SEQUENCE LISTING

<110> INSTITUT PASTEUR
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS)

<120> LASSA VACCINE

<130> B12929A - AD/HLQ/KN

<140> PCT/FRXX XXX XXX
<141> 2018-12-20

<150> US 62/609155
<151> 2017-12-21

<160> 17

<170> PatentIn version 3.5

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Lys Gly Leu Tyr Asn Phe Ala Thr Cys Gly Leu Val Gly Leu Val Thr
35 40 45

Phe Leu Leu Leu Cys Gly Arg Ser Cys Thr Thr Ser Leu Tyr Lys Gly
50 55 60

Val Tyr Glu Leu Gln Thr Leu Glu Leu Asn Met Glu Thr Leu Asn Met
65 70 75 80

Thr Met Pro Leu Ser Cys Thr Lys Asn Asn Ser His His Tyr Ile Met

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                85                  90                  95

Val Gly Asn Glu Thr Gly Leu Glu Leu Thr Leu Thr Asn Thr Ser Ile
            100                 105                 110

Ile Asn His Lys Phe Cys Asn Leu Ser Asp Ala His Lys Lys Asn Leu
        115                 120                 125

Tyr Asp His Ala Leu Met Ser Ile Ile Ser Thr Phe His Leu Ser Ile
    130                 135                 140

Pro Asn Phe Asn Gln Tyr Glu Ala Met Ser Cys Asp Phe Asn Gly Gly
145                 150                 155                 160

Lys Ile Ser Val Gln Tyr Asn Leu Ser His Ser Tyr Ala Gly Asp Ala
                165                 170                 175

Ala Asn His Cys Gly Thr Val Ala Asn Gly Val Leu Gln Thr Phe Met
            180                 185                 190

Arg Met Ala Trp Gly Gly Ser Tyr Ile Ala Leu Asp Ser Gly Arg Gly
        195                 200                 205

Asn Trp Asp Cys Ile Met Thr Ser Tyr Gln Tyr Leu Ile Ile Gln Asn
    210                 215                 220

Thr Thr Trp Glu Asp His Cys Gln Phe Ser Arg Pro Ser Pro Ile Gly
225                 230                 235                 240

Tyr Leu Gly Leu Leu Ser Gln Arg Thr Arg Asp Ile Tyr Ile Ser Arg
                245                 250                 255

Arg Leu Leu Gly Thr Phe Thr Trp Thr Leu Ser Asp Ser Glu Gly Lys
            260                 265                 270

Asp Thr Pro Gly Gly Tyr Cys Leu Thr Arg Trp Met Leu Ile Glu Ala
        275                 280                 285
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Glu Leu Lys Cys Phe Gly Asn Thr Ala Val Ala Lys Cys Asn Glu Lys
    290                 295                 300

His Asp Glu Glu Phe Cys Asp Met Leu Arg Leu Phe Asp Phe Asn Lys
305                 310                 315                 320

Gln Ala Ile Gln Arg Leu Lys Ala Glu Ala Gln Met Ser Ile Gln Leu
                325                 330                 335

Ile Asn Lys Ala Val Asn Ala Leu Ile Asn Asp Gln Leu Ile Met Lys
            340                 345                 350

Asn His Leu Arg Asp Ile Met Gly Ile Pro Tyr Cys Asn Tyr Ser Lys
        355                 360                 365

Tyr Trp Tyr Leu Asn His Thr Thr Thr Gly Arg Thr Ser Leu Pro Lys
    370                 375                 380

Cys Trp Leu Val Ser Asn Gly Ser Tyr Leu Asn Glu Thr His Phe Ser
385                 390                 395                 400

Asp Asp Ile Glu Gln Gln Ala Asp Asn Met Ile Thr Glu Met Leu Gln
                405                 410                 415

Lys Glu Tyr Met Glu Arg Gln Gly Lys Thr Pro Leu Gly Leu Val Asp
            420                 425                 430

Leu Phe Val Phe Ser Thr Ser Phe Tyr Leu Ile Ser Ile Phe Leu His
        435                 440                 445

Leu Val Lys Ile Pro Thr His Arg His Ile Val Gly Lys Ser Cys Pro
    450                 455                 460

Lys Pro His Arg Leu Asn His Met Gly Ile Cys Ser Cys Gly Leu Tyr
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Lys Gln Pro Gly Val Pro Val Lys Trp Lys Arg
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485 490

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cacctgtcca tccccaattt caaccagtac gaggcaatgt catgcgactt caacgggggc 480

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Lys Asp Ala Gln Ala Leu Leu His Gly Leu Asp Phe Ser Glu Val Ser
35 40 45

Asn Val Gln Arg Leu Met Arg Lys Glu Arg Arg Asp Asp Asn Asp Leu
50 55 60

Lys Arg Leu Arg Asp Leu Asn Gln Ala Val Asn Asn Leu Val Glu Leu
65 70 75 80

Lys Ser Thr Gln Gln Lys Ser Ile Leu Arg Val Gly Thr Leu Thr Ser
85 90 95

Asp Asp Leu Leu Ile Leu Ala Ala Asp Leu Glu Lys Leu Lys Ser Lys
100 105 110

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Val Ile Arg Thr Glu Arg Pro Leu Ser Ala Gly Val Tyr Met Gly Asn
        115                 120                 125

Leu Ser Ser Gln Gln Leu Asp Gln Arg Arg Ala Leu Leu Asn Met Ile
    130                 135                 140

Gly Met Ser Gly Gly Asn Gln Gly Ala Arg Ala Gly Arg Asp Gly Val
145                 150                 155                 160

Val Arg Val Trp Asp Val Lys Asn Ala Glu Leu Leu Asn Asn Gln Phe
                165                 170                 175

Gly Thr Met Pro Ser Leu Thr Leu Ala Cys Leu Thr Lys Gln Gly Gln
            180                 185                 190

Val Asp Leu Asn Asp Ala Val Gln Ala Leu Thr Asp Leu Gly Leu Ile
        195                 200                 205

Tyr Thr Ala Lys Tyr Pro Asn Thr Ser Asp Leu Asp Arg Leu Thr Gln
    210                 215                 220

Ser His Pro Ile Leu Asn Met Ile Asp Thr Lys Lys Ser Ser Leu Asn
225                 230                 235                 240

Ile Ser Gly Tyr Asn Phe Ser Leu Gly Ala Ala Val Lys Ala Gly Ala
                245                 250                 255

Cys Met Leu Asp Gly Gly Asn Met Leu Glu Thr Ile Lys Val Ser Pro
            260                 265                 270

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

Leu Gly Met Phe Ile Ser Asp Thr Pro Gly Glu Arg Asn Pro Tyr Glu
    290                 295                 300

Asn Ile Leu Tyr Lys Ile Cys Leu Ser Gly Asp Gly Trp Pro Tyr Ile
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305                 310                 315                 320

Ala Ser Arg Thr Ser Ile Thr Gly Arg Ala Trp Glu Asn Thr Val Val
                325                 330                 335

Asp Leu Glu Ser Asp Gly Lys Pro Gln Lys Ala Asp Ser Asn Asn Ser
            340                 345                 350

Ser Lys Ser Leu Gln Ser Ala Gly Phe Thr Ala Gly Leu Thr Tyr Ser
        355                 360                 365

Gln Leu Met Thr Leu Lys Asp Ala Met Leu Gln Leu Asp Pro Asn Ala
    370                 375                 380

Lys Thr Trp Met Asp Ile Glu Gly Arg Pro Glu Asp Pro Val Glu Ile
385                 390                 395                 400

Ala Leu Tyr Gln Pro Ser Ser Gly Cys Tyr Ile His Phe Phe Arg Glu
                405                 410                 415

Pro Thr Asp Leu Lys Gln Phe Lys Gln Asp Ala Lys Tyr Ser His Gly
            420                 425                 430

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

Val Ile Asp Ala Leu Pro Arg Asn Met Val Ile Thr Cys Gln Gly Ser
    450                 455                 460

Asp Asp Ile Arg Lys Leu Leu Glu Ser Gln Gly Arg Lys Asp Ile Lys
465                 470                 475                 480

Leu Ile Asp Ile Ala Leu Ser Lys Thr Asp Ser Arg Lys Tyr Glu Asn
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Ala Val Trp Asp Gln Tyr Lys Asp Leu Cys His Met His Thr Gly Val
            500                 505                 510
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Val Val Glu Lys Lys Lys Arg Gly Gly Lys Glu Glu Ile Thr Pro His
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Cys Ala Leu Met Asp Cys Ile Met Phe Asp Ala Ala Val Ser Gly Gly
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Arg Thr Ser Thr Pro Arg Val Val Leu
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Lys Asp Ala Gln Ala Leu Leu His Gly Leu Asp Phe Ser Glu Val Ser
        35                  40                  45

Asn Val Gln Arg Leu Met Arg Lys Glu Arg Arg Asp Asp Asn Asp Leu
    50                  55                  60

Lys Arg Leu Arg Asp Leu Asn Gln Ala Val Asn Asn Leu Val Glu Leu
65                  70                  75                  80

Lys Ser Thr Gln Gln Lys Ser Ile Leu Arg Val Gly Thr Leu Thr Ser
                85                  90                  95

Asp Asp Leu Leu Ile Leu Ala Ala Asp Leu Glu Lys Leu Lys Ser Lys
            100                 105                 110

Val Ile Arg Thr Glu Arg Pro Leu Ser Ala Gly Val Tyr Met Gly Asn
        115                 120                 125

Leu Ser Ser Gln Gln Leu Asp Gln Arg Arg Ala Leu Leu Asn Met Ile
    130                 135                 140

Gly Met Ser Gly Gly Asn Gln Gly Ala Arg Ala Gly Arg Asp Gly Val
145                 150                 155                 160

Val Arg Val Trp Asp Val Lys Asn Ala Glu Leu Leu Asn Asn Gln Phe
                165                 170                 175

Gly Thr Met Pro Ser Leu Thr Leu Ala Cys Leu Thr Lys Gln Gly Gln
            180                 185                 190

Val Asp Leu Asn Asp Ala Val Gln Ala Leu Thr Asp Leu Gly Leu Ile
        195                 200                 205

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

Cys Met Leu Asp Gly Gly Asn Met Leu Glu Thr Ile Lys Val Ser Pro
            260                 265                 270

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

Leu Gly Met Phe Ile Ser Asp Thr Pro Gly Glu Arg Asn Pro Tyr Glu
    290                 295                 300

Asn Ile Leu Tyr Lys Ile Cys Leu Ser Gly Asp Gly Trp Pro Tyr Ile
305                 310                 315                 320

Ala Ser Arg Thr Ser Ile Thr Gly Arg Ala Trp Glu Asn Thr Val Val
                325                 330                 335

Asp Leu Glu Ser Asp Gly Lys Pro Gln Lys Ala Asp Ser Asn Asn Ser
            340                 345                 350

Ser Lys Ser Leu Gln Ser Ala Gly Phe Thr Ala Gly Leu Thr Tyr Ser
        355                 360                 365

Gln Leu Met Thr Leu Lys Asp Ala Met Leu Gln Leu Asp Pro Asn Ala
    370                 375                 380

Lys Thr Trp Met Ala Ile Glu Ala Arg Pro Glu Asp Pro Val Glu Ile
385                 390                 395                 400

Ala Leu Tyr Gln Pro Ser Ser Gly Cys Tyr Ile His Phe Phe Arg Glu
                405                 410                 415

Pro Thr Asp Leu Lys Gln Phe Lys Gln Asp Ala Lys Tyr Ser His Gly
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420 425 430

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

Val Ile Asp Ala Leu Pro Arg Asn Met Val Ile Thr Cys Gln Gly Ser
450 455 460

Asp Asp Ile Arg Lys Leu Leu Glu Ser Gln Gly Arg Lys Asp Ile Lys
465 470 475 480

Leu Ile Asp Ile Ala Leu Ser Lys Thr Asp Ser Arg Lys Tyr Glu Asn
485 490 495

Ala Val Trp Asp Gln Tyr Lys Asp Leu Cys His Met His Thr Gly Val
500 505 510

Val Val Glu Lys Lys Lys Arg Gly Gly Lys Glu Glu Ile Thr Pro His
515 520 525

Cys Ala Leu Met Asp Cys Ile Met Phe Asp Ala Ala Val Ser Gly Gly
530 535 540

Leu Asn Thr Ser Val Leu Arg Ala Val Leu Pro Arg Asp Met Val Phe
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Arg Thr Ser Thr Pro Arg Val Val Leu
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<213> Artificial Sequence

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<223> Codon-optimized cDNA mutated NP

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Ser Cys Trp Phe Glu Asn Lys Gly Leu Val Glu Cys Asn Asn His Tyr
35 40 45

Leu Cys Leu Asn Cys Leu Thr Leu Leu Leu Ser Val Ser Asn Arg Cys
50 55 60

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

Pro Thr Ala Pro Pro Thr Gly Ala Ala Asp Ser Ile Arg Pro Pro Pro
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Tyr Ser Pro

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