucleotides 5345 to 5485 of SEQ ID NO: 6 that confers improved cell culture characteristics to said polynucleotide.

19. The polynucleotide of claim 18, wherein the polynucleotide is capable of replication in a HeLa cell.

20. The polynucleotide of claim 18, wherein the HCV is impaired in its ability to cause disease, establish chronic infections, trigger autoimmune responses, and transform cells.

21. The polynucleotide of claim 18, having a transfection efficiency into mammalian cells of greater than 0.01%.

22. The polynucleotide of claim 18, wherein the transfection efficiency into mammalian cells is greater than 0.1%.

23. The polynucleotide of claim 18, wherein the transfection efficiency into mammalian cells is greater than 1%.

24. The polynucleotide of claim 18, wherein the transfection efficiency into mammalian cells is greater than 5%.

25. The polynucleotide of claim 18, wherein the transfection efficiency into mammalian cells is about 6%.

26. The polynucleotide of claim 18, wherein the polynucleotide is double-stranded DNA.

27. A vector comprising the polynucleotide of claim 26 operably associated with a promoter.

28. An isolated host cell or a non-human transgenic organism comprising the vector of claim 27.

29. An isolated host cell or an isolated host cell engrafted in a host organism comprising the polynucleotide of claim 18, wherein the isolated host cell is a mammalian cell.

30. The isolated host cell of claim 29 wherein the isolated host cell is a human cell.

31. The isolated host cell of claim 30 wherein the isolated host cell is a liver cell.

32. The polynucleotide of claim 18, further comprising a mutation in the NS3 or NS4B coding region.

33. The polynucleotide of claim 18, further comprising a mutation in the coding region of NS3 that results in a change in the NS3 amino acid sequence selected from the group consisting of Gin (87) to Arg and Lys (584) to Glu of SEQ ID NO:3.

34. The polynucleotide of claim 18, further comprising a mutation the coding region of NS4B that results in a Ser(925) to Gly change in the NS4B amino acid sequence of SEQ ID NO:3.

35. The polynucleotide of claim 18, further comprising both a mutation in the coding region of NS3 that results in a Lys (584) to Glu change in the NS3 amino acid sequence of SEQ ID NO:3 and a mutation in the coding region of NS4B that results in a Ser(926) to Gly change in the NS4B amino acid sequence of SEQ ID NO:3.

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