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<110> Spicona Inc.

<120> COMBINATION VACCINE

<130> P67254WO

<150> GB 2010425.3
<151> 2020-07-07

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<170> PatentIn version 3.5

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


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

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Gly Pro Val Ser Ile Ser Ala Val Ala Val Leu Ala Pro His Ser Ala
225                 230                 235                 240

Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val Asn
                245                 250                 255

Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe Thr
            260                 265                 270

Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu His
        275                 280                 285

Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp Phe
    290                 295                 300

His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp Asn
305                 310                 315                 320

Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu Lys
                325                 330                 335

Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser Lys
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Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile Lys
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Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr Tyr
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Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe Val
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Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr Pro
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Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser Gly
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Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro Arg
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Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala Val
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Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys Ser
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Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys Pro
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Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn Gly
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Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val Asn
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Asp Ala  Gly Phe Ile Lys Gln  Tyr Gly Asp Cys Leu  Gly Asp Ile
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Ala Ala  Arg Asp Leu Ile Cys  Ala Gln Lys Phe Asn  Gly Leu Thr
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Val Leu  Pro Pro Leu Leu Thr  Asp Glu Met Ile Ala  Gln Tyr Thr
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Ser Ala  Leu Leu Ala Gly Thr  Ile Thr Ser Gly Trp  Thr Phe Gly
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Arg Phe  Asn Gly Ile Gly Val  Thr Gln Asn Val Leu  Tyr Glu Asn
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Gln Asp  Ser Leu Ser Ser Thr  Ala Ser Ala Leu Gly  Lys Leu Gln
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Gln Leu  Ser Ser Asn Phe Gly  Ala Ile Ser Ser Val  Leu Asn Asp
    1205                1210                1215

Ile Leu  Ser Arg Leu Asp Lys  Val Glu Ala Glu Val  Gln Ile Asp
    1220                1225                1230
```

```
Arg Leu  Ile Thr Gly Arg Leu  Gln Ser Leu Gln Thr  Tyr Val Thr
    1235                1240                1245

Gln Gln  Leu Ile Arg Ala Ala  Glu Ile Arg Ala Ser  Ala Asn Leu
    1250                1255                1260

Ala Ala  Thr Lys Met Ser Glu  Cys Val Leu Gly Gln  Ser Lys Arg
    1265                1270                1275

Val Asp  Phe Cys Gly Lys Gly  Tyr His Leu Met Ser  Phe Pro Gln
    1280                1285                1290

Ser Ala  Pro His Gly Val Val  Phe Leu His Val Thr  Tyr Val Pro
    1295                1300                1305

Ala Gln  Glu Lys Asn Phe Thr  Thr Ala Pro Ala Ile  Cys His Asp
    1310                1315                1320

Gly Lys  Ala His Phe Pro Arg  Glu Gly Val Phe Val  Ser Asn Gly
    1325                1330                1335

Thr His  Trp Phe Val Thr Gln  Arg Asn Phe Tyr Glu  Pro Gln Ile
    1340                1345                1350

Ile Thr  Thr Asp Asn Thr Phe  Val Ser Gly Asn Cys  Asp Val Val
    1355                1360                1365

Ile Gly  Ile Val Asn Asn Thr  Val Tyr Asp Pro Leu  Gln Pro Glu
    1370                1375                1380

Leu Asp  Ser Phe Lys Glu Glu  Leu Asp Lys Tyr Phe  Lys Asn His
    1385                1390                1395

Thr Ser  Pro Asp Val Asp Leu  Gly Asp Ile Ser Gly  Ile Asn Ala
    1400                1405                1410

Ser Val  Val Asn Ile Gln Lys  Glu Ile Asp Arg Leu  Asn Glu Val
    1415                1420                1425

Ala Lys  Asn Leu Asn Glu Ser  Leu Ile Asp Leu Gln  Glu Leu Gly
```

```
    1430                1435                1440

Lys Tyr  Glu Gln Tyr Ile Lys  Trp Pro Trp Tyr Ile  Trp Leu Gly
    1445                1450                1455

Phe Ile  Ala Gly Leu Ile Ala  Ile Val Met Val Thr  Ile Met Leu
    1460                1465                1470

Cys Cys  Met Thr Ser Cys Cys  Ser Cys Leu Lys Gly  Cys Cys Ser
    1475                1480                1485

Cys Gly  Ser Cys Cys Lys Phe  Asp Glu Asp Asp Ser  Glu Pro Val
    1490                1495                1500

Leu Lys  Gly Val Lys Leu His  Tyr Thr
    1505                1510
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<210> 10
<211> 1779
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein HPV18L1/SARS-CoV-2 spike protein

<400> 10

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Met Ala Leu Trp Arg Pro Ser Asp Asn Thr Val Tyr Leu Pro Pro Pro
1               5                   10                  15

Ser Val Ala Arg Val Val Asn Thr Asp Asp Tyr Val Thr Arg Thr Ser
            20                  25                  30

Ile Phe Tyr His Ala Gly Ser Ser Arg Leu Leu Thr Val Gly Asn Pro
        35                  40                  45

Tyr Phe Arg Val Pro Ala Gly Gly Gly Asn Lys Gln Asp Ile Pro Lys
    50                  55                  60

Val Ser Ala Tyr Gln Tyr Arg Val Phe Arg Val Gln Leu Pro Asp Pro
65                  70                  75                  80

Asn Lys Phe Gly Leu Pro Asp Thr Ser Ile Tyr Asn Pro Glu Thr Gln
```

```
                85                  90                  95

Arg Leu Val Trp Ala Cys Ala Gly Val Glu Ile Gly Arg Gly Gln Pro
            100                 105                 110

Leu Gly Val Gly Leu Ser Gly His Pro Phe Tyr Asn Lys Leu Asp Asp
        115                 120                 125

Thr Glu Ser Ser His Ala Ala Thr Ser Asn Val Ser Glu Asp Val Arg
    130                 135                 140

Asp Asn Val Ser Val Asp Tyr Lys Gln Thr Gln Leu Cys Ile Leu Gly
145                 150                 155                 160

Cys Ala Pro Ala Ile Gly Glu His Trp Ala Lys Gly Thr Ala Cys Lys
                165                 170                 175

Ser Arg Pro Leu Ser Gln Gly Asp Cys Pro Pro Leu Glu Leu Lys Asn
            180                 185                 190

Thr Val Leu Glu Asp Gly Asp Met Val Asp Thr Gly Tyr Gly Ala Met
        195                 200                 205

Asp Phe Ser Thr Leu Gln Asp Thr Lys Cys Glu Val Pro Leu Asp Ile
    210                 215                 220

Cys Gln Ser Ile Cys Lys Tyr Pro Asp Tyr Leu Gln Met Ser Ala Asp
225                 230                 235                 240

Pro Tyr Gly Asp Ser Met Phe Phe Cys Leu Arg Arg Glu Gln Leu Phe
                245                 250                 255

Ala Arg His Phe Trp Asn Arg Ala Gly Thr Met Gly Asp Thr Val Pro
            260                 265                 270

Gln Ser Leu Tyr Ile Lys Gly Thr Gly Met Arg Ala Ser Pro Gly Ser
        275                 280                 285

Cys Val Tyr Ser Pro Ser Pro Ser Gly Ser Ile Val Thr Ser Asp Ser
    290                 295                 300
```

```
Gln Leu Phe Asn Lys Pro Tyr Trp Leu His Lys Ala Gln Gly His Asn
305                 310                 315                 320

Asn Gly Val Cys Trp His Asn Gln Leu Phe Val Thr Val Val Asp Thr
                325                 330                 335

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

Pro Gly Gln Tyr Asp Ala Thr Lys Phe Lys Gln Tyr Ser Arg His Val
        355                 360                 365

Glu Glu Tyr Asp Leu Gln Phe Ile Phe Gln Leu Cys Thr Ile Thr Leu
    370                 375                 380

Thr Ala Asp Val Met Ser Tyr Ile His Ser Met Asn Ser Ser Ile Leu
385                 390                 395                 400

Glu Asp Trp Asn Phe Gly Val Pro Pro Pro Pro Thr Thr Ser Leu Val
                405                 410                 415

Asp Thr Tyr Arg Phe Val Gln Ser Val Ala Ile Thr Cys Gln Lys Asp
            420                 425                 430

Ala Ala Pro Ala Glu Asn Lys Asp Pro Tyr Asp Lys Leu Lys Phe Trp
        435                 440                 445

Asn Val Asp Leu Lys Glu Lys Phe Ser Leu Asp Leu Asp Gln Tyr Pro
    450                 455                 460

Leu Gly Arg Lys Phe Leu Val Gln Ala Gly Leu Arg Arg Lys Pro Thr
465                 470                 475                 480

Ile Gly Pro Arg Lys Arg Ser Ala Pro Ser Ala Thr Thr Ser Ser Lys
                485                 490                 495

Pro Ala Lys Arg Val Arg Val Arg Ala Arg Lys Phe Val Phe Leu Val
            500                 505                 510

Leu Leu Pro Leu Val Ser Ser Gln Cys Val Asn Leu Thr Thr Arg Thr
```

```
        515                 520                 525

Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe Thr Arg Gly Val Tyr Tyr
    530                 535                 540

Pro Asp Lys Val Phe Arg Ser Ser Val Leu His Ser Thr Gln Asp Leu
545                 550                 555                 560

Phe Leu Pro Phe Phe Ser Asn Val Thr Trp Phe His Ala Ile His Val
                565                 570                 575

Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp Asn Pro Val Leu Pro Phe
            580                 585                 590

Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu Lys Ser Asn Ile Ile Arg
        595                 600                 605

Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser Lys Thr Gln Ser Leu Leu
    610                 615                 620

Ile Val Asn Asn Ala Thr Asn Val Val Ile Lys Val Cys Glu Phe Gln
625                 630                 635                 640

Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr Tyr His Lys Asn Asn Lys
                645                 650                 655

Ser Trp Met Glu Ser Glu Phe Arg Val Tyr Ser Ser Ala Asn Asn Cys
            660                 665                 670

Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu Met Asp Leu Glu Gly Lys
        675                 680                 685

Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe Val Phe Lys Asn Ile Asp
    690                 695                 700

Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr Pro Ile Asn Leu Val Arg
705                 710                 715                 720

Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu Pro Leu Val Asp Leu Pro
                725                 730                 735
```

```
Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr Leu Leu Ala Leu His Arg
            740                 745                 750

Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser Gly Trp Thr Ala Gly Ala
        755                 760                 765

Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro Arg Thr Phe Leu Leu Lys
    770                 775                 780

Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala Val Asp Cys Ala Leu Asp
785                 790                 795                 800

Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys Ser Phe Thr Val Glu Lys
                805                 810                 815

Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val Gln Pro Thr Glu Ser Ile
            820                 825                 830

Val Arg Phe Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe
        835                 840                 845

Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala Trp Asn Arg Lys Arg Ile
    850                 855                 860

Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser Ala Ser Phe
865                 870                 875                 880

Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro Thr Lys Leu Asn Asp Leu
                885                 890                 895

Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe Val Ile Arg Gly Asp Glu
            900                 905                 910

Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp Tyr Asn
        915                 920                 925

Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys Val Ile Ala Trp Asn Ser
    930                 935                 940

Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg
```

```
945                 950                 955                 960

Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile Ser Thr
                965                 970                 975

Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe
            980                 985                 990

Asn Cys Tyr Phe Pro Leu Gln Ser  Tyr Gly Phe Gln Pro  Thr Asn Gly
        995                 1000                1005

Val Gly  Tyr Gln Pro Tyr Arg  Val Val Val Leu Ser  Phe Glu Leu
    1010                1015                1020

Leu His  Ala Pro Ala Thr Val  Cys Gly Pro Lys Lys  Ser Thr Asn
    1025                1030                1035

Leu Val  Lys Asn Lys Cys Val  Asn Phe Asn Phe Asn  Gly Leu Thr
    1040                1045                1050

Gly Thr  Gly Val Leu Thr Glu  Ser Asn Lys Lys Phe  Leu Pro Phe
    1055                1060                1065

Gln Gln  Phe Gly Arg Asp Ile  Ala Asp Thr Thr Asp  Ala Val Arg
    1070                1075                1080

Asp Pro  Gln Thr Leu Glu Ile  Leu Asp Ile Thr Pro  Cys Ser Phe
    1085                1090                1095

Gly Gly  Val Ser Val Ile Thr  Pro Gly Thr Asn Thr  Ser Asn Gln
    1100                1105                1110

Val Ala  Val Leu Tyr Gln Asp  Val Asn Cys Thr Glu  Val Pro Val
    1115                1120                1125

Ala Ile  His Ala Asp Gln Leu  Thr Pro Thr Trp Arg  Val Tyr Ser
    1130                1135                1140

Thr Gly  Ser Asn Val Phe Gln  Thr Arg Ala Gly Cys  Leu Ile Gly
    1145                1150                1155
```

```
Ala Glu  His Val Asn Asn Ser  Tyr Glu Cys Asp Ile  Pro Ile Gly
    1160                1165                1170

Ala Gly  Ile Cys Ala Ser Tyr  Gln Thr Gln Thr Asn  Ser Pro Arg
    1175                1180                1185

Arg Ala  Arg Ser Val Ala Ser  Gln Ser Ile Ile Ala  Tyr Thr Met
    1190                1195                1200

Ser Leu  Gly Ala Glu Asn Ser  Val Ala Tyr Ser Asn  Asn Ser Ile
    1205                1210                1215

Ala Ile  Pro Thr Asn Phe Thr  Ile Ser Val Thr Thr  Glu Ile Leu
    1220                1225                1230

Pro Val  Ser Met Thr Lys Thr  Ser Val Asp Cys Thr  Met Tyr Ile
    1235                1240                1245

Cys Gly  Asp Ser Thr Glu Cys  Ser Asn Leu Leu Leu  Gln Tyr Gly
    1250                1255                1260

Ser Phe  Cys Thr Gln Leu Asn  Arg Ala Leu Thr Gly  Ile Ala Val
    1265                1270                1275

Glu Gln  Asp Lys Asn Thr Gln  Glu Val Phe Ala Gln  Val Lys Gln
    1280                1285                1290

Ile Tyr  Lys Thr Pro Pro Ile  Lys Asp Phe Gly Gly  Phe Asn Phe
    1295                1300                1305

Ser Gln  Ile Leu Pro Asp Pro  Ser Lys Pro Ser Lys  Arg Ser Phe
    1310                1315                1320

Ile Glu  Asp Leu Leu Phe Asn  Lys Val Thr Leu Ala  Asp Ala Gly
    1325                1330                1335

Phe Ile  Lys Gln Tyr Gly Asp  Cys Leu Gly Asp Ile  Ala Ala Arg
    1340                1345                1350

Asp Leu  Ile Cys Ala Gln Lys  Phe Asn Gly Leu Thr  Val Leu Pro
```

```
    1355                1360                1365

Pro Leu  Leu Thr Asp Glu Met  Ile Ala Gln Tyr Thr  Ser Ala Leu
    1370                1375                1380

Leu Ala  Gly Thr Ile Thr Ser  Gly Trp Thr Phe Gly  Ala Gly Ala
    1385                1390                1395

Ala Leu  Gln Ile Pro Phe Ala  Met Gln Met Ala Tyr  Arg Phe Asn
    1400                1405                1410

Gly Ile  Gly Val Thr Gln Asn  Val Leu Tyr Glu Asn  Gln Lys Leu
    1415                1420                1425

Ile Ala  Asn Gln Phe Asn Ser  Ala Ile Gly Lys Ile  Gln Asp Ser
    1430                1435                1440

Leu Ser  Ser Thr Ala Ser Ala  Leu Gly Lys Leu Gln  Asp Val Val
    1445                1450                1455

Asn Gln  Asn Ala Gln Ala Leu  Asn Thr Leu Val Lys  Gln Leu Ser
    1460                1465                1470

Ser Asn  Phe Gly Ala Ile Ser  Ser Val Leu Asn Asp  Ile Leu Ser
    1475                1480                1485

Arg Leu  Asp Lys Val Glu Ala  Glu Val Gln Ile Asp  Arg Leu Ile
    1490                1495                1500

Thr Gly  Arg Leu Gln Ser Leu  Gln Thr Tyr Val Thr  Gln Gln Leu
    1505                1510                1515

Ile Arg  Ala Ala Glu Ile Arg  Ala Ser Ala Asn Leu  Ala Ala Thr
    1520                1525                1530

Lys Met  Ser Glu Cys Val Leu  Gly Gln Ser Lys Arg  Val Asp Phe
    1535                1540                1545

Cys Gly  Lys Gly Tyr His Leu  Met Ser Phe Pro Gln  Ser Ala Pro
    1550                1555                1560
```

```
His Gly  Val Val Phe Leu His  Val Thr Tyr Val Pro  Ala Gln Glu
    1565                1570                1575

Lys Asn  Phe Thr Thr Ala Pro  Ala Ile Cys His Asp  Gly Lys Ala
    1580                1585                1590

His Phe  Pro Arg Glu Gly Val  Phe Val Ser Asn Gly  Thr His Trp
    1595                1600                1605

Phe Val  Thr Gln Arg Asn Phe  Tyr Glu Pro Gln Ile  Ile Thr Thr
    1610                1615                1620

Asp Asn  Thr Phe Val Ser Gly  Asn Cys Asp Val Val  Ile Gly Ile
    1625                1630                1635

Val Asn  Asn Thr Val Tyr Asp  Pro Leu Gln Pro Glu  Leu Asp Ser
    1640                1645                1650

Phe Lys  Glu Glu Leu Asp Lys  Tyr Phe Lys Asn His  Thr Ser Pro
    1655                1660                1665

Asp Val  Asp Leu Gly Asp Ile  Ser Gly Ile Asn Ala  Ser Val Val
    1670                1675                1680

Asn Ile  Gln Lys Glu Ile Asp  Arg Leu Asn Glu Val  Ala Lys Asn
    1685                1690                1695

Leu Asn  Glu Ser Leu Ile Asp  Leu Gln Glu Leu Gly  Lys Tyr Glu
    1700                1705                1710

Gln Tyr  Ile Lys Trp Pro Trp  Tyr Ile Trp Leu Gly  Phe Ile Ala
    1715                1720                1725

Gly Leu  Ile Ala Ile Val Met  Val Thr Ile Met Leu  Cys Cys Met
    1730                1735                1740

Thr Ser  Cys Cys Ser Cys Leu  Lys Gly Cys Cys Ser  Cys Gly Ser
    1745                1750                1755

Cys Cys  Lys Phe Asp Glu Asp  Asp Ser Glu Pro Val  Leu Lys Gly
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1760 1765 1770

Val Lys Leu His Tyr Thr
1775

<210> 11
<211> 1777
<212> PRT
<213> Artificial Sequence

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<223> fusion protein HPV16L1/SARS-CoV-2 spike protein

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Met Ser Leu Trp Leu Pro Ser Glu Ala Thr Val Tyr Leu Pro Pro Val
1 5 10 15

Pro Val Ser Lys Val Val Ser Thr Asp Glu Tyr Val Ala Arg Thr Asn
20 25 30

Ile Tyr Tyr His Ala Gly Thr Ser Arg Leu Leu Ala Val Gly His Pro
35 40 45

Tyr Phe Pro Ile Lys Lys Pro Asn Asn Asn Lys Ile Leu Val Pro Lys
50 55 60

Val Ser Gly Leu Gln Tyr Arg Val Phe Arg Ile His Leu Pro Asp Pro
65 70 75 80

Asn Lys Phe Gly Phe Pro Asp Thr Ser Phe Tyr Asn Pro Asp Thr Gln
85 90 95

Arg Leu Val Trp Ala Cys Val Gly Val Glu Val Gly Arg Gly Gln Pro
100 105 110

Leu Gly Val Gly Ile Ser Gly His Pro Leu Leu Asn Lys Leu Asp Asp
115 120 125

Thr Glu Asn Ala Ser Ala Tyr Ala Ala Asn Ala Gly Val Asp Asn Arg
130 135 140

Glu Cys Ile Ser Met Asp Tyr Lys Gln Thr Gln Leu Cys Leu Ile Gly

```
145                 150                 155                 160

Cys Lys Pro Pro Ile Gly Glu His Trp Gly Lys Gly Ser Pro Cys Thr
                165                 170                 175

Asn Val Ala Val Asn Pro Gly Asp Cys Pro Pro Leu Glu Leu Ile Asn
            180                 185                 190

Thr Val Ile Gln Asp Gly Asp Met Val Asp Thr Gly Phe Gly Ala Met
        195                 200                 205

Asp Phe Thr Thr Leu Gln Ala Asn Lys Ser Glu Val Pro Leu Asp Ile
    210                 215                 220

Cys Thr Ser Ile Cys Lys Tyr Pro Asp Tyr Ile Lys Met Val Ser Glu
225                 230                 235                 240

Pro Tyr Gly Asp Ser Leu Phe Phe Tyr Leu Arg Arg Glu Gln Met Phe
                245                 250                 255

Val Arg His Leu Phe Asn Arg Ala Gly Ala Val Gly Glu Asn Val Pro
            260                 265                 270

Asp Asp Leu Tyr Ile Lys Gly Ser Gly Ser Thr Ala Asn Leu Ala Ser
        275                 280                 285

Ser Asn Tyr Phe Pro Thr Pro Ser Gly Ser Met Val Thr Ser Asp Ala
    290                 295                 300

Gln Ile Phe Asn Lys Pro Tyr Trp Leu Gln Arg Ala Gln Gly His Asn
305                 310                 315                 320

Asn Gly Ile Cys Trp Gly Asn Gln Leu Phe Val Thr Val Val Asp Thr
                325                 330                 335

Thr Arg Ser Thr Asn Met Ser Leu Cys Ala Ala Ile Ser Thr Ser Glu
            340                 345                 350

Thr Thr Tyr Lys Asn Thr Asn Phe Lys Glu Tyr Leu Arg His Gly Glu
        355                 360                 365
```

```
Glu Tyr Asp Leu Gln Phe Ile Phe Gln Leu Cys Lys Ile Thr Leu Thr
    370                 375                 380

Ala Asp Val Met Thr Tyr Ile His Ser Met Asn Ser Thr Ile Leu Glu
385                 390                 395                 400

Asp Trp Asn Phe Gly Leu Gln Pro Pro Pro Gly Gly Thr Leu Glu Asp
                405                 410                 415

Thr Tyr Arg Phe Val Thr Ser Gln Ala Ile Ala Cys Gln Lys His Thr
            420                 425                 430

Pro Pro Ala Pro Lys Glu Asp Pro Leu Lys Lys Tyr Thr Phe Trp Glu
        435                 440                 445

Val Asn Leu Lys Glu Lys Phe Ser Ala Asp Leu Asp Gln Phe Pro Leu
    450                 455                 460

Gly Arg Lys Phe Leu Leu Gln Ala Gly Leu Lys Ala Lys Pro Lys Phe
465                 470                 475                 480

Thr Leu Gly Lys Arg Lys Ala Thr Pro Thr Thr Ser Ser Thr Ser Thr
                485                 490                 495

Thr Ala Lys Arg Lys Lys Arg Lys Leu Phe Val Phe Leu Val Leu Leu
            500                 505                 510

Pro Leu Val Ser Ser Gln Cys Val Asn Leu Thr Thr Arg Thr Gln Leu
        515                 520                 525

Pro Pro Ala Tyr Thr Asn Ser Phe Thr Arg Gly Val Tyr Tyr Pro Asp
    530                 535                 540

Lys Val Phe Arg Ser Ser Val Leu His Ser Thr Gln Asp Leu Phe Leu
545                 550                 555                 560

Pro Phe Phe Ser Asn Val Thr Trp Phe His Ala Ile His Val Ser Gly
                565                 570                 575

Thr Asn Gly Thr Lys Arg Phe Asp Asn Pro Val Leu Pro Phe Asn Asp
```

```
            580                 585                 590

Gly Val Tyr Phe Ala Ser Thr Glu Lys Ser Asn Ile Ile Arg Gly Trp
        595                 600                 605

Ile Phe Gly Thr Thr Leu Asp Ser Lys Thr Gln Ser Leu Leu Ile Val
    610                 615                 620

Asn Asn Ala Thr Asn Val Val Ile Lys Val Cys Glu Phe Gln Phe Cys
625                 630                 635                 640

Asn Asp Pro Phe Leu Gly Val Tyr Tyr His Lys Asn Asn Lys Ser Trp
                645                 650                 655

Met Glu Ser Glu Phe Arg Val Tyr Ser Ser Ala Asn Asn Cys Thr Phe
            660                 665                 670

Glu Tyr Val Ser Gln Pro Phe Leu Met Asp Leu Glu Gly Lys Gln Gly
        675                 680                 685

Asn Phe Lys Asn Leu Arg Glu Phe Val Phe Lys Asn Ile Asp Gly Tyr
    690                 695                 700

Phe Lys Ile Tyr Ser Lys His Thr Pro Ile Asn Leu Val Arg Asp Leu
705                 710                 715                 720

Pro Gln Gly Phe Ser Ala Leu Glu Pro Leu Val Asp Leu Pro Ile Gly
                725                 730                 735

Ile Asn Ile Thr Arg Phe Gln Thr Leu Leu Ala Leu His Arg Ser Tyr
            740                 745                 750

Leu Thr Pro Gly Asp Ser Ser Ser Gly Trp Thr Ala Gly Ala Ala Ala
        755                 760                 765

Tyr Tyr Val Gly Tyr Leu Gln Pro Arg Thr Phe Leu Leu Lys Tyr Asn
    770                 775                 780

Glu Asn Gly Thr Ile Thr Asp Ala Val Asp Cys Ala Leu Asp Pro Leu
785                 790                 795                 800
```

```
Ser Glu Thr Lys Cys Thr Leu Lys Ser Phe Thr Val Glu Lys Gly Ile
                805                 810                 815

Tyr Gln Thr Ser Asn Phe Arg Val Gln Pro Thr Glu Ser Ile Val Arg
            820                 825                 830

Phe Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala
        835                 840                 845

Thr Arg Phe Ala Ser Val Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn
    850                 855                 860

Cys Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr
865                 870                 875                 880

Phe Lys Cys Tyr Gly Val Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe
                885                 890                 895

Thr Asn Val Tyr Ala Asp Ser Phe Val Ile Arg Gly Asp Glu Val Arg
            900                 905                 910

Gln Ile Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys
        915                 920                 925

Leu Pro Asp Asp Phe Thr Gly Cys Val Ile Ala Trp Asn Ser Asn Asn
    930                 935                 940

Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe
945                 950                 955                 960

Arg Lys Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile
                965                 970                 975

Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys
            980                 985                 990

Tyr Phe Pro Leu Gln Ser Tyr Gly  Phe Gln Pro Thr Asn  Gly Val Gly
        995                 1000                1005

Tyr Gln  Pro Tyr Arg Val Val  Val Leu Ser Phe Glu  Leu Leu His
```

```
    1010                1015                1020

Ala Pro  Ala Thr Val Cys Gly  Pro Lys Lys Ser Thr  Asn Leu Val
    1025                1030                1035

Lys Asn  Lys Cys Val Asn Phe  Asn Phe Asn Gly Leu  Thr Gly Thr
    1040                1045                1050

Gly Val  Leu Thr Glu Ser Asn  Lys Lys Phe Leu Pro  Phe Gln Gln
    1055                1060                1065

Phe Gly  Arg Asp Ile Ala Asp  Thr Thr Asp Ala Val  Arg Asp Pro
    1070                1075                1080

Gln Thr  Leu Glu Ile Leu Asp  Ile Thr Pro Cys Ser  Phe Gly Gly
    1085                1090                1095

Val Ser  Val Ile Thr Pro Gly  Thr Asn Thr Ser Asn  Gln Val Ala
    1100                1105                1110

Val Leu  Tyr Gln Asp Val Asn  Cys Thr Glu Val Pro  Val Ala Ile
    1115                1120                1125

His Ala  Asp Gln Leu Thr Pro  Thr Trp Arg Val Tyr  Ser Thr Gly
    1130                1135                1140

Ser Asn  Val Phe Gln Thr Arg  Ala Gly Cys Leu Ile  Gly Ala Glu
    1145                1150                1155

His Val  Asn Asn Ser Tyr Glu  Cys Asp Ile Pro Ile  Gly Ala Gly
    1160                1165                1170

Ile Cys  Ala Ser Tyr Gln Thr  Gln Thr Asn Ser Pro  Arg Arg Ala
    1175                1180                1185

Arg Ser  Val Ala Ser Gln Ser  Ile Ile Ala Tyr Thr  Met Ser Leu
    1190                1195                1200

Gly Ala  Glu Asn Ser Val Ala  Tyr Ser Asn Asn Ser  Ile Ala Ile
    1205                1210                1215
```

```
Pro Thr  Asn Phe Thr Ile Ser  Val Thr Thr Glu Ile  Leu Pro Val
    1220                1225                1230

Ser Met  Thr Lys Thr Ser Val  Asp Cys Thr Met Tyr  Ile Cys Gly
    1235                1240                1245

Asp Ser  Thr Glu Cys Ser Asn  Leu Leu Leu Gln Tyr  Gly Ser Phe
    1250                1255                1260

Cys Thr  Gln Leu Asn Arg Ala  Leu Thr Gly Ile Ala  Val Glu Gln
    1265                1270                1275

Asp Lys  Asn Thr Gln Glu Val  Phe Ala Gln Val Lys  Gln Ile Tyr
    1280                1285                1290

Lys Thr  Pro Pro Ile Lys Asp  Phe Gly Gly Phe Asn  Phe Ser Gln
    1295                1300                1305

Ile Leu  Pro Asp Pro Ser Lys  Pro Ser Lys Arg Ser  Phe Ile Glu
    1310                1315                1320

Asp Leu  Leu Phe Asn Lys Val  Thr Leu Ala Asp Ala  Gly Phe Ile
    1325                1330                1335

Lys Gln  Tyr Gly Asp Cys Leu  Gly Asp Ile Ala Ala  Arg Asp Leu
    1340                1345                1350

Ile Cys  Ala Gln Lys Phe Asn  Gly Leu Thr Val Leu  Pro Pro Leu
    1355                1360                1365

Leu Thr  Asp Glu Met Ile Ala  Gln Tyr Thr Ser Ala  Leu Leu Ala
    1370                1375                1380

Gly Thr  Ile Thr Ser Gly Trp  Thr Phe Gly Ala Gly  Ala Ala Leu
    1385                1390                1395

Gln Ile  Pro Phe Ala Met Gln  Met Ala Tyr Arg Phe  Asn Gly Ile
    1400                1405                1410

Gly Val  Thr Gln Asn Val Leu  Tyr Glu Asn Gln Lys  Leu Ile Ala
```

```
    1415                1420                1425

Asn Gln  Phe Asn Ser Ala Ile  Gly Lys Ile Gln Asp  Ser Leu Ser
    1430                1435                1440

Ser Thr  Ala Ser Ala Leu Gly  Lys Leu Gln Asp Val  Val Asn Gln
    1445                1450                1455

Asn Ala  Gln Ala Leu Asn Thr  Leu Val Lys Gln Leu  Ser Ser Asn
    1460                1465                1470

Phe Gly  Ala Ile Ser Ser Val  Leu Asn Asp Ile Leu  Ser Arg Leu
    1475                1480                1485

Asp Lys  Val Glu Ala Glu Val  Gln Ile Asp Arg Leu  Ile Thr Gly
    1490                1495                1500

Arg Leu  Gln Ser Leu Gln Thr  Tyr Val Thr Gln Gln  Leu Ile Arg
    1505                1510                1515

Ala Ala  Glu Ile Arg Ala Ser  Ala Asn Leu Ala Ala  Thr Lys Met
    1520                1525                1530

Ser Glu  Cys Val Leu Gly Gln  Ser Lys Arg Val Asp  Phe Cys Gly
    1535                1540                1545

Lys Gly  Tyr His Leu Met Ser  Phe Pro Gln Ser Ala  Pro His Gly
    1550                1555                1560

Val Val  Phe Leu His Val Thr  Tyr Val Pro Ala Gln  Glu Lys Asn
    1565                1570                1575

Phe Thr  Thr Ala Pro Ala Ile  Cys His Asp Gly Lys  Ala His Phe
    1580                1585                1590

Pro Arg  Glu Gly Val Phe Val  Ser Asn Gly Thr His  Trp Phe Val
    1595                1600                1605

Thr Gln  Arg Asn Phe Tyr Glu  Pro Gln Ile Ile Thr  Thr Asp Asn
    1610                1615                1620
```

```
Thr Phe  Val Ser Gly Asn Cys  Asp Val Val Ile Gly  Ile Val Asn
    1625                1630                1635

Asn Thr  Val Tyr Asp Pro Leu  Gln Pro Glu Leu Asp  Ser Phe Lys
    1640                1645                1650

Glu Glu  Leu Asp Lys Tyr Phe  Lys Asn His Thr Ser  Pro Asp Val
    1655                1660                1665

Asp Leu  Gly Asp Ile Ser Gly  Ile Asn Ala Ser Val  Val Asn Ile
    1670                1675                1680

Gln Lys  Glu Ile Asp Arg Leu  Asn Glu Val Ala Lys  Asn Leu Asn
    1685                1690                1695

Glu Ser  Leu Ile Asp Leu Gln  Glu Leu Gly Lys Tyr  Glu Gln Tyr
    1700                1705                1710

Ile Lys  Trp Pro Trp Tyr Ile  Trp Leu Gly Phe Ile  Ala Gly Leu
    1715                1720                1725

Ile Ala  Ile Val Met Val Thr  Ile Met Leu Cys Cys  Met Thr Ser
    1730                1735                1740

Cys Cys  Ser Cys Leu Lys Gly  Cys Cys Ser Cys Gly  Ser Cys Cys
    1745                1750                1755

Lys Phe  Asp Glu Asp Asp Ser  Glu Pro Val Leu Lys  Gly Val Lys
    1760                1765                1770

Leu His  Tyr Thr
    1775
```

<210> 12
<211> 1407
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein HBSAg/SARS-CoV-2 spike protein

<400> 12

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Met Asn Phe Leu Gly Gly Thr Thr Val Cys Leu Gly Gln Asn Ser Gln
1               5                  10                  15

Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Thr Cys Pro
            20                  25                  30

Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile
        35                  40                  45

Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly
    50                  55                  60

Met Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Thr Ser Thr
65                  70                  75                  80

Gly Pro Cys Arg Thr Cys Thr Thr Pro Ala Gln Gly Thr Ser Met Tyr
                85                  90                  95

Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile
            100                 105                 110

Pro Ile Pro Ser Ser Trp Ala Phe Gly Lys Phe Leu Trp Glu Trp Ala
        115                 120                 125

Ser Ala Arg Phe Ser Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser
    130                 135                 140

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

Thr Asn Ser Phe Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg
                165                 170                 175

Ser Ser Val Leu His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser
            180                 185                 190

Asn Val Thr Trp Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr
        195                 200                 205

Lys Arg Phe Asp Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe
```

```
    210                 215                 220

Ala Ser Thr Glu Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr
225                 230                 235                 240

Thr Leu Asp Ser Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr
                245                 250                 255

Asn Val Val Ile Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe
            260                 265                 270

Leu Gly Val Tyr Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu
        275                 280                 285

Phe Arg Val Tyr Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser
    290                 295                 300

Gln Pro Phe Leu Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn
305                 310                 315                 320

Leu Arg Glu Phe Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr
                325                 330                 335

Ser Lys His Thr Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe
            340                 345                 350

Ser Ala Leu Glu Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr
        355                 360                 365

Arg Phe Gln Thr Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly
    370                 375                 380

Asp Ser Ser Ser Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly
385                 390                 395                 400

Tyr Leu Gln Pro Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr
                405                 410                 415

Ile Thr Asp Ala Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys
            420                 425                 430
```

```
Cys Thr Leu Lys Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser
        435                 440                 445

Asn Phe Arg Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile
    450                 455                 460

Thr Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala
465                 470                 475                 480

Ser Val Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp
                485                 490                 495

Tyr Ser Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr
            500                 505                 510

Gly Val Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr
        515                 520                 525

Ala Asp Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro
    530                 535                 540

Gly Gln Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp
545                 550                 555                 560

Phe Thr Gly Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys
                565                 570                 575

Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn
            580                 585                 590

Leu Lys Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly
        595                 600                 605

Ser Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu
    610                 615                 620

Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr
625                 630                 635                 640

Arg Val Val Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val
```

```
               645                 650                 655

Cys Gly Pro Lys Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn
            660                 665                 670

Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn
        675                 680                 685

Lys Lys Phe Leu Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr
    690                 695                 700

Thr Asp Ala Val Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr
705                 710                 715                 720

Pro Cys Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr
                725                 730                 735

Ser Asn Gln Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val
            740                 745                 750

Pro Val Ala Ile His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr
        755                 760                 765

Ser Thr Gly Ser Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly
    770                 775                 780

Ala Glu His Val Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala
785                 790                 795                 800

Gly Ile Cys Ala Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala
                805                 810                 815

Arg Ser Val Ala Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly
            820                 825                 830

Ala Glu Asn Ser Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr
        835                 840                 845

Asn Phe Thr Ile Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr
    850                 855                 860
```

```
Lys Thr Ser Val Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu
865                 870                 875                 880


Cys Ser Asn Leu Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn
                885                 890                 895


Arg Ala Leu Thr Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu
            900                 905                 910


Val Phe Ala Gln Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp
        915                 920                 925


Phe Gly Gly Phe Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro
    930                 935                 940


Ser Lys Arg Ser Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu
945                 950                 955                 960


Ala Asp Ala Gly Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile
                965                 970                 975


Ala Ala Arg Asp Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val
            980                 985                 990


Leu Pro Pro Leu Leu Thr Asp Glu  Met Ile Ala Gln Tyr  Thr Ser Ala
        995                 1000                1005


Leu Leu  Ala Gly Thr Ile Thr  Ser Gly Trp Thr Phe  Gly Ala Gly
    1010                1015                1020


Ala Ala  Leu Gln Ile Pro Phe  Ala Met Gln Met Ala  Tyr Arg Phe
    1025                1030                1035


Asn Gly  Ile Gly Val Thr Gln  Asn Val Leu Tyr Glu  Asn Gln Lys
    1040                1045                1050


Leu Ile  Ala Asn Gln Phe Asn  Ser Ala Ile Gly Lys  Ile Gln Asp
    1055                1060                1065


Ser Leu  Ser Ser Thr Ala Ser  Ala Leu Gly Lys Leu  Gln Asp Val
```

```
    1070                1075                1080

Val Asn  Gln Asn Ala Gln Ala  Leu Asn Thr Leu Val  Lys Gln Leu
    1085                1090                1095

Ser Ser  Asn Phe Gly Ala Ile  Ser Ser Val Leu Asn  Asp Ile Leu
    1100                1105                1110

Ser Arg  Leu Asp Lys Val Glu  Ala Glu Val Gln Ile  Asp Arg Leu
    1115                1120                1125

Ile Thr  Gly Arg Leu Gln Ser  Leu Gln Thr Tyr Val  Thr Gln Gln
    1130                1135                1140

Leu Ile  Arg Ala Ala Glu Ile  Arg Ala Ser Ala Asn  Leu Ala Ala
    1145                1150                1155

Thr Lys  Met Ser Glu Cys Val  Leu Gly Gln Ser Lys  Arg Val Asp
    1160                1165                1170

Phe Cys  Gly Lys Gly Tyr His  Leu Met Ser Phe Pro  Gln Ser Ala
    1175                1180                1185

Pro His  Gly Val Val Phe Leu  His Val Thr Tyr Val  Pro Ala Gln
    1190                1195                1200

Glu Lys  Asn Phe Thr Thr Ala  Pro Ala Ile Cys His  Asp Gly Lys
    1205                1210                1215

Ala His  Phe Pro Arg Glu Gly  Val Phe Val Ser Asn  Gly Thr His
    1220                1225                1230

Trp Phe  Val Thr Gln Arg Asn  Phe Tyr Glu Pro Gln  Ile Ile Thr
    1235                1240                1245

Thr Asp  Asn Thr Phe Val Ser  Gly Asn Cys Asp Val  Val Ile Gly
    1250                1255                1260

Ile Val  Asn Asn Thr Val Tyr  Asp Pro Leu Gln Pro  Glu Leu Asp
    1265                1270                1275
```

Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser
    1280   1285   1290

Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala Ser Val
    1295   1300   1305

Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val Ala Lys
    1310   1315   1320

Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr
    1325   1330   1335

Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile Trp Leu Gly Phe Ile
    1340   1345   1350

Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Met Leu Cys Cys
    1355   1360   1365

Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys Ser Cys Gly
    1370   1375   1380

Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val Leu Lys
    1385   1390   1395

Gly Val Lys Leu His Tyr Thr Ala Ala
    1400   1405

<210> 13
<211> 665
<212> DNA
<213> Artificial Sequence

<220>
<223> RBD SARS-CoV-2 spike protein nucleic acid

<400> 13
gctagcgacg ccaccatgag agtccaacca acagaatcta ttgttagatt tcctaatatt 60

acaaacttgt gccctttttgg tgaagttttt aacgccacca gatttgcatc tgtttatgct 120

tggaacagga agagaatcag caactgtgtt gctgattatt ctgtcctata taattccgca 180

tcattttcca cttttaagtg ttatggagtg tctcctacta aattaaatga tctctgcttt 240

actaatgtct atgcagattc atttgtaatt agaggtgatg aagtcagaca aatcgctcca 300

gggcaaactg gaaagattgc tgattataat tataaattac cagatgattt tacaggctgc 360

gttatagctt ggaattctaa caatcttgat tctaaggttg gtggtaatta taattacctg 420

tatagattgt ttaggaagtc taatctcaaa ccttttgaga gagatatttc aactgaaatc 480

tatcaggccg gtagcacacc ttgtaatggt gttgaaggtt ttaattgtta ctttccttta 540

caatcatatg gtttccaacc cactaatggt gttggttacc aaccatacag agtagtagta 600

ctttcttttg aacttctaca tgcaccagca actgtttgtg gacctaaaaa gtgataagcg 660

gccgc 665

<210> 14
<211> 665
<212> DNA
<213> Artificial Sequence

<220>
<223> RBD SARS-CoV-2 spike protein nucleic acid sequence - human codon optimized

<400> 14
gctagcgacg ccaccatgag agtgcagcct acagagtcta tcgtgcggtt ccccaacatc 60

accaatctgt gccctttcgg cgaggtgttc aacgccacaa gatttgccag cgtgtacgcc 120

tggaaccgga agagaatcag caactgcgtg gccgactaca gcgtgctgta caatagcgcc 180

agcttcagca ccttcaagtg ctacggcgtg tcccctacca agctgaacga cctgtgcttc 240

accaatgtgt acgccgacag cttcgtgatc agaggcgacg aagttcggca gatcgctcct 300

ggacagacag gcaagatcgc cgattacaac tacaagctgc ccgacgactt caccggctgc 360

gtgatcgcct ggaatagcaa caacctggac agcaaagtcg gcggcaacta caactacctg 420

taccggctgt tccggaagtc caacctgaag cctttcgagc gggacatcag caccgagatc 480

tatcaggccg gcagcacccc ttgtaatggc gtggaaggct tcaactgcta cttcccactg 540

cagtcctacg gcttccagcc tacaaacggc gtgggctacc agccttatag agtggtggtg 600

ctgagcttcg aactgctgca tgcccctgct acagtgtgcg gccccaagaa gtgataagcg 660

gccgc 665

<210> 15
<211> 212

<212> PRT
<213> SARS-CoV-2

<400> 15

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Met Arg Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr
1               5                  10                  15


Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser
            20                  25                  30


Val Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr
        35                  40                  45


Ser Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly
    50                  55                  60


Val Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala
65                  70                  75                  80


Asp Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly
                85                  90                  95


Gln Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
            100                 105                 110


Thr Gly Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val
        115                 120                 125


Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu
    130                 135                 140


Lys Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser
145                 150                 155                 160


Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln
                165                 170                 175


Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg
            180                 185                 190


Val Val Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys
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195 200 205

Gly Pro Lys Lys
210

<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> EAAAK linker consensus sequence

<400> 16

Ala Glu Ala Ala Ala Lys Ala
1 5

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> (EAAAK)3 linker

<400> 17
gaagccgccg ctaaagaggc cgctgccaaa gaagctgctg ctaag 45

<210> 18
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> (EAAAK)3 linker

<400> 18

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

<210> 19
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> GS linker consensus sequence

<400> 19

Gly Gly Gly Gly Ser
1 5

<210> 20
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> GS5 linker

<400> 20

Gly Gly Gly Gly Ser
1 5

<210> 21
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> GS10 linker

<400> 21

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

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

<220>
<223> GS15 linker

<400> 22
ggtggtggtg gtagcggtgg tggcggttca ggtggcggtg gttca 45

<210> 23
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> GS15 linker

<400> 23

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 24
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> GS20 linker

<400> 24

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 25
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> GS25 linker

<400> 25

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 26
<211> 1427
<212> DNA
<213> Artificial Sequence

<220>
<223> HBSAg-(EAAAK)3-RBD

<400> 26
gctagcgacg ccaccatgat tgcactgacc ctgtttaatc tggcagatac cctgttaggt 60

ggtctgccga ccgaactgat tagcagtgcc ggtggtcagc tgttttatag ccgtccggtt 120

gttagcgcaa atggtgaacc gaccgttaaa ctgtatacca gcgttgaaaa tgcacagcag 180

gataaaggta ttgcaattcc gcatgatatt gatctgggtg aaagccgtgt tgtgattcag 240

gattatgata atcagcatga acaggatcgt ccgacaccga gtccggcacc gagccgtccg 300

tttagcgttc tgcgtgcaaa tgatgttctg tggctgagcc tgaccgcagc agaatatgat 360

cagagcacct atggtagcag caccggtccg gtttatgtta gcgatagcgt taccctggtt 420

aatgttgcaa ccggtgcaca ggcagttgca cgtagcctgg attggaccaa agtgaccctg 480

gatggtcgtc cgctgagcac cattcagcag tatagcaaaa ccttttttgt tctgccgctg 540

cgtggtaaac tgagcttttg ggaagcaggc accaccaaag caggttatcc gtataactat 600

aataccaccg caagcgatca gctgctggtt gaaaacgcag caggtcatcg tgttgcaatt 660

agcacctata ccaccagttt aggtgcaggt ccggttagca ttagcgcagt tgcagttctg 720

gcaccgcatt cagccgaagc agccgctaaa gaagcagccg ctaaagaagc agccgctaaa 780

agagtccaac caacagaatc tattgttaga tttcctaata ttacaaactt gtgccctttt 840

ggtgaagttt ttaacgccac cagatttgca tctgtttatg cttggaacag gaagagaatc 900

agcaactgtg ttgctgatta ttctgtccta tataattccg catcattttc cacttttaag 960

tgttatggag tgtctcctac taaattaaat gatctctgct ttactaatgt ctatgcagat 1020

tcatttgtaa ttagaggtga tgaagtcaga caaatcgctc cagggcaaac tggaaagatt 1080

gctgattata attataaatt accagatgat tttacaggct gcgttatagc ttggaattct 1140

aacaatcttg attctaaggt tggtggtaat tataattacc tgtatagatt gtttaggaag 1200

tctaatctca aacctttga gagagatatt tcaactgaaa tctatcaggc cggtagcaca 1260

ccttgtaatg gtgttgaagg ttttaattgt tactttcctt tacaatcata tggtttccaa 1320

cccactaatg gtgttggtta ccaaccatac agagtagtag tactttcttt tgaacttcta 1380

catgcaccag caactgtttg tggacctaaa aagtgataag cggccgc 1427

<210> 27
<211> 1106
<212> DNA
<213> Artificial Sequence

<220>
<223> HBSAg-(EAAAK)3-RBD nucleic acid sequence human codon optimised

<400> 27
gctagcgacg ccaccatgaa ttttctcggc ggcacaacag tgtgcctggg ccagaatagc 60

cagtctccta ccagcaatca cagccccacc agctgtcctc caacctgtcc tggctacaga 120

tggatgtgcc tgcggcggtt catcatcttt ctgttcatcc tgctgctgtg cctgatcttc 180

ctgctggtgc tgctggatta ccagggaatg ctgcctgtgt gtcctctgat ccctggcagc 240

agcacaacaa gcacaggccc ttgcagaacc tgcacaacac cagctcaggg caccagcatg 300

taccctagct gctgttgtac caagcctagc gacggcaact gcacatgcat ccccattcct 360

agcagctggg ccttcggcaa gtttctgtgg gaatgggcca gcgccagatt ttccgaagcc 420

gccgctaaag aggccgctgc caaagaagct gctgctaaga gagtgcagcc caccgagtct 480

atcgtgcggt tccccaacat caccaatctg tgcccttttcg gcgaggtgtt caacgccaca 540

agatttgcca gcgtgtacgc ctggaaccgg aagagaatca gcaactgcgt ggccgactac 600

agcgtgctgt acaatagcgc cagcttcagc accttcaagt gctacggcgt gtcccctacc 660

aagctgaacg acctgtgctt caccaatgtg tacgccgaca gcttcgtgat cagaggcgac 720

gaagttcggc agatcgctcc tggacagaca ggcaagatcg ccgattacaa ctacaagctg 780

cccgacgact tcaccggctg cgtgatcgcc tggaatagca acaacctgga cagcaaagtc 840

ggcggcaact acaactacct gtaccggctg ttccggaagt ccaacctgaa gcctttcgag 900

cgggacatca gcaccgaaat ctaccaggcc ggcagcaccc cttgtaatgg cgtggaaggc 960

ttcaactgct acttcccact gcagtcctac ggcttccagc ctacaaacgg cgtgggctac 1020

cagccttata gagtggtggt gctgagcttc gaactgctgc atgcccctgc tacagtgtgc 1080

ggccccaaga agtgataagc ggccgc 1106

<210> 28
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> HBSAg-(EAAAK)3-RBD

<400> 28

Met Asn Phe Leu Gly Gly Thr Thr Val Cys Leu Gly Gln Asn Ser Gln
1 5 10 15

```
Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Thr Cys Pro
            20                  25                  30

Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile
        35                  40                  45

Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly
    50                  55                  60

Met Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Thr Ser Thr
65                  70                  75                  80

Gly Pro Cys Arg Thr Cys Thr Thr Pro Ala Gln Gly Thr Ser Met Tyr
                85                  90                  95

Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile
            100                 105                 110

Pro Ile Pro Ser Ser Trp Ala Phe Gly Lys Phe Leu Trp Glu Trp Ala
        115                 120                 125

Ser Ala Arg Phe Ser Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
    130                 135                 140

Ala Ala Ala Lys Arg Val Gln Pro Thr Glu Ser Ile Val Arg Phe Pro
145                 150                 155                 160

Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Arg
                165                 170                 175

Phe Ala Ser Val Tyr Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val
            180                 185                 190

Ala Asp Tyr Ser Val Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys
        195                 200                 205

Cys Tyr Gly Val Ser Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn
    210                 215                 220

Val Tyr Ala Asp Ser Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile
```

225 230 235 240

Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro
245 250 255

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

Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys
275 280 285

Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln
290 295 300

Ala Gly Ser Thr Pro Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe
305 310 315 320

Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln
325 330 335

Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala
340 345 350

Thr Val Cys Gly Pro Lys Lys
355

<210> 29
<211> 1418
<212> DNA
<213> Artificial Sequence

<220>
<223> HEV-GS15-RBD

<400> 29
gagctcatga ttgcactgac cctgtttaat ctggcagata ccctgctggg tggtctgccg 60

accgaactga ttagcagtgc cggtggtcag ctgttttata gccgtccggt tgttagcgca 120

aatggtgaac cgaccgttaa actgtatacc agcgttgaaa atgcacagca ggataaaggt 180

attgcaattc cgcatgatat tgatctgggt gaaagccgtg ttgtgattca ggattatgat 240

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ctgcgtgcaa atgatgttct gtggctgagc ctgaccgcag cagaatatga tcagagcacc 360

tatggtagca gcaccggtcc ggtttatgtt agcgatagcg ttaccctggt taatgttgca 420

accggtgcac aggcagttgc acgtagcctg gattggacca aagtgaccct ggatggtcgt 480

ccgctgagca ccattcagca gtatagcaaa acctttttg ttctgccgct gcgtggtaaa 540

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gcaactgttt gtggacctaa aaagtgataa gcggccgc 1418

<210> 30
<211> 1418
<212> DNA
<213> Artificial Sequence

<220>
<223> HEV-GS15-RBD nucleic acid sequence optimized for E.coli expression

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aatggtgaac cgaccgttaa actgtatacc agcgttgaaa atgcacagca ggataaaggt 180

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ctgcgtgcaa atgatgttct gtggctgagc ctgaccgcag cagaatatga tcagagcacc 360

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accggtgcac aggcagttgc acgtagcctg gattggacca aagtgaccct ggatggtcgt 480

ccgctgagca ccattcagca gtatagcaaa acctttttg ttctgccgct gcgtggtaaa 540

ctgagctttt gggaagcagg caccaccaaa gcaggttatc cgtataacta taataccacc 600

gcaagcgatc agctgctggt tgaaaacgca gcaggtcatc gtgttgcaat tagcacctat 660

accaccagtt taggtgcagg tccggttagc attagcgcag ttgcagttct ggcaccgcat 720

tcagccggtg gtggtggtag cggtggtggc ggttcaggtg gcggtggttc acgtgttcag 780

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aactacaaac tgccggatga ttttacgggt tgtgttattg catggaatag caataacctg 1140

gatagcaaag ttggtggcaa ctataactat ctgtatcgcc tgtttcgtaa gagcaatctg 1200

aaaccgtttg aacgtgatat tagcaccgaa atttatcagg caggtagcac cccgtgcaat 1260

ggtgttgaag gttttaattg ttattttccg ctgcagagct atggttttca gcctaccaat 1320

ggtgtgggtt atcagccgta tcgtgttgtt gttctgtcat ttgaactgct gcatgcaccg 1380

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<210> 31
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> HEV-GS15-RBD

<400> 31

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1               5                  10                  15

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

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

Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp
    50                  55                  60

Ile Asp Leu Gly Glu Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln
65                  70                  75                  80

His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe
                85                  90                  95

Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala
            100                 105                 110

Glu Tyr Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Val
        115                 120                 125

Ser Asp Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val
    130                 135                 140

Ala Arg Ser Leu Asp Trp Thr Lys Val Thr Leu Asp Gly Arg Pro Leu
145                 150                 155                 160

Ser Thr Ile Gln Gln Tyr Ser Lys Thr Phe Phe Val Leu Pro Leu Arg
                165                 170                 175

Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro
            180                 185                 190

Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Leu Leu Val Glu Asn Ala
        195                 200                 205

Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala
    210                 215                 220
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Gly Pro Val Ser Ile Ser Ala Val Ala Val Leu Ala Pro His Ser Ala
225                 230                 235                 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg
                245                 250                 255

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

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

Ala Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val
    290                 295                 300

Leu Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser
305                 310                 315                 320

Pro Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser
                325                 330                 335

Phe Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr
            340                 345                 350

Gly Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly
        355                 360                 365

Cys Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly
    370                 375                 380

Asn Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro
385                 390                 395                 400

Phe Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro
                405                 410                 415

Cys Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr
            420                 425                 430
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Gly Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val
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Val Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro
450 455 460

Lys Lys
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<210> 32
<211> 4566
<212> DNA
<213> Artificial Sequence

<220>
<223> HBSAg-(EAAAK)3-full-length SARS-CoV-2 spike protein nucleic acid sequence human codon optimised

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tggacttctc tcaattttct agggggatca cccgtgtgtc tgggccaaaa ttcgcagtcc 180

ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 240

tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttgttg 300

gttcttctgg actaccaggg tatgttgccc gtttgtcctc taattccagg atcaacaact 360

accaacacgg gaccatgcaa gacctgcacg actcctgctc aaggaaactc tatgtttccc 420

tcttgttgct gtacaaaacc taccgacgga aactgcactt gtattcccat cccatcatcc 480

tgggctttcg caaaatacct atgggagtgg gcctcagtcc gtttctcctg gctcagttta 540

ctagtgccat ttgttcagtg gttcgtaggg ctttccccca ctgtttggct ttccgctata 600

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ttaccaattt tcttttgtct ttgggtatac attgaggctg ccgcaaagga agccgcagct 720

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<210> 33
<211> 1513
<212> PRT
<213> Artificial Sequence

<220>
<223> HBSAg-(EAAAK)3-full-length SARS-CoV-2 spike protein

<400> 33

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

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ser Pro Val Cys
35 40 45

Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
50 55 60

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
65 70 75 80

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
85 90 95

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly
100 105 110

Ser Thr Thr Thr Asn Thr Gly Pro Cys Lys Thr Cys Thr Thr Pro Ala

```
        115                 120                 125

Gln Gly Asn Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Thr Asp
    130                 135                 140

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Lys
145                 150                 155                 160

Tyr Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
                165                 170                 175

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
            180                 185                 190

Ser Ala Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Ser Ile
        195                 200                 205

Val Ser Pro Phe Ile Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
    210                 215                 220

Tyr Ile Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala
225                 230                 235                 240

Lys Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
                245                 250                 255

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
            260                 265                 270

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
        275                 280                 285

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
    290                 295                 300

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
305                 310                 315                 320

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
                325                 330                 335
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Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
            340                 345                 350

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
        355                 360                 365

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
    370                 375                 380

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
385                 390                 395                 400

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
                405                 410                 415

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
            420                 425                 430

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
        435                 440                 445

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
    450                 455                 460

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
465                 470                 475                 480

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
                485                 490                 495

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
            500                 505                 510

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
        515                 520                 525

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
    530                 535                 540

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
```

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545                 550                 555                 560

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
                565                 570                 575

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
            580                 585                 590

Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
        595                 600                 605

Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
    610                 615                 620

Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
625                 630                 635                 640

Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
                645                 650                 655

Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
            660                 665                 670

Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
        675                 680                 685

Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
    690                 695                 700

Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
705                 710                 715                 720

Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
                725                 730                 735

Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
            740                 745                 750

Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
        755                 760                 765
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Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
    770                 775                 780

Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
785                 790                 795                 800

Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
                805                 810                 815

Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
            820                 825                 830

Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
        835                 840                 845

Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile
    850                 855                 860

His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
865                 870                 875                 880

Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
                885                 890                 895

Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
            900                 905                 910

Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
        915                 920                 925

Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
    930                 935                 940

Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
945                 950                 955                 960

Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
                965                 970                 975

Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
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            980                 985                 990

Leu Leu Gln Tyr Gly Ser Phe Cys  Thr Gln Leu Asn Arg  Ala Leu Thr
        995                 1000                1005

Gly Ile  Ala Val Glu Gln Asp  Lys Asn Thr Gln Glu  Val Phe Ala
    1010                1015                1020

Gln Val  Lys Gln Ile Tyr Lys  Thr Pro Pro Ile Lys  Asp Phe Gly
    1025                1030                1035

Gly Phe  Asn Phe Ser Gln Ile  Leu Pro Asp Pro Ser  Lys Pro Ser
    1040                1045                1050

Lys Arg  Ser Phe Ile Glu Asp  Leu Leu Phe Asn Lys  Val Thr Leu
    1055                1060                1065

Ala Asp  Ala Gly Phe Ile Lys  Gln Tyr Gly Asp Cys  Leu Gly Asp
    1070                1075                1080

Ile Ala  Ala Arg Asp Leu Ile  Cys Ala Gln Lys Phe  Asn Gly Leu
    1085                1090                1095

Thr Val  Leu Pro Pro Leu Leu  Thr Asp Glu Met Ile  Ala Gln Tyr
    1100                1105                1110

Thr Ser  Ala Leu Leu Ala Gly  Thr Ile Thr Ser Gly  Trp Thr Phe
    1115                1120                1125

Gly Ala  Gly Ala Ala Leu Gln  Ile Pro Phe Ala Met  Gln Met Ala
    1130                1135                1140

Tyr Arg  Phe Asn Gly Ile Gly  Val Thr Gln Asn Val  Leu Tyr Glu
    1145                1150                1155

Asn Gln  Lys Leu Ile Ala Asn  Gln Phe Asn Ser Ala  Ile Gly Lys
    1160                1165                1170

Ile Gln  Asp Ser Leu Ser Ser  Thr Ala Ser Ala Leu  Gly Lys Leu
    1175                1180                1185
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Gln Asp  Val Val Asn Gln Asn  Ala Gln Ala Leu Asn  Thr Leu Val
    1190                1195                1200

Lys Gln  Leu Ser Ser Asn Phe  Gly Ala Ile Ser Ser  Val Leu Asn
    1205                1210                1215

Asp Ile  Leu Ser Arg Leu Asp  Lys Val Glu Ala Glu  Val Gln Ile
    1220                1225                1230

Asp Arg  Leu Ile Thr Gly Arg  Leu Gln Ser Leu Gln  Thr Tyr Val
    1235                1240                1245

Thr Gln  Gln Leu Ile Arg Ala  Ala Glu Ile Arg Ala  Ser Ala Asn
    1250                1255                1260

Leu Ala  Ala Thr Lys Met Ser  Glu Cys Val Leu Gly  Gln Ser Lys
    1265                1270                1275

Arg Val  Asp Phe Cys Gly Lys  Gly Tyr His Leu Met  Ser Phe Pro
    1280                1285                1290

Gln Ser  Ala Pro His Gly Val  Val Phe Leu His Val  Thr Tyr Val
    1295                1300                1305

Pro Ala  Gln Glu Lys Asn Phe  Thr Thr Ala Pro Ala  Ile Cys His
    1310                1315                1320

Asp Gly  Lys Ala His Phe Pro  Arg Glu Gly Val Phe  Val Ser Asn
    1325                1330                1335

Gly Thr  His Trp Phe Val Thr  Gln Arg Asn Phe Tyr  Glu Pro Gln
    1340                1345                1350

Ile Ile  Thr Thr Asp Asn Thr  Phe Val Ser Gly Asn  Cys Asp Val
    1355                1360                1365

Val Ile  Gly Ile Val Asn Asn  Thr Val Tyr Asp Pro  Leu Gln Pro
    1370                1375                1380

Glu Leu  Asp Ser Phe Lys Glu  Glu Leu Asp Lys Tyr  Phe Lys Asn
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    1385                1390                1395

His Thr  Ser Pro Asp Val Asp  Leu Gly Asp Ile Ser  Gly Ile Asn
    1400                1405                1410

Ala Ser  Val Val Asn Ile Gln  Lys Glu Ile Asp Arg  Leu Asn Glu
    1415                1420                1425

Val Ala  Lys Asn Leu Asn Glu  Ser Leu Ile Asp Leu  Gln Glu Leu
    1430                1435                1440

Gly Lys  Tyr Glu Gln Tyr Ile  Lys Trp Pro Trp Tyr  Ile Trp Leu
    1445                1450                1455

Gly Phe  Ile Ala Gly Leu Ile  Ala Ile Val Met Val  Thr Ile Met
    1460                1465                1470

Leu Cys  Cys Met Thr Ser Cys  Cys Ser Cys Leu Lys  Gly Cys Cys
    1475                1480                1485

Ser Cys  Gly Ser Cys Cys Lys  Phe Asp Glu Asp Asp  Ser Glu Pro
    1490                1495                1500

Val Leu  Lys Gly Val Lys Leu  His Tyr Thr
    1505                1510
```