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(54) 발명의 명칭 **항종양 아레나바이러스 및 아레나바이러스 돌연변이체의 제조 방법**

(57) 요 약

본 발명은 개선된 항종양 특성을 갖는 아레나바이러스의 돌연변이에 관한 것이다. 본 발명은 또한 그러한 아레나바이러스 돌연변이체를 생산하는 방법, 관련 약학적 조성물, 의학적 용도, 치료 방법, 및 단리된 단백질 및 핵산에 관한 것이다.

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명 세 서

청구범위

청구항 1

림프구성 맥락수막염 바이러스의 돌연변이체로서, 여기서 돌연변이체는 야생형 림프구성 맥락수막염 바이러스 균주 WE와 비교하여 종양 세포에서 더 강한 증식을 겪을 수 있고, 돌연변이체는 당단백질을 인코딩하는 핵산을 포함하고, 상기 당단백질은 서열 번호 10에 제시된 야생형 당단백질 서열과 비교하여 돌연변이 Arg 185 → Trp 및 Ile 181 → Met 중 적어도 하나를 포함하는 것인, 돌연변이체.

청구항 2

제1항에 있어서, 돌연변이체는 서열 번호 10에 제시된 야생형 당단백질 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖는 당단백질을 인코딩하는 핵산을 포함하는 것인, 돌연변이체.

청구항 3

제1항 또는 제2항에 있어서, 돌연변이체는 당단백질을 인코딩하는 핵산을 포함하며, 여기서 상기 당단백질은 서열 번호 10에 제시된 야생형 당단백질과 비교하여 돌연변이 Arg 185 → Trp 및 Ile 181 → Met를 포함하는 것인, 돌연변이체.

청구항 4

제1항 내지 제3항 중 어느 한 항에 있어서, 돌연변이체는 당단백질을 인코딩하는 핵산을 포함하며, 여기서 상기 당단백질은 서열 번호 18, 26, 34, 42, 50 및 58 중 어느 하나에 제시된 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가지거나 또는 바람직하게는 그와 동일한 것인, 돌연변이체.

청구항 5

제1항 내지 제4항 중 어느 한 항에 있어서, 돌연변이체는 당단백질을 인코딩하는 핵산을 포함하며, 여기서 상기 핵산은 서열 번호 17, 25, 33, 41, 49 및 57에 제시된 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가지거나 또는 바람직하게는 그와 동일한 서열을 포함하는 것인, 돌연변이체.

청구항 6

제1항에 있어서, 돌연변이체는 L-단백질을 인코딩하는 핵산을 포함하며, 여기서 상기 L-단백질은 서열 번호 16에 제시된 야생형 L-단백질 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖는 것인, 돌연변이체.

청구항 7

제1항 내지 제6항 중 어느 한 항에 있어서, 돌연변이체는 L-단백질을 인코딩하는 핵산을 포함하며, 여기서 상기 L-단백질은 서열 번호 24, 32, 40, 48, 56 및 64 중 어느 하나에 제시된 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는

적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%, 바람직하게는 적어도 약 99.8%, 바람직하게는 적어도 약 99.9%의 서열 동일성을 가지거나 또는 바람직하게는 그와 동일한 것인, 돌연변이체.

청구항 8

제1항 내지 제7항 중 어느 한 항에 있어서, 돌연변이체는 L-단백질을 인코딩하는 핵산을 포함하며, 여기서 상기 L-단백질은 서열 번호 16에 제시된 야생형 L-단백질 서열과 비교하여 다음 돌연변이 세트: Lys 253 → Arg; Lys 1512 → Met; Lys 1513 → Glu; Ser 1758 → Phe; Phe 1995 → Ser; Ile 2094 → Val; Lys 2115 → Glu; Thr 2141 → Ala; Arg 2175 → Lys; Thr 2185 → Ala 중 1, 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개를 포함하는 것인, 돌연변이체.

청구항 9

제1항 내지 제8항 중 어느 한 항에 있어서, 돌연변이체는 L-단백질을 인코딩하는 핵산을 포함하며, 상기 L-단백질은 서열 번호 16에 제시된 야생형 L-단백질 서열과 비교하여 다음 돌연변이 세트 중 하나를 포함하는 것인, 돌연변이체:

(a) Ser 1758 → Phe;

(b) Phe 1995 → Ser; 선택적으로 Ile 2094 → Val; 및 선택적으로 Thr 2141 → Ala;

(c) Lys 1513 → Glu; Phe 1995 → Ser; 및 선택적으로 Arg 2175 → Lys;

(d) Lys 253 → Arg; Lys 1512 → Met; Lys 2115 → Glu; 선택적으로 Thr 2141 → Ala; Thr 2185 → Ala

(e) Phe 1995 → Ser; 또는

(f) Lys 2115 → Glu.

청구항 10

제1항 내지 제9항 중 어느 한 항에 있어서, 돌연변이체는 L-단백질을 인코딩하는 핵산을 포함하며, 여기서 상기 핵산은 서열 번호 17, 25, 33, 41, 49 및 57에 제시된 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%, 바람직하게는 적어도 약 99.8%, 바람직하게는 적어도 약 99.9%의 서열 동일성을 가지거나 또는 바람직하게는 그와 동일한 서열에 상보적인 것인, 돌연변이체.

청구항 11

제1항 내지 제10항 중 어느 한 항에 있어서, 돌연변이체는 핵단백질을 인코딩하는 핵산을 포함하며, 여기서 상기 핵단백질은 서열 번호 12, 20, 28, 36, 44, 52, 및 60 중 어느 하나에 제시된 핵단백질에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가지거나 또는 바람직하게는 그와 동일한 것인, 돌연변이체.

청구항 12

제1항 내지 제11항 중 어느 한 항에 있어서, 돌연변이체는 핵단백질을 인코딩하는 핵산을 포함하며, 여기서 상기 핵산은 서열 번호 11, 19, 27, 35, 43, 51, 및 59 중 어느 하나에 제시된 핵단백질에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가지거나 또는 바람직하게는 그와 동일한 서열에 상보적인 것인, 돌연변이체.

청구항 13

제1항 내지 제12항 중 어느 한 항에 있어서, 돌연변이체는 Z-단백질을 인코딩하는 핵산을 포함하며, 여기서 상기 Z-단백질은 서열 번호 14, 22, 30, 38, 46, 54, 및 62 중 어느 하나에 제시된 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가지거나 또는 바람직하게는 그와 동일한 것인, 돌연변이체.

청구항 14

제1항 내지 제13항 중 어느 한 항에 있어서, 돌연변이체는 Z-단백질을 인코딩하는 핵산을 포함하며, 여기서 상기 핵산은 서열 번호 13, 21, 29, 37, 45, 53, 및 61 중 어느 하나에 제시된 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가지거나 또는 그와 동일한 서열을 포함하는 것인, 돌연변이체.

청구항 15

항종양 아레나바이러스, 특히 오리지널 아레나바이러스에 비해 개선된 항종양 특성을 갖는 아레나바이러스의 생산 방법으로서, 상기 방법은

a) 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포를 영양 배지 상에 및/또는 내에 플레이팅하는 단계,

b) 플레이팅된 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포를 오리지널 아레나바이러스로 접종하는 단계,

c) 접종된 원발성 종양 세포 또는 접종된 세포주 H1975, C643 또는 Tramp-C2의 세포의 적어도 일부를 오리지널 아레나바이러스로 감염시키기에 적합한 조건 하에서, 접종된 원발성 종양 세포 또는 접종된 세포주 H1975, C643 또는 Tramp-C2의 세포를 인큐베이팅하는 단계,

d) 인큐베이팅된 원발성 종양 세포 또는 인큐베이팅된 세포주 H1975, C643 또는 Tramp-C2의 세포를 함유하는 세포 배양물로부터 아레나바이러스 함유 세포 배양 상청액을 추출하는 단계를 포함하며,

여기서 단계 순서 a) 내지 d)는 여러번 반복되고, 단계 순서 a) 내지 d)의 첫 번째 반복을 수행할 때의 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포는, 단계 b)를 수행하기 위해, 단계 순서 a) 내지 d)의 첫 번째 반복 전 단계 d)를 수행할 때 추출된 아레나바이러스 함유 세포 배양 상청액 또는 그 일부로 접종되고, 단계 순서 a) 내지 d)의 각각의 추가의 반복을 수행할 때의 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포는, 단계 b)를 수행하기 위해, 단계 순서 a) 내지 d)의 이전의 반복의 단계 d)를 수행할 때 추출된 아레나바이러스 함유 세포 배양 상청액 또는 그 일부로 접종되는 것인, 방법.

청구항 16

제15항에 있어서, 원발성 종양 세포는 단계 a)를 수행하기 전에, 최대 1000 회, 특히 최대 100 회, 바람직하게는 최대 10 회 계대되는 것을 특징으로 하는, 방법.

청구항 17

제15항 또는 제16항에 있어서, 단계 c)는 다음과 같이 수행되는 것을 특징으로 하는, 방법:

- 1 시간 내지 1000 시간, 특히 3 시간 내지 300 시간, 바람직하게는 12 시간 내지 96 시간의 기간 내에, 및/또는

- 4 ℃ 내지 50 ℃, 특히 20 ℃ 내지 42 ℃, 바람직하게는 34 ℃ 내지 39 ℃의 온도에서, 및/또는

- RPMI-1640, DMEM 및 IMDM으로 이루어진 군으부터 선택되는 영양 배지 중에서 - 상기 영양 배지는 태아 소 혈청 또는 인간 혈청과 같은 혈청, 및/또는 글루타메이트 및/또는 글루타민과 같은 아미노산, 및/또는 항생제를 추가적으로 포함함 -, 및/또는

- 0% 내지 20%, 특히 2% 내지 10%, 바람직하게는 4% 내지 6%의 이산화탄소 분위기 하에서.

청구항 18

제15항 내지 제17항 중 어느 한 항에 있어서, 단계의 순서는 3 내지 1000 회, 특히 10 내지 100 회, 바람직하게는 20 내지 50 회 반복되는 것인, 방법.

청구항 19

제15항 내지 제18항 중 어느 한 항에 있어서,

- 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포 및/또는

- 오리지널 아레나바이러스 및/또는 추출된 세포 배양 상청액 또는 그 일부에 포함된 아레나바이러스는 단계 d)를 수행하기 전에 적어도 하나의 화학요법제로 처리되고/되거나 방사선 처리를 받음, 및/또는

- 적어도 하나의 화학요법제에 대해 내성이 있는 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포가 사용됨, 및/또는

- 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포 및/또는 오리지널 아레나바이러스 및/또는 추출된 세포 배양 상청액 또는 그 일부에 함유된 아레나바이러스는 단계 d)를 수행하기 전에 적어도 하나의 항바이러스 화합물, 특히 알파-인터페론 및/또는 감마-인터페론으로 처리됨을 특징으로 하는, 방법.

청구항 20

제15항 내지 제19항 중 어느 한 항에 있어서, 원발성 종양 세포는 원발성 맥락막 흑색종 세포, 원발성 항문 암종 세포, 원발성 혈관 육종 세포, 원발성 성상세포종 세포, 원발성 기저 세포 암종 세포, 원발성 자궁경부 암종 세포, 원발성 연골육종 세포, 원발성 융모막 암종 세포, 원발성 진피 편평 세포 암종 세포, 원발성 소장 암종 세포, 원발성 자궁내막 암종 세포, 원발성 Ewing 육종 세포, 원발성 섬유 육종 세포, 원발성 담낭 암종 세포, 원발성 담관 암종 세포, 원발성 교모세포종 세포, 원발성 방광 암종 세포, 원발성 요관 암종 세포, 원발성 요도 암종 세포, 원발성 간세포 암종 세포, 원발성 고환 종양 세포, 원발성 하인두 암종 세포, 원발성 뇌하수체 암종 세포, 원발성 카포시 육종 세포, 원발성 소세포 기관지 암종 세포, 원발성 결장 암종 세포, 원발성 결장직장 암종 세포, 원발성 후두 암종 세포, 원발성 평활근 육종 세포, 원발성 지방 육종 세포, 원발성 위 암종 세포, 원발성 악성 섬유성 조직구종 세포, 원발성 유방 암종 세포, 원발성 수모세포종 세포, 원발성 흑색종 세포, 원발성 구강 저 암종 세포, 원발성 부비동 암종 세포, 원발성 비인두 암종 세포, 원발성 부신 피질 암종 세포, 원발성 부갑상선 암종 세포, 원발성 신경성 육종 세포, 원발성 비소세포 기관지 암종 세포, 원발성 신장 암종 세포, 원발성 구강 인두 암종 세포, 원발성 골육종 세포, 원발성 난소 암종 세포, 원발성 췌장 종양 세포, 원발성 음경 암종 세포, 원발성 갈색세포종 세포, 원발성 흉막중피종 세포, 원발성 전립선 암종 세포, 원발성 직장 암종 세포, 원발성 망막 모세포종 세포, 원발성 횡문근 육종 세포, 원발성 갑상선 암종 세포, 원발성 타액선 암종 세포, 원발성 식도 암종 세포, 원발성 편도선 암종 세포, 원발성 질 암종 세포, 원발성 외음부 암종 세포, 원발성 Wilms 종양 세포, 원발성 신경 내분비 종양의 세포 및 원발성 혀 암종 세포로 이루어진 군으로부터 선택되는 것을 특징으로 하는, 방법.

청구항 21

제15항 내지 제20항 중 어느 한 항에 있어서, 오리지널 아레나바이러스로서 야생형 아레나바이러스, 특히 야생형 림프구성 맥락수막염 바이러스가 사용되는 것을 특징으로 하는, 방법.

청구항 22

하기를 포함하는 림프구성 맥락수막염 바이러스 돌연변이체:

- 적어도 하나의 돌연변이를 갖는 당단백질, 여기서 적어도 하나의 돌연변이는 당단백질의 위치 181에서의 이소류신의 다른 아미노산에 의한, 바람직하게는 메티오닌에 의한 아미노산 치환, 및/또는 당단백질의 위치 185에서의 아르기닌의 다른 아미노산에 의한, 바람직하게는 트립토판에 의한 아미노산 치환임, 및/또는

- 적어도 하나의 돌연변이를 갖는 L-단백질, 여기서 적어도 하나의 돌연변이는 L-단백질의 위치 1513에서의 라이신의 다른 아미노산에 의한, 바람직하게는 글루타메이트에 의한 아미노산 치환, 및/또는 L-단백질의 위치 1995에서의 페닐알라닌의 다른 아미노산에 의한, 바람직하게는 세린에 의한 아미노산 치환, 및/또는 L-단백질의

위치 2094에서의 이소류신의 다른 아미노산에 의한, 바람직하게는 발린에 의한 아미노산 치환, 및/또는 L-단백질의 위치 2141에서의 트레오닌의 다른 아미노산에 의한, 바람직하게는 알라닌에 의한 아미노산 치환, 및/또는 L-단백질의 위치 2175에서의 아르기닌의 다른 아미노산에 의한, 바람직하게는 라이신에 의한 아미노산 치환임.

청구항 23

제22항에 있어서, 림프구성 맥락수막염 바이러스 돌연변이체는 서열 번호 1, 서열 번호 3, 서열 번호 5, 서열 번호 18, 서열 번호 26, 서열 번호 34, 서열 번호 42, 서열 번호 50, 서열 번호 58, 서열 번호 24, 서열 번호 32, 서열 번호 40, 서열 번호 48, 서열 번호 56, 또는 서열 번호 64에 따른 아미노산 서열을 갖거나 또는 이로 이루어진, 단백질 또는 펩티드, 특히 당단백질 또는 L-단백질을 포함하는 것을 특징으로 하는, 림프구성 맥락수막염 바이러스 돌연변이체.

청구항 24

제22항 또는 제23항에 있어서, 림프구성 맥락수막염 바이러스 돌연변이체는 서열 번호 1, 서열 번호 3, 서열 번호 5, 서열 번호 18, 서열 번호 26, 서열 번호 34, 서열 번호 42, 서열 번호 50, 서열 번호 58, 서열 번호 24, 서열 번호 32, 서열 번호 40, 서열 번호 48, 서열 번호 56, 또는 서열 번호 64에 따른 아미노산 서열을 포함하거나 이로 이루어진 단백질 또는 펩티드를 코딩하는 핵산을 포함하고/하거나, 림프구성 맥락수막염 바이러스 돌연변이체는 서열 번호 2, 서열 번호 4, 서열 번호 6, 서열 번호 17, 서열 번호 25, 서열 번호 33, 서열 번호 41, 서열 번호 49, 서열 번호 57, 서열 번호 23, 서열 번호 31, 서열 번호 39, 서열 번호 47, 서열 번호 55, 또는 서열 번호 63에 따른 핵산 서열이거나 그에 상보적인 핵산 서열을 갖거나 또는 핵산 서열로 이루어진 핵산을 포함하는 것을 특징으로 하는, 림프구성 맥락수막염 바이러스 돌연변이체.

청구항 25

제1항 내지 제14항 및 제22항 내지 제24항 중 어느 한 항에 있어서, 약제에 사용하기 위한, 특히 종양, 바람직하게는 항문 암종, 기관지 암종, 폐 암종, 자궁 내막 암종, 담낭 암종, 방광 암종, 간세포 암종, 고환 암종, 결장 암종, 결장직장 암종, 결장직장 암종, 간세포 암종, 고환 암종, 결장 암종, 방광의 종양, 방광 암종, 방광의 종양, 간세포 암종, 폐 암종, 폐 암종, 자궁 내막 암종, 결장직장 암종, 직장 암종, 후두 암종, 식도 암종, 위 암종, 유방 암종, 신장 암종, 난소 암종, 췌장 암종, 인두 암종, 안인두 안종, 전립선 암종, 갑상선 암종, 자궁경부 암종, 혈관 육종, 연골 육종, Ewing 육종, 섬유 육종, 카포시 육종, 지방 육종, 평활근 육종, 악성 섬유성 조직구종, 림프종, 백혈병, 신경성 육종, 골육종 및 횡문근 육종으로 이루어진 군으로부터 선택되는 종양의 치료 및/또는 예방에 사용하기 위한 림프구성 맥락수막염 바이러스 돌연변이체.

청구항 26

제1항 내지 제14항 및 제22항 내지 제24항 중 어느 한 항의 림프구성 맥락수막염 바이러스 돌연변이체를 포함하는 의약 또는 약학적 조성물.

청구항 27

제26항에 있어서, 의약이 PD-1과 같은 관문 차단제 및/또는 아폽토시스 조절제, 특히 SMAC mimeticum과 같은 아폽토시스 억제제를 추가로 포함하는 것을 특징으로 하는, 의약.

청구항 28

서열 번호 1, 서열 번호 3, 서열 번호 5, 서열 번호 7, 서열 번호 10, 서열 번호 18, 서열 번호 26, 서열 번호 34, 서열 번호 42, 서열 번호 50, 서열 번호 58, 서열 번호 24, 서열 번호 32, 서열 번호 40, 서열 번호 48, 서열 번호 56, 또는 서열 번호 64, 서열 번호 12, 서열 번호 20, 서열 번호 28, 서열 번호 36, 서열 번호 44, 서열 번호 52, 서열 번호 60, 서열 번호 14, 서열 번호 22, 서열 번호 30, 서열 번호 38, 서열 번호 46, 서열 번호 54, 또는 서열 번호 62에 따른 아미노산 서열을 포함하거나 이로 이루어진, 단리된 단백질 또는 펩티드, 특히 당단백질, L-단백질, 핵단백질, 또는 Z-단백질.

청구항 29

특히 당단백질, L-단백질, 핵단백질, 또는 Z-단백질을 인코딩하는 단리된 핵산으로서, 여기서 핵산은 서열 번호 2, 서열 번호 4, 서열 번호 6 또는 서열 번호 8, 서열 번호 9, 서열 번호 17, 서열 번호 25, 서열 번호 33, 서

열 번호 41, 서열 번호 49, 서열 번호 57, 서열 번호 23, 서열 번호 31, 서열 번호 39, 서열 번호 47, 서열 번호 55, 서열 번호 63, 서열 번호 11, 서열 번호 19, 서열 번호 27, 서열 번호 35, 서열 번호 43, 서열 번호 51, 서열 번호 59, 서열 번호 13, 서열 번호 21, 서열 번호 29, 서열 번호 37, 서열 번호 45, 서열 번호 53, 또는 서열 번호 61에 따른 핵산 서열이거나 이에 상보적인 핵산 서열을 갖거나 또는 핵산 서열로 이루어지는 것인, 단리된 핵산.

발명의 설명

기 술 분 야

[0001] 관련 출원의 상호 참조

[0002] 본 출원은 2018년 9월 12자로 출원된 독일 특허 출원 제DE10 2018 215 551.8호의 우선권을 주장하며, 상기 출원은 그 전체 내용이 모든 목적으로 본 명세서에 참고로서 포함된다.

[0003] 본 발명은 항종양 아레나바이러스, 아레나바이러스 돌연변이체, 단리된 단백질 또는 펩티드, 특히 단리된 당단백질, 아레나바이러스 및 해당 단백질 또는 펩티드를 인코딩하는 핵산의 제조 방법에 관한 것이다.

배 경 기 술

[0004] 아레나바이러스는 인간 병원성 다형태 RNA 바이러스의 패밀리(family)에 속한다. 이들 바이러스를 갖는 질병은 이의 동물, 주로 설치류 내 자연적 저장으로 인해 인수공통전염병에 속한다. 인수공통전염병은 동물로부터 인간으로 전염될 수 있고 그 반대로 인간으로부터 동물로 전염될 수 있는 질병이다.

[0005] 적어도 8가지의 아레나바이러스가 인간에서의 질병, 전형적으로 무균 수막염 및 출혈열을 유발하는 것으로 알려져 있다. 인간에게 질병을 일으킬 수 있는 알려진 바이러스는 림프구성 맥락수막염 바이러스(LCMV), 구아나리토 바이러스(GTOV), 후닌 바이러스(JUNV), 라사 바이러스(LASV), 루조 바이러스(LUJV), 마추포 바이러스(MACV), 사비아 바이러스(SABV) 및 화이트워터 아로요 바이러스(WWAV)이다.

[0006] 맘마레나바이러스(mammarenavirus) 속의 아레나바이러스는 Old World Arenaviruses와 New World Arenaviruses의 두 그룹으로 나뉜다. 이 그룹은 지리적 및 유전적으로 다르다. 림프구성 맥락수막염 바이러스와 같은 Old World Arenaviruses는 주로 유럽, 아시아 및 아프리카 국가와 같은 동반구 국가에서 발견되었다. 대조적으로, New World Arenavirus는 아르헨티나, 볼리비아, 베네수엘라, 브라질 및 미국과 같은 서반구 국가에서 발견되었다.

[0007] 아레나바이러스는 세포 내 복제되어 비리온(감염성 입자)으로서 세포외 공간으로 들어간다. 비리온은 주로 110 nm 내지 130 nm, 최대 50 nm 내지 300 nm의 직경을 가진 다형성의, 종종 둥근 모양을 가진다. 비리온의 캡시드는 이중 지질 막과 스파이크 모양으로 튀어 나온 당단백질(GP1 및 GP2)의 동종 삼량체로 구성된 외피 단백질로 둘러싸여 있다. GP1은 바깥쪽으로 향하고 감염시 세포 수용체에 결합한다. GP2는 반대 방향으로 향하고 세포와의 융합을 매개한다. Z-단백질은 뉴클레오캡시드 내부에 위치된 지질층 아래에 고리처럼 놓여 있으며, 리보핵산 단백질(RNP)-복합체는 각각 더 짧은 RNA 세그먼트(S 세그먼트 3.5kb), 더 긴 RNA 세그먼트(L 세그먼트 7.2kb) 및 핵단백질로 이루어진다. 바이러스 중합효소인 L-단백질은 RNP 복합체와 관련이 있다. L- 및 S-세그먼트는 각각 2개의 단백질에 대한 유전 정보와 코드를 전달한다. 단일 가닥 RNA는 혼합(즉, 음양공존성 극성)을 가지며, 3' 미번역 말단에서 서열(약 19-30 bp)은 또한 바이러스 패밀리 내에서 보존된다. 먼저, 핵단백질 및 L-단백질의 mRNA가 전사되고, 이어서 Z-단백질 및 당단백질 전구체의 복제 및 mRNA 전사가 뒤따르고, 마지막으로 바이러스 단백질의 번역 및 변형이 뒤따른다.

[0008] 백신 접종 벡터로서 아레나바이러스의 사용은 잘 알려져 있다. 대표적인 예는 아르헨티나 출혈열에 대해 사용된 백신 접종 바이러스 Candid #1이다. 이것은 후닌 바이러스의 백신 접종 변종이다.

[0009] WO 2009/083210 A1호로부터, 특히 흑색종, 전립선 암종, 유방 암종 및 폐 암종과 같은 종양성 질환의 치료를 위한 복제 결함, 즉 유전적으로 변형된 아레나바이러스 입자(비리온)의 사용이 알려져 있다. 간행물 "Development of replication-defective lymphocytic choriomeningitis virus vectors for the induction of potent CD8+ T cell immunity" (Nature Medicine, vol. 16, no. 3, March 2010, p. 339-345; doi: 10.1038/nm.2104)에서는 이러한 바이러스 입자 암 면역요법에 대한 잠재적인 적용으로서 언급하고 있다.

[0010] 추가로 WO 2006/008074 A1로부터, 고형 종양의 유전자 치료를 위한 레트로바이러스 및 아레나바이러스-당단백질 위형(pseudotyped) 비리온을 모두 생산하는 패키징 세포의 사용이 알려져 있다.

[0011] 상기 기술된 종양 치료를 위한 최첨단 방법은 유전 공학에 의해 생성하기에 매우 복잡한 바이러스 입자의 사용을 기반으로 한다. 또한, 유전자 요법 치료 방법의 경우, 유전적으로 조작된 비리온 또는 비리온을 생성하는 패키징 세포로 종양 조직의 충분하고 치료 효과적인 형질도입은 종종 달성되지 않고 있다.

[0012] 그러나, WO 2016/166285 A1호로부터, 종양의 치료 및/또는 예방을 위한 아레나바이러스가 알려져 있으며, 여기서 상기 아레나바이러스에는 게놈 외래 RNA가 없다. 추가로, WO 2016/166285 A1호로부터 종양 퇴행 특성을 갖는 아레나바이러스의 생산 방법이 알려져 있다.

[0013] 그럼에도 불구하고, 종양의 치료 및/또는 예방에 사용하기 위한 특정한, 특히 치료 효과적인 아레나바이러스에 대한 요구가 여전히 존재한다.

발명의 내용

해결하려는 과제

[0014] 본 발명의 근본적인 목적은 항종양 특성 및/또는 개선된 항종양 특성을 갖는 아레나바이러스를 생산하는 것이다. 더욱이, 본 발명의 근본적인 목적은 아레나바이러스의 상응하는 아레나바이러스 돌연변이체, 단리된 단백질 또는 펩티드, 특히 아레나바이러스의 당단백질 및/또는 L-단백질 뿐만 아니라 이들을 코딩하는 핵산을 제공하는 것이다.

[0015] 상기 목적은 독립 청구항 1에 따른 림프구성 맥락수막염 바이러스 돌연변이체, 독립 청구항 15에 따른 방법, 청구항 22에 따른 림프구성 맥락수막염 바이러스 돌연변이체, 청구항 26에 따른 의약 또는 약제학적 조성물, 청구항 28에 따른 단리된 단백질 또는 펩티드 및 청구항 29에 따른 단리된 핵산에 의해 해결된다. 방법 및 림프구성 맥락수막염 바이러스 돌연변이체의 바람직한 실시양태는 종속 청구항 및 본 설명의 대상이다. 본 발명의 추가적인 양태가 본 설명에 개시되어 있다. 모든 청구항의 표현은 본 설명의 내용에 대한 명시적인 참고로서 본 명세서에 포함된다.

과제의 해결 수단

[0016] 본 발명은 아레나바이러스, 특히 림프구성 맥락수막염 바이러스(LCMV)의 특정 돌연변이체가 야생형 바이러스에 비해 개선된 항종양 알티바이트(altivite)를 가질 수 있다는 놀라운 발견에 기초한다.

[0017] 따라서, 본 발명은 일반적으로 림프구성 맥락수막염 바이러스의 돌연변이체, 바람직하게는 균주 WE의 돌연변이체에 관한 것이다.

[0018] 돌연변이체는 야생형 림프구성 맥락수막염 바이러스 균주 WE와 비교하여 H1975 세포, HCC1954 세포, 뮤린 췌장암 세포 또는 인간 흑색종 세포와 같은 종양 세포에서 더 강력한 증식을 겪을 수 있다. 돌연변이체는 또한 생체 내에서 LCMV-WE 야생형보다 더 강한 선천적 면역 활성화를 유도할 수 있다. 돌연변이체는 또한 LCMV-WE 야생형보다 생체 내에서 더 강한 항종양 효과를 가질 수 있다. 돌연변이체는 또한 LCMV-WE 야생형과 비교하여 종양 특이적 CD8+ T 세포의 확장을 증가시킬 수 있다. 돌연변이체는 또한 종양 특이적 CD8+ T 세포의 기능을 증가시킬 수 있다. 돌연변이체는 또한 LCMV-WE 야생형과 비교하여 종양 특이적 T 세포를 자극하는 더 높은 능력을 가질 수 있다.

[0019] 본 발명의 림프구성 맥락수막염 바이러스의 돌연변이체는 바람직하게는 당단백질을 인코딩하는 핵산 - 여기서 상기 당단백질은 서열 번호 10에 제시된 야생형 당단백질 서열의 위치 181 및 185에 대응하는 위치에서의 적어도 하나의 돌연변이를 포함함. 바람직한 돌연변이는 서열번호 10에 제시된 야생형 당단백질 서열과 비교하여 Arg 185 → Trp 및/또는 Ile 181 → Met (예컨대 Arg 185 → Trp 만, Ile 181 → Met 만 또는 Arg 185 → Trp 및 Ile 181 → Met) 임 - 및/또는 상기 핵산에 의해 인코딩되는 각각의 단백질(들)을 포함한다. 본 출원의 예는 돌연변이 중 어느 하나의 존재가 야생형 림프구성 맥락수막염 바이러스에 비해 개선된 기능을 제공하기 위해 이미 충분할 수 있음을 입증하고 있지만, 언급된 두 돌연변이 모두의 존재는 LCMV의 기능을 더욱 향상시킬 것이며, 이는 부가적으로 또는 심지어 시너지로 작용할 수 있다. 따라서, 바람직한 실시양태에서, 두 돌연변이 모두가 본 발명의 LCMV에 존재한다.

[0020] 이론에 얽매이지 않고, 당단백질에서 1개 또는 2개의 상기 언급된 돌연변이의 존재가, 다른 돌연변이, 특히

LCMV의 다른 유전자 또는 단백질의 다른 돌연변이의 존재와 무관하게, LCMV의 기능(예를 들어, 상기 기재된 바와 같은 종양 세포에서의 복제 또는 증식 및/또는 항종양 활성 및/또는 면역계 자극)을 개선할 수 있다. 이 가정은 당단백질의 돌연변이 Arg 185 → Trp 및 Ile 181 → Met가 보존된 상태로 유지되는 반면, 일부 다른 돌연변이는 연속 계대 동안 나타나고 사라지고, 다른 돌연변이 균주간에 보존되지 않는다는 사실을 기반으로 한다. 이 가정은 추가로 LCMV의 당단백질(들)이 비리온 외피에 스파이크를 형성하고 따라서 바이러스가 종양 세포를 감염시키는 능력에서 우세한 역할을 하는 것으로 믿어진다는 사실을 기반으로 한다.

[0021] 본 발명의 LCMV 돌연변이체는 당단백질을 인코딩하는 핵산을 포함할 수 있고/있거나 - 여기서 상기 당단백질은 서열 번호 10에 제시된 야생형 당단백질 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가짐 -, 상기 핵산에 의해 인코딩된 각각의 단백질(들)을 포함할 수 있다.

[0022] 본 발명의 LCMV 돌연변이체는 당단백질을 인코딩하는 핵산을 포함할 수 있으며, 여기서 당단백질은 서열 번호 10에 제시된 야생형 당단백질과 비교하여 돌연변이 Arg 185 → Trp 및 Ile 181 → Met를 포함한다.

[0023] 본 발명의 LCMV 돌연변이체는 당단백질을 인코딩하는 핵산을 포함할 수 있고/있거나 - 여기서 상기 당단백질은 서열 번호 18, 26, 34, 42, 50 및 58 중 어느 하나에 제시된 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가지거나 또는 바람직하게는 그와 동일함 -, 상기 핵산에 의해 인코딩된 각각의 단백질(들)을 포함할 수 있다.

[0024] 본 발명의 LCMV 돌연변이체는 당단백질을 인코딩하는 핵산을 포함할 수 있고/있거나 - 여기서 상기 핵산은 서열 번호 17, 25, 33, 41, 49 및 57에 제시된 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가지거나 또는 바람직하게는 그와 동일한 서열을 포함함 -, 상기 핵산에 의해 인코딩된 각각의 단백질(들)을 포함할 수 있다.

[0025] 상기에서 이미 지적한 바와 같이, 비리온 외피에 스파이크를 형성하는 LCMV의 당단백질(들)은 바이러스가 종양 세포를 감염시키는 능력 면에서 우세한 역할을 하는 것으로 믿어진다. 그러나, 추가의 단백질들은 바람직하게는 LCMV에 존재한다.

[0026] 본 발명의 LCMV 돌연변이체는 서열 번호 16에 제시된 야생형 L-단백질 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖는 L-단백질을 인코딩하는 핵산을 포함할 수 있고/있거나, 상기 핵산에 의해 인코딩된 각각의 단백질(들)을 포함할 수 있다.

[0027] 본 발명의 LCMV 돌연변이체는 L-단백질을 인코딩하는 핵산을 포함할 수 있고/있거나 - 여기서 상기 L-단백질은 서열 번호 24, 32, 40, 48, 56 및 64 중 어느 하나에 제시된 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%, 바람직하게는 적어도 약 99.8%, 바람직하게는 적어도 약 99.9%의 서열 동일성을 가지거나 또는 바람직하게는 그와 동일함 -, 상기 핵산에 의해 인코딩된 각각의 단백질을 포함할 수 있다.

[0028] 본 발명의 LCMV 돌연변이체는 L-단백질을 인코딩하는 핵산을 포함할 수 있고/있거나 - 여기서 상기 L-단백질은 서열 번호 16에 제시된 야생형 L-단백질 서열의 위치 253, 1512, 1513, 1758, 1995, 2094, 2115, 2141, 2175 및 2185에 상응하는 위치에서 1, 2, 3, 4, 5, 6, 7, 8, 9 또는 10개의 돌연변이를 포함하며, 이들 위치에서의

돌연변이의 바람직한 실시양태는, 서열 번호 16에 제시된 야생형 L-단백질 서열과 비교하여 Lys 253 → Arg; Lys 1512 → Met; Lys 1513 → Glu; Ser 1758 → Phe; Phe 1995 → Ser; Ile 2094 → Val; Lys 2115 → Glu; Thr 2141 > Ala; Arg 2175 → Lys; Thr 2185 → Ala임 -, 상기 핵산에 의해 인코딩된 각각의 단백질을 포함할 수 있다. 바람직하게는, LCMV 뮤테인은 전술한 돌연변이 중 1, 2, 3, 4 또는 5개를 포함한다.

[0029] 본 발명의 LCMV 돌연변이체는 L-단백질을 인코딩하는 핵산을 포함할 수 있고/있거나 - 여기서 상기 L-단백질은 서열 번호 16에 제시된 야생형 L-단백질 서열과 비교하여 다음 돌연변이 세트 중 하나: Ser 1758 → Phe (돌연변이 균주 P42의 돌연변이에 해당); Phe 1995 → Ser, 선택적으로 Ile 2094 → Val 및 선택적으로 Thr 2141 → Ala (위치 2094 및 2141에 대해 올리고클론(oligoclonal)인 돌연변이 균주 P52의 돌연변이에 해당); Lys 1513 → Glu, Phe 1995 → Ser 및 선택적으로 Arg 2175 → Lys (위치 2175에 대해 올리고클론인 돌연변이 균주 P91의 돌연변이에 해당); Lys 253 → Arg; Lys 1512 → Met; Lys 2115 → Glu; Thr 2185 → Ala (돌연변이 균주 P52-1의 돌연변이에 해당); Phe 1995 → Ser (변이 균주 P52-1.3의 돌연변이에 해당); 또는 Lys 2115 → Glu (돌연변이 균주 P52-2.1의 돌연변이에 해당)를 포함함 -, 상기 핵산에 의해 인코팅된 각각의 단백질을 포함할 수 있다.

[0030] 본 발명의 LCMV 돌연변이체는 L-단백질을 인코딩하는 핵산을 포함할 수 있고/있거나 - 여기서 상기 핵산은 서열 번호 17, 25, 33, 41, 49 및 57에 제시된 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%, 바람직하게는 적어도 약 99.8%, 바람직하게는 적어도 약 99.9%의 서열 동일성을 가지거나 또는 바람직하게는 그와 동일한 서열을 갖거나 또는 바람직하게는 그에 상보적임 -, 상기 핵산에 의해 인코딩된 각각의 단백질을 포함할 수 있다.

[0031] 본 발명의 LCMV 돌연변이체는 핵단백질을 인코딩하는 핵산을 포함할 수 있고/있거나 - 여기서 상기 핵단백질은 서열 번호 12, 20, 28, 36, 44, 52, 및 60 중 어느 하나에 제시된 핵단백질에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가지거나 또는 그와 동일함 -, 상기 핵산에 의해 인코딩된 각각의 단백질을 포함할 수 있다.

[0032] 본 발명의 LCMV 돌연변이체는 핵단백질을 인코딩하는 핵산을 포함할 수 있고/있거나 - 여기서 상기 핵산은 서열 번호 11, 19, 27, 35, 43, 51, 및 59 중 어느 하나에 제시된 핵단백질에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가지거나 또는 그와 동일한 서열을 갖거나 또는 바람직하게는 그에 상보적임 -, 상기 핵산에 의해 인코딩된 각각의 단백질을 포함할 수 있다.

[0033] 본 발명의 LCMV 돌연변이체는 Z-단백질을 인코딩하는 핵산을 포함할 수 있고/있거나 - 여기서 상기 Z-단백질은 서열 번호 14, 22, 30, 38, 46, 54, 및 62 중 어느 하나에 제시된 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가지거나 또는 그와 동일함 -, 상기 핵산에 의해 인코딩된 각각의 단백질을 포함할 수 있다.

[0034] 본 발명의 LCMV 돌연변이체는 Z-단백질을 인코딩하는 핵산을 포함할 수 있고/있거나 - 여기서 상기 핵산은 서열 번호 13, 21, 29, 37, 45, 53, 및 61 중 어느 하나에 제시된 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 가지거나 또는 그와 동일한 서열을 포함함 -, 상기 핵산에 의해 인코딩된 각각의 단백질을 포함할 수 있다.

[0035] 본 발명의 LCMV 돌연변이체는 바람직하게는 본원에 정의된 당단백질(들), 바람직하게는 본원에 정의된 L 단백질, 바람직하게는 본원에 정의된 Z 단백질, 및 바람직하게는 본원에 정의된 핵단백질을 포함 할 수 있다.

본 발명의 LCMV 돌연변이체는 바람직하게는 본원에 정의된 당단백질(들), 바람직하게는 본원에 정의된 L 단백질, 바람직하게는 본원에 정의된 Z 단백질, 및 바람직하게는 본원에 정의된 핵단백질을 인코딩하는 핵산(들)을 포함할 수 있다.

[0036] 본 발명의 LCMV 돌연변이체는 서열 번호 18, 20, 22 및 24의 단백질 또는 이들 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖는 단백질을 인코딩하는 핵산(들)을 포함할 수 있다. 당단백질은 Ile 181 → Met 돌연변이를 포함할 수 있다. L-단백질은 Ser 1758 → Phe 돌연변이를 포함할 수 있다. 본 발명의 LCMV 돌연변이체는 서열 번호 17 및 21에 제시된 서열을 포함하고 서열 번호 19 및 23에 제시된 서열에 상보적인 서열을 포함하는 핵산(들)을 포함할 수 있다.

[0037] 본 발명의 LCMV 돌연변이체는 서열 번호 26, 28, 30 및 32의 단백질 또는 이들 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖는 단백질을 인코딩하는 핵산(들)을 포함할 수 있다. 당단백질은 Ile 181 → Met 및 Arg 185 → Trp 돌연변이를 포함할 수 있다. L 단백질은 다음의 돌연변이들: Phe 1995 → Ser, 선택적으로 Ile 2094 → Val 및 선택적으로 Thr 2141> Ala를 포함할 수 있다. 본 발명의 LCMV 돌연변이체는 서열 번호 25 및 29에 제시된 서열을 포함하고 서열 번호 27 및 31에 제시된 서열에 상보적인 서열을 포함하는 핵산(들)을 포함할 수 있다.

[0038] 본 발명의 LCMV 돌연변이체는 서열 번호 34, 36, 38 및 40의 단백질 또는 이들 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖는 단백질을 인코딩하는 핵산(들)을 포함할 수 있다. 당단백질은 Ile 181 → Met 및 Arg 185 → Trp 돌연변이를 포함할 수 있다. L 단백질은 다음의 돌연변이들: Lys 1513 → Glu, Phe 1995 → Ser, 및 선택적으로 Arg 2175 → Lys를 포함할 수 있다. 본 발명의 LCMV 돌연변이체는 서열 번호 33 및 37에 제시된 서열을 포함하고 서열 번호 35 및 39에 제시된 서열에 상보적인 서열을 포함하는 핵산(들)을 포함할 수 있다.

[0039] 본 발명의 LCMV 돌연변이체는 서열 번호 50, 52, 54 및 56의 단백질 또는 이들 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖는 단백질을 인코딩하는 핵산(들)을 포함할 수 있다. 당단백질은 Ile 181 → Met 및 Arg 185 → Trp 돌연변이를 포함할 수 있다. L 단백질은 다음의 돌연변이들: Lys 253 → Arg; Lys 1512 → Met; Lys 2115 → Glu; Thr 2185 → Ala를 포함할 수 있다. 본 발명의 LCMV 돌연변이체는 서열 번호 41 및 45에 제시된 서열을 포함하고 서열 번호 43 및 47에 제시된 서열에 상보적인 서열을 포함하는 핵산(들)을 포함할 수 있다.

[0040] 본 발명의 LCMV 돌연변이체는 서열 번호 58, 60, 62 및 64의 단백질 또는 이들 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖는 단백질을 인코딩하는 핵산(들)을 포함할 수 있다. 당단백질은 Arg 185 → Trp 돌연변이를 포함할 수 있다. L 단백질은 Phe 1995 → Ser 돌연변이를 포함할 수 있다. 본 발명의 LCMV 돌연변이체는 서열 번호 49 및 53에 제시된 서열을 포함하고 서열 번호 51 및 55에 제시된 서열에 상보적인 서열을 포함하는 핵산(들)을 포함할 수 있다.

[0041] 본 발명의 LCMV 돌연변이체는 서열 번호 66, 68, 70 및 72의 단백질 또는 이들 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약

99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖는 단백질을 인코딩하는 핵산(들)을 포함할 수 있다. 당단백질은 Ile 181 → Met 돌연변이를 포함할 수 있다. L 단백질은 Lys 2115 → Glu 돌연변이를 포함할 수 있다. 본 발명의 LCMV 돌연변이체는 서열 번호 57 및 61에 제시된 서열을 포함하고 서열 번호 59 및 63에 제시된 서열에 상보적인 서열을 포함하는 핵산(들)을 포함할 수 있다.

[0042] 본 발명의 LCMV 돌연변이체는 서열 번호 10, 12, 14 및 18의 단백질 또는 이들 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖는 단백질을 인코딩하는 핵산(들)을 포함할 수 있다. 본 개시내용의 LCMV 돌연변이체는 서열 번호 10 및 14에 제시된 서열을 포함하고 서열 번호 12 및 16에 제시된 서열에 상보적인 서열을 포함하는 핵산(들)을 포함할 수 있다.

[0043] 본 발명은 또한 일반적으로 치료에 사용하기 위한 본 개시내용의 LCMV, 특히 본 개시내용의 LCMV 돌연변이체에 관한 것이다.

[0044] 특히, 본 개시내용의 LCMV 돌연변이체가 사용되는 경우, 이러한 사용은 야생형 림프구성 맥락수막염 바이러스 균주 WE를 사용하는 것과 비교하여 종양 (세포)에서 LCMV 돌연변이체의 더 강력한 증식을 포함할 수 있다. 이러한 사용은 또한 생체 내 LCMV-WE 야생형의 사용과 비교하여 더 강한 선천적 면역 활성화를 유도하는 것을 포함할 수 있다. 이러한 사용은 또한 LCMV-WE 야생형의 사용과 비교하여 생체 내에서 더 강한 항종양 효과를 촉진하는 것을 포함할 수 있다. 이러한 사용은 또한 LCMV-WE 야생형의 사용과 비교하여 종양 특이적 CD8+ T 세포의 확장을 증가시키는 것을 포함할 수 있다. 사용은 또한 종양-특이적 CD8+ T 세포의 기능을 증가시키는 것을 포함할 수 있다. 사용은 또한 LCMV-WE 야생형과 비교하여 더 큰 정도로 종양 특이적 T 세포를 자극하는 것을 포함할 수 있다.

[0045] 본 개시내용의 LCMV (돌연변이체)는 종양의 치료 및/또는 예방에 사용하기 위한 것일 수 있다. 종양은 본 명세서에 개시된 임의의 종양일 수 있다. 종양은 바람직하게는 암종, 흑색종, 모세포종, 림프종 및 육종으로 이루어진 군으로부터 선택된다.

[0046] 제1 양태에 따르면, 본 발명은 항종양 아레나바이러스, 즉 종양 퇴치 또는 반발 아레나바이러스(소위 종양 퇴행 아레나바이러스), 특히 오리지널 아레나바이러스에 비해 개선된 항종양 특성, 즉 개선된 종양 퇴치 또는 반발 특성을 갖는 아레나바이러스의 생산 방법에 관한 것이다.

[0047] 상기 방법은,

[0048] a) 원발성 종양 세포를 영양 배지, 바람직하게는 액체 영양 배지에 플레이팅하거나, 또는 세포주 H1975, C643 또는 Tramp-C2의 세포를 영양 배지, 바람직하게는 액체 영양 배지에 플레이팅하는 단계,

[0049] b) 플레이팅된 원발성 종양 세포를 오리지널 아레나바이러스로 접종하거나 또는 플레이팅된 세포주 H1975, C643 또는 Tramp-C2의 세포를 오리지널 아레나바이러스로 접종하는 단계,

[0050] c) 접종된 원발성 종양 세포의 적어도 일부 또는 접종된 세포주 H1975, C643 또는 Tramp-C2의 세포의 적어도 일부, 특히 접종된 원발성 종양 세포의 일부만 또는 접종된 세포주 H1975, C643 또는 Tramp-C2의 세포의 일부만, 또는 접종된 원발성 종양 세포 모두 또는 접종된 세포주 H1975, C643 또는 Tramp-C2의 세포 모두가 오리지널 아레나바이러스에 감염되도록 하기에 적합한 조건 하에서, 접종된 원발성 종양 세포를 인큐베이팅하거나 접종된 세포주 H1975, C643 또는 Tramp-C2의 세포를 인큐베이팅하는 단계, 즉 원발성 종양 세포와 오리지널 아레나바이러스를 인큐베이팅하거나 또는 세포주 H1975, C643 또는 Tramp-C2의 세포와 오리지널 아레나바이러스를 인큐베이팅하는 단계,

[0051] d) 인큐베이팅된 원발성 종양 세포 배양물로부터 아레나바이러스 함유 세포 배양 상청액을 추출하거나, 또는 인큐베이팅된 세포주 H1975, C643 또는 Tramp-C2의 세포 함유 세포 배양물로부터 아레나바이러스 함유 세포 배양 상청액을 추출하는 단계를 포함하며,

[0052] 여기서 단계 순서 a) 내지 d)는 여러번 반복되고, 단계 순서 a) 내지 d)의 첫 번째 반복을 수행할 때의 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포는, 단계 b)를 수행하기 위해, 단계 순서 a) 내지 d)

의 첫 번째 반복 전 단계 d)를 수행할 때 추출된 아레나바이러스 함유 세포 배양 상청액 또는 그 일부로 접종되고, 단계 순서 a) 내지 d)의 각각의 추가의 반복을 수행할 때의 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포는, 단계 b)를 수행하기 위해, 단계 순서 a) 내지 d)의 이전의 반복의 단계 d)를 수행할 때 추출된 아레나바이러스 함유 세포 배양 상청액 또는 그 일부로 접종된다.

[0053] 단계 순서 a) 내지 d)의 첫 번째 수행은 또한 본 발명의 의미 내에서 "제1 계대"로 지칭될 수 있다. 따라서 제1 계대는 오리지널 아레나바이러스를 접종물로 사용하여 수행된다. 이어서, 각각의 추가 계대는 선행하는, 바람직하게는 직전 계대의 단계 d)에서 추출된 아레나바이러스 함유 세포 배양 상청액 또는 그의 일부를 이용해 수행된다. 본 발명의 의미 내에서, 제2 계대 이후 수행하는 것으로부터 상기 계대는 "반복 계대"로 지칭될 수 있다.

[0054] 본 발명의 맥락에서 용어 "오리지널 아레나바이러스"는 단계 순서 a) 내지 d)의 첫 번째 반복 이전에, 즉 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포의 접종(단계 b))을 위해 제1 계대 이전에 사용되는 아레나바이러스를 의미하는 것으로 이해될 수 있다. "오리지널 아레나바이러스"는 야생형 아레나바이러스 또는 이의 돌연변이체를 의미할 수 있으며, 아래에서 더 자세히 설명한다. 특히, 이 용어는 항종양 특성이 없거나 항종양 특성이 있는 오리지널 아레나바이러스를 지칭할 수 있다.

[0055] 본 발명의 맥락에서 용어 "야생형 아레나바이러스"는 유전적으로 정상적인 형태로 자연에서 발생하는 게놈을 갖는 아레나바이러스를 의미하는 것으로 이해되어야 한다.

[0056] 본 발명의 맥락에서 용어 "원발성 종양 세포"는 미계대 또는 계대하지 않은 종양 세포, 즉 종양 조직으로부터 직접 단리된 종양 세포 또는 단계 a)를 수행하기 전에 최대 1000회, 특히 최대 100회, 바람직하게는 최대 10회 계대된 종양 조직으로부터 직접 단리된 종양 세포, 또는 상이한 세포 클론들을 갖는 것을 특징으로 하는 원발성 종양 세포를 의미하는 것으로 이해되어야 한다. 후자의 경우, 이질성은 상이한 단백질 발현과 상이한 DNA 서열(유전자 지문)에 의해 입증될 수 있다.

[0057] 본 발명의 맥락에서 용어 "세포주 H1975"는 인간 선암으로부터 단리되었으며 NCI-H1975(ATCC® CRL-5908®)라는 명칭 및 수탁 또는 기탁 번호 CVCL-1511로 ATCC (American Type Culture Collection)에 기탁되어 있는 세포주를 의미하는 것으로 이해되어야 한다.

[0058] 본 발명의 맥락에서 용어 "세포주 C643"은 C643라는 명칭 및 수탁 또는 기탁 번호 CVCL-5969 (ExPASy Cellosaurus)로 기탁된 인간 역형성 갑상선 암종으로부터 단리된 세포주를 의미하는 것으로 이해되어야 한다.

[0059] 본 발명의 맥락에서 용어 "세포주 Tramp-C2"은 Tramp-C2라는 명칭 및 수탁 또는 기탁 번호 CVCL-3615 (ExPASy Cellosaurus)로 기탁된 쥐의 선암으로부터 단리된 세포주를 의미하는 것으로 이해되어야 한다.

[0060] 본 발명의 맥락에서 용어 "플레이팅 아웃"은 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포를 배양 배지, 바람직하게는 액체 배양 배지 상으로 및/또는 내로 파종 또는 도입하는 것을 의미하는 것으로 이해되어야 한다. 다시 말해, 본 발명의 의미에서 용어 "플레이팅"은 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포의 배양 배지, 바람직하게는 액체 배양 배지 상에 및/또는 내에서의 배양, 특히 초기 배양을 의미하는 것으로 이해되어야 한다.

[0061] 용어 "림프구성 맥락수막염 바이러스 WE 균주"는 문헌[Seiler,P., et al., J. Immunol. 162 (8), 4536-4541 (1999)]에 기재된 LCMV-WE 균주를 지칭할 수 있다. 본 명세서에 사용된 용어 "림프구성 맥락수막염 바이러스 WE 균주"는 바람직하게는 서열 번호 10의 위치 59-265 및 266-498의 서열을 갖는 당단백질, 서열 번호 12의 서열을 갖는 핵단백질; 서열 번호 14의 서열을 갖는 Z-단백질; 및/또는 서열 번호 16의 서열을 갖는 L-단백질을 포함하는 LCMV를 지칭한다. 본 명세서에 사용된 용어 "림프구성 맥락수막염 바이러스 WE 균주"는 또한 바람직하게는 서열번호 9, 11, 13 및/또는 15의 서열이거나 이에 상보적인 서열을 포함하는, 하나 이상의, 바람직하게는 2개의 핵산 분자를 포함하는 LCMV를 지칭한다.

[0062] 본 발명의 맥락에서 용어 "아레나바이러스 돌연변이체" 또는 "아레나바이러스의 돌연변이체"는 게놈 및/또는 프로테옴이 야생형의 게놈 및/또는 프로테옴에 대해 적어도 하나의 돌연변이, 특히 적어도 하나의 점 돌연변이를 갖는 아레나바이러스를 의미하는 것으로 이해되어야 한다. 바람직하게는, 용어 "아레나바이러스 돌연변이체" 또는 "아레나바이러스의 돌연변이체"는 상응하는 야생형 아레나바이러스의 상응하는 단백질, 특히 당단백질 및/또는 L-단백질에 대해 적어도 하나의 돌연변이를 바람직하게는 아미노산 치환 형태로 갖는 단백질, 특히 당단백질 및/또는 L-단백질을 갖는 아레나바이러스로 이해되어야 한다.

[0063] 따라서, 용어 "림프구성 맥락수막염 바이러스 돌연변이체"는 게놈 및/또는 프로테옴이 야생형 림프구성 맥락수

막염 바이러스의 게놈 및/또는 프로테옴에 대해 적어도 하나의 돌연변이, 특히 적어도 하나의 점 돌연변이를 갖는 림프구성 맥락수막염 바이러스의 돌연변이로 이해되어야 한다. 바람직하게는 용어 "림프구성 맥락수막염 바이러스 돌연변이체"는 야생형 림프구성 맥락수막염 바이러스의 상응하는 단백질, 특히 당단백질 및/또는 L-단백질에 대해 적어도 하나의 돌연변이를 바람직하게는 아미노산 치환 형태로 갖는 단백질, 특히 당단백질 및/또는 L-단백질을 갖는 아레나바이러스를 의미하는 것으로 이해되어야 한다.

[0064] 본 발명의 맥락에서 용어 "당단백질"은 특정 맥락에서 또한 단백질 모이어티, 또는 단백질 성분 및 적어도 하나의 공유결합된 탄수화물 기들(당 기들), 특히 모노- 및/또는 올리고- 및/또는 폴리사카라이드 기들로 지칭될 수 있는, 단백질로 이루어진 거대분자를 의미하는 것으로 이해되어야 한다.

[0065] 본 발명의 맥락에서 용어 "반복 계대" 또는 "반복 계대하는"은 달리 언급되지 않는 한, 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포가 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포로부터 생산된 아레나바이러스로 처리되는 단일 또는 반복 공정으로 이해되어야 한다. 이를 위해 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포를 위한 배양 배지, 예컨대 10% 소태아 혈청(FKS) 및 1% 페니실린/스트렙토마이신/글루타민(1 unit/ml 페니실린, 100 microg/ml 스트렙토마이신 및 2mM L-글루타민에 상응)을 포함하는 DMEM (둘베코 수정 이글 배지)가 사용되어야 한다. 비감염 원발성 종양 세포 또는 비감염 세포주 H1975, C643 또는 Tramp-C2의 세포는 접종 단계(단계 b) 전 바람직하게는 0 내지 7 일; 특히 1 내지 7 일 플레이팅된다. 바람직하게는, 세포 플레이팅에 사용되는 배양 배지는 접종 단계 전에 신선한 배양 배지로 교체된다. 경우에 따라 접종 단계(단계 b) 후 1, 10 또는 100 분 후에 배양 배지를 추출하고 새로운 배양 배지로 교체할 수 있다. 24, 48, 72 또는 96 시간의 배양 기간 후, 돌연변이된 아레나바이러스의 축적을 함유하는 세포 배양 상청액을 추출한다. 이 상청액의 일부는 감염되지 않은 새로운 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포에 추가된다.

[0066] 본 명세서에 사용된 용어 "핵산"은 일반적으로 DNA 또는 RNA로 지칭될 수 있다. DNA와 RNA는 무엇보다도 핵 염기가 다르다. 아데닌에 대한 상보적 염기가 DNA에서는 티민인 반면, RNA에서는 우라실이다. 단순화를 위해 아데닌에 해당하는 염기는 본 개시내용 전반에 걸쳐 "t"로 표시되며, 문맥에 따라 티민(DNA에서) 또는 우라실(RNA에서)을 지칭할 수 있다.

[0067] 핵산과 관련하여 본 명세서에 사용된 용어 "인코딩" 또는 "인코딩하다"는 핵산에 의해 인코딩되는 특정 아미노산 서열로 번역될 수 있는 서열을 갖는 핵산과 관련있다. 핵산 서열은 코딩 가닥의 서열을 포함할 수 있고 또한 코딩 가닥에 상보적인 가닥의 서열을 포함할 수 있다.

[0068] 본 명세서에 개시된 서열에 대한 "퍼센트(%) 서열 동일성"은, 서열을 얼라인먼트하고 필요한 경우 갭을 도입한 후, 어떠한 보존적 치환도 서열 동일성의 일부로 고려하지 않고 최대 퍼센트 서열 동일성을 달성하는, 참조 서열의 아미노산 잔기 또는 뉴클레오티드와 쌍으로 동일한 후보 서열의 아미노산 잔기 또는 뉴클레오티드의 백분율로 정의된다. 퍼센트 아미노산 서열 동일성을 결정하기 위한 얼라인먼트는, 예를 들어 공중이 이용가능한 컴퓨터 소프트웨어, 예컨대 BLAST, BLAST-2, ALIGN 또는 Megalign(DNASTAR) 소프트웨어를 사용하여 당업계의 기술 범위 내의 다양한 방법으로 달성될 수 있다. 당업자는 비교되는 서열의 전장에 걸쳐서 최대 얼라인먼트를 달성하는 데 필요한 임의의 알고리즘을 포함한, 얼라인먼트 측정을 위한 적절한 매개변수를 결정할 수 있다. 본 명세서에 개시된 뉴클레오티드 서열에 대해서도 동일하다. 서열 동일성을 결정하기 위해, 우라실(예를 들어, RNA에서)은 티민(예를 들어, DNA에서)과 동일한 것으로 간주될 수 있다.

[0069] 본 발명은 또한 아레나바이러스로 감염된 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포의 계대를 통해 항종양 특성을 갖는 아레나바이러스, 특히 사용된 아레나바이러스에 비해 개선된 항종양 특성을 갖는 아레나바이러스가 생산될 수 있다. 이러한 아레나바이러스의 생산은 오리지널 아레나바이러스, 일반적으로 야생형 아레나바이러스가 원발성 종양 세포 또는 세포주 H1975의 세포에서 증식하기 어렵다는 사실에 근거한다. 동일하게 제한된 증식이 세포주 C643 및 Tramp-C2에서 관찰되었다. 제한된 증식은 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포 내 감염 및 복제시 아레나바이러스에서의 증가된 선택 또는 적응 압력을 촉발시킨다. 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포에서 증식할 수 있는 무작위로 출현한 바이러스 돌연변이체는 오리지널 아레나바이러스, 일반적으로 야생형 아레나바이러스를 과도하게 증식시킨다. 계대, 특히 반복 계대(단계 순서 a) 내지 d)의 다수 반복)를 통해, 바람직하게는 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포에 대해 항종양 효과를 가지거나 또는 오리지널 아레나바이러스와 비교하여 개선된 항종양 특성을 갖는, 아레나바이러스의 농축이 일어난다. 아레나바이러스 돌연변이체의 항종양 효과는 그것이 세포를 더 잘 감염시킬 수 있고 세포 내에서 더 잘 복제된다는 사실에 근거한다. 그렇게 함으로써,

아레나바이러스 돌연변이체는 오리지널 아레나바이러스에 비해 사용된 세포에서 더 성공적으로 확산될 수 있으며, 특히 강화된 면역 활성화를 촉진할 수 있다. 많은 종양 세포가 항바이러스 인자를 갖지 않아 제한된 바이러스 내성을 보여주기 때문에, 본 발명에 따른 방법은 항종양 아레나바이러스의 생산뿐만 아니라 종양 특이적 아레나바이러스의 생산에, 즉 항종양 및 종양 특이적 아레나바이러스의 생산에 유리할 수 있다.

[0070] 원발성 종양 세포뿐만 아니라 세포주 H1975, C643 및 Tramp-C2의 세포는 놀랍게도 아레나바이러스의 복제 감소만을 허용하고 계대 과정에서 특히 높은 아레나바이러스의 선택 압력 또는 적응 강제를 촉발시키는 세포로서 본 발명자들에 의해 확인되었다.

[0071] 본 발명의 일 실시양태에서, 원발성 종양 세포는 단계 a)를 수행하기 전에 최대 1000 회, 특히 최대 100 회, 바람직하게는 최대 10 회 계대된다. 이 문맥에서 용어 "계대"는 세포 배양물에 세포를 희석하고 따라서 세포를 현탁액 내에 흡수시키고 세포 일부를 새로운 영양 배지에 플레이팅(예컨대 50%, 10% 또는 1%)하는 것으로 이해되어야 한다. 단계 a) 전에 원발성 종양 세포가 덜 계대될수록, 더 많은 세포가 환자의 종양 세포의 특성에 상응한다. 특히, 형태, RNA 발현 패턴, 단백질 발현 및 DNA 서열에서의 개별 원발성 종양 세포들 간의 큰 차이(이질성)는 생체 내 종양 세포를 매핑한다. 이에 의해, 아레나바이러스는 유리한 방식으로 생산될 수 있으며, 이는 특히 각각의 종양 환자, 특히 그의 환자 그룹의 치료 적 치료에 적합하다.

[0072] 특히, 원발성 종양 세포는 단계 a) 전에 계대되지 않을 수 있다. 즉, 단계 a)를 수행하기 위해 미계대된, 즉 계대되지 않은 원발성 종양 세포가 사용될 수 있다. 이에 의해 오리지널 아레나바이러스 또는 추출된 세포 배양 상청액 또는 그 일부에 포함된 아레나바이러스는 특히 환자의 종양 세포를 대표하는 세포에 잘 적응하도록 강요된다. 그렇게 함으로써, 각각의 종양 환자, 특히 그의 환자 그룹의 치료적 처리를 위해 특히 적합한 아레나바이러스를 생성하는 것이 가능하다.

[0073] 세포주 H1975, C643 및 Tramp-C2의 이미 종종 계대된 세포는 이미 수년 동안 시험관 내에서 계대되었음에도 불구하고 동등하게 적합한 세포인 것으로 본 발명자들에 의해 확인되었다.

[0074] 본 발명의 추가 실시양태에서, 단계 c)는 1 시간 내지 1000 시간, 특히 3 시간 내지 300 시간, 바람직하게는 12 시간 내지 96 시간 동안 수행된다. 이 단락에 개시된 기간은 오리지널 아레나바이러스 또는 추출된 세포 배양 상청액 또는 이의 일부에 포함된 아레나바이러스로 접종된 원발성 종양 세포 또는 접종된 세포주 H1975, C643 또는 Tramp-C2의 세포의 효율적인 인큐베이션 및 결과적으로 감염에 특히 유익한 것으로 나타났다.

[0075] 본 발명의 추가 실시양태에서, 단계 (b) 및/또는 단계 (c)는 4 ℃ 내지 50 ℃, 특히 20 ℃ 내지 42 ℃, 바람직하게는 34 ℃ 내지 39 ℃의 온도에서 수행된다. 이 단락에 개시된 온도 범위는 오리지널 아레나바이러스 또는 추출된 세포 배양 상청액 또는 이의 일부에 포함된 아레나바이러스로의 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포의 효율적인 접종 및/또는 인큐베이션(및 결과적으로 감염)에 특히 유리한 것으로 나타났다.

[0076] 본 발명의 추가 실시양태에서, 단계 a) 및/또는 단계 b) 및/또는 단계 c) 및/또는 단계 d)는 바람직하게는 RPMI-1640 (Roswell Park Memorial Institute), DMEM (Dulbecco의 Modified Eagle's Medium) 및 IMDM (Iscove의 Modified Dulbecco 's Medium)으로 이루어진 군으부터 선택되는 영양 배지에서 수행된다. 영양 배지는 태아 소 혈청 및/또는 인간 혈청과 같은 혈청(0.1 - 20%), 및/또는 글루타메이트 및/또는 글루타민과 같은 아미노산, 및/또는 항생제를 추가로 함유할 수 있다. 배양 배지는 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포의 배양을 가능하게 한다. 특히, 배양 배지는 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포의 성장 및/또는 세포 분열에 특히 유리하다. 이 단락에 언급된 배양 배지는 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포의 배양에 특히 적합하다.

[0077] 본 발명의 추가 실시양태에서, 단계 a) 및/또는 단계 b) 및/또는 단계 c)는 0% 내지 20%, 특히 0.1% 내지 20%, 바람직하게는 2% 내지 10%, 더 바람직하게는 4% 내지 6%의 이산화탄소 분위기(CO2 분위기) 하에서 수행된다. 이것은 단계 a) 및/또는 단계 b) 및/또는 단계 c)에 사용되는 영양 배지의 pH가 일정하게 유지되도록한다. 이는 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포를 오리지널 아레나바이러스 또는 추출된 세포 배양 상청액 또는 그 일부에 포함된 아레나바이러스로 효율적으로 플레이팅 및/또는 접종 및/또는 인큐베이션(및 결과적으로 감염)할 수 있게 한다.

[0078] 바람직하게는 단계 a) 및/또는 단계 b) 및/또는 단계 c)는 인큐베이터에서 수행되며, 이에 의해 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포의 성장 및/또는 세포 분열을 위한 제어된 외부 조건이 생성될 수 있다.

[0079] 본 발명의 추가 실시양태에서, 단계 a) 내지 d)의 순서는 3 회 내지 1000 회, 특히 10 회 내지 100 회, 바람직하게는 20 회 내지 50 회 반복된다. 특히 이 단락에 개시된 바와 같이 단계 순서 a) 내지 d)의 다회 반복은 항종양 특성, 특히 점 돌연변이와 관련한 유익한 돌연변이의 발달의 관점에서 특히 유익하고 결과적으로 항종양 아레나바이러스의 생산에 유익한 것으로 나타났다.

[0080] 본 발명의 추가 실시양태에서, 영양 배지는 단계 b)를 수행하기 전에 신선한 또는 새로운 배양 배지로 교체된다. 이 단계를 통해 감염 상태를 유리하게 표준화 할 수 있다.

[0081] 본 발명의 추가 실시양태에서, 배양 배지는 단계 b) 후 0.1 분 내지 600 분, 특히 1 분 내지 30 분, 바람직하게는 5 분 내지 15 분의 기간 내에 신선한 또는 새로운 배양 배지로 교체된다. 이 단계는 감염 시간이 제한되어 있기 때문에 감염의 선택 압력을 유리하게 증가시킨다.

[0082] 본 발명의 추가 실시양태에서 다수의 영양 배지 변경이 수행된다. 예를 들어, 영양 배지는 단계 b) 전에 신선한 또는 새로운 영양 배지로 교체될 수 있으며 후자는 단계 b)를 수행한 후 0.1 분 내지 600 분, 특히 1 분 내지 30 분, 바람직하게는 5 분 내지 15 분의 기간 내에 신선한 또는 새로운 영양 배지로 교체될 수 있다.

[0083] 본 발명의 추가 실시양태에서, 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포 및/또는 오리지널 아레나바이러스 및/또는 추출된 세포 배양 상청액 또는 이의 일부에 함유된 아레나바이러스는 단계 d)를 수행하기 전에, 특히 단계 c)를 수행하기 전에, 특히 단계 b)를 수행하기 전에, 특히 단계 a)를 수행하기 전에 적어도 하나의 화학요법제로 치료된다. 이에 의해 이미 화학요법으로 치료된 종양 세포를 시뮬레이션할 수 있다. 이는 유리하게는 이미 화학요법으로 치료되었거나/되었고 이미 모든 치료 옵션을 받은 것으로 간주되는 종양 환자의 치료에 특히 적합한 아레나바이러스의 생산을 가능하게 한다.

[0084] 본 발명의 추가 실시양태에서, 오리지널 아레나바이러스 및/또는 추출된 세포 배양 상청액 또는 그의 일부에 포함된 아레나바이러스는 단계 b)를 수행하기 전에 적어도 하나의 화학요법제로 치료된다. 따라서 아레나바이러스의 자연 돌연변이율이 유리하게 증가될 수 있으며, 이에 의해 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포에 대한 적응을 가속화할 수 있다.

[0085] 적어도 하나의 화학요법제는 특히 알킬화제, 토포이소머라제 억제제, 유사 분열 억제제, 항대사성물질, 항생제, 키나아제 억제제, 탈리도마이드 유도체, 세포 아폽토시스 유도제, 생물학적 정균제와 같은 생물학적 치료제, 동위원소 함유 화합물, 호르몬, 호르몬 길항제, 히스톤 데아세틸라제 억제제 및 다른 세포 증식 억제제로 이루어진 군으로부터 선택될 수 있다.

[0086] 알킬화제는 옥사자포스포린, N-손실 유도체, 알킬 설포네이트, 히드라진, 백금 함유 물질, 안트라사이클린 및 상기 알킬화제 중 적어도 2종의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0087] 옥사자포스포린은 예를 들어 사이클로포스파미드, 이포스파미드 및 이들의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0088] N-손실 유도체는 클로람부실(chlorambucil), 멜팔란(melphalan) 및 이들의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0089] 알킬 설포네이트는 예를 들어 후설판(husulfan)일 수 있다.

[0090] 예를 들어, 히드라진은 테모졸로미드, 다카르바진, 프로카르바진 및 상기 히드라진 중 적어도 2종의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0091] 백금 함유 물질은 예를 들어 시스플라틴, 카보플라틴, 옥살리플라틴 및 상기 백금 함유 물질 중 적어도 2종의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0092] 안트라사이클린은 예를 들어 독소루비신, 다우노루비신, 이다루비신, 엘리루비신 및 상기 안트라사이클린 중 적어도 2종의 혼합물로 이루어진 군으로부터 선택 될 수 있다.

[0093] 상기 언급된 토포이소머라제 억제제는 토포이소머라제 I 억제제, 토포이소머라제 II 억제제 (에토포사이드) 및 이들의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0094] 예를 들어, 토포이소머라제 I 억제제는 이리노테칸, 토포테칸 및 이들의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0095] 토포이소머라제 II 억제제는 예를 들어 에토포사이드일 수 있다.

[0096] 상기 언급된 유사 분열 억제제 또는 항대사성물질은 빈카 알칼로이드, 탁산, 엽산 길항제, 피리미딘 길항제, 퓨린 길항제, 리보뉴클레오타이드 환원 효소 억제제 및 상기 언급된 유사 분열 억제제 또는 항대사성물질 중 적어도 2종의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0097] 예를 들어, 빈카 알칼로이드는 빈크리스틴, 빈블라스틴 및 이들의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0098] 탁산은 도세탁셀, 파클리탁셀 및 이들의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0099] 예를 들어, 엽산 길항제는 메토트렉세이트, 페메트렉세드 및 이들의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0100] 피리미딘 길항제는 예를 들어 시타라빈, 5-플루오로우라실, 젬시타빈, 카페시타빈 및 상기 피리미딘 길항제 중 적어도 2종의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0101] 퓨린 길항제는 예를 들어 5-아자시티딘, 아자티오프린, 6-머캅토퓨린, 플루다라빈 및 상기 퓨린 길항제 중 적어도 2종의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0102] 예를 들어, 리보뉴클레오타이드 환원 효소 억제제는 하이드록시우레아일 수 있다.

[0103] 상기 항생제는 블레오마이신, 악티노마이신 D, 미토마이신 및 상기 항생제 중 적어도 2종의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0104] 상기 언급된 키나아제 억제제는 아파티닙(afatinib), 알렉티닙(alectinib), 악시티닙(axitinib), 크리조티닙(crizotinib), 코비메티닙(cobimetinib), 다사티닙(dasatinib), 다브라페닙(dabrafenib), 에를로티닙(erlotinib), 게피티닙(gefitinib), 이마티닙(imatinib), 익사조밉(Ixazomib), 렌바티닙(lenvatinib), 닐로티닙(nilotinib), 오시머티닙(osimertinib), 팔보시클립(palbociclib), 파조파닙(pazopanib), 포나티닙(ponatinib), 레고라페닙(regorafenib), 수니티닙(sunitinib), 베무라페닙(vemurafenib), 트라메티닙(trametinib), 에베롤리무스(everolimus) 및 상기 키나아제 억제제 중 적어도 2종의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0105] 상기 언급된 탈리도마이드 유도체는 레날리도마이드, 포말리도마이드 및 이들의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0106] 상기 언급된 세포 아폽토시스 유도제는 메톡살, 베네토클락스 및 이들의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0107] 상기 언급된 생물학적 치료제는 리툭시맙(rituximab), 트라스투주맙(trastuzumab), 세툭시맙(cetuximab), 파니투무맙(panitumumab), 이필리무맙(ipilimumab), 펨브롤리주맙(pembrolizumab), 니볼루맙(nivolumab), 아테졸리주맙(atezolizumab), 아벨루맙(avelumab), 니볼루맙(nivolumab), 올라라투맙(olaratumab), 라무시루맙(ramucirumab) 및 상기 언급된 생물학적 치료제 중 적어도 2종의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0108] 상기 언급된 호르몬 및/또는 호르몬 길항제는 부세렐린(buserelin), 고세렐린(goserelin), 류프로렐린(leuprorelin), 트립토렐린(triptorelin), 에스트라무스틴(estramustin), 타목시펜(tamoxifen), 아로마타제 억제제 예를 들어 아나타스트로졸(anastrozole), 안티안드로겐 예를 들어 엔잘루타미드(enzalutamide), 플루타미드(flutamide), 비카-루타미드(bica-lutamide), 프로게스틴 예를 들어 메게스트롤 아세테이트 및 메드록시프로게스테론 아세테이트, 글루코코르티코이드 및 상기 언급된 호르몬 및/또는 호르몬 길항제 중 적어도 2종의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0109] 상기 언급된 다른 세포 증식 억제제는 벡사로텐(bexarotene), 아파티닙(afatinib), 크리조티닙(crizotinib), 에를로티닙(erlotinib), 게피티닙(gefitinib), 라파티닙(lapatinib), 다사티닙(dasatinib), 이마티닙(imatinib), 닐로티닙(nilotinib), 포나티닙(ponatinib), 레고라페닙(regorafenib), 소니데깁(sonidegib), 하이드록시카르바마이드, 트라메티닙(trametinib), 트레티니노인(tretininoin), 이소트레티노인(isotretinoin), 알리트레티노인(alitretinoin), MAOP (5-아미노-4-옥소펜타노산 메틸 에스테르) 및 상기 다른 세포 증식 억제제 중 적어도 2종의 혼합물로 이루어진 군으로부터 선택될 수 있다.

[0110] 또한, 단계 d)를 수행하기 전에, 특히 단계 c)를 수행하기 전에, 특히 단계 b)를 수행하기 전에, 특히 단계 a)를 수행하기 전에, 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포 및/또는 오리지널 아레나

바이러스 및/또는 추출된 세포 배양 상청액 또는 그 일부에 포함된 아레나바이러스는 특히 자외선 (UV), 특히 UVA 선 및/또는 UVB 선, 알파 선, 베타 선, 감마 선 및 X 선으로 이루어진 군으로부터 선택된 방사선으로 처리할 수 있다. 이에 의해, 이미 치료 방사선을 받은 종양 세포가 유리하게 시뮬레이션될 수 있다. 이는 유리하게는 이미 방사선 요법으로 치료된 종양 환자의 치료에 특히 사용될 수 있는, 아레나바이러스의 생산을 가능하게 한다.

[0111] 또한, 단계 b)를 수행하기 전에 오리지널 아레나바이러스 및/또는 추출된 세포 배양 상청액 또는 이의 일부에 포함된 아레나바이러스는 특히 자외선 (UV), 특히 UVA 선 및/또는 UVB 선, 알파 선, 베타 선, 감마 선 및 X 선으로 이루어진 군으로부터 선택되는 방사선으로 처리된다. 이에 의해, 아레나바이러스의 자연적인 돌연변이율 및 따라서 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포에 대한 그의 적응이 유리하게 증가될 수 있다.

[0112] 본 발명의 또 다른 실시양태에서, 적어도 하나의 화학요법제에 내성이 있는 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포가 사용된다. 예를 들어, 파클리탁셀 및/또는 트라메티닙에 내성이 있는 원발성 종양 세포가 사용될 수 있다. 이에 의해, 종양 치료 동안 적어도 하나의 화학요법제에 내성이 있는 환자의 종양 세포가 유리하게 시뮬레이션될 수 있다. 따라서, 이 단락에 기재된 본 발명의 실시양태는 강력한 항종양 아레나바이러스의 생산을 위한 추가 가능성을 나타낸다.

[0113] 본 발명의 추가 실시양태에서, 원발성 종양 세포 또는 세포주 H1975, C643 또는 Tramp-C2의 세포 및/또는 오리지널 아레나바이러스 및/또는 추출된 세포 배양 상청액 또는 그 일부에 포함된 아레나바이러스는 단계 d)를 수행하기 전, 특히 단계 c)를 수행하기 전, 특히 단계 b)를 수행하기 전, 특히 단계 a)를 수행하기 전에 적어도 하나의 항바이러스 화합물, 특히 알파-인터페론 및/또는 감마-인터페론으로 치료된다. 이에 의해, 오리지널 아레나바이러스 또는 추출된 세포 배양 상청액 또는 그 일부에 포함된 아레나바이러스를 항바이러스 환경에 강제로 적응시킬 수 있어 동시에 내성을 나타내는 항종양 아레나바이러스를 생산할 수 있다. 이러한 아레나바이러스는 바이러스 내성을 나타낼 수 있는 종양 조직을 퇴치하는 데에도 사용될 수 있으므로 치료적 관점에서 특히 효과적이다.

[0114] 또한, 상기 방법은 추출된 세포 배양 상청액 또는 이의 일부로부터의 항종양 아레나바이러스, 특히 오리지널 아레나바이러스에 비해 개선된 항종양 특성을 갖는 아레나바이러스를 클로닝 및/또는 PCR (중합효소 연쇄 반응) 및/또는 시퀀싱에 의해 단리 및/또는 동정하는 추가의 단계 e)를 포함할 수 있다.

[0115] 바람직하게 사용되는 원발성 종양 세포는 원발성 악성 종양 세포, 특히 원발성 암종 세포, 원발성 흑색종 세포, 원발성 모세포종 세포, 원발성 림프종 세포 또는 원발성 육종 세포이다.

[0116] 본 발명의 추가 실시양태에서, 원발성 종양 세포는 원발성 맥락막 흑색종 세포, 원발성 항문 암종 세포, 원발성 혈관 육종 세포, 원발성 성상세포종 세포, 원발성 기저 세포 암종 세포, 원발성 자궁경부 암종 세포, 원발성 연골육종 세포, 원발성 융모막 암종 세포, 원발성 진피 편평 세포 암종 세포, 원발성 소장 암종 세포, 원발성 자궁내막 암종 세포, 원발성 Ewing 육종 세포, 원발성 섬유 육종 세포, 원발성 담낭 암종 세포, 원발성 담관 암종 세포, 원발성 교모세포종 세포, 원발성 방광 암종 세포, 원발성 요관 암종 세포, 원발성 요도 암종 세포, 원발성 간세포 암종 세포, 원발성 고환 종양 세포, 원발성 하인두 암종 세포, 원발성 뇌하수체 암종 세포, 원발성 카포시 육종 세포, 원발성 소세포 기관지 암종 세포, 원발성 결장 암종 세포, 원발성 결장직장 암종 세포, 원발성 후두 암종 세포, 원발성 평활근 육종 세포, 원발성 지방 육종 세포, 원발성 위 암종 세포, 원발성 악성 섬유성 조직구종 세포, 원발성 유방 암종 세포, 원발성 수모세포종 세포, 원발성 흑색종 세포, 원발성 구강 저 암종 세포, 원발성 부비동 암종 세포, 원발성 비인두 암종 세포, 원발성 부신 피질 암종 세포, 원발성 부갑상선 암종 세포, 원발성 신경성 육종 세포, 원발성 비소세포 기관지 암종 세포, 원발성 신장 암종 세포, 원발성 구강 인두 암종 세포, 원발성 골육종 세포, 원발성 난소 암종 세포, 원발성 췌장 종양 세포, 원발성 음경 암종 세포, 원발성 갈색세포종 세포, 원발성 흉막중피종 세포, 원발성 전립선 암종 세포, 원발성 직장 암종 세포, 원발성 망막모세포종 세포, 원발성 횡문근 육종 세포, 원발성 갑상선 암종 세포, 원발성 타액선 암종 세포, 원발성 식도 암종 세포, 원발성 편도선 암종 세포, 원발성 질 암종 세포, 원발성 외음부 암종 세포, 원발성 Wilms 종양 세포, 원발성 신경 내분비 종양의 세포 또는 원발성 혀 암종 세포이다.

[0117] 특히 바람직한 것은 원발성 흑색종 세포, 원발성 폐 암종 세포, 원발성 췌장 암종 세포, 원발성 결장 암종 세포, 원발성 위 암종 세포, 원발성 인두 암종 세포, 원발성 후두 암종 세포, 원발성 신장 세포 암종 세포가 원발성 종양 세포로서 특히 바람직하고, 원발성 난소 암종 세포, 원발성 자궁 내막 암종 세포, 원발성 갑상선 암종 세포, 원발성 전립선 암종 세포, 원발성 간 암종 세포, 또는 원발성 육종 세포 예를 들어 원발성 신경성 육

종 세포, 원발성 골육종 세포 또는 원발성 횡문근 육종 세포가 특히 바람직하다.

[0118] 본 발명의 추가 실시양태에서, 야생형 아레나바이러스, 즉 소위 야생형 아레나바이러스가 오리지널 아레나바이러스로서 사용된다.

[0119] 본 발명의 추가 실시양태에서, Old world 아레나바이러스가 오리지널 아레나바이러스로 사용된다. Old world 아레나바이러스는 바람직하게는 Catarina 바이러스, Danfenong 바이러스, Ippy 바이러스 (IP-PYV), Kodoko 바이러스, Lassa 바이러스 (LASV), 림프구성 맥락수막염 바이러스 (LCMV), Morogoro 바이러스, Mobala 바이러스 (MOBV), Gairo 바이러스, Mopeia 바이러스 (MOPV), Pinhal 바이러스, Skinner Tank 바이러스로 이루어진 군으로부터 선택된다.

[0120] 오리지널 아레나바이러스로서 바람직한 것은 림프구성 맥락수막염 바이러스, 특히 야생형의 림프구성 맥락수막염 바이러스이다. 예를 들어, 특히 WE, Armstrong, Clone 13 (Clone 13) 및 Docile로 이루어진 군으로부터 선택된 림프구성 맥락수막염 바이러스의 균주가 오리지널 아레나바이러스로 사용될 수 있다.

[0121] 특히 바람직한 것은 야생형 림프구성 맥락수막염 바이러스, 즉 서열 번호 7에 따른 아미노산 서열을 포함하거나 이로 이루어진 L-단백질, 및/또는 서열 번호 8에 따른 핵산 서열에 상보적인, 핵산 서열, 특히 리보핵산 서열, 바람직하게는 L-리보핵산 서열을 포함하거나 이로 이루어진, 핵산, 특히 리보핵산, 바람직하게는 L-리보핵산을 포함하는 야생형 림프구성 맥락수막염 바이러스이다.

[0122] 또한, New world 아레나바이러스가 오리지널 아레나바이러스로 사용될 수 있다. New world 아레나바이러스는 바람직하게는 Allpahuayo 바이러스 (ALLV), Amapari 바이러스 (AMAV), Bear Canyon 바이러스 (BCNV), Chapare 바이러스, Cupixi 바이러스 (CPXV), Flexal 바이러스 (FLEV), Guanarito 바이러스 (GTOV), Junin 바이러스 (JUNV), Candid # 1 (Candid No.1).), Latino 바이러스 (LATV), Machupo 바이러스 (MACV), Oliveros 바이러스 (OLVV), Parana 바이러스 (PARV), Pichinide 바이러스 (PICV), Pirital 바이러스 (PIRV), Sabia 바이러스 (SABV), Tacaribe 바이러스 (TCRV), Tamiami 바이러스 (TAMV) 및 Whitewater arroyo 바이러스 (WWAV)로 이루어진 군으로부터 선택된다.

[0123] 또한, 항종양 특성이 없는 아레나바이러스를 오리지널 아레나바이러스로 사용할 수 있다.

[0124] 대안적으로, 항종양 특성을 갖는 오리지널 아레나바이러스가 사용될 수 있다.

[0125] 제2 양태에 따르면, 본 발명은 림프구성 맥락수막염 바이러스 돌연변이체, 즉 림프구성 맥락수막염 바이러스의 돌연변이체에 관한 것이다.

[0126] 림프구성 맥락수막염 바이러스 돌연변이체는 단백질 또는 펩티드, 특히 당단백질을 포함한다. 단백질 또는 펩티드는 돌연변이, 특히 점 돌연변이를 포함한다. 돌연변이, 특히 점 돌연변이는 바람직하게는 서열 AJ297484, AJ233196 및 참조 서열 LCMV (균주 WE-Essen)와 상이하다.

[0127] 바람직하게는, 림프구성 맥락수막염 바이러스 돌연변이체는 적어도 하나의 돌연변이를 갖는 당단백질, 특히 당단백질의 단백질 성분 또는 단백질 모이어티를 가지며, 여기서 적어도 하나의 돌연변이는 당단백질의 위치 181에서의 이소류신의 다른 아미노산, 바람직하게는 메티오닌에 의한 아미노산 치환, 및/또는 위치 185에서의 아르기닌의 다른 아미노산, 바람직하게는 트립토판에 의한 아미노산 치환이다.

[0128] 대안적으로 또는 조합하여, 림프구성 맥락수막염 바이러스 돌연변이체는 바람직하게는 적어도 하나의 돌연변이를 갖는 L-단백질을 포함하고, 여기서 적어도 하나의 돌연변이는 L-단백질의 위치 1513에서의 라이신의 다른 아미노산, 바람직하게는 글루타메이트에 의한 아미노산 치환, 및/또는 L-단백질의 위치 1995에서의 페닐알라닌의 다른 아미노산, 바람직하게는 세린에 의한 아미노산 치환, 및/또는 L-단백질의 위치 2094에서의 이소류신의 다른 아미노산, 바람직하게는 발린에 의한 아미노산 치환, 및/또는 L-단백질의 위치 2141에서의 트레오닌의 다른 아미노산, 바람직하게는 알라닌에 의한 아미노산 치환, 및/또는 L-단백질의 위치 2175에서의 아르기닌의 다른 아미노산, 바람직하게는 라이신에 의한 아미노산 치환이다.

[0129] 대안적으로 또는 조합하여, 림프구성 맥락수막염 바이러스 돌연변이체는 바람직하게는 서열 번호 1, 서열 번호 3, 서열 번호 5, 서열 번호 18, 서열 번호 26, 서열 번호 34, 서열 번호 42, 서열 번호 50, 서열 번호 58, 서열 번호 24, 서열 번호 32, 서열 번호 40, 서열 번호 48, 서열 번호 56, 및 서열 번호 64에 따른 아미노산 서열을 포함하거나 이로 이루어진 단백질 또는 펩티드, 특히 당단백질, 특히 당단백질의 단백질 성분 또는 단백질 모이어티, 또는 L-단백질을 포함한다. 서열 번호 1, 서열 번호 3, 서열 번호 18, 서열 번호 26, 서열 번호 34, 서열 번호 42, 서열 번호 50 및 서열 번호 58에 따른 아미노산 서열은 바람직하게는 림프구성 맥락수막염 바이러스

돌연변이체의 당단백질의 아미노산 서열이다. 서열 번호 5, 서열 번호 24, 서열 번호 32, 서열 번호 40, 서열 번호 48, 서열 번호 56 및 서열 번호 64의 아미노산 서열은 바람직하게는 림프구성 맥락수막염 바이러스 돌연변이체의 L-단백질의 아미노산 서열이다.

[0130] 대안적으로 또는 조합하여, 림프구성 맥락수막염 바이러스 돌연변이체는 바람직하게는 서열 번호 1, 서열 번호 3, 서열 번호 5, 서열 번호 18, 서열 번호 26, 서열 번호 34, 서열 번호 42, 서열 번호 50, 서열 번호 58, 서열 번호 24, 서열 번호 32, 서열 번호 40, 서열 번호 48, 서열 번호 56, 또는 서열 번호 64에 따른 아미노산 서열을 포함하거나 이로 이루어진, 단백질 또는 펩티드, 특히 당단백질, 또는 L-단백질을 인코딩하는, 핵산, 특히 리보핵산을 포함한다.

[0131] 대안적으로 또는 조합하여, 림프구성 맥락수막염 바이러스 돌연변이체는 바람직하게는 서열 번호 2, 서열 번호 4, 서열 번호 6, 서열 번호 17, 서열 번호 25, 서열 번호 33, 서열 번호 41, 서열 번호 49, 서열 번호 57, 서열 번호 23, 서열 번호 31, 서열 번호 39, 서열 번호 47, 서열 번호 55, 또는 서열 번호 63에 따른 핵산 서열에 상보적인, 핵산 서열, 특히 리보핵산 서열을 포함하거나 또는 핵산 서열, 특히 리보핵산 서열로 이루어지는, 핵산, 특히 리보핵산을 포함한다.

[0132] 놀랍게도 림프구성 맥락수막염 바이러스의 각각의 돌연변이체/각각의 돌연변이체들은 - 이전 단락에 기재된 바와 같이 - 원발성 종양 세포 또는 세포주 H1975의 세포에서의 개선된 복제 능력 뿐만 아니라 특히 야생형의 림프구성 맥락수막염 바이러스에 비해 항종양 또는 개선된 항종양 특성을 갖는다는 것을 발견하였다.

[0133] 또한, 당단백질의 위치 181에서의 이소류신에 대한 코돈이 다른 코돈, 바람직하게는 메티오닌에 대한 코돈으로 대체되는 것이 바람직하다.

[0134] 또한, 당단백질의 위치 185에서의 아르기닌에 대한 코돈이 다른 코돈, 바람직하게는 트립토판에 대한 코돈으로 대체되는 것이 바람직하다.

[0135] 또한, 당단백질의 위치 155에서의 히스티딘에 대한 코돈이 다른 코돈, 바람직하게는 티로신에 대한 코돈으로 대체되는 것이 바람직하다.

[0136] 또한, 당단백질의 위치 358에서의 아르기닌에 대한 코돈이 다른 코돈, 바람직하게는 리신에 대한 코돈으로 대체되는 것이 바람직하다.

[0137] 또한, 림프구성 맥락수막염 바이러스 돌연변이체는 돌연변이를 포함하는 핵산, 특히 리보핵산, 바람직하게는 L-리보핵산을 포함하는 것이 또한 바람직하며, 여기서 돌연변이는 핵산, 특히 리보핵산, L-리보핵산의 위치 4537에서의 아데닌의 구아닌에 의한 뉴클레오티드 치환이다.

[0138] 또한, 림프구성 맥락수막염 바이러스 돌연변이체는 돌연변이를 포함하는 L-단백질을 인코딩하는, 핵산, 특히 리보핵산, 바람직하게는 L-리보핵산을 포함하는 것이 바람직하며, 여기서 돌연변이는 L-단백질의 위치 1513에서의 라이신의 다른 아미노산에 의한, 바람직하게는 글루타메이트에 의한 아미노산 치환이다.

[0139] 또한, 림프구성 맥락수막염 바이러스 돌연변이체는 돌연변이를 포함하는 L-단백질을 인코딩하는, 핵산, 특히 리보핵산, 바람직하게는 L-리보핵산을 포함하는 것이 바람직하며, 여기서 돌연변이는 L-단백질의 위치 1995에서의 페닐알라닌의 다른 아미노산에 의한, 바람직하게는 세린에 의한 아미노산 치환이다.

[0140] 또한, 림프구성 맥락수막염 바이러스 돌연변이체는 돌연변이를 포함하는 핵산, 특히 리보핵산, 바람직하게는 L-리보핵산을 포함하는 것이 또한 바람직하며, 여기서 돌연변이는 핵산, 특히 리보핵산, 바람직하게는 L-리보핵산의 위치 5984에서의 티민의, 바람직하게는 뉴클레오티드 사이토신에 의한 뉴클레오티드 치환이다.

[0141] 또한, 림프구성 맥락수막염 바이러스 돌연변이체는 돌연변이를 포함하는 L-단백질을 인코딩하는, 핵산, 특히 리보핵산, 바람직하게는 L-리보핵산을 포함하는 것이 또한 바람직하며, 여기서 돌연변이는 L-단백질의 위치 2094에서의 이소류신의 다른 아미노산에 의한, 바람직하게는 발린에 의한 아미노산 치환이다.

[0142] 또한, 림프구성 맥락수막염 바이러스 돌연변이체는 돌연변이를 포함하는 핵산, 특히 리보핵산, 바람직하게는 L-리보핵산을 포함하는 것이 바람직하며, 여기서 돌연변이는 핵산, 리보핵산, 바람직하게는 L-리보핵산의 뉴클레오티드 위치 6280에서의 아데닌의, 다른 뉴클레오티드에 의한, 바람직하게는 구아닌에 의한 뉴클레오티드 치환이다.

[0143] 또한, 림프구성 맥락수막염 바이러스 돌연변이체는 돌연변이를 포함하는 L-단백질을 인코딩하는, 핵산, 특히 리보핵산, 바람직하게는 L-리보핵산을 포함하는 것이 바람직하며, 여기서 돌연변이는 L-단백질의 위치 2141에서의

트레오닌의 다른 아미노산에 의한, 바람직하게는 알라닌에 의한 아미노산 치환이다.

[0144] 또한, 림프구성 맥락수막염 바이러스 돌연변이체는 돌연변이를 포함하는 핵산, 특히 리보핵산, 바람직하게는 L-리보핵산을 포함하는 것이 또한 바람직하며, 여기서 돌연변이는 핵산, 리보핵산, 바람직하게는 L-리보핵산의 위치 6421에서의 아데닌의, 다른 뉴클레오티드에 의한, 바람직하게는 구아닌에 의한 뉴클레오티드 치환이다.

[0145] 또한, 림프구성 맥락수막염 바이러스 돌연변이체는 돌연변이를 포함하는 L-단백질을 인코딩하는, 핵산, 특히 리보핵산, 바람직하게는 L-리보핵산을 포함하는 것이 또한 바람직하며, 여기서 돌연변이는 L-단백질의 위치 2175에서의 아르기닌의, 바람직하게는 라이신에 의한 아미노산 치환이다.

[0146] 또한, 림프구성 맥락수막염 바이러스 돌연변이체는 돌연변이를 포함하는 핵산, 특히 리보핵산, 바람직하게는 L-리보핵산을 포함하는 것이 또한 바람직하며, 여기서 돌연변이는 핵산, 리보핵산, 바람직하게는 L-리보핵산의 위치 6524에서의 구아닌의, 뉴클레오티드 아데닌에 의한 뉴클레오티드 치환이다.

[0147] 본 발명의 또 다른 실시 양태에서, 림프구성 맥락수막염 바이러스 돌연변이 체는 의약에 적용 또는 사용하기 위한 본 개시내용의 임의의 림프구성 맥락수막염 바이러스 돌연변이체를 비롯한, 림프구성 맥락수막염 바이러스 돌연변이체이다.

[0148] 바람직하게는 림프구성 맥락수막염 바이러스 돌연변이체는 종양의 치료 및/또는 예방에 적용 또는 사용하기 위한 림프구성 맥락수막염 바이러스 돌연변이체이다.

[0149] 종양은 바람직하게는 암종, 흑색종, 모세포종, 림프종 및 육종으로 이루어진 군으로부터 선택된다.

[0150] 본 발명의 맥락에서 용어 "암종"은 상피 기원의 악성 신생물을 의미하는 것으로 이해되어야 한다.

[0151] 본 발명의 맥락에서 용어 "육종"은 중배엽 기원의 악성 신생물을 의미하는 것으로 이해되어야 한다.

[0152] 본 발명의 맥락에서 용어 "흑색종"은 멜라닌 세포 기원의 악성 신생물을 의미하는 것으로 이해되어야 한다.

[0153] 본 발명의 맥락에서 용어 "림프종"은 림프구 기원의 악성 신생물을 의미하는 것으로 이해되어야 한다.

[0154] 본 발명의 맥락에서 용어 "모세포종"은 배아 기원의 악성 신생물을 의미하는 것으로 이해되어야 한다.

[0155] 암종은 바람직하게는 항문 암종, 기관지 암종, 폐 암종, 자궁 내막 암종, 담낭 암종, 방광 암종, 간세포 암종, 고환 암종, 결장 암종, 결장직장 암종, 직장 암종, 후두 암종, 식도 암종, 위 암종, 유방 암종, 신장 암종, 난소 암종, 췌장 암종, 인두 암종, 구강 인두 암종, 전립선 암종, 갑상선 암종 및 자궁 경부 암종으로 이루어진 군으로부터 선택된다.

[0156] 육종은 혈관 육종, 연골 육종, Ewing 육종, 섬유 육종, 카포시 육종, 지방 육종, 평활근 육종, 악성 섬유성 조직구종, 신경성 육종, 골육종 및 횡문근 육종으로 이루어진 군으로부터 선택될 수 있다.

[0157] 추가로, 림프구성 맥락수막염 바이러스 돌연변이체는 국소, 특히 근육 내, 복강 내 또는 피하 투여를 위해 제조되거나 사용될 수 있다.

[0158] 대안적으로, 림프구성 맥락수막염 바이러스 돌연변이체는 전신, 특히 정맥 내 투여를 위해 제조되거나 사용될 수 있다.

[0159] 림프구성 맥락수막염 바이러스 돌연변이체의 추가 특성 및 이점에 대해서는 이전 및 다음 설명을 완전히 참조한다.

[0160] 제3 양태에 따르면, 본 발명은 서열 번호 1 서열 번호 3, 서열 번호 5, 서열 번호 18, 서열 번호 26, 서열 번호 34, 서열 번호 42, 서열 번호 50, 서열 번호 58, 서열 번호 66, 서열 번호 24, 서열 번호 32, 서열 번호 40, 서열 번호 48, 서열 번호 56, 또는 서열 번호 64에 따른 아미노산 서열을 포함하거나 이로 이루어진, 단백질 또는 펩티드, 특히 당단백질 또는 L-단백질을 포함하거나 이로 이루어진 림프구성 맥락수막염 바이러스 돌연변이체에 관한 것이다.

[0161] 대안적으로 또는 조합하여, 림프구성 맥락수막염 바이러스 돌연변이체는 핵산, 특히 리보핵산을 포함하며, 여기서 핵산, 특히 리보핵산은 서열 번호 2, 서열 번호 4, 서열 번호 6, 서열 번호 17, 서열 번호 25, 서열 번호 33, 서열 번호 41, 서열 번호 49, 서열 번호 57, 서열 번호 65, 서열 번호 23, 서열 번호 31, 서열 번호 39, 서열 번호 47, 서열 번호 55, 또는 서열 번호 63에 따른 핵산 서열이거나 그에 상보적인, 핵산 서열, 특히 리보핵산 서열을 포함하거나 또는 핵산 서열, 특히 리보핵산 서열로 이루어진다.

[0162] 바람직하게는 림프구성 맥락수막염 바이러스 돌연변이체는 의약에 적용 또는 사용하기 위한 림프구성 맥락수막염 바이러스 돌연변이체이다.

[0163] 림프구성 맥락수막염 바이러스 돌연변이체는 특히 바람직하게는 종양의 치료 및/또는 예방에 사용 또는 적용하기 위한 림프구성 맥락수막염 바이러스 돌연변이체이다.

[0164] 종양은 바람직하게는 암종, 흑색종, 모세포종, 림프종 및 육종으로 이루어진 군으로부터 선택된다.

[0165] 본 발명의 맥락에서 용어 "암종"은 상피 기원의 악성 신생물을 의미하는 것으로 이해되어야 한다.

[0166] 본 발명의 맥락에서 용어 "육종"은 중배엽 기원의 악성 신생물을 의미하는 것으로 이해되어야 한다.

[0167] 본 발명의 맥락에서 용어 "흑색종"은 멜라닌 세포 기원의 악성 신생물을 의미하는 것으로 이해되어야 한다.

[0168] 본 발명의 맥락에서 용어 "림프종"은 림프구 기원의 악성 신생물을 의미하는 것으로 이해되어야 한다.

[0169] 본 발명의 맥락에서 용어 "모세포종"은 배아 기원의 악성 신생물을 의미하는 것으로 이해되어야 한다.

[0170] 암종은 바람직하게는 항문 암종, 기관지 암종, 폐 암종, 자궁 내막 암종, 담낭 암종, 방광 암종, 간세포 암종, 고환 암종, 결장 암종, 결장직장 암종, 직장 암종, 후두 암종, 식도 암종, 위 암종, 유방 암종, 신장 암종, 난소 암종, 췌장 암종, 인두 암종, 구강 인두 암종, 전립선 암종, 갑상선 암종 및 자궁 경부 암종으로 이루어진 군으로부터 선택된다.

[0171] 육종은 혈관 육종, 연골 육종, Ewing 육종, 섬유 육종, 카포시 육종, 지방 육종, 평활근 육종, 악성 섬유성 조직구종, 신경성 육종, 골육종 및 횡문근 육종으로 이루어진 군으로부터 선택될 수 있다.

[0172] 추가로, 림프구성 맥락수막염 바이러스 돌연변이체는 국소, 특히 근육 내, 복강 내 또는 피하 투여를 위해 제조되거나 사용될 수 있다.

[0173] 대안적으로, 림프구성 맥락수막염 바이러스 돌연변이체는 전신, 특히 정맥 내 투여를 위해 제조되거나 사용될 수 있다.

[0174] 림프구성 맥락수막염 바이러스 돌연변이체의 다른 특징 및 이점과 관련하여, 반복을 피하기 위해, 이전 설명, 특히 본 발명의 제2 양태의 맥락에서 이루어진 진술을 완전히 참조한다. 특히 림프구성 맥락수막염 바이러스 돌연변이체, 단백질 또는 펩티드, 특히 당단백질, 및 핵산, 특히 리보핵산과 관련하여 거기에 기술된 특징 및 장점은 본 발명의 제3 양태에 따른 림프구성 맥락수막염 바이러스 돌연변이체에도 준용된다.

[0175] 제4 양태에 따르면, 본 발명은 본 발명의 제2 또는 제3 양태에 따른 림프구성 맥락수막염 바이러스 돌연변이체를 포함하는 약물 또는 약제에 관한 것이다.

[0176] 약물 또는 약제는 PD-1(프로그램된 세포 사멸 단백질 1)과 같은 관문 차단제, 및/또는 아폽토시스 조절제, 특히 SMAC-mimeticum (LCL-161)와 같은 아폽토시스 억제제를 추가로 포함할 수 있다.

[0177] 약물 또는 약제는 바람직하게는 약학적으로 허용되는 담체를 추가로 포함한다. 담체는 물, 염수 수용액, 완충 수용액, 세포 배양 배지 및 상기 담체 중 적어도 2종의 조합으로 이루어진 군으로부터 선택될 수 있다.

[0178] 약물 또는 약제의 다른 특징 및 이점과 관련하여, 반복을 피하기 위해, 이전 설명, 특히 본 발명의 제2 및 제3 양태의 맥락에서 이루어진 진술을 완전히 참조한다. 특히 림프구성 맥락수막염 바이러스 돌연변이체와 관련하여 거기에 기술된 특징 및 장점은 본 발명의 제4 양태에서 언급된 약물 또는 약제에도 준용된다.

[0179] 제5 양태에 따르면, 본 발명은 서열 번호 1, 서열 번호 3, 서열 번호 5, 서열 번호 7, 서열 번호 10, 서열 번호 18, 서열 번호 26, 서열 번호 34, 서열 번호 42, 서열 번호 50, 서열 번호 58, 서열 번호 24, 서열 번호 32, 서열 번호 40, 서열 번호 48, 서열 번호 56, 또는 서열 번호 64에 따른 아미노산 서열을 포함하거나 이로 이루어진, 바람직하게는 단리된 단백질 또는 펩티드, 특히 당단백질 또는 L-단백질인, 단백질 또는 펩티드에 관한 것이다. 본 발명은 또한 서열 번호 1, 서열 번호 3, 서열 번호 5, 서열 번호 7, 서열 번호 10, 서열 번호 18, 서열 번호 26, 서열 번호 34, 서열 번호 42, 서열 번호 50, 서열 번호 58, 서열 번호 24, 서열 번호 32, 서열 번호 40, 서열 번호 48, 서열 번호 56, 또는 서열 번호 64에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖

는 단리된 단백질 또는 펩티드에 관한 것이다.

[0180] 서열 번호 1 및 서열 번호 3에 따른 아미노산 서열은 바람직하게는 림프구성 맥락수막염 바이러스 돌연변이체의 당단백질, 특히 당단백질의 단백질 성분 또는 단백질 모이어티의 아미노산 서열이다. 서열 번호 5에 따른 아미노산 서열은 바람직하게는 림프구성 맥락수막염 바이러스 돌연변이체의 L-단백질의 아미노산 서열이다. 서열 번호 7의 아미노산 서열은 바람직하게는 야생형 림프구성 맥락수막염 바이러스의 L-단백질의 아미노산 서열이다.

[0181] 본 발명은 또한 서열 번호 12, 서열 번호 20, 서열 번호 28, 서열 번호 36, 서열 번호 44, 서열 번호 52, 서열 번호 60, 서열 번호 14, 서열 번호 22, 서열 번호 30, 서열 번호 38, 서열 번호 46, 서열 번호 54, 또는 서열 번호 62에 따른 아미노산 서열을 포함하거나 이로 이루어진, 바람직하게는 단리된 단백질 또는 펩티드, 특히 핵단백질 또는 Z-단백질인 단백질 또는 펩티드에 관한 것이다. 본 발명은 또한 서열 번호 12, 서열 번호 20, 서열 번호 28, 서열 번호 36, 서열 번호 44, 서열 번호 52, 서열 번호 60, 서열 번호 14, 서열 번호 22, 서열 번호 30, 서열 번호 38, 서열 번호 46, 서열 번호 54, 또는 서열 번호 62에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖는 단리된 단백질 또는 펩티드에 관한 것이다.

[0182] 단백질 또는 펩티드의 다른 특징 및 이점과 관련하여, 반복을 피하기 위해, 이전 설명, 특히 본 발명의 제2 및 제3 양태의 맥락에서 이루어진 진술을 완전히 참조한다. 특히 단백질 또는 펩티드, 특히 당단백질과 관련하여 거기에 기술된 특징 및 장점은 본 발명의 제5 양태에 따른 단리된 단백질 또는 펩티드에도 준용된다.

[0183] 제6 양태에 따르면, 본 발명은 서열 번호 2, 서열 번호 4, 서열 번호 6, 서열 번호 8 서열 번호 9, 서열 번호 17, 서열 번호 25, 서열 번호 33, 서열 번호 41, 서열 번호 49, 서열 번호 57, 서열 번호 23, 서열 번호 31, 서열 번호 39, 서열 번호 47, 서열 번호 55, 또는 서열 번호 63에 따른 또는 이에 상보적인, 핵산 서열, 특히 리보핵산 서열을 포함하거나 이로 이루어진, 바람직하게는 단리된 핵산, 특히 리보핵산인 핵산에 관한 것이다. 본 발명은 또한 서열 번호 2, 서열 번호 4, 서열 번호 6, 서열 번호 8 서열 번호 9, 서열 번호 17, 서열 번호 25, 서열 번호 33, 서열 번호 41, 서열 번호 49, 서열 번호 57, 서열 번호 23, 서열 번호 31, 서열 번호 39, 서열 번호 47, 서열 번호 55, 또는 서열 번호 63, 또는 각각의 상보적 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%, 바람직하게는 적어도 약 99.5%, 바람직하게는 적어도 약 99.6%, 바람직하게는 적어도 약 99.7%의 서열 동일성을 갖는 단리된 단백질 또는 펩티드에 관한 것이다.

[0184] 본 발명은 또한 서열 번호 11, 서열 번호 19, 서열 번호 27, 서열 번호 35, 서열 번호 43, 서열 번호 51, 서열 번호 59, 서열 번호 13, 서열 번호 21, 서열 번호 29, 서열 번호 37, 서열 번호 45, 서열 번호 53, 또는 서열 번호 61에 따른 또는 이에 상보적인, 핵산 서열, 특히 리보핵산 서열을 포함하거나 이로 이루어진, 바람직하게는 단리된 핵산, 특히 리보핵산인 핵산에 관한 것이다. 본 발명은 또한 서열 번호 11, 서열 번호 19, 서열 번호 27, 서열 번호 35, 서열 번호 43, 서열 번호 51, 서열 번호 59, 서열 번호 13, 서열 번호 21, 서열 번호 29, 서열 번호 37, 서열 번호 45, 서열 번호 53, 또는 서열 번호 61, 또는 각각의 상보적 서열에 대해 적어도 약 95%, 바람직하게는 적어도 약 96%, 바람직하게는 적어도 약 97%, 바람직하게는 적어도 약 98%, 바람직하게는 적어도 약 99%, 바람직하게는 적어도 약 99.1%, 바람직하게는 적어도 약 99.2%, 바람직하게는 적어도 약 99.3%, 바람직하게는 적어도 약 99.4%의 서열 동일성을 갖는 단리된 단백질 또는 펩티드에 관한 것이다.

[0185] 서열 번호 2 및 서열 번호 4에 따른 핵산 서열은 각각 바람직하게는 림프구성 맥락수막염 바이러스 돌연변이체의 당단백질, 특히 당단백질의 단백질 성분 또는 단백질 모이어티를 인코딩한다.

[0186] 서열 번호 6에 따른 핵산 서열은 바람직하게는 림프구성 맥락수막염 바이러스 돌연변이체의 L-단백질을 인코딩한다.

[0187] 서열 번호 8의 핵산 서열은 바람직하게는 야생형 림프구성 맥락수막염 바이러스의 L-단백질을 인코딩한다.

[0188] 상기 단리된 핵산의 추가 특징 및 이점과 관련하여, 반복을 피하기 위해, 이전 설명, 특히 본 발명의 제2 및 제3 양태의 맥락에서 이루어진 진술을 완전히 참조한다. 특히 핵산, 특히 리보핵산과 관련하여 거기에 기술된 특징 및 장점은 본 발명의 제6 양태에 따른 단리된 핵산에도 준용된다.

[0189] 제7 양태에 따르면, 본 발명은 본 발명의 제5 양태에 따른 적어도 하나의 핵산, 특히 리보핵산을 함유하는 단리

된 유전자 클러스터 또는 오페론에 관한 것이다.

[0190] 유전자 클러스터 또는 오페론의 추가 특징 및 장점과 관련하여, 반복을 피하기 위해, 이전 설명, 특히 본 발명의 제6 양태의 맥락에서 이루어진 진술을 또한 완전히 참조한다. 특히 핵산, 특히 리보핵산과 관련하여 거기에 기술된 특징 및 장점은 본 발명의 제7 양태에 따른 단리된 유전자 클러스터 또는 오페론에도 준용된다.

[0191] 제8 양태에 따르면, 본 발명은 본 발명의 제6 양태에 따른 적어도 하나의 핵산 또는 본 발명의 제7 양태에 따른 유전자 클러스터 또는 오페론을 함유하는 발현 벡터에 관한 것이다.

[0192] 발현 벡터의 추가 특징 및 장점과 관련하여, 반복을 피하기 위해, 이전 설명, 특히 본 발명의 제6 및 제7 양태의 맥락에서 이루어진 진술을 또한 완전히 참조한다. 특히 핵산 및 유전자 클러스터 또는 오페론과 관련하여 거기에 기술된 특징 및 장점은 본 발명의 제8 양태에 따른 발현 벡터에도 준용된다.

[0193] 제9 양태에 따르면, 본 발명은 본 발명의 제5 양태에 따른 단백질 또는 펩티드를 발현하거나 함유하고/하거나 본 발명의 제6 양태에 따른 핵산, 특히 리보핵산을 함유하는 유기체, 바이러스, 벡터 또는 플라스미드에 관한 것이다.

[0194] 유기체는 숙주 세포, 진균 또는 세균일 수 있다.

[0195] 숙주 세포는 예를 들어 진핵 또는 원핵 세포일 수 있다. 더욱이, 숙주 세포는 유기체 및/또는 벡터 및/또는 플라스미드의 생산에 사용될 수 있는 세포일 수 있다.

[0196] 세균은 예를 들어 백신 벡터 또는 다른 치료용 세균일 수 있다.

[0197] 바이러스는 예를 들어 백신 벡터 또는 다른 치료용 바이러스일 수 있다.

[0198] 숙주 세포의 추가 특징 및 장점과 관련하여, 반복을 피하기 위해, 특히 본 발명의 제5 및 제6 양태에서 이루어진 진술을 완전히 참조한다. 특히 단백질 또는 펩티드, 특히 당단백질, 및 핵산, 특히 리보핵산과 관련하여 거기에 기술된 특징 및 장점은 본 발명의 제9 양태에 따른 숙주 세포에도 준용된다.

[0199] 본 발명의 추가 특징 및 이점은 실시예, 상응하는 도면 및 청구 범위의 형태로 바람직한 실시양태에 대한 하기 설명으로부터 이루어진다. 이하에 기술된 실시양태는 본 발명의 추가 설명 및 더 나은 이해를 제공하기 위한 것일 뿐이며 결코 제한적인 것으로 해석되어서는 안된다.

[0200] 본 발명은 또한 본 개시내용의 LCMV, 바람직하게는 본 개시내용의 LCMV 돌연변이체를 포함하는 약학적 조성물에 관한 것이다. 상기 조성물은 약학적으로 허용되는 부형제를 추가로 포함할 수 있다. 약학적 조성물은 PD-1(프로그램된 세포 사멸 단백질 1)과 같은 관문 차단제, 및/또는 아폽토시스 조절제, 특히 SMAC-mimeticum (LCL-161)와 같은 아폽토시스 억제제를 추가로 포함할 수 있다. 약학적 조성물은 약학적으로 허용되는 담체를 추가로 포함할 수 있다. 담체는 물, 염수 수용액, 완충 수용액, 세포 배양 배지 및 상기 담체 중 적어도 2종의 조합으로 이루어진 군으로부터 선택될 수 있다.

[0201] 본 개시내용은 또한 약제의 제조를 위한 개시내용의 LCMV, 바람직하게는 개시내용의 LCMV 돌연변이체의 용도에 관한 것이다. 약제는 종양 치료를 위한 것일 수 있다. 약제는 본 발명의 제4 양태에 따른 약제일 수 있다.

[0202] 본 개시내용은 또한 유효량의 개시내용의 LCMV, 바람직하게는 개시내용의 LCMV 돌연변이체, 또는 개시내용의 약제 또는 개시내용의 약학적 조성물을 이를 필요로 하는 대상체에게 투여하는 것을 포함하는, 종양 치료 방법에 관한 것이다.

[0203] 달리 표시되지 않는 한, 일련의 요소 앞에 나오는 "적어도"라는 용어는 일련의 모든 요소를 지칭하는 것으로 이해되어야 한다. 당업자는 단지 일상적인 실험을 사용하여 본원에 기술된 본 발명의 특정 실시양태에 대한 많은 등가물을 인식하거나 확인할 수 있을 것이다. 이러한 등가물은 본 발명에 포함되는 것으로 의도된다.

[0204] 본 명세서에서 사용된 용어 "및/또는" 은 "및", "또는" 및 "상기 용어에 의해 연결된 요소의 전부 또는 임의의 다른 조합"의 의미를 포함한다.

[0205] 본 명세서에 사용된 용어 "약" 또는 "대략"은 주어진 값 또는 범위의 20% 이내, 바람직하게는 10% 이내, 더욱 바람직하게는 5% 이내를 의미한다. 그러나 여기에는 구체적인 숫자도 포함되며, 예를 들어 약 20은 20을 포함한다.

[0206] 문맥이 달리 요구하지 않는 한, 본 명세서 및 이어지는 청구 범위 전체에 걸쳐, "포함하다"라는 단어 및 "포함하다" 및 "포함하는"과 같은 변형은 언급된 정수 또는 단계 또는 정수 또는 단계의 그룹을 포함하지만 임의의

다른 정수 또는 단계 또는 정수 또는 단계의 그룹이 제외되지 않는 것을 의미하는 것으로 이해되어야 할 것이다. 본 명세서 사용된 용어 "포함하는"은 용어 "함유하는" 또는 "포함하는"으로 대체될 수 있거나 때때로 본 명세서에서 사용시 용어 "갖는"으로 대체될 수 있다.

[0207] 본 명세서에 사용될 때 "으로 이루어진"은 청구 요소에 명시되지 않은 임의의 요소, 단계 또는 성분을 배제한다. 본 명세서에서 사용될 때 "으로 본질적으로 이루어진"은 청구물의 기본적 및 신규한 특징에 실질적으로 영향을 미치지 않는 물질 또는 단계를 배제하지 않는다.

[0208] 본 명세서의 각 경우에서 "포함하는", "으로 본질적으로 이루어진" 및 "으로 이루어진"이라는 용어 중 어느 하나는 다른 두 용어 중 하나로 대체될 수 있다. 예를 들어, 용어 "포함하는"은 "으로 본질적으로 이루어진" 및 "으로 이루어진"에 대한 명시적 지원도 제공하는 것을 의미하고, 용어 "으로 본질적으로 이루어진"은 "포함하는" 및 "으로 이루어진"에 대한 명시적 지원도 제공하는 것을 의미하고, 용어 "으로 이루어진"은 "으로 본질적으로 이루어진" 및 "포함하는"에 대한 명시적 지원도 제공하는 것을 의미한다.

[0209] 본 발명은 본 명세서에 기술된 특정 방법론, 프로토콜, 재료, 시약 및 물질 등에 제한되지 않고 그 자체가 다양할 수 있음을 이해해야 한다. 본 명세서에서 사용된 용어는 특정 실시양태를 설명하기 위한 것이며, 청구 범위에 의해서만 정의되는 본 발명의 범위를 제한하려는 의도가 아니다.

[0210] 본 명세서 전체에서 인용된 모든 간행물(모든 특허, 특허출원, 과학 간행물, 제조업체의 사양, 지침 등을 포함)은 그 전체가 여기에 참조로 포함된다. 본 명세서의 어떠한 것도 본 발명이 선행 발명으로 인해 그러한 개시를 선행할 자격이 없다는 것을 인정하는 것으로 해석되어서는 안된다. 참조로 포함된 자료가 본 명세서와 모순되거나 일치하지 않는 한, 명세서는 그러한 자료를 대체할 것이다.

발명을 실시하기 위한 구체적인 내용

[0211] **실시예**

[0212] **1. 방법 및 재료**

[0213] **1.1 마우스**

[0214] 생체 내 항종양 분석을 위해 WT 동물(C57BL/6 배경) 또는 적응성 면역계가 없는 NOD.SCID 마우스가 사용되었다. OT-1 마우스는 오브알부민(ovalbumin)-특이적 MHC-1 제한 T 세포 수용체를 이식 유전자로서 가지고 있다.

[0215] **1.2 세포주**

[0216] MC57 (CVCL_4985)은 아레나바이러스 LCMV가 잘 증식할 수 있는 뮤린 섬유아세포 세포주이다. C643 (CVCL_5969)은 인간 역형성 갑상선 암종 세포주이다. H1975는 인간 폐 암종 세포주(CVCL_1511, ATCC, CRL-5908, 선암)이다. TrampC2는 뮤린 선암 세포주이다(CVCL_3615). MOPC는 뮤린 구인두 세포주이다. CMT167 (CVCL_2405)은 뮤린 폐 암종 세포주이다. B16F10-OVA는 모델 항원으로서 오브알부민을 발현하는 뮤린 흑색종 세포주 (CVCL_0159)이다. UKE-Mel-13a는 인간 흑색종 전이에서 단리된 원발성 종양 세포이며 100x 미만으로 계대된 것이다. 511950은 트랜스제닉 뮤린 췌장 암종으로부터 단리된 원발성 종양 세포이며(Mazur PK et al Nat Med. 2015 Oct; 21 (10) : 1163-71.) 20x 미만으로 계대된 것이다. 511950R은 511950 세포에서 유래하며 MEK 억제제 트라메티닙으로 처리하여 100x 미만으로 계대된 것이다.

[0217] **1.3 바이러스**

[0218] LCMV 균주 WE는 Prof. Zinkernagel (Experimental Immunology, Zurich, Switzerland)의 실험실에서 획득했으며 2008 년부터 L929 세포 또는 BHK 세포에서 증식되었다. 클론 LCMV-P42, LCMV-P52 및 LCMV-P91은 다른 계대 후에 단리 및 시퀀싱되었다.

[0219] **1.4 시약**

[0220] LCL161 (Selleckchem) 및 항-PD1 (BioXcell)을 각각 LCMV 및 LCMV-P52와 조합하여 항종양 활성에 대해 시험했다.

[0221] **1.5 면역형광에 의한 LCMV 감염된 세포의 결정**

[0222] 세포에서 LCMV를 검출하기 위해 면역형광을 사용하였다. 세포를 각각 커버 유리를 포함하는 24 웰 플레이트에 파종하였다. 24 시간 후 세포를 LCMV로 감염시키고 24 시간 후에 형광색소 표지된 항-LCMV-NP 항체(클론 VL4)로

염색하고, 형광 현미경으로 시각화하고 일체형 CCD 카메라로 사진을 찍었다.

[0223] 1.6 플라크 분석에 의한 상청액 중의 LCMV 측정

[0224] 세포의 LCMV 생산을 결정하기 위해, 세포를 24-웰 플레이트에 파종하고 24 시간 후에 LCMV로 감염시켰다. 24 시간 후에 상청액을 추출하였다. 상청액을 24-웰 플레이트에서 적정하고 MC57 세포(150,000 세포/홀)를 첨가하였다. 4 시간 후에 메틸 셀룰로오스를 첨가하였다. 추가 48 시간 후, 세포 잔디(cell lawn)를 항-LCMV-NP 항체(클론 KL53)가 있는 LCMV 플라크에 대해 분석했다. 상청액 내 감염성 입자의 수/ml 를 결정하기 위해 플라크를 계수하였다.

[0225] 1.7 바이러스 계대

[0226] 바이러스를 종양에 적응시키기 위해, 상이한 원발성 종양 세포 또는 종양 세포주를 LCMV-WE로 감염시켰다. 세포를 24-웰 플레이트(1 mL 배지 중 약 100,000 세포/웰)에 플레이팅하였다. 24 시간 후, 100 μL 중 감염다중도(MOI) = 1로 바이러스를 첨가했다. 설정에 따라 1 ~ 30 분 사이에 초기 접종물을 제거하고, 새로운 배지를 추가했다. 24 시간 또는 48 시간 또는 72 시간 후 세포 배양 상청액을 추출하고 추가 분석을 위해 동결했다. 새로 플레이팅된 세포를 추출된 상청액 100 μL로 감염시켰다. 이 절차를 30 ~ 100 회 반복하였다.

[0227] 1.8 시퀀싱

[0228] 바이러스 RNA의 역전사 후, 중합 효소 연쇄 반응(PCR)에서 서열 특이적 프라이머 쌍(올리고뉴클레오티드)으로 cDNA를 증폭시켰다. PCR 산물을 정제하고, 사이클 시퀀싱(modified singer method)에 의해 시퀀싱하고, 산물을 모세관 전기 영동으로 분리하고 시퀀스를 전기 영동도로 기록했다. 핵산 서열을 번역하여 단백질 서열을 얻었다.

[0229] 1.9 선천성 면역 활성

[0230] 선천성 면역계를 활성화시키는 LCMV의 능력은 뮤린 IFN-알파 ELISA (ThermoFisher)를 사용하여 바이오마커 IFN-알파에 의해 측정하였다.

[0231] 1.10 적응성 면역 활성화

[0232] 적응성 면역계를 활성화하는 LCMV의 능력은 활성화된 림프구의 4량체 염색(NIH, Tetramer Facility)에 의해 시험하였다.

[0233] 1.11 종양 성장 및 처리

[0234] 항종양 효과를 측정하기 위해 C57BL/6 또는 NOD.SCID 마우스(6-12 주령) 5 x 10^5 종양 세포(100 μL)를 오른쪽 또는 왼쪽 옆구리에 피하 주사했다. 가시적인 종양이 형성된 후, 동물을 처리하고 평균 종양 직경 또는 종양 부피를 결정했다. 전이 모델의 경우 B16F10-OVA 세포를 정맥 내로 적용했다.

[0235] 1.12 오브알부민(종양)-특이적 CD8+ T 세포의 분리 및 전달

[0236] 종양 특이적 CD8+ T 세포의 분석을 위해, OT-1 마우스의 비장 세포를 오브알부민 발현 종양(B16F10-OVA) 세포를 보유한 C57BL/6 마우스로 옮겼다. 비장은 기계적으로 분쇄하였다. 여과 후, 마우스 당 10^7 개의 비장 세포를 정맥 내 주사하였다.

[0237] 1.13 종양 특이적 CD8+ T 세포의 측정

[0238] 종양 특이적 CD8+ T 세포의 수를 분석하기 위해, 혈액으로부터의 세포를 형광 오브알부민 4량체(펩티드 SIINFEKL를 보유하는 4개의 결합된 H-2 Kb MHC-I 분자, NIH Tetramer Facility) 및 형광색 결합된 항-CD8 항체(eBioscience) 및 유세포 분석기로 세척 후 분석하였다. T 세포 기능 분석을 위해, 비장 세포를 기계적으로 분쇄하고 Brefeldin A로 여과한 후 SIINFEKL 펩티드 유무에 관계없이 인큐베이션했다. 6 시간 후 세포를 고정하고, 침투시키고, CD8(항-CD8, eBioscience) 및 세포내 인터페론-감마(항-인터페론-감마, eBioscience)에 특이적인 형광 항체로 염색했다. IFN-감마 생산 세포의 빈도는 유세포 분석기로 분석하였다.

[0239] 1.14 통계 분석

[0240] 평균 값은 짝을 이루지 않은 2-샘플 스튜던트 t-검정을 사용하여 비교하였다. 데이터는 평균±SEM으로 표시된다. 통계적 유의 수준은 $p < 0.05$로 결정되었다.

[0241] 1.15 LCMV-P42의 생성:

[0242] LCMV-WE를 원발성 종양 세포 배양물(UKE-Mel-13a)에서 42 회 계대하였다. 42 계대 후, 새로운 바이러스(LCMV-P42)에서 기능적 돌연변이가 발견되었다. LCMV-WE 및 돌연변이체 P42의 핵산 및 아미노산 서열이 도 25(A 및 B)에 도시되어 있다.

[0243] 1.16 LCMV-P91, LCMV-P52 및 서브클론의 생성:

[0244] LCMV-WE를 종양 세포주 H1975에서 52 회 계대했다. 52 계대 후, 돌연변이 I181M, R185W가 새로운 바이러스의 당단백질에서 검출되었다. 또한 일부 관련성이 없거나 올리고클론성 돌연변이(준종)가 발견되었다. 이 바이러스는 "LCMV-P52"로 명명된다. I181M 및 R185W 돌연변이의 안정성과 중요성을 결정하기 위해 계대 P52의 상청액을 39 회 더 계대했다. 이 계대에서 파생된 바이러스는 "LCMV-P91"로 명명되었으며 여전히 돌연변이 I181M 및 R185W를 포함하고 있다. 바이러스 LCMV-P52는 제한 희석에 의해 서브클로닝되었다. 이 클론 바이러스는 "LCMV-P52.1"로 명명된다. 돌연변이 I181M, R185W는 안정적으로 유지되었다. 관련이 없는 것으로 간주되고/되거나 올리고클론성 돌연변이(준종)는 약간의 변화를 보였다. 단일 돌연변이 I181M 및 R185W의 역할을 결정하기 위해 일부 이전 계대를 분석했다. 계대 P29에는 개별 I181M 및 R185W 돌연변이를 가진 바이러스가 포함되어 있다. 계대 P29로부터의 바이러스는 제한 희석에 의해 서브클로닝되었다. 단일 돌연변이 R185W를 갖는 하나의 서브클론은 "LCMV-P52-1.3"으로 명명되었으며; 단일 돌연변이 I181M을 갖는 하나의 서브클론은 "LCMV-P52-2.1"로 명명되었다. LCMV 돌연변이체 P52, P92, P52-1, P52-1.3 및 P52-2.1의 핵산 및 아미노산 서열이 도 25(C-G)에 도시되어 있다. 핵산 및 아미노산 서열 LCMV-WE 및 돌연변이체 P42, P52, P92, P52-1, P52-1.3 및 P52-2.1의 얼라인먼트는 도 26(A-H)에 도시되어 있다.

[0245] 2. 조사

[0246] 2.1 종양 세포주 MC57, C643, H1975 및 원발성 종양 세포 배양물(UKE Mel-13a)을 LCMV(균주 WE, MOI 1)로 감염시켰다. 복제는 24 시간 후에 측정되었다(n = 3).

[0247] 이에 의해 LCMV(균주 WE)가 다르게 퍼짐이 입증되었다. 종양 세포주 MC57과 비교하여, 원발성 종양 세포 배양물(UKE-Mel-13a) 뿐만 아니라 세포주 C643 및 H1975에서 확산이 감소했다. 얻은 결과는 도 1에 그래픽으로 도시되어 있다.

[0248] 흰색에서는 MC57, C643, H1975 및 UKE-Mel-13a이 있는 배양물 내 LCMV 감염된 세포를 볼 수 있다. ∅ = 감염 없음, LCMV = LCMV 감염됨.

[0249] 2.2 종양 세포주 MC57 및 원발성 종양 세포 배양물 511950을 LCMV(균주 WE, MOI 0,1)(왼쪽 그래프)로 감염시켰다. 종양 세포주 MC57, Tramp-C2 및 원발성 종양 세포 배양물(511950 및 511950R)을 LCMV(균주 WE, MOI 1)(오른쪽 그래프)로 감염시켰다. 감염성 바이러스 입자의 수를 상청액에서 24 시간 후에 측정하였다.

[0250] 이에 의해, LCMV(균주 WE)는 Tramp-C2 세포주 및 원발성 종양 세포 배양물(511950 및 511950R)에서 MC57 종양 세포주와 비교하여 덜 증식하는 것으로 입증되었다. 결과는 도 2에 도시되어 있다.

[0251] 도 2는 다음 범례를 갖는다:

[0252] 세포 좌표: 상청액 중 감염성 LCMV 입자 (PFU/mL),

[0253] 가로 좌표: 처리 그룹; MC57, Tramp-C2, 511950, 511950R.

[0254] 2.3 LCMV-WE는 원발성 종양 세포 배양물(UKE-Mel-13a)에서 42 회 계대되었다. 42 계대 후, 새로운 바이러스(LCMV-P42)에서 기능적 돌연변이가 발견되었다.

[0255] 이에 의해, 원발성 종양 세포가 계대에 의해 아레나바이러스를 변형하는데 적합하다는 것이 입증될 수 있다. 실험 절차는 도 3에 도시되어 있다.

[0256] 2.4 LCMV-WE는 종양 세포주 H1975에서 52 회 계대되었다. 52 계대 후, 새로운 바이러스 LCMV-P52에서 기능적 돌연변이들이 발견되었다.

[0257] 이에 의해, H1975의 예를 사용하여, (세포주 MC57에 비해) 감소된 LCMV 복제를 갖는 종양 세포주가 계대에 의해 아레나바이러스를 변경하는데 적합하다는 것이 입증되었다. 실험 절차는 도 4에 도시되어 있다.

[0258] 2.5 LCMV-P52는 종양 세포주 H1975에서 39 회 계대되었다. 39 계대 후 새로운 바이러스 LCMV-P91에서 추가 기능

적 돌연변이들이 검출되었다.

[0259] 이에 의해 H1975 세포가 계대에 의해 아레나바이러스를 변경할 수 있다는 것이 입증되었다. 실험 절차는 도 5에 그래픽으로 도시되어 있다.

[0260] 2.6 세포주 H1975를 LCMV-WE 및 LCMV-P52(MOI 1)로 감염시켰다. 바이러스는 상청액에서 12 시간 후에 결정되었다 (n = 6).

[0261] 이에 의해 H1975 세포에서 LCMV-P52가 LCMV-WE보다 더 잘 복제된다는 것이 입증되었다. 얻은 결과는 도 6에 그래픽으로 도시되어 있다.

[0262] 도 6은 다음 범례를 갖는다:

[0263] 세포 좌표: 상청액 중 감염성 LCMV 입자 (PFU/mL),

[0264] 가로 좌표 : 처리 그룹; LCMV-WE 또는 LCMV-P52

[0265] 2.7 뮤린 골수 유래 수지상 세포를 LCMV-WE 및 LCMV-P52 (MOI 1)로 감염시켰다. 바이러스는 상청액에서 24 시간 후에 결정되었다 (n = 3).

[0266] 이에 의해 항원 제시 세포에서 LCMV-P52가 LCMV-WE보다 더 잘 복제된다는 것이 입증되었다. 도 7에 그래픽으로 도시되어 있다.

[0267] 도 7은 다음 범례를 갖는다:

[0268] 세포 좌표: 상청액 중 감염성 LCMV 입자 (PFU/mL),

[0269] 가로 좌표 : 처리 그룹; LCMV-WE 또는 LCMV-P52

[0270] 2.8 종양 세포주 H1975를 LCMV-WE 또는 LCMV-P52(MOI 1)로 감염시켰다. 바이러스 확산은 24 시간 후 면역 형광으로 측정하였다.

[0271] 이에 의해, LCMV-P52는 H1975의 예를 사용한 LCMV WE에 비해 종양 세포주에서 더 잘 퍼질 수 있다는 것이 입증되었다. 얻은 결과는 도 8에 그래픽으로 도시되어 있다.

[0272] LCMV-WE 또는 LCMV-P52로 감염된 배양물에 대한 LCMV 감염된 세포는 흰색으로 표시된다.

[0273] 2.9 원발성 종양 세포(UKE-Mel-13a)를 LCMV-WE 또는 LCMV-P52(MOI 1)로 감염시켰다. 바이러스의 확산은 24 시간 후 면역 형광으로 측정하였다.

[0274] 이에 의해 LCMV-P52가 LCMV-WE에 비해 원발성 종양 세포에서 더 잘 퍼질 수 있다는 것이 입증되었다. 얻은 결과는 도 9에 그래픽으로 도시되어 있다.

[0275] LCMV-WE 또는 LCMV-P52로 감염된 배양물에 대한 LCMV 감염된 세포는 흰색으로 표시된다.

[0276] 2.10 C57BL/6 마우스를 LCMV-WE 또는 LCMV-P52(2 x 10^4 PFU 정맥 내)로 감염시켰다. 감염 1 일 후 혈청에서 IFN-알파를 측정하여 선천성 면역계의 활성화를 결정하였다.

[0277] 이에 의해 LCMV-P52가 LCMV-WE보다 더 강한 선천적 면역 활성화를 유발한다는 것이 입증되었다. 얻은 결과는 도 10에 그래픽으로 도시되어 있다.

[0278] 도 10은 다음 범례를 갖는다:

[0279] 세로 좌표: IFN-알파 농도 (ng/mL 혈청)

[0280] 가로 좌표: 처리 그룹; LCMV-WE 또는 LCMV-P52 감염된 동물.

[0281] 2.11 C57BL/6 마우스를 LCMV-WE 또는 LCMV-P52 (2 x 10^4 PFU 정맥 내)로 감염시켰다. 적응성 면역계의 활성화는 4량체를 사용하여 유세포 분석에 의해 결정되었다(바이러스 특이적 CD8+ T 세포 측정).

[0282] 이에 의해 LCMV-P52가 LCMV-WE보다 더 강한 적응성 면역 활성화를 유도한다는 것이 입증되었다. 얻은 결과는 도 11에 그래픽으로 도시되어 있다.

[0283] 도 11은 다음 범례를 갖는다:

[0284] 세로 좌표: 바이러스 특이적 CD8+ T 세포 (혈액 내 총 CD8+ T 세포의 %),

[0285] 가로 좌표: 시간 (감염 후 일수)

[0286] 2.12 NOD.SCID 마우스를 5 x 10^5 H1975 세포로 피하 처리하였다(-7 일). 마우스를 종양 내로 2 x 10^4 PFU LCMV-WE 또는 LCMV-P52로 추가로 감염시켰다(0 일). 종양 성장을 분석하였다.

[0287] 이에 의해 LCMV-P52 처리가 LCMV-WE 처리보다 더 강한 항종양 효과가 있다는 것이 입증되었다. 얻은 결과는 도 12에 그래픽으로 도시되어 있다.

[0288] 도 12는 다음 범례를 갖는다:

[0289] 세로 좌표: 평균 종양 직경(cm),

[0290] 가로 좌표: 시간(LCMV 처리 후 일수)

[0291] 2.13 C57BL/6 마우스를 5 x 10^5 MOPC 세포로 피하 처리하였다(-7 일). 마우스 그룹을 추가로 2 x 10^4 PFU LCMV-P52로 정맥 내로 감염시켰다(n = 3, 0 일). 종양 성장을 분석하였다.

[0292] 이에 의해 LCMV-P52 처리가 강한 항종양 효과가 있다는 것이 입증되었다. 결과는 도 13에 그래픽으로 도시되어 있다.

[0293] 도 13은 다음 범례를 갖는다:

[0294] 세로 좌표: 종양 부피 (mm^3),

[0295] 가로 좌표: 시간 (LCMV 처리 후 일수)

[0296] 2.14 C57BL/6 마우스를 5 x 10^5 CMT167 세포로 피하 처리하였다(-7 일). 한 그룹의 마우스를 추가로 2 x 10^4 PFU LCMV-P52로 정맥 내로 감염시켰다(n = 3, 0 일). 종양 성장을 분석하였다.

[0297] 이에 의해 LCMV-P52 처리가 강력한 항종양 효과가 있다는 것이 입증되었다. 결과는 도 14에 도시되어 있다.

[0298] 도 14는 다음 범례를 갖는다:

[0299] 세로 좌표: 종양 부피 (mm^3),

[0300] 가로 좌표: 시간 (LCMV 처리 후 일수)

[0301] 이에 의해 LCMV-P52 처리가 강력한 항종양 효과가 있다는 것이 입증되었다. 얻은 결과는 도 15에 그래픽으로 도시되어 있다.

[0302] 검은 색에는 폐 내 종양 세포가 표시된다; ∅ = 감염 없음.

[0303] 2.15 C57BL/6 마우스를 5 x 10^5 B16F10-OVA 세포로 정맥 내 처리하였다(-7 일). OT-1 마우스의 비장에서 단리된 종양 특이적 CD8+ T 세포를 옮겼다(-4 일). 한 그룹의 동물을 추가로 LCMV-P52로 정맥 내 처리하였다(2 x 10^4 PFU, n = 4). 9 일째에 폐를 제거하고 사진을 찍었다.

[0304] ∅ = 대조군 동물, 각 4 개의 폐; LCMV-P52 = LCMV-P52로 처리된 LCMV-P52, 각 4 개의 폐.

[0305] 2.16 C57BL/6 마우스를 5 x 10^5 B16F10-OVA 세포로 정맥 내 처리하였다(-7 일). OT-1 마우스의 비장에서 단리된 종양 특이적 CD8+ T 세포를 옮겼다(-4 일). 한 그룹의 동물을 추가로 LCMV-P52를 정맥 내 처리하였다(2 x 10^4 PFU, n = 4). 3 일째에 혈액 내 종양 특이적 CD8+ T 세포의 빈도를 측정했다.

[0306] 이에 의해 LCMV-P52 처리가 종양 특이적 CD8+ T 세포의 확장을 증가시킨다는 것이 입증되었다. 얻은 결과는 도 16에 그래픽으로 도시되어 있다.

[0307] 도 16은 다음과 같은 범례를 갖는다:

[0308] 세로 좌표: 혈액 내 종양 특이적 CD8+ T 세포의 빈도(총 CD8+ T 세포의 %),

[0309] 가로 좌표: 처리군 ∅ = 감염이 없는 상태 LCMV-P52 = LCMV-P52로 처리됨

[0310] **2.17** C57BL/6 마우스를 5 x 10^5 B16F10-OVA 세포로 정맥 내 처리하였다(-7 일). OT-1 마우스의 비장에서 단리된 종양 특이적 CD8+ T 세포를 옮겼다(-4 일). 한 그룹의 동물을 추가로 LCMV-P52로 정맥 내 처리하였다(2 x 10^4 PFU, n = 4). 9 일째에, 비장 내 종양 특이적 CD8+ T 세포의 기능을 시험관 내 재 자극에 의해 결정하였다.

[0311] 이에 의해 LCMV-P52 처리가 종양 특이적 CD8+ T 세포의 기능을 증가시킨다는 것이 입증되었다. 얻은 결과는 도 17에 그래픽으로 도시되어 있다.

[0312] 도 17은 다음과 같은 범례를 갖는다:

[0313] 세로 좌표: IFN- 감마 생성 종양 특이적 CD8+ T 세포의 빈도(총 CD8+ T 세포의 %),

[0314] 가로 좌표: 처리군 ∅ = LCMV-P52 처리 없음; LCMV-P52 = LCMV-P52로 처리; 범례: -: 항원 없음; +: 항원 재자극(SIINFEKL 펩티드).

[0315] **2.18** C57BL/6 마우스를 5 x 10^5 B16F10-OVA 세포로 피하 처리하였다(-7 일). 한 그룹의 동물은 더 이상 처리되지 않았다(n = 3). 한 그룹의 동물을 0 일부터 일주일에 두 번 억제제 LCL-161(경구 50 mg/kg 체중)으로 처리하였다. 한 그룹은 0 일에 LCMV-WE로 종양 내 처리하였다(2 x 10^4 PFU, n = 4). 한 그룹은 LCL-161 및 LCMV로 처리하였다. 종양 성장을 분석했다.

[0316] 이에 의해 LCMV-WE 처리가 LCL-161과 상승 효과가 있음이 입증되었다. 얻은 결과는 도 18에 그래픽으로 도시되어 있다.

[0317] 도 18은 다음 범례를 갖는다:

[0318] 세로 좌표: 종양 부피 (mm^3),

[0319] 가로 좌표: 시간 (LCMV 투여 후 일수)

[0320] **2.19** C57BL/6 마우스를 5 x 10^5 B16F10-OVA 세포로 피하 처리하였다(-7 일). 한 그룹의 동물은 더 이상 처리되지 않았다(n = 3). 한 그룹의 동물을 0 일부터 일주일에 두 번 억제제 LCL-161(경구 50 mg/kg 체중)으로 처리하였다. 한 그룹은 0 일에 LCMV-WE로 종양 내 처리하였다(2 x 10^4 PFU, n = 4). 한 그룹은 LCL-161 및 LCMV로 처리하였다. 동물의 생존율을 분석하였다.

[0321] LCMV-WE에 의한 처리가 LCL-161과 상승 효과가 있음을 알 수 있다. 얻은 결과는 도 19에 그래픽으로 도시되어 있다.

[0322] 도 19는 다음 범례를 갖는다:

[0323] 세로 좌표: 동물의 생존율(%),

[0324] 가로 좌표: 시간 (LCMV 투여 후 일수)

[0325] **2.20** C57BL/6 마우스를 5 x 10^5 B16F10-OVA 세포로 피하 처리하였다(-9 일). 한 그룹의 동물은 더 이상 처리되지 않았다(n = 3). 한 그룹은 0 일(2 x 10^4 PFU, n = 6-8)에 LCMV-P52로 종양 내 처리하였다. 동물 그룹은 1, 5 및 8 일에 관문 차단제 항-PD-1 (200 μg. 복강 내)로 처리하였다. 한 그룹은 관문 차단제 항 PD-1 및 LCMV-P52로 처리하였다. 종양 성장을 분석하였다.

[0326] 이에 의해 LCMV-P52 처리가 관문 차단제(예: 항-PD-1)와 시너지 효과가 있음이 입증되었다. 얻은 결과는 도 20에 그래픽으로 도시되어 있다.

[0327] 도 20은 다음과 같은 범례를 갖는다:

[0328] 세로 좌표: 종양 부피 (mm^3),

[0329] 가로 좌표: 시간 (LCMV 처리 후 일수)

[0330] 본 명세서에 언급된 아미노산 및 핵산 서열은 하기 서열 목록에 개시된 아미노산 및 핵산 서열에 상응한다.

[0331] **2.21** 10^5 개의 H1975 세포를 24 웰 플레이트에 파종하였다. 24 시간 후 세포를 바이러스 LCMV-WE, LCMV-P52.1(I181M, R185W), LCMV-P52-1.3(R185W) 및 LCMV-P52-2.1(I181M)로 감염다중도(MOI) 0.1로 감염시켰다. 바이러스를 24 시간 후에 상청액에서 분석하였다. 결과는 도 21에 도시되어 있다(평균+SEM, n = 6, $^*p < 0.05$, t-테스트).

[0332] 데이터는 돌연변이 I181M 및 R185W가 종양 세포에서 바이러스 증식을 개별적으로 증가시킨다는 것을 보여준다.

[0333] 도 21은 다음 범례를 갖는다:

[0334] X-축: 여러가지 바이러스

[0335] Y-축: 상청액 중 LCMV($\log_{10}$ PFU/ml)

[0336] **2.22** 2.5 x 10^5 개의 HCC1954 세포를 24 웰 플레이트에 파종한 후 LCMV-WE, LCMV-P52.1(I181M, R185W), LCMV-P52-1.3(R185W) 및 LCMV-P52-2.1(I181M)으로 감염다중도(MOI) 0.001로 감염시켰다. 바이러스를 48 시간 후에 상청액에서 분석하였다. 결과는 도 22에 도시되어 있다(오차 막대는 SEM, n = 4, $^{**}p < 0.001$, n.s.는 유의하지 않음을 나타낸다, 추가 Tukey 사후 테스트가 사용된 일원 분산 분석(one-way ANOVA이 사용되었다).

[0337] 데이터는 돌연변이 I181M 또는 돌연변이 185W가 HCC1954 종양 세포에서 바이러스 증식을 증가시킨다는 것을 보여준다.

[0338] 도 22는 다음 범례를 갖는다:

[0339] X-축: 여러가지 바이러스

[0340] Y-축: 상청액 중 LCMV($\log_{10}$ PFU/ml)

[0341] **2.23** 뮤린 췌장암 세포(511950, 4 x 10^5 세포), 인간 흑색종 세포(UKE118b, 4 x 10^5 세포) 또는 (UKE118c, 4 x 10^5 세포)를 24 웰 플레이트에 파종한 후 LCMV-WE(흰색 막대) 또는 LCMV-P42(I181M, 검은 색 막대)로 감염다중도(MOI) 0.1로 감염시켰다. 바이러스를 24 시간 후에 상청액에서 분석하였다. 결과는 도 23에 도시되어 있다(평균+SEM, n = 3, $^*p < 0.05$, t-테스트).

[0342] 데이터는 돌연변이 I181M이 종양 세포에서 바이러스 증식을 증가시킨다는 것을 보여준다.

[0343] 도 23은 다음 범례를 갖는다:

[0344] X-축: 여러가지 세포 유형

[0345] Y-축: 상청액 중 LCMV($\log_{10}$ PFU/ml)

[0346] **2.24** C57BL/6 마우스를 LCMV-WE, LCMV-P52.1(I181M, R185W), LCMV-P52-1.3(R185W) 및 LCMV-P52-2.1(I181M) 중 하나의 2 x 10^4 PFU로 정맥 내 감염시켰다. 8 일(흰색 막대) 및 10 일(검은 색 막대)에 혈액을 유세포 분석으로 4량체를 사용하여 LCMV-GP33-특이적 CD8+ T 세포의 빈도에 대해 분석하였다. 결과는 도 24에 도시되어 있다(평균+SEM, n = 6-12, 4 개의 개별 실험에서 풀링됨, $^*p < 0.05$, t-테스트).

[0347] 데이터는 돌연변이 I181M 및 R185W가 특정 T 세포를 자극하는 LCMV의 능력을 증가시킨다는 것을 보여준다. 돌연변이 I181M 및 R185W의 조합은 초기 T 세포 자극에 대한 상승적 특성을 가질 수 있다.

[0348] 도 24는 다음 범례를 갖는다:

[0349] X-축: 여러가지 바이러스

[0350] Y-축: 4량체-GP33-결합 CD8+ T 세포의 빈도(총 CD8+ T 세포의 %).

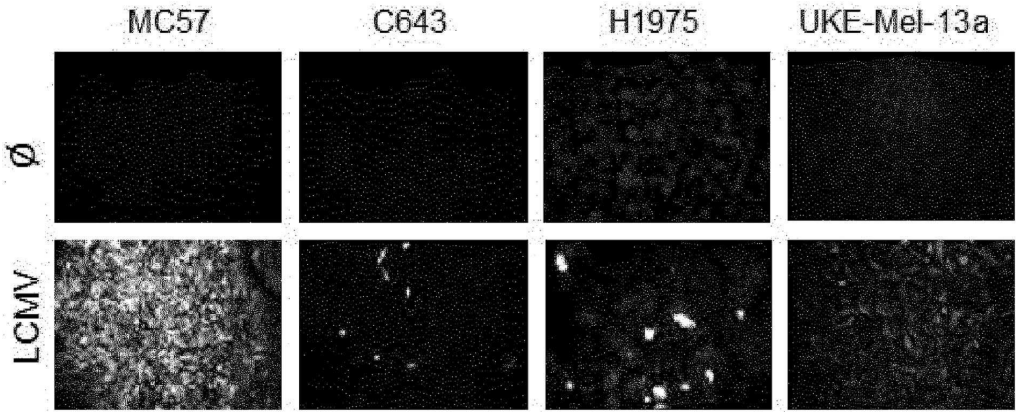
[0351] 본 명세서에 예시적으로 설명된 본 발명은 본 명세서에 구체적으로 개시되지 않은 임의의 요소 또는 요소들, 제한 또는 제한들 없이 적합하게 실시될 수 있다. 또한, 여기에 사용된 용어 및 표현은 제한이 아닌 설명의 용어로 사용되었으며, 이러한 용어 및 표현을 사용하여 제시 및 설명된 특징의 균등물 또는 그 일부를 배제하려는

의도는 없으며, 다만 청구된 본 발명의 범위 내에서 다양한 변형이 가능하다는 것은 인식할 수 있다. 따라서, 본 발명이 예시적인 실시양태 및 선택적 특징에 의해 구체적으로 개시되었지만, 본 명세서에 개시된 발명의 수정 및 변형은 당업자에 의해 의존될 수 있으며, 그러한 수정 및 변형은 본 발명의 범위 내에 있는 것으로 간주된다.

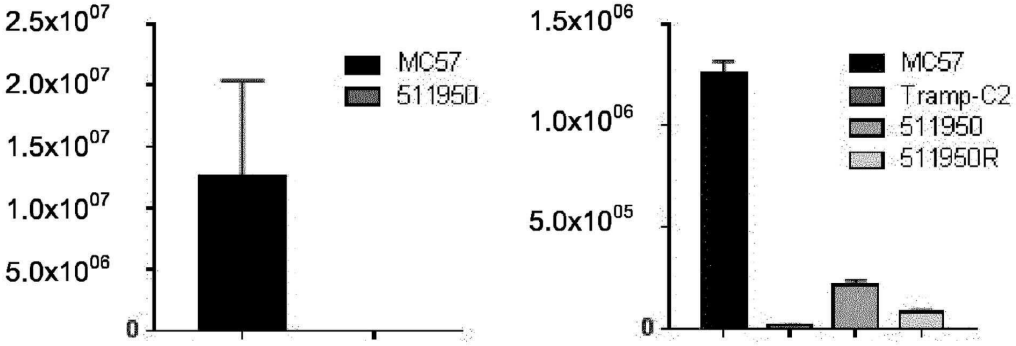
[0352] 본 발명은 본 명세서에서 광범위하고 일반적으로 설명되었다. 일반적인 개시에 속하는 각각의 더 좁은 종 및 하위 그룹도 본 발명의 일부를 형성한다. 여기에는, 청구된 물질이 본 명세서에서 구체적으로 언급되고 있는지 여부에 관계없이, 속으로부터 임의의 대상물을 제거하는 단서적 또는 부정적 제한과 함께 본 발명의 일반적인 설명이 포함된다.

도면

도면1



도면2



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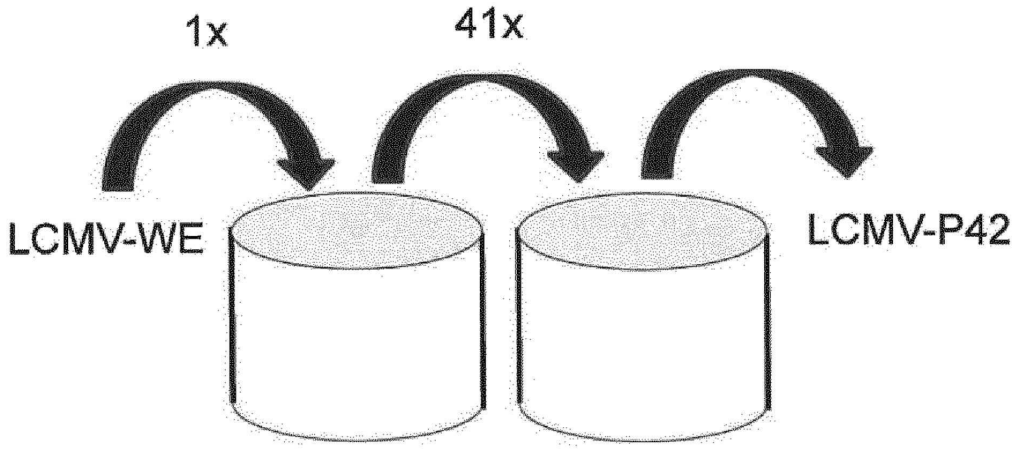
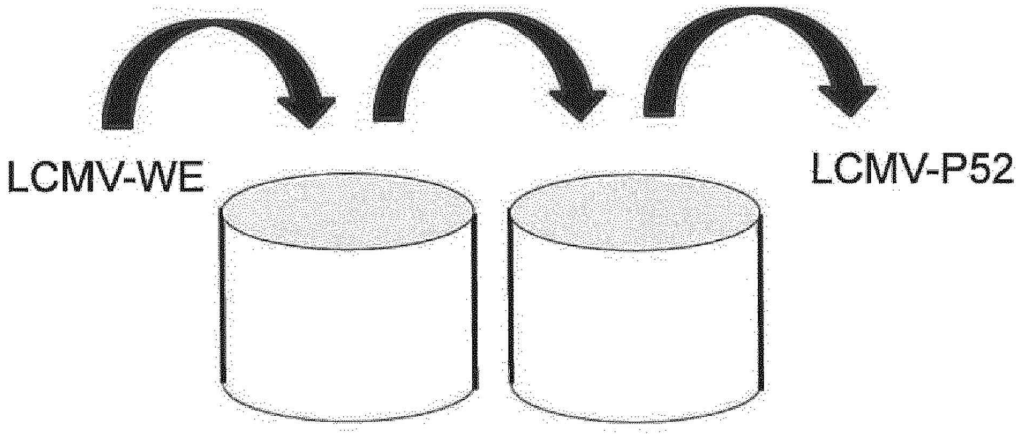
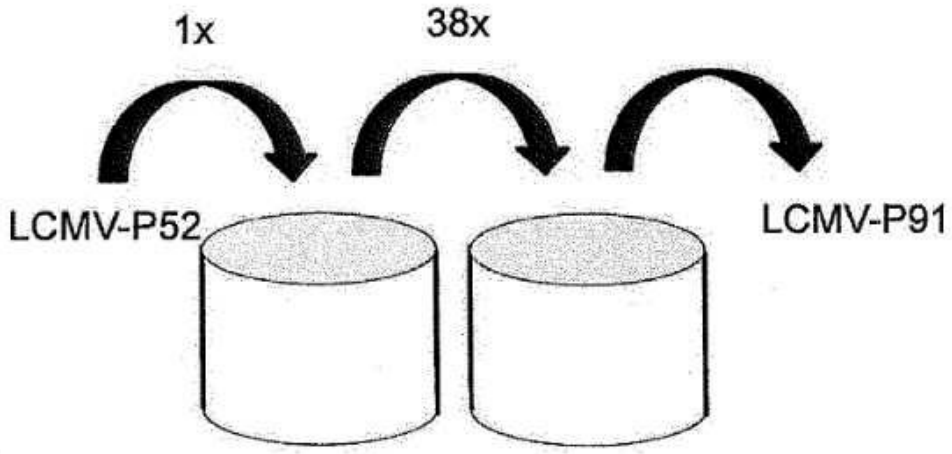

1x
41x
LCMV-WE
LCMV-P42

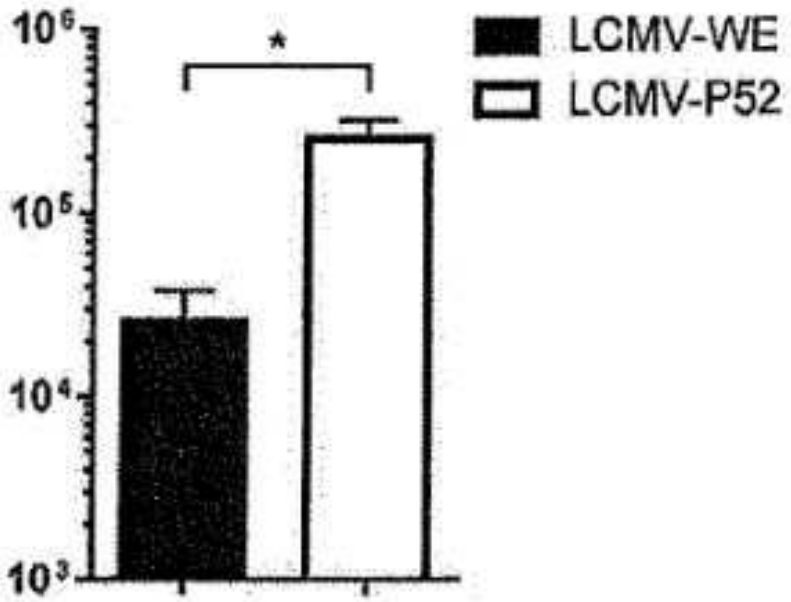
도면4


LCMV-WE
LCMV-P52

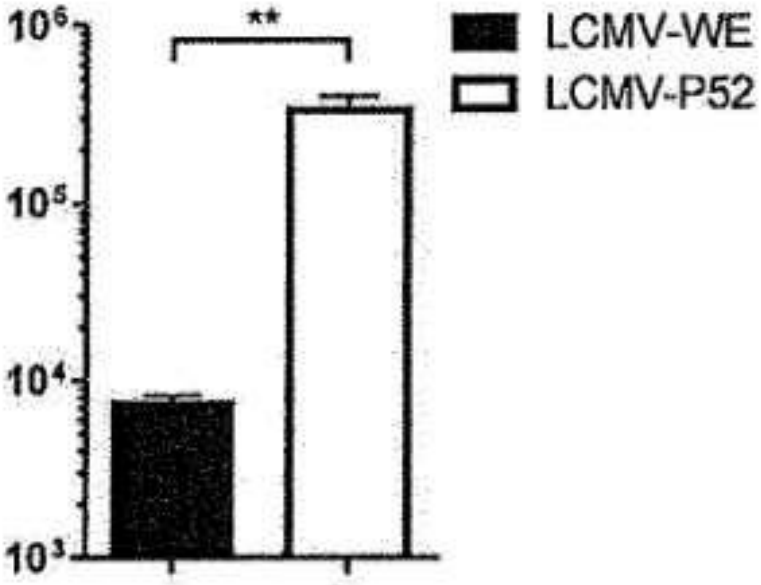
도면5


1x
38x
LCMV-P52
LCMV-P91

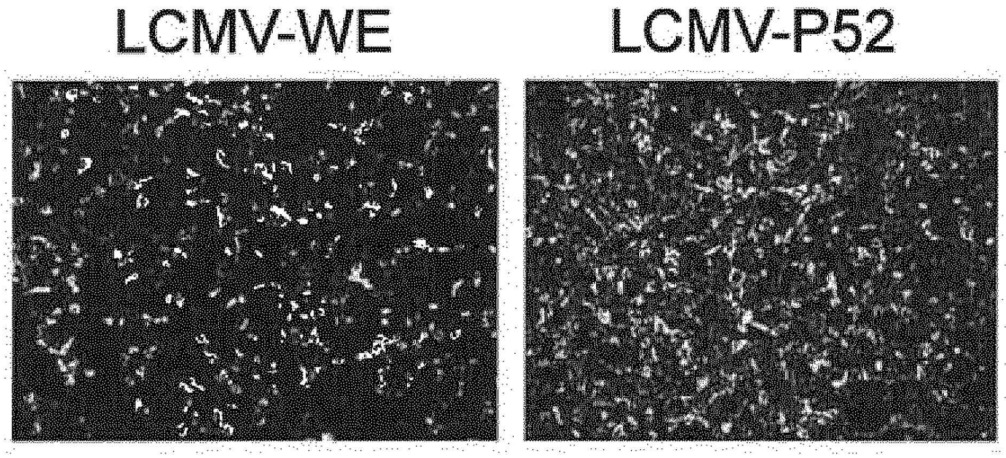
도면6


10⁶
10⁵
10⁴
10³
*
LCMV-WE
LCMV-P52

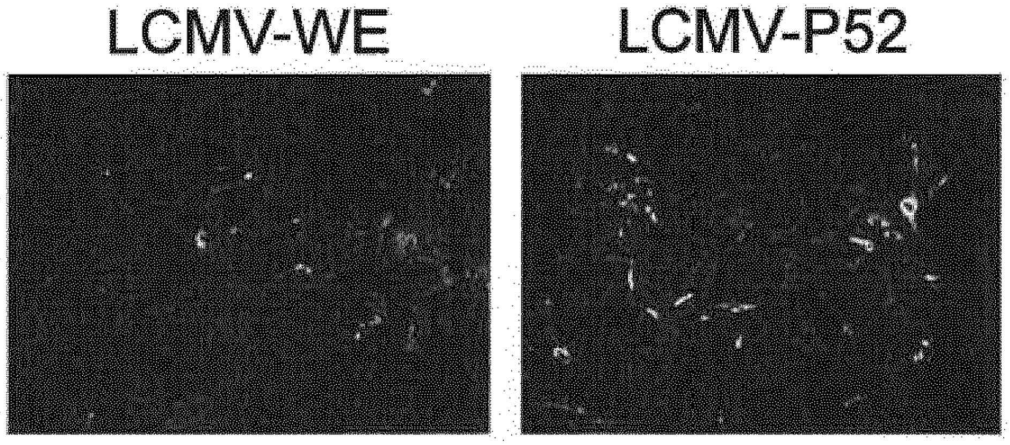
도면7


10⁶
10⁵
10⁴
10³
**
LCMV-WE
LCMV-P52

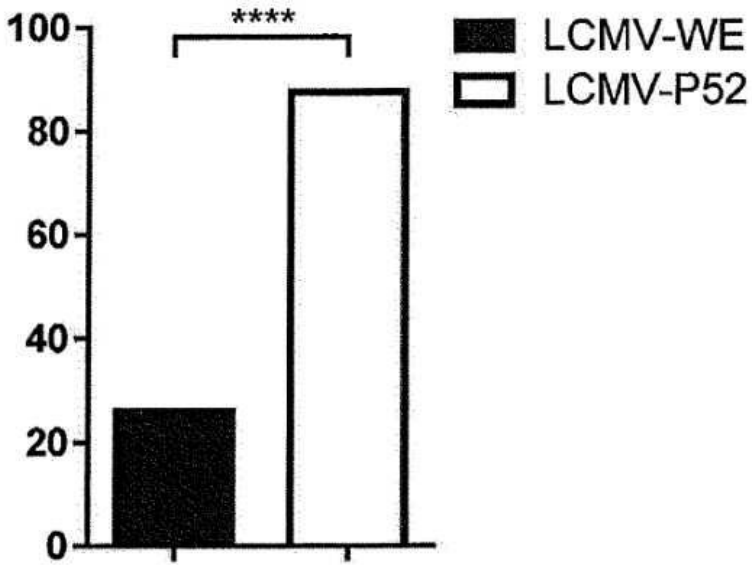
도면8


LCMV-WE
LCMV-P52

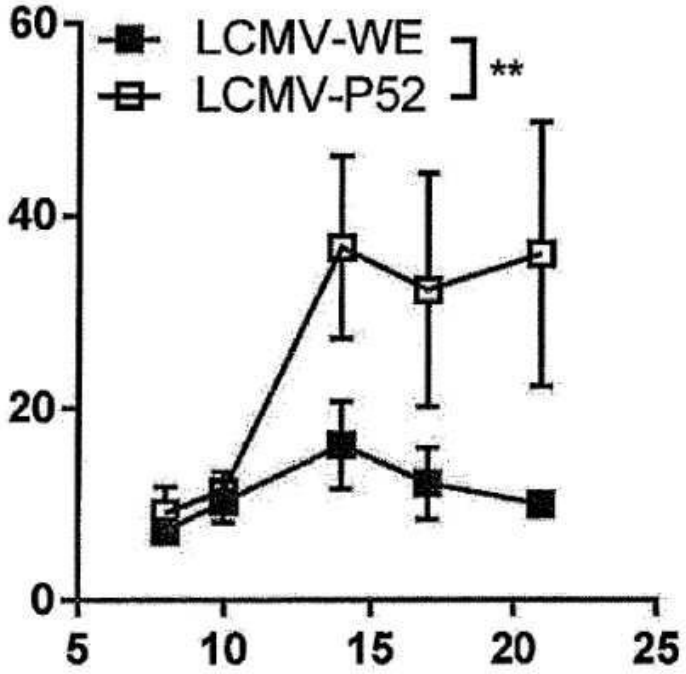
도면9


LCMV-WE
LCMV-P52

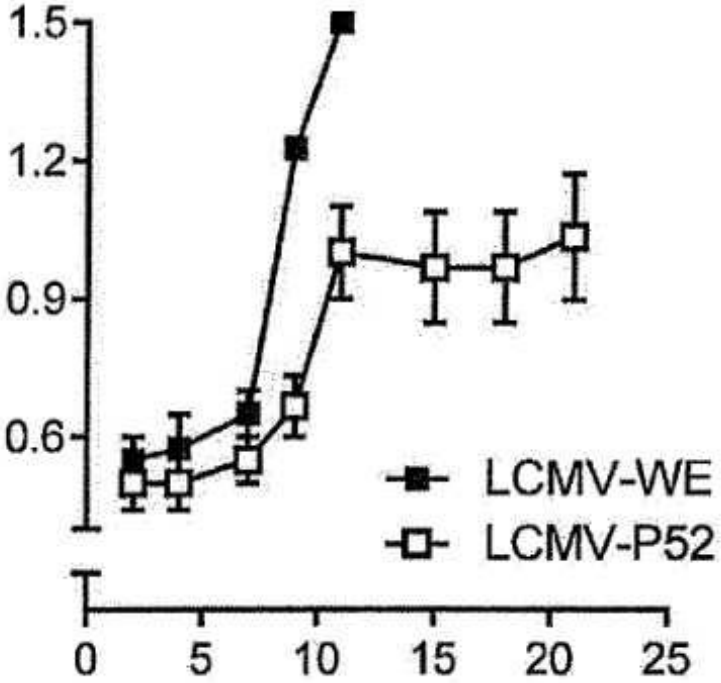
도면10


****
LCMV-WE
LCMV-P52
100
80
60
40
20
0

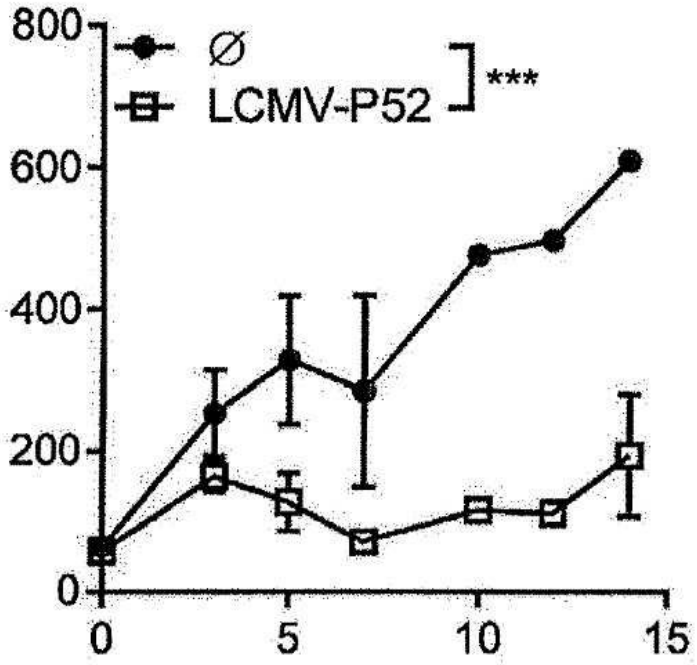
도면11


60
40
20
0
LCMV-WE
LCMV-P52
**
5
10
15
20
25

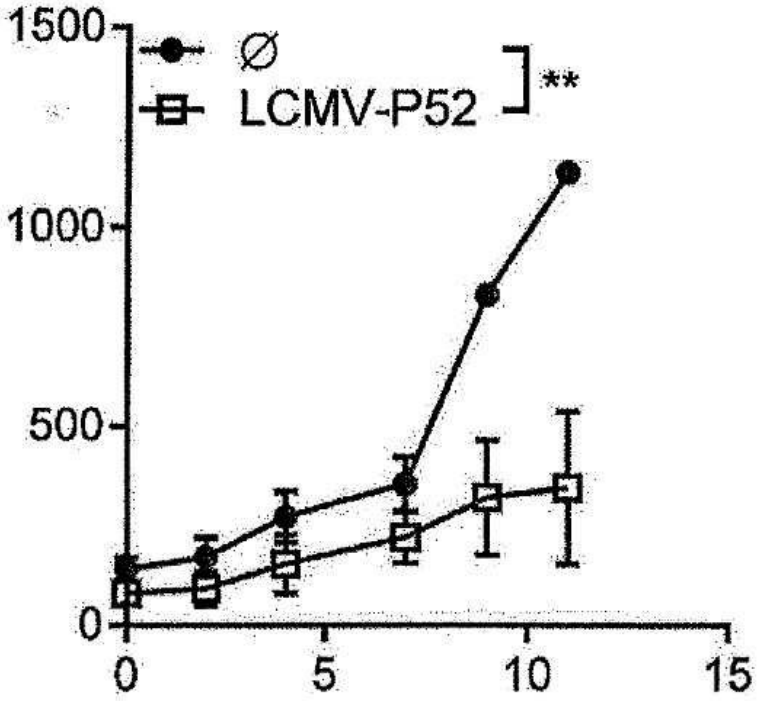
도면12


1.5
1.2
0.9
0.6
LCMV-WE
LCMV-P52
0
5
10
15
20
25

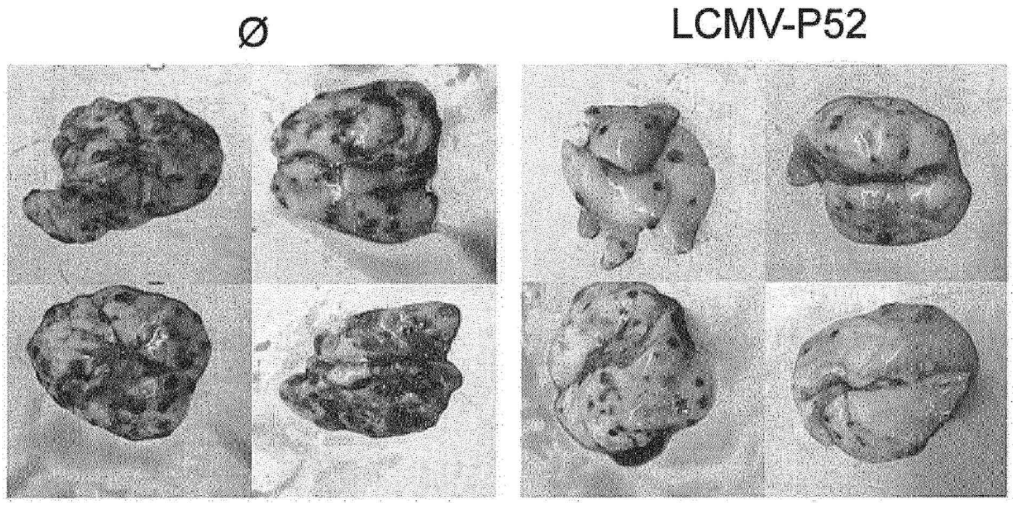
도면13


800
600
400
200
0
∅
LCMV-P52
***
0
5
10
15

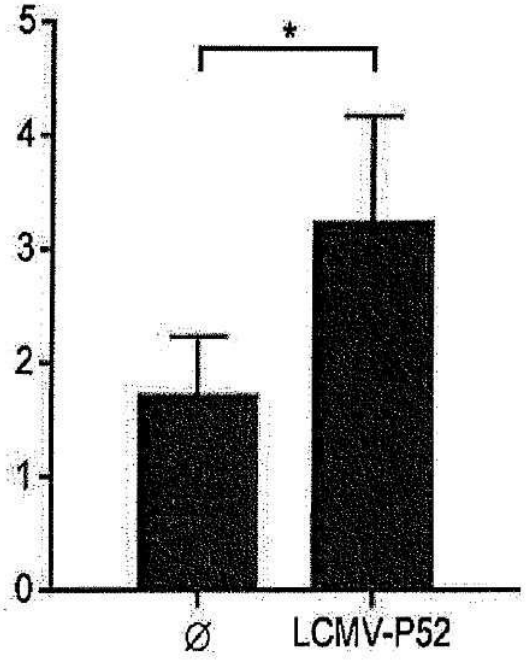
도면14


1500
1000
500
0
∅
LCMV-P52
**
0
5
10
15

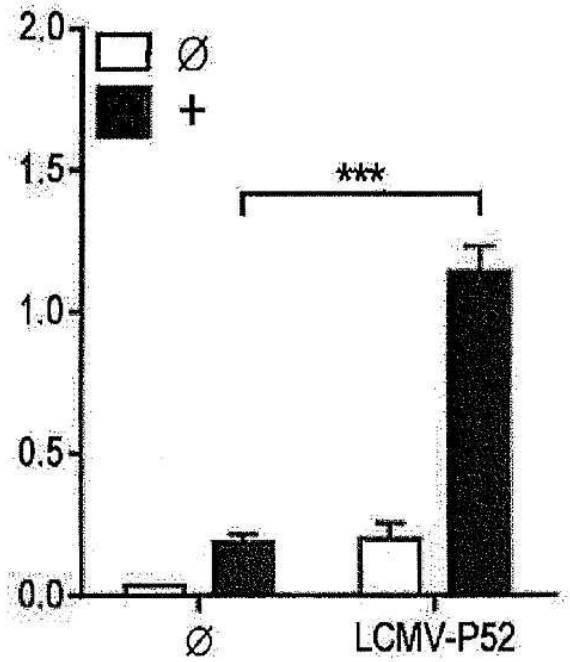
도면15



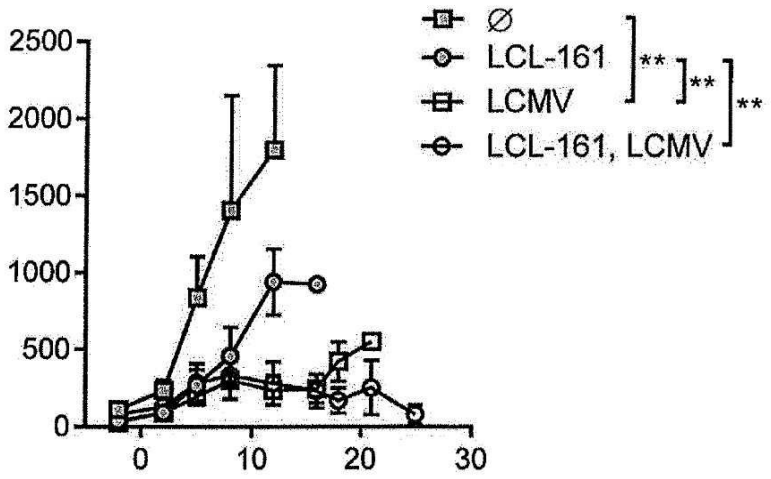
도면16



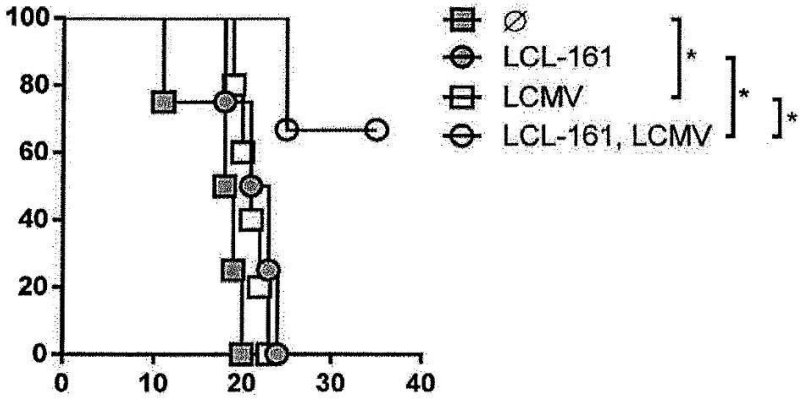
도면17



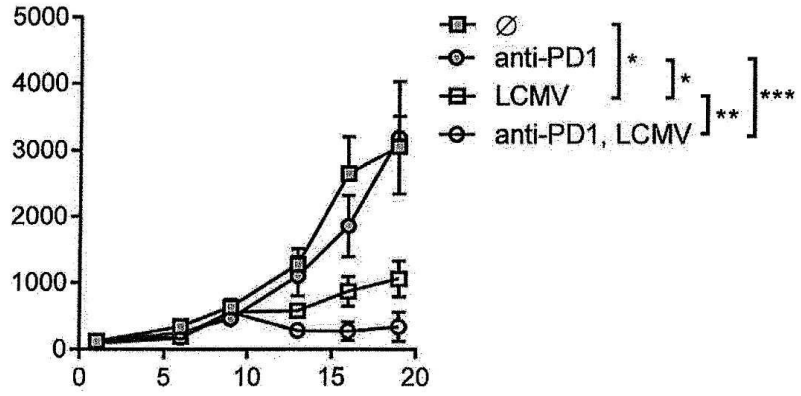
도면18



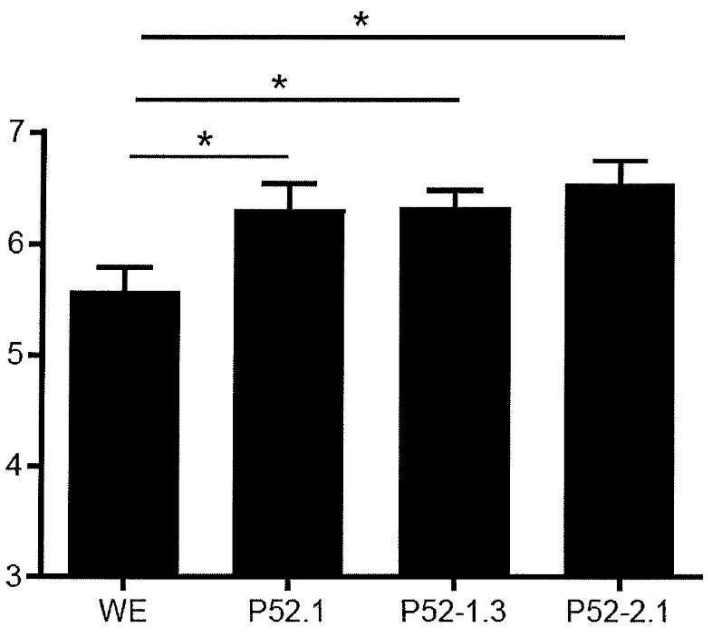
도면19



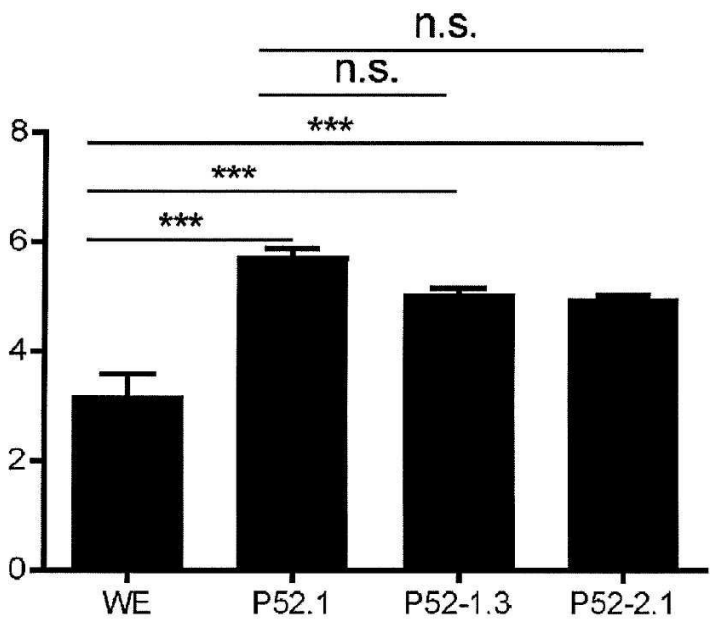
도면20


5000
4000
3000
2000
1000
0
0
5
10
15
20
∅
anti-PD1
LCMV
anti-PD1, LCMV
*
*
**
***

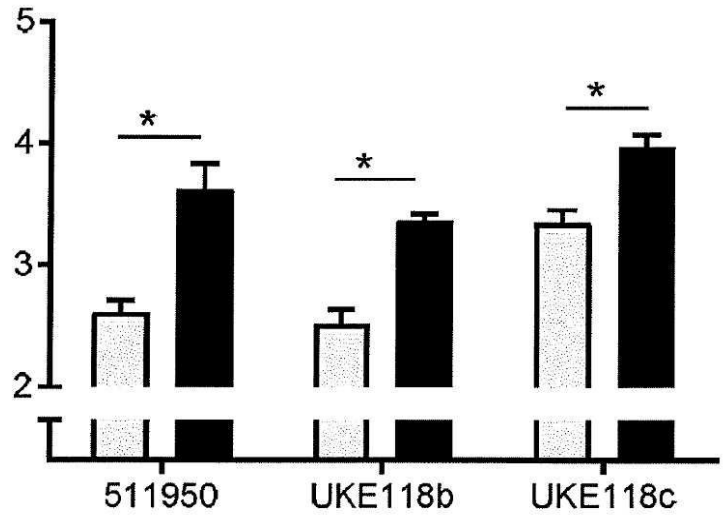
도면21


*
*
*
7
6
5
4
3
WE
P52.1
P52-1.3
P52-2.1

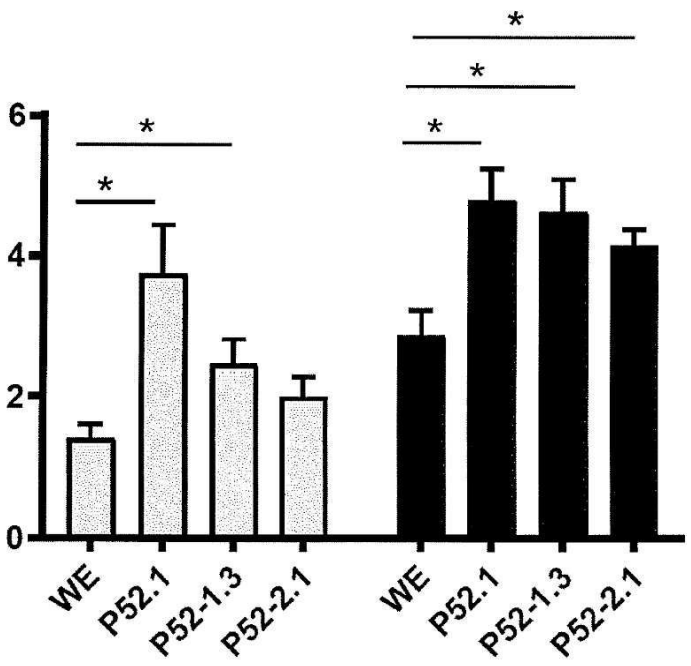
도면22



도면23



도면24



도면25a

A. Lymphocytic choriomeningitis virus (LCMV) strain WE

Source: 1-3376 **Segment = S**
Protein: **Pre-glycoprotein polyprotein GP complex**
Gene: GPC
Gene: 79-1575

```
>LCMV-WE-DUE_GP
ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC
ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC
TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT
ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC
ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC
AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT
ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATTCCAACCACAAAGCAGTGTCTTGT
GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT
ATAAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA
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AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA
TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC
ACTAGGAGACTTGCAGGCACATTCACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT
CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG
AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA
CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG
CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT
GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG
AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG
TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA
CATAGACACATAAAGGGCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAAACTATCTGGAAAAGACGCTGA
(SEQ ID NO: 9)
```

CDS: **79-1575**
Codon Start = 1; Codons 1-498

Chain:	*1-498*	*Pre-glycoprotein polyprotein GP complex*
Chain:	*1-58*	*Stable signal peptide*
Chain:	*59-265*	*Glycoprotein G1*
Chain:	*266-498*	*Glycoprotein G2*

Translation=

```
>LCMV-WE-DUE_GP
MGQIVTMFEALPHIIDEVINIVIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGMY
GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGSSGLELTFTNDSILNH
NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA
ISQCRTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR
YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG
NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH
LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM
LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI
CSCGAFKVPGVKTIWKRR
(SEQ ID NO:10)
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도면25b

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

>LCMV-WE-DUE_NP
ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG
CAGAGTTTTACATCAGATGTAAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT
GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT
GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG
AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG
ACCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA
GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACTTGATCAAAGATCCCAAATA
CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG
GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAATGCCAAGCCTGACAATG
GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC
CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT
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GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT
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AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT
GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA
AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA
TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
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AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA
ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC
ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAACATCCTGCCACATCATTTAATCTTCAGAGCACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 11)

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558

Translation=

>LCMV-WE-DUE_NP
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DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ
ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY
NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE
NILYKVCLSGEGWPYTACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY
SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGPNVVTL
(SEQ ID NO: 12)

도면25c

Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

>LCMV-WE-DUE_ZP
ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT
TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC
AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 13)

CDS: 90-362
Codon Start = 1; Codons 1-91
Translation=

>LCMV-WE-DUE_ZP
MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE

도면25d

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

>LCMV-WE-DUE_LP
ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG
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GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC
ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCCTTATTCTT
CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC
AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA
GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATGGGTGAATTTTAAGTTC
AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG
TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG
GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAATG
TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC
TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAAACTCAAAAGGAATTTCCAAAAG
GTCAGCCCTGGGGGCTTAATCAAGGAATTCTCTGAACTTTATGAAACCCTTACTGATAAT
GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCCTTAATGAGGTTCATT
ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA
CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAATTATTAAACACTAGAAGGAGACAGCTG
CTGAACTTAGATGTCTTATGTCTTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG
GAAAATGATAAACATTGGGTTGGTTGTTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC
CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAAGAAAATCAAGAGTG
CACAAAAAGGCATCTCTTGATGAGCTTTTTAGGGTATCCATAAATGAGTTCATAGCAAAA
ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC
CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAACTTTATGAGAGCCGGGACT
CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA
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CTACTATATCAGAAAACTGGAGAATCATCGAGGTGTTATTCCATACAAGGTCCGGATGGT
CACTTGATTTCCTTTTACGCAGATCCAAAAAGGTTCTTTTTACCAATTTTTTCAGATGAG
GTGTTGCACAACATGATAGACACAATGATTTCATGGATTAGGTCATGCCCTGACTTAAAA
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CCAACAAAGAGAAATCAAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGTC
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TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCACTAGCCTTAATGAA
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TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTTCATTTCATCTAGTA
GAGGACTTTGATCCATCCTGTCTCACCAATGACGACATGAGGTTTATTTGTGAGGCTGTT
GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT
CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTTCTTCTCAGAGGGTGATTGGTTCTCA
TGTATGAAGATGATCTTGTTACAGATGAATGCAAATGCGTATTCAGGGAAGTACAGACAC

도면25e

ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA
ATTAGTGAAAGGGAAAGCAATTCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC
ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCAACATCATACACT
TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG
GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCACAAGATTGGTAGAA
GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG
TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC
ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA
AATCTCAAACTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG
TTGACTTGGCATATGCATAAACTTGTTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG
AAATCATATGTTAAATCAAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG
AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT
GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG
TTTATCAATTATTGTATTGGTGTCATTTTTGGAGAGAGGCCAGAAGCCTATACATCAAGT
GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA
GAAGTCCTTGTCTTGCTGGAATTCCACTCTCACTTAAGTGGTTTGTTGAACAAGTTCATC
AGTCCAAAAAGTGTGGTTGGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG
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GGAGTTCCAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAAATAT
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GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA
AAGATCATGAGAAAACTTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC
GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA
GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG
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AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG
AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA
AATAAAAACAGGGAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA
CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA
CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCCTTCTCTGGGACTACATT
TGCATCTCATTGAGCAACTCTTTTGAGCTGGGTGTTTGGGTTTTAGCAGAACCTGTGAAA
GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTGATTATGTAGCAAGA
AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCAATCT
GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTCTGATGTG
AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAAATTCCTTGACCTTTGTGTGCTGATT
GACATCAACTCAGAGTCTTTGTCACTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA
CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA
GTTGATGAATTTGTTGTCAGCACAAGGGATGTCTGCAAGAACTTTTTGAAGCAAGTGTAT
TTCGAATCATTTGTACGAGAGTTTGTTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG
TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCCTTCCAA
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CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG
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TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC
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AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCTTTG
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AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG
AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAGAATATCTCTGTGAAATTGGAGACA
AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATTGGTGATGTCCTC
GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT
ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG
CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA
ATGTATGAGACAACTGGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG

도면25f

GCGGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 15)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210
Translation=

>LCMV-WE-DUE_LP
MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC
IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT
NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE
SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS
FFGRFRRDLLNGKLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL
ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ
LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK
DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF
EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG
TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI
TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS
LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS
CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC
MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ
NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE
RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS
DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW
GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY
ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFLDLFNREKKEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM
TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR
NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI
CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS
VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE
HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW
FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ
LQSPGVADYLSCSHFFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL
TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNISVKLET
KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMESEISTVLQELCMDRSVMLTPLSFV
PDWFTFRDCRLCFSRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID
(SEQ ID NO: 16)

도면25g

B. Lymphocytic choriomeningitis virus (LCMV) P42 mutant

Source: 1-3376 **Segment = S**
Protein: **Pre-glycoprotein polyprotein GP complex**
Gene: **GPC**
Gene: **79-1575**

>LCMV-P42_GP
ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC
ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC
TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT
ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC
ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC
AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT
ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATTCCAACCACAAAGCAGTGTCTTGT
GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT
ATGAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA
GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTCAGATGGCAAGACCACTTGGTGC
AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA
TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC
ACTAGGAGACTTGCAGGCACATTCACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT
CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG
AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA
CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG
CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT
GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG
AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG
TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA
CATAGACACATAAAGGGCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAAACTATCTGGAAAAGACGCTGA
(SEQ ID NO: 17)

CDS: **79-1575**
Codon Start = 1; Codons 1-498
Chain: *1-498* *Pre-glycoprotein polyprotein GP complex*
Chain: *1-58* *Stable signal peptide*
Chain: *59-265* *Glycoprotein G1*
Chain: *266-498* *Glycoprotein G2*

Translation=

>LCMV-P42_GP
MGQIVTMFEALPHIIDEVINIVIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGMY
GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGSSGLELTFTNDSILNH
NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA
MSQCRTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR
YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG
NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH
LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM
LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI
CSCGAFKVPGVKTIWKRR
(SEQ ID NO: 18)

도면25h

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

>LCMV-P42_NP
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GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT
GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG
AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG
ACCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA
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CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG
GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAATGCCAAGCCTGACAATG
GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC
CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT
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CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG
GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT
GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC
AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT
GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA
AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA
TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC
AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA
ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC
ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 19)

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558
Translation=

>LCMV-P42_NP
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DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ
ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY
NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE
NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY
SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGPNVVTL
(SEQ ID NO: 20)

도면25i

Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

>LCMV-P42_ZP
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TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC
AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 21)

CDS: 90-362
Codon Start = 1; Codons 1-91
Translation=

>LCMV-P42_ZP
MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE
(SEQ ID NO: 22)

도면25j

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

>LCMV-P42_LP

ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG
AGGCTGTCAAGGCAAAAACTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGCTAATT
GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC
ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCCTTATTCTT
CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC
AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA
GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATGGGTGAATTTTAAGTTC
AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG
TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG
GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAATG
TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC
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ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC
CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAACTTTATGAGAGCCGGGACT
CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA
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GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT
CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTTCTTCTCAGAGGGTGATTGGTTCTCA
TGTATGAAGATGATCTTGTTACAGATGAATGCAAATGCGTATTCAGGGAAGTACAGACAC

도면25k

ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA
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AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT
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GAAGTCCTTGTCTTGCTGGAATTCCACTCTCACTTAAGTGGTTTGTTGAACAAGTTCATC
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CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCCTTCTCTGGGACTACATT
TGCATCTCATTGAGCAACTCTTTTGAGCTGGGTGTTTGGGTTTTAGCAGAACCTGTGAAA
GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTGATTATGTAGCAAGA
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AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAAATTCCTTGACCTTTGTGTGCTGATT
GACATCAACTCAGAGTCTTTGTCACTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA
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ACACTTGGTGATTCACTAGAACTTGAACTAATAGGTTCTAGAAGCATTCTGAATGAGATC
AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG
AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAGAATATCTCTGTGAAATTGGAGACA
AAGGACATGAGRGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATTGGTGATGTCCTC
GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT
ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG
CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTR
ATGTATGAGACAACTGGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG

도면251

GCGGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 23)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210
Translation=

>LCMV-P42_LP
MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC
IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT
NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE
SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS
FFGRFRRDLLNGKLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL
ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ
LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK
DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF
EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG
TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI
TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS
LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS
CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC
MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ
NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE
RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS
DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW
GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY
ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFLDLFNREKKEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM
TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR
NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI
CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS
VRRLYPKIFEDQLLPFMFDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE
HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW
FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ
LQSPGVADYLSCSHFFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL
TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNISVKLET
KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMESEISTVLQELCMDRSVMLTPLSFV
PDWFTFRDCRLCFSRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID
(SEQ ID NO: 24)

도면25m

C. Lymphocytic choriomeningitis virus (LCMV) P52 mutant

Source: 1-3376 Segment = S
Protein: Pre-glycoprotein polyprotein GP complex
Gene: GPC
Gene: 79-1575

>LCMV-P52_GP
ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC
ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC
TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT
ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC
ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC
AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT
ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATTCCAACCACAAAGCAGTGTCTTGT
GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT
ATGAGCCAGTGTTGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA
GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTCAGATGGCAAGACCACTTGGTGC
AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA
TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC
ACTAGGAGACTTGCAGGCACATTCACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT
CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG
AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA
CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG
CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT
GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG
AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG
TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
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CATAGACACATAAAGGGCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAAACTATCTGGAAAAGACGCTGA
(SEQ ID NO: 25)

CDS: 79-1575
Codon Start = 1; Codons 1-498

Chain:	*1-498*	*Pre-glycoprotein polyprotein GP complex*
Chain:	*1-58*	*Stable signal peptide*
Chain:	*59-265*	*Glycoprotein G1*
Chain:	*266-498*	*Glycoprotein G2*

Translation=

>LCMV-P52_GP
MGQIVTMFEALPHIIDEVINIVIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGMY
GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGSSGLELTFTNDSILNH
NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA
MSQCWTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR
YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG
NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH
LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM
LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI
CSCGAFKVPGVKTIWKRR
(SEQ ID NO: 26)

도면25n

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

>LCMV-P52_NP
ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG
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GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT
GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG
AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG
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CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG
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AATTTCAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG
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GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT
GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC
AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT
GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA
AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA
TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
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AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA
ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC
ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 27)

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558
Translation=

>LCMV-P52_NP
MSLSKEVKSFQWTQALRRELQSFTSDVKAAVIKDATSLLNGLDFSEVSNVQRIMRKERRD
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ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY
NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE
NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY
SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQ[illegible]RRDIKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGPNVVTL
(SEQ ID NO: 28)

도면25o

Organism: Lymphocytic choriomeningitis virus (LCMV strain WE)
Subtype: P52
Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

>LCMV-P52_ZP
ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT
TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC
AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 29)

CDS: 90-362
Codon Start = 1; Codons 1-91
Translation=

>LCMV-P52_ZP
MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE
(SEQ ID NO: 30)

도면25p

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

>LCMV-P52_LP
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AGGCTGTCAAGGCAAAAACTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGCTAATT
GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC
ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCCTTATTCTT
CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC
AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA
GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATGGGTGAATTTTAAGTTC
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TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC
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GTCAGCCCTGGGGGCTTAATCAAGGAATTCTCTGAACTTTATGAAACCCTTACTGATAAT
GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCCTTAATGAGGTTCATT
ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA
CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAATTATTAAACACTAGAAGGAGACAGCTG
CTGAACTTAGATGTCTTATGTCTTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG
GAAAATGATAAACATTGGGTTGGTTGTTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC
CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAAGAAAATCAAGAGTG
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ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC
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CACTTGATTTCCTTTTACGCAGATCCAAAAAGGTTCTTTTTACCAATTTTTTCAGATGAG
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GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC
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GGGCAAGGGGAGGGAGAATTCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG
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GAGGACTTTGATCCATCCTGTCTCACCAATGACGACATGAGGTTTATTTGTGAGGCTGTT
GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT
CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTTCTTCTCAGAGGGTGATTGGTTCTCA
TGTATGAAGATGATCTTGTTACAGATGAATGCAAATGCGTATTCAGGGAAGTACAGACAC

도면25q

ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA
ATTAGTGAAAGGGAAAGCAATTCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC
ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCAACATCATACACT
TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG
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CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCCTTCTCTGGGACTACATT
TGCATCTCATTGAGCAACTCTTTTGAGCTGGGTGTTTGGGTTTTAGCAGAACCTGTGAAA
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GACATCAACTCAGAGTCTTTGTCACTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA
CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA
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AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG
AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAGAATRTCTCTGTGAAATTGGAGACA
AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATTGGTGATGTCCTC
GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT
RCAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG
CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA
ATGTATGAGACAACTGGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG

도면25r

GCGGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 31)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210
Translation=

>LCMV-P52_LP
MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC
IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT
NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE
SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS
FFGRFRRDLLNGKLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL
ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ
LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK
DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF
EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG
TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI
TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS
LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS
CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC
MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ
NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE
RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS
DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW
GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY
ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFLDLFNREKKEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM
TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR
NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI
CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS
VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE
HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW
FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ
LQSPGVADYLSCSHSFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL
TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQN**X**SVKLET X=I/V
KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMESEIS**X**VLQELCMDRSVMLTPLSFV X=T/A
PDWFTFRDCRLCFSRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID
(SEQ ID NO: 32)

도면25s

D. Lymphocytic choriomeningitis virus (LCMV) P91 mutant

Source: 1-3376 Segment = S
Protein: Pre-glycoprotein polyprotein GP complex
Gene: GPC
Gene: 79-1575

>LCMV-P91_GP
ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC
ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC
TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT
ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC
ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC
AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT
ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATTCCAACCACAAAGCAGTGTCTTGT
GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT
ATGAGCCAGTGTTGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA
GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTCAGATGGCAAGACCACTTGGTGC
AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA
TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC
ACTAGGAGACTTGCAGGCACATTCACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT
CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG
AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA
CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG
CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT
GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG
AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG
TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA
CATAGACACATAAAGGGCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAAACTATCTGGAAAAGACGCTGA
(SEQ ID NO: 33)

CDS: 79-1575
Codon Start = 1; Codons 1-498
Chain: *1-498* *Pre-glycoprotein polyprotein GP complex*
Chain: *1-58* *Stable signal peptide*
Chain: *59-265* *Glycoprotein G1*
Chain: *266-498* *Glycoprotein G2*

Translation=

>LCMV-P91_GP
MGQIVTMFEALPHIIDEVINIVIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGMY
GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGSSGLELTFTNDSILNH
NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA
MSQCWTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR
YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG
NTAVAXCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH
LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM
LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI
CSCGAFKVPGVKTIWKRR
(SEQ ID NO: 34)

도면25t

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

>LCMV-P91_NP
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GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT
GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG
AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG
ACCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA
GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACTTGATCAAAGATCCCAAATA
CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG
GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAATGCCAAGCCTGACAATG
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AATTTCAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG
CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG
GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT
GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC
AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT
GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA
AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA
TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC
AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA
ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC
ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 35)

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558
Translation=

>LCMV-P91_NP
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ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY
NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE
NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY
SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGPNVVTL
(SEQ ID NO: 36)

도면25u

Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

>LCMV-P91_ZP
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TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC
AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 37)

CDS: 90-362
Codon Start = 1; Codons 1-91
Translation=

>LCMV-P91_ZP
MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE
(SEQ ID NO: 38)

도면25v

Source: 1-7235 Segment = L

Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

>LCMV-P91_LP
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AGGCTGTCAAGGCAAAAACTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGCTAATT
GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC
ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCCTTATTCTT
CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC
AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA
GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATGGGTGAATTTTAAGTTC
AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG
TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG
GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAATG
TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC
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GTCAGCCCTGGGGGCTTAATCAAGGAATTCTCTGAACTTTATGAAACCCTTACTGATAAT
GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCCTTAATGAGGTTCATT
ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA
CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAATTATTAAACACTAGAAGGAGACAGCTG
CTGAACTTAGATGTCTTATGTCTTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG
GAAAATGATAAACATTGGGTTGGTTGCTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC
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CACAAAAAGGCATCTCTTGATGAGCTTTTTAGGGTATCCATAAATGAGTTCATAGCAAAA
ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC
CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAACTTTATGAGAGCCGGGACT
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CTACTATATCAGAAAACTGGAGAATCATCGAGGTGTTATTCCATACAAGGTCCGGATGGT
CACTTGATTTCCTTTTACGCAGATCCAAAAAGGTTCTTTTTACCAATTTTTTCAGATGAG
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GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC
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GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTTAGTGCTGTGAGCCAAATT
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GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTG
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GGGCAAGGGGAGGGAGAATTCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG
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GAGGACTTTGATCCATCCTGTCTCACCAATGACGACATGAGGTTTATTTGTGAGGCTGTT
GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT
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TGTATGAAGATGATCTTGTTACAGATGAATGCAAATGCGTATTCAGGGAAGTACAGACAC

도면25w

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ATTAGTGAAAGGGAAAGCAATTCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC
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AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAGAATATCTCTGTGAAATTGGAGACA
AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATTGGTGATGTCCTC
GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT
ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG
CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCARGTCAAAGAACACTGTA
ATGTATGAGACAACTGGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG

도면25x

GCGGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 39)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210
Translation=

>LCMV-P91_LP
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NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE
SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS
FFGRFRRDLLNGKLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI
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ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ
LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK
DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF
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TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI
TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS
LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS
CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC
MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
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NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE
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DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW
GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY
ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFLDLFNREKEEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM
TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR
NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI
CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS
VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE
HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW
FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ
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TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNISVKLET
KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMESEISTVLQELCMDRSVMLTPLSFV
PDWFTFRDCRLCFS**X**SKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID X=R/K
(SEQ ID NO: 40)

도면25y

E. Lymphocytic choriomeningitis virus (LCMV) P52-1 mutant

Source: **1-3376 Segment = S**
Protein: **Pre-glycoprotein polyprotein GP complex**
Gene: **GPC**
Gene: **79-1575**

```
>LCMV-P52-1
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ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC
TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
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ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC
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GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT
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TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC
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CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG
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CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG
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GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG
AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG
TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA
CATAGACACATAAAGGGCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAAACTATCTGGAAAAGACGCTGA
(SEQ ID NO: 41)
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CDS: **79-1575**
Codon Start = 1; Codons 1-498

Chain:	*1-498*	*Pre-glycoprotein polyprotein GP complex*
Chain:	*1-58*	*Stable signal peptide*
Chain:	*59-265*	*Glycoprotein G1*
Chain:	*266-498*	*Glycoprotein G2*

Translation=

```
>LCMV-P52-1
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GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGSSGLELTFTNDSILNH
NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA
MSQCWTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR
YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG
NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH
LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM
LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI
CSCGAFKVPGVKTIWKRR
(SEQ ID NO: 42)
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도면25z

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

>LCMV-P52-1_NP
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GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT
GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC
AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT
GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA
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TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
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AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA
ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC
ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 43)

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558
Translation=

>LCMV-P52-1_NP
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ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY
NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE
NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY
SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGPNVVTL
(SEQ ID NO: 44)

도면25aa

Source: 1-7235 **Segment = L**
Protein: **RING finger protein Z**
Gene: **ZP**
Gene: **90-362**

>LCMV-P52-1_ZP
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AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 45)

CDS: **90-362**
Codon Start = 1; Codons 1-91
Translation=

>LCMV-P52-1_ZP
MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE
(SEQ ID NO: 46)

도면25bb

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

```
>LCMV-P52-1_LP
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도면25cc

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AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG
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AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAAATTCCTTGACCTTTGTGTGCTGATT
GACATCAACTCAGAGTCTTTGTCACTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA
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GTTGATGAATTTGTTGTCAGCACAAGGGATGTCTGCAAGAACTTTTTGAAGCAAGTGTAT
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AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAGAATATCTCTGTGAAATTGGAGACA
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GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT
RCAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG
CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA
ATGTATGAGACAGCTGGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG

도면25dd

GCGGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 47)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210
Translation=

>LCMV-P52-1_LP
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NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE
SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS
FFGRFRRDLLNGRLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL
ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ
LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK
DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF
EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG
TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI
TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS
LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS
CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC
MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ
NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE
RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS
DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW
GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY
ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFLDLFNREMKEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM
TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR
NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI
CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS
VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE
HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW
FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ
LQSPGVADYLSCSHFFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL
TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNISVKLET
KDMRVFLAELEGCGEIGDVLGSLLLHRFRTGEHLMESEISTVLQELCMDRSVMLTPLSFV
PDWFTFRDCRLCFSRSKNTVMYETAGGRFRLKGKSCDDWLAERVAEEID
(SEQ ID NO: 48)

도면25ee

F. Lymphocytic choriomeningitis virus (LCMV) p52-1.3

Source: **1-3376 Segment = S**
Protein: **Pre-glycoprotein polyprotein GP complex**
Gene: **GPC**
Gene: **79-1575**

```
>LCMV-p52-1.3_GP
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ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC
TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT
ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC
ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC
AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT
ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATTCCAACCACAAAGCAGTGTCTTGT
GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT
ATAAGCCAGTGTTGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA
GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTCAGATGGCAAGACCACTTGGTGC
AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA
TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC
ACTAGGAGACTTGCAGGCACATTCACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT
CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG
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CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG
CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT
GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGCCTCCTACTTG
AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG
TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA
CATAGACACATAAAGGGCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
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(SEQ ID NO: 49)
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CDS: **79-1575**
Codon Start = 1; Codons 1-498

Chain:	*1-498*	*Pre-glycoprotein polyprotein GP complex*
Chain:	*1-58*	*Stable signal peptide*
Chain:	*59-265*	*Glycoprotein G1*
Chain:	*266-498*	*Glycoprotein G2*

Translation=

```
>LCMV-p52-1.3_GP
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NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA
ISQCWTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR
YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG
NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH
LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM
LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI
CSCGAFKVPGVKTIWKRR
(SEQ ID NO: 50)
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도면25ff

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

>LCMV-p52-1.3_NP
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GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT
GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG
AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG
ACCCTTGCAGCTGATCTCGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA
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CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG
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AATTTCAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG
CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG
GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT
GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC
AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT
GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA
AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACACCCTGGGCTGACCTCA
TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC
AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA
ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC
ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 51)

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558
Translation=

>LCMV-p52-1.3_NP
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ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY
NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE
NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY
SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGPNVVTL
(SEQ ID NO: 52)

도면25gg

Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

>LCMV-p52-1.3_ZP
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AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 53)

CDS: 90-362
Codon Start = 1; Codons 1-91
Translation=

>LCMV-p52-1.3_ZP
MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE
(SEQ ID NO: 54)

도면25hh

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

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>LCMV-p52-1.3_LP
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GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC
ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCCTTATTCTT
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AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA
GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATGCGTGAATTTTAAGTTC
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도면25ii

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GTTGATGAATTTGTTGTCAGCACAAGGGATGTCTGCAAGAACTTTTTGAAGCAAGTGTAT
TTCGAATCATTTGTACGAGAGTTTGTTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG
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TCATTTATTTTGAAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG
CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG
TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTTGTGGGAT
TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC
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GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG
AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCTTTG
ACACTTGGTGATTCACTAGAACTTGAACTAATAGGTTCTAGAAGGATTCTGAATGAGATC
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AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAGAATATCTCTGTGAAATTGGAGACA
AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATTGGTGATGTCCTC
GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATCGAGTCAGAAATAAGT
ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG
CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA
ATGTATGAGACAACTGGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG

도면25jj

GCGGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 55)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210
Translation=

>LCMV-p52-1.3_LP
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NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE
SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS
FFGRFRRDLLNGKLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL
ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ
LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK
DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF
EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG
TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI
TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS
LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS
CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC
MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ
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RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS
DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW
GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY
ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFLDLFNREKKEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM
TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR
NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI
CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS
VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE
HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW
FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ
LQSPGVADYLSCSHSFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL
TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNISVKLET
KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMESEISTVLQELCMDRSVMLTPLSFV
PDWFTFRDCRLCFSRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID
(SEQ ID NO: 56)

도면25kk

G. Lymphocytic choriomeningitis virus (LCMV) P52-2.1

Source: 1-3376 Segment = S
Protein: Pre-glycoprotein polyprotein GP complex
Gene: GPC
Gene: 79-1575

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>LCMV-p52-2.1_GP
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TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT
ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC
ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC
AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT
ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATTCCAACCACAAAGCAGTGTCTTGT
GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT
ATGAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA
GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTCAGATGGCAAGACCACTTGGTGC
AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA
TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC
ACTAGGAGACTTGCAGGCACATTCACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT
CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG
AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA
CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG
CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT
GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG
AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG
TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA
CATAGACACATAAAGGGCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAAACTATCTGGAAAAGACGCTGA
(SEQ ID NO: 57)
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CDS: 79-1575
Codon Start = 1; Codons 1-498

Chain:	*1-498*	*Pre-glycoprotein polyprotein GP complex*
Chain:	*1-58*	*Stable signal peptide*
Chain:	*59-265*	*Glycoprotein G1*
Chain:	*266-498*	*Glycoprotein G2*

Translation=

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>LCMV-p52-2.1_GP
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NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA
MSQCRTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR
YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG
NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH
LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM
LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI
CSCGAFKVPGVKTIWKRR
(SEQ ID NO: 58)
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도면2511

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

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GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT
GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG
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ACCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA
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CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG
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AATTTCAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG
CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG
GCCAAAAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT
GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC
AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT
GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA
AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA
TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC
AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA
ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC
ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 59)

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558
Translation=

>LCMV-p52-2.1_NP
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ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY
NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE
NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY
SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGPNVVTL
(SEQ ID NO: 60)

도면25mm

Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

>LCMV-p52-2.1_ZP
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AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 61)

CDS: 90-362
Codon Start = 1; Codons 1-91
Translation=

>LCMV-p52-2.1_ZP
MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE
(SEQ ID NO: 62)

도면25nn

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

>LCMV-p52-2.1_LP
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GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC
ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
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CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC
AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA
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TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC
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GTCAGCCCTGGGGGCTTAATCAAGGAATTCTCTGAACTTTATGAAACCCTTACTGATAAT
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GCGGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 63)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210
Translation=

>LCMV-p52-2.1_LP
MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC
IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT
NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE
SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS
FFGRFRRDLLNGKLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL
ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ
LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK
DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF
EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG
TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI
TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS
LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS
CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC
MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ
NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE
RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS
DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW
GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY
ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFLDLFNREKKEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM
TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR
NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI
CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS
VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE
HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW
FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ
LQSPGVADYLSCSHFFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL
TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNISVKLET
KDMRVFLAELEGCGEIGDVLGSLLLHRFRTGEHLMESEISTVLQELCMDRSVMLTPLSFV
PDWFTFRDCRLCFSRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID
(SEQ ID NO: 64)

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A.

Source: 1-3376 Segment = S
Protein: Pre-glycoprotein polyprotein GP complex
Gene: GPC
Gene: 79-1575
Sequence Alignment: Nucleotide

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LCMV-WE_GP          ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC    60
LCMV-P42_GP         ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC    60
LCMV-P52_GP         ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC    60
LCMV-P91_GP         ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC    60
LCMV-P52-1          ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC    60
LCMV-P52-1.3_GP     ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC    60
LCMV-P52-2.1_GP     ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC    60
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LCMV-WE_GP          ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC   120
LCMV-P42_GP         ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC   120
LCMV-P52_GP         ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC   120
LCMV-P91_GP         ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC   120
LCMV-P52-1          ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC   120
LCMV-P52-1.3_GP     ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC   120
LCMV-P52-2.1_GP     ATTGTTATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTCGCCACC   120
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LCMV-WE_GP          TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC   180
LCMV-P42_GP         TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC   180
LCMV-P52_GP         TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC   180
LCMV-P91_GP         TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC   180
LCMV-P52-1          TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC   180
LCMV-P52-1.3_GP     TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC   180
LCMV-P52-2.1_GP     TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC   180
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LCMV-WE_GP          GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT   240
LCMV-P42_GP         GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT   240
LCMV-P52_GP         GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT   240
LCMV-P91_GP         GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT   240
LCMV-P52-1          GGCCTCAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT   240
LCMV-P52-1.3_GP     GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT   240
LCMV-P52-2.1_GP     GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT   240
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LCMV-WE_GP          ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC   300
LCMV-P42_GP         ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC   300
LCMV-P52_GP         ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC   300
LCMV-P91_GP         ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC   300
LCMV-P52-1          ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC   300
LCMV-P52-1.3_GP     ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC   300
LCMV-P52-2.1_GP     ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACTCTCATCACTAC   300
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LCMV-WE_GP          ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC   360
LCMV-P42_GP         ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC   360
LCMV-P52_GP         ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC   360
LCMV-P91_GP         ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC   360
LCMV-P52-1          ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC   360
LCMV-P52-1.3_GP     ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC   360
LCMV-P52-2.1_GP     ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC   360
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LCMV-WE_GP          AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT   420
LCMV-P42_GP         AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT   420
LCMV-P52_GP         AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT   420
LCMV-P91_GP         AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT   420
LCMV-P52-1          AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT   420
LCMV-P52-1.3_GP     AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT   420
LCMV-P52-2.1_GP     AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT   420
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LCMV-WE_GP          ATAGTCTCGAGTCTGCACCTCAGTATTACAGGGAATTCCAACCACAAAGCAGTGTCTTGT    480
LCMV-P42_GP         ATAGTCTCGAGTCTGCACCTCAGTATTACAGGGAATTCCAACCACAAAGCAGTGTCTTGT    480
LCMV-P52_GP         ATAGTCTCGAGTCTGCACCTCAGTATTACAGGGAATTCCAACCACAAAGCAGTGTCTTGT    480
LCMV-P91_GP         ATAGTCTCGAGTCTGCACCTCAGTATTACAGGGAATTCCAACCACAAAGCAGTGTCTTGT    480
LCMV-P52-1          ATAGTCTCGAGTCTGCACCTCAGTATTACAGGGAATTCCAACCACAAAGCAGTGTCTTGT    480
LCMV-P52-1.3_GP     ATAGTCTCGAGTCTGCACCTCAGTATTACAGGGAATTCCAACCACAAAGCAGTGTCTTGT    480
LCMV-P52-2.1_GP     ATAGTCTCGAGTCTGCACCTCAGTATTACAGGGAATTCCAACCACAAAGCAGTGTCTTGT    480
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LCMV-WE_GP          GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT    540
LCMV-P42_GP         GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT    540
LCMV-P52_GP         GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT    540
LCMV-P91_GP         GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT    540
LCMV-P52-1          GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT    540
LCMV-P52-1.3_GP     GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT    540
LCMV-P52-2.1_GP     GATTTTAACAATGGCATCACCATTCAATACAACTTGTCATTTTCGGACCCACAGAGCGCT    540
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LCMV-WE_GP          ATAAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA    600
LCMV-P42_GP         ATGAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA    600
LCMV-P52_GP         ATGAGCCAGTGTTGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA    600
LCMV-P91_GP         ATGAGCCAGTGTTGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA    600
LCMV-P52-1          ATGAGCCAGTGTTGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA    600
LCMV-P52-1.3_GP     ATAAGCCAGTGTTGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA    600
LCMV-P52-2.1_GP     ATGAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA    600
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LCMV-WE_GP          GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTCAGATGGCAAGACCACTTGGTGC    660
LCMV-P42_GP         GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTCAGATGGCAAGACCACTTGGTGC    660
LCMV-P52_GP         GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTCAGATGGCAAGACCACTTGGTGC    660
LCMV-P91_GP         GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTCAGATGGCAAGACCACTTGGTGC    660
LCMV-P52-1          GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTCAGATGGCAAGACCACTTGGTGC    660
LCMV-P52-1.3_GP     GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTCAGATGGCAAGACCACTTGGTGC    660
LCMV-P52-2.1_GP     GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTCAGATGGCAAGACCACTTGGTGC    660
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LCMV-WE_GP          AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA    720
LCMV-P42_GP         AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA    720
LCMV-P52_GP         AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA    720
LCMV-P91_GP         AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA    720
LCMV-P52-1          AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA    720
LCMV-P52-1.3_GP     AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA    720
LCMV-P52-2.1_GP     AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA    720
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LCMV-WE_GP          TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC    780
LCMV-P42_GP         TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC    780
LCMV-P52_GP         TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC    780
LCMV-P91_GP         TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC    780
LCMV-P52-1          TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC    780
LCMV-P52-1.3_GP     TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC    780
LCMV-P52-2.1_GP     TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC    780
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LCMV-WE_GP          ACTAGGAGACTTGCAGGCACATTCACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT    840
LCMV-P42_GP         ACTAGGAGACTTGCAGGCACATTCACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT    840
LCMV-P52_GP         ACTAGGAGACTTGCACCCACATTCACCTGCACCCTGTCAGACTCCTCAGGAGTAGAAAAT    840
LCMV-P91_GP         ACTAGGAGACTTGCAGGCACATTCACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT    840
LCMV-P52-1          ACTAGGAGACTTGCAGGCACATTCACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT    840
LCMV-P52-1.3_GP     ACTAGGAGACTTGCAGGCACATTCACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT    840
LCMV-P52-2.1_GP     ACTAGGAGACTTGCAGGCACATTCACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT    840
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LCMV-WE_GP          CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG    900
LCMV-P42_GP         CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG    900
LCMV-P52_GP         CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG    900
LCMV-P91_GP         CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG    900
LCMV-P52-1          CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG    900
LCMV-P52-1.3_GP     CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG    900
LCMV-P52-2.1_GP     CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG    900
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LCMV-WE_GP        AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA    960
LCMV-P42_GP       AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA    960
LCMV-P52_GP       AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA    960
LCMV-P91_GP       AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA    960
LCMV-P52-1        AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA    960
LCMV-P52-1.3_GP   AACACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA    960
LCMV-P52-2.1_GP   AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA    960
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LCMV-WE_GP        CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG    1020
LCMV-P42_GP       CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG    1020
LCMV-P52_GP       CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG    1020
LCMV-P91_GP       CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG    1020
LCMV-P52-1        CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG    1020
LCMV-P52-1.3_GP   CTAATTGATTACAACAAGGCCCCCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG    1020
LCMV-P52-2.1_GP   CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG    1020
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LCMV-WE_GP        CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT    1080
LCMV-P42_GP       CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT    1080
LCMV-P52_GP       CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT    1080
LCMV-P91_GP       CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT    1080
LCMV-P52-1        CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT    1080
LCMV-P52-1.3_GP   CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT    1080
LCMV-P52-2.1_GP   CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT    1080
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LCMV-WE_GP        CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT    1140
LCMV-P42_GP       CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT    1140
LCMV-P52_GP       CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT    1140
LCMV-P91_GP       CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT    1140
LCMV-P52-1        CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT    1140
LCMV-P52-1.3_GP   CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT    1140
LCMV-P52-2.1_GP   CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT    1140
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LCMV-WE_GP        GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG    1200
LCMV-P42_GP       GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG    1200
LCMV-P52_GP       GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG    1200
LCMV-P91_GP       GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG    1200
LCMV-P52-1        GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG    1200
LCMV-P52-1.3_GP   GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG    1200
LCMV-P52-2.1_GP   GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG    1200
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LCMV-WE_GP        AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG    1260
LCMV-P42_GP       AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG    1260
LCMV-P52_GP       AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG    1260
LCMV-P91_GP       AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG    1260
LCMV-P52-1        AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG    1260
LCMV-P52-1.3_GP   AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGACATG    1260
LCMV-P52-2.1_GP   AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG    1260
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LCMV-WE_GP        TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG    1320
LCMV-P42_GP       TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG    1320
LCMV-P52_GP       TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG    1320
LCMV-P91_GP       TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG    1320
LCMV-P52-1        TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG    1320
LCMV-P52-1.3_GP   TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG    1320
LCMV-P52-2.1_GP   TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG    1320
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LCMV-WE_GP        ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA    1380
LCMV-P42_GP       ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA    1380
LCMV-P52_GP       ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA    1380
LCMV-P91_GP       ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA    1380
LCMV-P52-1        ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA    1380
LCMV-P52-1.3_GP   ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA    1380
LCMV-P52-2.1_GP   ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA    1380
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도면26d

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LCMV-WE_GP        CATAGACACATAAAGGGCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC    1440
LCMV-P42_GP       CATAGACACATAAAGGGCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC    1440
LCMV-P52_GP       CATAGACACATAAAGGGCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC    1440
LCMV-P91_GP       CATAGACACATAAAGGGCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC    1440
LCMV-P52-1        CATAGACACATAAAGGGCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC    1440
LCMV-P52-1.3_GP   CATAGACACATAAAGGCCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC    1440
LCMV-P52-2.1_GP   CATAGACACATAAAGGCCGGTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC    1440
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LCMV-WE_GP        TGTAGTTGTGGTGCATTCAAGGTGCCTGCTGTAAAAACTATCTGGAAAAGACGCTGA      1497
LCMV-P42_GP       TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAAACTATCTGGAAAAGACGCTGA      1497
LCMV-P52_GP       TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAAACTATCTGGAAAAGACGCTGA      1497
LCMV-P91_GP       TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAAACTATCTGGAAAAGACGCTGA      1497
LCMV-P52-1        TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAAACTATCTGGAAAAGACGCTGA      1497
LCMV-P52-1.3_GP   TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAAACTATCTGGAAAAGACGCTGA      1497
LCMV-P52-2.1_GP   TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAAACTATCTGGAAAAGACGCTGA      1497
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LCMV-WE_GP:       SEQ ID NO: 9
LCMV-P42_GP:      SEQ ID NO: 17
LCMV-P52_GP:      SEQ ID NO: 25
LCMV-P91_GP:      SEQ ID NO: 33
LCMV-P52-1:       SEQ ID NO: 41
LCMV-P52-1.3_GP:  SEQ ID NO: 49
LCMV-P52-2.1_GP:  SEQ ID NO: 57
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도면26e

B.

Source: 1-3376 Segment = S
Protein: Pre-glycoprotein polyprotein GP complex
Gene: GPC
Gene: 79-1575
Sequence Alignment: Aminoacid

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LCMV-WE_GP          MGQIVTMFEALPHIIDEVINIVIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGMY    60
LCMV-P42_GP         MGQIVTMFEALPHIIDEVINIVIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGMY    60
LCMV-P52_GP         MGQIVTMFEALPHIIDEVINIVIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGMY    60
LCMV-P91_GP         MGQIVTMFEALPHIIDEVINIVIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGMY    60
LCMV-P52-1          MGQIVTMFEALPHIIDEVINIVIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGMY    60
LCMV-P52-1.3_GP     MGQIVTMFEALPHIIDEVINIVIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGMY    60
LCMV-P52-2.1_GP     MGQIVTMFEALPHIIDEVINIVIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGMY    60
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LCMV-WE_GP          GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGSSGLELTFTNDSILNH   120
LCMV-P42_GP         GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGSSGLELTFTNDSILNH   120
LCMV-P52_GP         GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGSSGLELTFTNDSILNH   120
LCMV-P91_GP         GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGSSGLELTFTNDSILNH   120
LCMV-P52-1          GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGSSGLELTFTNDSILNH   120
LCMV-P52-1.3_GP     GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGSSGLELTFTNDSILNH   120
LCMV-P52-2.1_GP     GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMGSSGLELTFTNDSILNH   120
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LCMV-WE_GP          NFCNLTSAFNKKTFDETLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA   180
LCMV-P42_GP         NFCNLTSAFNKKTFDETLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA   180
LCMV-P52_GP         NFCNLTSAFNKKTFDETLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA   180
LCMV-P91_GP         NFCNLTSAFNKKTFDETLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA   180
LCMV-P52-1          NFCNLTSAFNKKTFDETLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA   180
LCMV-P52-1.3_GP     NFCNLTSAFNKKTFDETLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA   180
LCMV-P52-2.1_GP     NFCNLTSAFNKKTFDETLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA   180
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LCMV-WE_GP          ISQCRTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR   240
LCMV-P42_GP         MSQCRTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR   240
LCMV-P52_GP         MSQCWTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR   240
LCMV-P91_GP         MSQCWTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR   240
LCMV-P52-1          MSQCWTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR   240
LCMV-P52-1.3_GP     ISQCWTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR   240
LCMV-P52-2.1_GP     MSQCRTFRGRVLDMFRTAFGGKYMRSGWGWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR   240
                     *** ***********************************************************

LCMV-WE_GP          YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG   300
LCMV-P42_GP         YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG   300
LCMV-P52_GP         YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG   300
LCMV-P91_GP         YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG   300
LCMV-P52-1          YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG   300
LCMV-P52-1.3_GP     YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG   300
LCMV-P52-2.1_GP     YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG   300
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LCMV-WE_GP          NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH   360
LCMV-P42_GP         NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH   360
LCMV-P52_GP         NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH   360
LCMV-P91_GP         NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH   360
LCMV-P52-1          NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH   360
LCMV-P52-1.3_GP     NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH   360
LCMV-P52-2.1_GP     NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH   360
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LCMV-WE_GP          LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM   420
LCMV-P42_GP         LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM   420
LCMV-P52_GP         LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM   420
LCMV-P91_GP         LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM   420
LCMV-P52-1          LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM   420
LCMV-P52-1.3_GP     LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM   420
LCMV-P52-2.1_GP     LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM   420
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도면26f

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LCMV-WE_GP          LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI   480
LCMV-P42_GP         LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI   480
LCMV-P52_GP         LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI   480
LCMV-P91_GP         LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI   480
LCMV-P52-1          LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI   480
LCMV-P52-1.3_GP     LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI   480
LCMV-P52-2.1_GP     LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI   480
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LCMV-WE_GP          CSCGAFKVPGVKTIWKRR          498
LCMV-P42_GP         CSCGAFKVPGVKTIWKRR          498
LCMV-P52_GP         CSCGAFKVPGVKTIWKRR          498
LCMV-P91_GP         CSCGAFKVPGVKTIWKRR          498
LCMV-P52-1          CSCGAFKVPGVKTIWKRR          498
LCMV-P52-1.3_GP     CSCGAFKVPGVKTIWKRR          498
LCMV-P52-2.1_GP     CSCGAFKVPGVKTIWKRR          498
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LCMV-WE_GP:      SEQ ID NO: 10
LCMV-P42_GP:     SEQ ID NO: 18
LCMV-P52_GP:     SEQ ID NO: 26
LCMV-P91_GP:     SEQ ID NO: 34
LCMV-P52-1:      SEQ ID NO: 42
LCMV-P52-1.3_GP: SEQ ID NO: 50
LCMV-P52-2.1_GP: SEQ ID NO: 58
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도면26g

C.

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement
Sequence Alignment: Nucleotide

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LCMV-WE_NP          ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG    60
LCMV-P42_NP         ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG    60
LCMV-P52_NP         ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG    60
LCMV-P91_NP         ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG    60
LCMV-P52-1_NP       ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG    60
LCMV-P52-1.3_NP     ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG    60
LCMV-P52-2.1_NP     ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG    60
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LCMV-WE_NP          CAGAGTTTTACATCAGATGTAAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT    120
LCMV-P42_NP         CAGAGTTTTACATCAGATGTAAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT    120
LCMV-P52_NP         CAGAGTTTTACATCAGATGTAAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT    120
LCMV-P91_NP         CAGAGTTTTACATCAGATGTAAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT    120
LCMV-P52-1_NP       CAGAGTTTTACATCAGATGTAAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT    120
LCMV-P52-1.3_NP     CAGAGTTTTACATCAGATGTAAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT    120
LCMV-P52-2.1_NP     CAGAGTTTTACATCAGATGTAAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT    120
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LCMV-WE_NP          GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT    180
LCMV-P42_NP         GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT    180
LCMV-P52_NP         GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT    180
LCMV-P91_NP         GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT    180
LCMV-P52-1_NP       GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT    180
LCMV-P52-1.3_NP     GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT    180
LCMV-P52-2.1_NP     GGGTTGGACTTTTCTGAAGTCAGCAACGTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT    180
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LCMV-WE_NP          GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG    240
LCMV-P42_NP         GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG    240
LCMV-P52_NP         GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG    240
LCMV-P91_NP         GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG    240
LCMV-P52-1_NP       GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG    240
LCMV-P52-1.3_NP     GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG    240
LCMV-P52-2.1_NP     GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTTGATCTG    240
                    ************************************************************

LCMV-WE_NP          AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG    300
LCMV-P42_NP         AAGTCTACATCAAAGAAAAATGTTCTGAAACTGCCAAGACTTAGTGCAGAGGAATTGATG    300
LCMV-P52_NP         AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG    300
LCMV-P91_NP         AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG    300
LCMV-P52-1_NP       AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG    300
LCMV-P52-1.3_NP     AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG    300
LCMV-P52-2.1_NP     AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG    300
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LCMV-WE_NP          ACCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA    360
LCMV-P42_NP         ACCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA    360
LCMV-P52_NP         ACCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA    360
LCMV-P91_NP         ACCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA    360
LCMV-P52-1_NP       ACCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA    360
LCMV-P52-1.3_NP     ACCCTTGCAGCTGATCTCGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA    360
LCMV-P52-2.1_NP     ACCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA    360
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LCMV-WE_NP          GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACTTGATCAAAGATCCCAAATA    420
LCMV-P42_NP         GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACTTGATCAAAGATCCCAAATA    420
LCMV-P52_NP         GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACTTGATCAAAGATCCCAAATA    420
LCMV-P91_NP         GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACTTGATCAAAGATCCCAAATA    420
LCMV-P52-1_NP       GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACTTGATCAAAGATCCCAAATA    420
LCMV-P52-1.3_NP     GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACTTGATCAAAGATCCCAAATA    420
LCMV-P52-2.1_NP     GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACTTGATCAAAGATCCCAAATA    420
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도면26h

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LCMV-WE_NP          CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG     480
LCMV-P42_NP         CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG     480
LCMV-P52_NP         CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG     480
LCMV-P91_NP         CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG     480
LCMV-P52-1_NP       CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG     480
LCMV-P52-1.3_NP     CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG     480
LCMV-P52-2.1_NP     CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG     480
                    ************************************************************

LCMV-WE_NP          GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAATGCCAAGCCTGACAATG     540
LCMV-P42_NP         GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAATGCCAAGCCTGACAATG     540
LCMV-P52_NP         GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAATGCCAAGCCTGACAATG     540
LCMV-P91_NP         GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAATGCCAAGCCTGACAATG     540
LCMV-P52-1_NP       GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAATGCCAAGCCTGACAATG     540
LCMV-P52-1.3_NP     GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAATGCCAAGCCTGACAATG     540
LCMV-P52-2.1_NP     GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAATGCCAAGCCTGACAATG     540
                    ************************************************************

LCMV-WE_NP          GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC     600
LCMV-P42_NP         GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC     600
LCMV-P52_NP         GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC     600
LCMV-P91_NP         GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC     600
LCMV-P52-1_NP       GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC     600
LCMV-P52-1.3_NP     GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC     600
LCMV-P52-2.1_NP     GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC     600
                    ************************************************************

LCMV-WE_NP          CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT     660
LCMV-P42_NP         CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT     660
LCMV-P52_NP         CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT     660
LCMV-P91_NP         CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT     660
LCMV-P52-1_NP       CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT     660
LCMV-P52-1.3_NP     CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT     660
LCMV-P52-2.1_NP     CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT     660
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LCMV-WE_NP          AAACACCCAGTTCTGGGGGTCATTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT     720
LCMV-P42_NP         AAACACCCAGTTCTGGGGGTCATTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT     720
LCMV-P52_NP         AAACACCCAGTTCTGGGGGTCATTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT     720
LCMV-P91_NP         AAACACCCAGTTCTGGGGGTCATTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT     720
LCMV-P52-1_NP       AAACACCCAGTTCTGGGGGTCATTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT     720
LCMV-P52-1.3_NP     AAACACCCAGTTCTGGGGGTCATTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT     720
LCMV-P52-2.1_NP     AAACACCCAGTTCTGGGGGTCATTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT     720
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LCMV-WE_NP          AATTTCAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG     780
LCMV-P42_NP         AATTTCAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG     780
LCMV-P52_NP         AATTTCAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG     780
LCMV-P91_NP         AATTTCAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG     780
LCMV-P52-1_NP       AATTTCAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG     780
LCMV-P52-1.3_NP     AATTTCAGTCTTGGTGCAGCTCTGAAACCGGGGGCAGCTCTGCTAGATGGAGGGAACATG     780
LCMV-P52-2.1_NP     AATTTCAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG     780
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LCMV-WE_NP          CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG     840
LCMV-P42_NP         CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG     840
LCMV-P52_NP         CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG     840
LCMV-P91_NP         CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG     840
LCMV-P52-1_NP       CTGGAATCTATCTTGATCAAACCCAGCAACACTCACGATCTCCTAAAAGCAGTCCTCGGG     840
LCMV-P52-1.3_NP     CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG     840
LCMV-P52-2.1_NP     CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG     840
                    ************************************************************

LCMV-WE_NP          GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA     900
LCMV-P42_NP         GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA     900
LCMV-P52_NP         GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA     900
LCMV-P91_NP         GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA     900
LCMV-P52-1_NP       GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA     900
LCMV-P52-1.3_NP     GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA     900
LCMV-P52-2.1_NP     GCCAAAAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA     900
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LCMV-WE_NP          AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG    960
LCMV-P42_NP         AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG    960
LCMV-P52_NP         AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG    960
LCMV-P91_NP         AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG    960
LCMV-P52-1_NP       AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG    960
LCMV-P52-1.3_NP     AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG    960
LCMV-P52-2.1_NP     AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG    960
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LCMV-WE_NP          TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT    1020
LCMV-P42_NP         TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT    1020
LCMV-P52_NP         TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT    1020
LCMV-P91_NP         TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT    1020
LCMV-P52-1_NP       TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT    1020
LCMV-P52-1.3_NP     TCAGTTGTGCGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT    1020
LCMV-P52-2.1_NP     TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAAACTTGTT    1020
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LCMV-WE_NP          GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC    1080
LCMV-P42_NP         GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC    1080
LCMV-P52_NP         GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC    1080
LCMV-P91_NP         GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC    1080
LCMV-P52-1_NP       GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC    1080
LCMV-P52-1.3_NP     GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC    1080
LCMV-P52-2.1_NP     GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCCACCTCAGGTGGGCTTGAGTTAC    1080
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LCMV-WE_NP          AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG    1140
LCMV-P42_NP         AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG    1140
LCMV-P52_NP         AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG    1140
LCMV-P91_NP         AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG    1140
LCMV-P52-1_NP       AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG    1140
LCMV-P52-1.3_NP     AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG    1140
LCMV-P52-2.1_NP     AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG    1140
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LCMV-WE_NP          ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT    1200
LCMV-P42_NP         ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT    1200
LCMV-P52_NP         ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT    1200
LCMV-P91_NP         ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT    1200
LCMV-P52-1_NP       ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT    1200
LCMV-P52-1.3_NP     ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT    1200
LCMV-P52-2.1_NP     ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT    1200
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LCMV-WE_NP          GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA    1260
LCMV-P42_NP         GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA    1260
LCMV-P52_NP         GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA    1260
LCMV-P91_NP         GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA    1260
LCMV-P52-1_NP       GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA    1260
LCMV-P52-1.3_NP     GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA    1260
LCMV-P52-2.1_NP     GGGCAATTCATACATTTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA    1260
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LCMV-WE_NP          AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA    1320
LCMV-P42_NP         AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA    1320
LCMV-P52_NP         AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA    1320
LCMV-P91_NP         AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA    1320
LCMV-P52-1_NP       AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA    1320
LCMV-P52-1.3_NP     AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA    1320
LCMV-P52-2.1_NP     AAGTATTCACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA    1320
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LCMV-WE_NP          TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC    1380
LCMV-P42_NP         TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC    1380
LCMV-P52_NP         TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC    1380
LCMV-P91_NP         TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC    1380
LCMV-P52-1_NP       TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC    1380
LCMV-P52-1.3_NP     TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC    1380
LCMV-P52-2.1_NP     TCAGTTATAGGTGCTCTCCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC    1380
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LCMV-WE_NP          AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC    1440
LCMV-P42_NP         AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC    1440
LCMV-P52_NP         AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC    1440
LCMV-P91_NP         AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC    1440
LCMV-P52-1_NP       AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC    1440
LCMV-P52-1.3_NP     AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC    1440
LCMV-P52-2.1_NP     AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC    1440
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LCMV-WE_NP          AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA    1500
LCMV-P42_NP         AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA    1500
LCMV-P52_NP         AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA    1500
LCMV-P91_NP         AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA    1500
LCMV-P52-1_NP       AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA    1500
LCMV-P52-1.3_NP     AAGCAGCCCTCAAGAGAATATGAACATAAACTCTCCCACAAATATGCCTGGCTATGCAAA    1500
LCMV-P52-2.1_NP     AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA    1500
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LCMV-WE_NP          ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC    1560
LCMV-P42_NP         ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC    1560
LCMV-P52_NP         ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC    1560
LCMV-P91_NP         ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC    1560
LCMV-P52-1_NP       ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC    1560
LCMV-P52-1.3_NP     ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC    1560
LCMV-P52-2.1_NP     ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCCACACTGTGCACTC    1560
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LCMV-WE_NP          ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT    1620
LCMV-P42_NP         ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT    1620
LCMV-P52_NP         ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT    1620
LCMV-P91_NP         ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT    1620
LCMV-P52-1_NP       ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT    1620
LCMV-P52-1.3_NP     ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT    1620
LCMV-P52-2.1_NP     ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT    1620
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LCMV-WE_NP          CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA       1677
LCMV-P42_NP         CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA       1677
LCMV-P52_NP         CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA       1677
LCMV-P91_NP         CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA       1677
LCMV-P52-1_NP       CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA       1677
LCMV-P52-1.3_NP     CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA       1677
LCMV-P52-2.1_NP     CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA       1677
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LCMV-WE_NP:       SEQ ID NO: 11
LCMV-P42_NP:      SEQ ID NO: 19
LCMV-P52_NP:      SEQ ID NO: 27
LCMV-P91_NP:      SEQ ID NO: 35
LCMV-P52-1_NP:    SEQ ID NO: 43
LCMV-P52-1.3_NP:  SEQ ID NO: 51
LCMV-P52-2.1_NP:  SEQ ID NO: 59
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D.

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement
Sequence Alignment: Aminoacid

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LCMV-WE_NP          MSLSKEVKSFQWTQALRRELQSFTSDVKAAVIKDATSLLNGLDFSEVSNVQRIMRKERRD    60
LCMV-P42_NP         MSLSKEVKSFQWTQALRRELQSFTSDVKAAVIKDATSLLNGLDFSEVSNVQRIMRKERRD    60
LCMV-P52_NP         MSLSKEVKSFQWTQALRRELQSFTSDVKAAVIKDATSLLNGLDFSEVSNVQRIMRKERRD    60
LCMV-P91_NP         MSLSKEVKSFQWTQALRRELQSFTSDVKAAVIKDATSLLNGLDFSEVSNVQRIMRKERRD    60
LCMV-P52-1_NP       MSLSKEVKSFQWTQALRRELQSFTSDVKAAVIKDATSLLNGLDFSEVSNVQRIMRKERRD    60
LCMV-P52-1.3_NP     MSLSKEVKSFQWTQALRRELQSFTSDVKAAVIKDATSLLNGLDFSEVSNVQRIMRKERRD    60
LCMV-P52-2.1_NP     MSLSKEVKSFQWTQALRRELQSFTSDVKAAVIKDATSLLNGLDFSEVSNVQRIMRKERRD    60
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LCMV-WE_NP          DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ    120
LCMV-P42_NP         DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ    120
LCMV-P52_NP         DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ    120
LCMV-P91_NP         DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ    120
LCMV-P52-1_NP       DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ    120
LCMV-P52-1.3_NP     DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ    120
LCMV-P52-2.1_NP     DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ    120
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LCMV-WE_NP          ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM    180
LCMV-P42_NP         ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM    180
LCMV-P52_NP         ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM    180
LCMV-P91_NP         ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM    180
LCMV-P52-1_NP       ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM    180
LCMV-P52-1.3_NP     ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM    180
LCMV-P52-2.1_NP     ASGVYMGNLTAQQLDQRSQILQMVGMRRPQQGASGVVRVWDVKDSSLLNNQFGTMPSLTM    180
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LCMV-WE_NP          ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY    240
LCMV-P42_NP         ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY    240
LCMV-P52_NP         ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY    240
LCMV-P91_NP         ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY    240
LCMV-P52-1_NP       ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY    240
LCMV-P52-1.3_NP     ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY    240
LCMV-P52-2.1_NP     ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGY    240
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LCMV-WE_NP          NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE    300
LCMV-P42_NP         NFSLGAAVKAGAALLDCGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVCDRNPYE    300
LCMV-P52_NP         NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE    300
LCMV-P91_NP         NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE    300
LCMV-P52-1_NP       NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE    300
LCMV-P52-1.3_NP     NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE    300
LCMV-P52-2.1_NP     NFSLGAAVKAGAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE    300
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LCMV-WE_NP          NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY    360
LCMV-P42_NP         NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY    360
LCMV-P52_NP         NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY    360
LCMV-P91_NP         NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY    360
LCMV-P52-1_NP       NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY    360
LCMV-P52-1.3_NP     NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY    360
LCMV-P52-2.1_NP     NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPGAAGPPQVGLSY    360
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LCMV-WE_NP          SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS    420
LCMV-P42_NP         SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS    420
LCMV-P52_NP         SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS    420
LCMV-P91_NP         SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS    420
LCMV-P52-1_NP       SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS    420
LCMV-P52-1.3_NP     SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS    420
LCMV-P52-2.1_NP     SQTMLLKDLMGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS    420
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LCMV-WE_NP          KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT    480
LCMV-P42_NP         KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT    480
LCMV-P52_NP         KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT    480
LCMV-P91_NP         KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT    480
LCMV-P52-1_NP       KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT    480
LCMV-P52-1.3_NP     KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT    480
LCMV-P52-2.1_NP     KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRRDIKLIDVEMT    480
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LCMV-WE_NP          KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV    540
LCMV-P42_NP         KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV    540
LCMV-P52_NP         KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV    540
LCMV-P91_NP         KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV    540
LCMV-P52-1_NP       KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV    540
LCMV-P52-1.3_NP     KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV    540
LCMV-P52-2.1_NP     KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV    540
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LCMV-WE_NP          HNILPHDLIFRGPNVVTL          558
LCMV-P42_NP         HNILPHDLIFRGPNVVTL          558
LCMV-P52_NP         HNILPHDLIFRGPNVVTL          558
LCMV-P91_NP         HNILPHDLIFRGPNVVTL          558
LCMV-P52-1_NP       HNILPHDLIFRGPNVVTL          558
LCMV-P52-1.3_NP     HNILPHDLIFRGPNVVTL          558
LCMV-P52-2.1_NP     HNILPHDLIFRGPNVVTL          558
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LCMV-WE_NP:       SEQ ID NO: 12
LCMV-P42_NP:      SEQ ID NO: 20
LCMV-P52_NP:      SEQ ID NO: 28
LCMV-P91_NP:      SEQ ID NO: 36
LCMV-P52-1_NP:    SEQ ID NO: 44
LCMV-P52-1.3_NP:  SEQ ID NO: 52
LCMV-P52-2.1_NP:  SEQ ID NO: 60
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E.

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Source: 1-7235  Segment = L
Protein:        RING finger protein Z
Gene:   ZP
Gene:   90-362
Sequence Alignment: Nucleotide

LCMV-WE_ZP          ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT    60
LCMV-P42_ZP         ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT    60
LCMV-P52_ZP         ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT    60
LCMV-P91_ZP         ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT    60
LCMV-P52-1_ZP       ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT    60
LCMV-P52-1.3_ZP     ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT    60
LCMV-P52-2.1_ZP     ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT    60
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LCMV-WE_ZP          TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC    120
LCMV-P42_ZP         TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC    120
LCMV-P52_ZP         TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC    120
LCMV-P91_ZP         TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC    120
LCMV-P52-1_ZP       TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC    120
LCMV-P52-1.3_ZP     TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC    120
LCMV-P52-2.1_ZP     TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC    120
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LCMV-WE_ZP          AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA    180
LCMV-P42_ZP         AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA    180
LCMV-P52_ZP         AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA    180
LCMV-P91_ZP         AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA    180
LCMV-P52-1_ZP       AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA    180
LCMV-P52-1.3_ZP     AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA    180
LCMV-P52-2.1_ZP     AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA    180
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LCMV-WE_ZP          GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA    240
LCMV-P42_ZP         GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA    240
LCMV-P52_ZP         GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA    240
LCMV-P91_ZP         GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA    240
LCMV-P52-1_ZP       GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA    240
LCMV-P52-1.3_ZP     GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA    240
LCMV-P52-2.1_ZP     GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA    240
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LCMV-WE_ZP          GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA    273
LCMV-P42_ZP         GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA    273
LCMV-P52_ZP         GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA    273
LCMV-P91_ZP         GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA    273
LCMV-P52-1_ZP       GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA    273
LCMV-P52-1.3_ZP     GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA    273
LCMV-P52-2.1_ZP     GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA    273
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LCMV-WE_ZP:       SEQ ID NO: 13
LCMV-P42_ZP:      SEQ ID NO: 21
LCMV-P52_ZP:      SEQ ID NO: 29
LCMV-P91_ZP:      SEQ ID NO: 37
LCMV-P52-1_ZP:    SEQ ID NO: 45
LCMV-P52-1.3_ZP:  SEQ ID NO: 53
LCMV-P52-2.1_ZP:  SEQ ID NO: 61
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도면26n

F.

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Source: 1-7235  Segment = L
Protein:        RING finger protein Z
Gene:   ZP
Gene:   90-362
Sequence Alignment: Aminoacid

LCMV-WE_ZP          MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS    60
LCMV-P42_ZP         MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS    60
LCMV-P52_ZP         MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS    60
LCMV-P91_ZP         MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS    60
LCMV-P52-1_ZP       MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS    60
LCMV-P52-1.3_ZP     MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS    60
LCMV-P52-2.1_ZP     MGQGKSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS    60
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LCMV-WE_ZP          VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE    90
LCMV-P42_ZP         VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE    90
LCMV-P52_ZP         VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE    90
LCMV-P91_ZP         VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE    90
LCMV-P52-1_ZP       VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE    90
LCMV-P52-1.3_ZP     VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE    90
LCMV-P52-2.1_ZP     VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE    90
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LCMV-WE_ZP:       SEQ ID NO: 14
LCMV-P42_ZP:      SEQ ID NO: 22
LCMV-P52_ZP:      SEQ ID NO: 30
LCMV-P91_ZP:      SEQ ID NO: 38
LCMV-P52-1_ZP:    SEQ ID NO: 46
LCMV-P52-1.3_ZP:  SEQ ID NO: 54
LCMV-P52-2.1_ZP:  SEQ ID NO: 62
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G.

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement
Sequence Alignment: Nucleotide

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LCMV-WE_LP        ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG    60
LCMV-P42_LP       ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG    60
LCMV-P52_LP       ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG    60
LCMV-P91_LP       ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG    60
LCMV-P52-1_LP     ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG    60
LCMV-P52-1.3_LP   ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG    60
LCMV-P52-2.1_LP   ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAA    60
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LCMV-WE_LP        AGGCTGTCAAGGCAAAAACTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGCTAATT   120
LCMV-P42_LP       AGGCTGTCAAGGCAAAAACTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGCTAATT   120
LCMV-P52_LP       AGGCTGTCAAGGCAAAAACTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGCTAATT   120
LCMV-P91_LP       AGGCTGTCAAGGCAAAAACTCAACTTCCTCGCACAAACAGAACCCAGAATGGTCCTAATT   120
LCMV-P52-1_LP     AGGCTGTCAAGGCAAAAACTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGCTAATT   120
LCMV-P52-1.3_LP   AGGCTGTCAAGGCAAAAACTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGCTAATT   120
LCMV-P52-2.1_LP   AGGCTGTCAAGGCAAAAACTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGCTAATT   120
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LCMV-WE_LP        GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC   180
LCMV-P42_LP       GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC   180
LCMV-P52_LP       GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC   180
LCMV-P91_LP       GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC   180
LCMV-P52-1_LP     GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC   180
LCMV-P52-1.3_LP   GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC   180
LCMV-P52-2.1_LP   GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC   180
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LCMV-WE_LP        ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT   240
LCMV-P42_LP       ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT   240
LCMV-P52_LP       ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGCGATTGTGTGT   240
LCMV-P91_LP       ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT   240
LCMV-P52-1_LP     ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT   240
LCMV-P52-1.3_LP   ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT   240
LCMV-P52-2.1_LP   ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT   240
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LCMV-WE_LP        CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCCTTATTCTT   300
LCMV-P42_LP       CCAGGACTGCCACTCATCATCCCTGATGCTTATAAGTTGATTGACAATTCCCTTATTCTT   300
LCMV-P52_LP       CCAGGACTGCCACTCATCATCCCTGATGCTTATAAGTTGATTGACAATTCCCTTATTCTT   300
LCMV-P91_LP       CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCCTTATTCTT   300
LCMV-P52-1_LP     CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCCTTATTCTT   300
LCMV-P52-1.3_LP   CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCCTTATTCTT   300
LCMV-P52-2.1_LP   CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCCTTATTCTT   300
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LCMV-WE_LP        CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC   360
LCMV-P42_LP       CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC   360
LCMV-P52_LP       CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC   360
LCMV-P91_LP       CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC   360
LCMV-P52-1_LP     CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC   360
LCMV-P52-1.3_LP   CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC   360
LCMV-P52-2.1_LP   CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC   360
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LCMV-WE_LP        AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA   420
LCMV-P42_LP       AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA   420
LCMV-P52_LP       AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA   420
LCMV-P91_LP       AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA   420
LCMV-P52-1_LP     AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA   420
LCMV-P52-1.3_LP   AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA   420
LCMV-P52-2.1_LP   AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA   420
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LCMV-WE_LP          GTGGATGGTCGTTGTGATTATGATAACACTTTCATGCCAGAATGGGTGAATTTTAAGTTC    480
LCMV-P42_LP         GTGGATGGTCGTTGTGATTATGATAACACTTTCATGCCAGAATGGGTGAATTTTAAGTTC    480
LCMV-P52_LP         GTGGATGGTCGTTGTGATTATGATAACACTTTCATGCCAGAATGGGTGAATTTTAAGTTC    480
LCMV-P91_LP         GTGGATGGTCGTTGTGATTATGATAACACTTTCATGCCAGAATGGGTGAATTTTAAGTTC    480
LCMV-P52-1_LP       GTGGATGGTCGTTGTGATTATGATAACACTTTCATGCCAGAATGGGTGAATTTTAAGTTC    480
LCMV-P52-1.3_LP     GTGGATGGTCGTTGTGATTATGATAACACTTTCATGCCAGAATGGGTGAATTTTAAGTTC    480
LCMV-P52-2.1_LP     GTGGATGGTCGTTGTGATTATGATAACACTTTCATGCCAGAATGGGTGAATTTTAAGTTC    480
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LCMV-WE_LP          AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG    540
LCMV-P42_LP         AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG    540
LCMV-P52_LP         AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG    540
LCMV-P91_LP         AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG    540
LCMV-P52-1_LP       AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG    540
LCMV-P52-1.3_LP     AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG    540
LCMV-P52-2.1_LP     AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG    540
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LCMV-WE_LP          TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG    600
LCMV-P42_LP         TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG    600
LCMV-P52_LP         TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG    600
LCMV-P91_LP         TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG    600
LCMV-P52-1_LP       TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG    600
LCMV-P52-1.3_LP     TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG    600
LCMV-P52-2.1_LP     TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG    600
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LCMV-WE_LP          GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAATG    660
LCMV-P42_LP         GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAATG    660
LCMV-P52_LP         GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAATG    660
LCMV-P91_LP         GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAATG    660
LCMV-P52-1_LP       GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAATG    660
LCMV-P52-1.3_LP     GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAATG    660
LCMV-P52-2.1_LP     GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAATG    660
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LCMV-WE_LP          TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC    720
LCMV-P42_LP         TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC    720
LCMV-P52_LP         TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC    720
LCMV-P91_LP         TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC    720
LCMV-P52-1_LP       TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC    720
LCMV-P52-1.3_LP     TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC    720
LCMV-P52-2.1_LP     TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC    720
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LCMV-WE_LP          TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAAACTCAAAAGGAATTTCCAAAAG    780
LCMV-P42_LP         TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAAACTCAAAAGGAATTTCCAAAAG    780
LCMV-P52_LP         TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAAACTCAAAAGGAATTTCCAAAAG    780
LCMV-P91_LP         TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAAACTCAAAAGGAATTTCCAAAAG    780
LCMV-P52-1_LP       TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAGACTCAAAAGGAATTTCCAAAAG    780
LCMV-P52-1.3_LP     TTTTTTGGCAGGTTTAGGACGGACCTGTTAAATGGGAAACTCAAAAGGAATTTCCAAAAG    780
LCMV-P52-2.1_LP     TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAAACTCAAAAGGAATTTCCAAAAG    780
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LCMV-WE_LP          GTCAGCCCTGGGGGCTTAATCAAGGAATTCTCTGAACTTTATGAAACCCTTACTGATAAT    840
LCMV-P42_LP         GTCAGCCCTGGGGGCTTAATCAAGGAATTCTCTGAACTTTATGAAACCCTTACTGATAAT    840
LCMV-P52_LP         GTCAGCCCTGGGGGCTTAATCAAGGAATTCTCTGAACTTTATGAAACCCTTACTGATAAT    840
LCMV-P91_LP         GTCAGCCCTGGGGGCTTAATCAAGGAATTCTCTGAACTTTATGAAACCCTTACTGATAAT    840
LCMV-P52-1_LP       GTCAGCCCTGGGGGCTTAATCAAGGAATTCTCTGAACTTTATGAAACCCTTACTGATAAT    840
LCMV-P52-1.3_LP     GTCAGCCCTGGGGGCTTAATCAAGGAATTCTCTGAACTTTATGAAACCCTTACTGATAAT    840
LCMV-P52-2.1_LP     GTCAGCCCTGGGGGCTTAATCAAGGAATTCTCTGAACTTTATGAAACCCTTACTGATAAT    840
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LCMV-WE_LP          GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCCTTAATGAGGTTCATT    900
LCMV-P42_LP         GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCCTTAATGAGGTTCATT    900
LCMV-P52_LP         GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCCTTAATGAGGTTCATT    900
LCMV-P91_LP         GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCCTTAATGAGGTTCATT    900
LCMV-P52-1_LP       GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCCTTAATGAGGTTCATT    900
LCMV-P52-1.3_LP     GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCCTTAATGAGGTTCATT    900
LCMV-P52-2.1_LP     GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCCTTAATGAGGTTCATT    900
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LCMV-WE_LP          ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA    960
LCMV-P42_LP         ACAGCAGAGACCCATGGCCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA    960
LCMV-P52_LP         ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA    960
LCMV-P91_LP         ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA    960
LCMV-P52-1_LP       ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA    960
LCMV-P52-1.3_LP     ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA    960
LCMV-P52-2.1_LP     ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA    960
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LCMV-WE_LP          CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAATTATTAAACACTAGAAGGAGACAGCTG    1020
LCMV-P42_LP         CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAATTATTAAACACTAGAAGGAGACAGCTG    1020
LCMV-P52_LP         CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAATTATTAAACACTAGAAGGAGACAGCTG    1020
LCMV-P91_LP         CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAATTATTAAACACTAGAAGGAGACAGCTG    1020
LCMV-P52-1_LP       CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAATTATTAAACACTAGAAGGAGACAGCTG    1020
LCMV-P52-1.3_LP     CTCTCTATGTTAAACAAGGTGAAAAGTTTAAAATTATTAAACACTAGAAGGAGACAGCTG    1020
LCMV-P52-2.1_LP     CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAATTATTAAACACTAGAAGGAGACAGCTG    1020
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LCMV-WE_LP          CTGAACTTAGATGTCTTATGTCTTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG    1080
LCMV-P42_LP         CTGAACTTAGATGTCTTATGTCTTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG    1080
LCMV-P52_LP         CTGAACTTAGATGTCTTATGTCTTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG    1080
LCMV-P91_LP         CTGAACTTAGATGTCTTATGTCTTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG    1080
LCMV-P52-1_LP       CTGAACTTAGATGTCTTATGTCTTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG    1080
LCMV-P52-1.3_LP     CTGAACTTAGATGTCTTATGTCTTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG    1080
LCMV-P52-2.1_LP     CTGAACTTAGATGTCTTATGTCTTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG    1080
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LCMV-WE_LP          GAAAATGATAAACATTGGGTTGGTTGTTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC    1140
LCMV-P42_LP         GAAAATGATAAACATTGGGTTGGTTGTTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC    1140
LCMV-P52_LP         GAAAATGATAAACATTGGGTTGGTTGTTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC    1140
LCMV-P91_LP         GAAAATGATAAACATTGGGTTGGTTGCTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC    1140
LCMV-P52-1_LP       GAAAATGATAAACATTGGGTTGGTTGTTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC    1140
LCMV-P52-1.3_LP     GAAAATGATAAACATTGGGTTGGTTGTTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC    1140
LCMV-P52-2.1_LP     GAAAATGATAAACATTGGGTTGGTTGTTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC    1140
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LCMV-WE_LP          CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAAGAAAATCAAGAGTG    1200
LCMV-P42_LP         CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAAGAAAATCAAGAGTG    1200
LCMV-P52_LP         CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAAGAAAATCAAGAGTG    1200
LCMV-P91_LP         CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAAGAAAATCAAGAGTG    1200
LCMV-P52-1_LP       CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAAGAAAATCAAGAGTG    1200
LCMV-P52-1.3_LP     CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAAGAAAATCAAGAGTG    1200
LCMV-P52-2.1_LP     CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAAGAAAATCAAGAGTG    1200
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LCMV-WE_LP          CACAAAAAGGCATCTCTTGATGAGCTTTTTAGGGTATCCATAAATGAGTTCATAGCAAAA    1260
LCMV-P42_LP         CACAAAAAGGCATCTCTTGATGAGCTTTTTAGGGTATCCATAAATGAGTTCATAGCAAAA    1260
LCMV-P52_LP         CACAAAAAGGCATCTCTTGATGAGCTTTTTAGGGTATCCATAAATGAGTTCATAGCAAAA    1260
LCMV-P91_LP         CACAAAAAGGCATCTCTTGATGAGCTTTTTAGGGTATCCATAAATGAGTTCATAGCAAAA    1260
LCMV-P52-1_LP       CACAAAAAGGCATCTCTTGATGAGCTTTTTAGGGTATCCATAAATGAGTTCATAGCAAAA    1260
LCMV-P52-1.3_LP     CACAAAAAGGCATCTCTTGATGAGCTTTTTAGGGTATCCATAAATGAGTTCATAGCAAAA    1260
LCMV-P52-2.1_LP     CACAAAAAGGCATCTCTTGATGAGCTTTTTAGGGTATCCATAAATGAGTTCATAGCAAAA    1260
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LCMV-WE_LP          ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC    1320
LCMV-P42_LP         ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC    1320
LCMV-P52_LP         ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC    1320
LCMV-P91_LP         ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC    1320
LCMV-P52-1_LP       ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC    1320
LCMV-P52-1.3_LP     ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC    1320
LCMV-P52-2.1_LP     ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC    1320
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LCMV-WE_LP          CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAACTTTATGAGAGCCGGGACT    1380
LCMV-P42_LP         CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAACTTTATGAGAGCCGGGACT    1380
LCMV-P52_LP         CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAACTTTATGAGAGCCGGGACT    1380
LCMV-P91_LP         CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAACTTTATGAGAGCCGGGACT    1380
LCMV-P52-1_LP       CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAACTTTATGAGAGCCGGGACT    1380
LCMV-P52-1.3_LP     CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAACTTTATGAGAGCCGGGACT    1380
LCMV-P52-2.1_LP     CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAACTTTATGAGAGCCGGGACT    1380
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LCMV-WE_LP          CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA    1440
LCMV-P42_LP         CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA    1440
LCMV-P52_LP         CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA    1440
LCMV-P91_LP         CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA    1440
LCMV-P52-1_LP       CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA    1440
LCMV-P52-1.3_LP     CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA    1440
LCMV-P52-2.1_LP     CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA    1440
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LCMV-WE_LP          TTGAGGGGTTTACAGAGTTTGAGAAAACTGTCATCTGTTTGTTTGGCTCTAACAAACAGC    1500
LCMV-P42_LP         TTGAGGGGTTTACAGAGTTTGAGAAAACTGTCATCTGTTTGTTTGGCTCTAACAAACAGC    1500
LCMV-P52_LP         TTGAGGGGTTTACAGAGTTTGAGAAAACTGTCATCTGTTTGTTTGGCTCTAACAAACAGC    1500
LCMV-P91_LP         TTGAGGGGTTTACAGAGTTTGAGAAAACTGTCATCTGTTTGTTTGGCTCTAACAAACAGC    1500
LCMV-P52-1_LP       TTGAGGGGTTTACAGAGTTTGAGAAAACTGTCATCTGTTTGTTTGGCTCTAACAAACAGC    1500
LCMV-P52-1.3_LP     TTGAGGGGTTTACAGAGTTTGAGAAAACTGTCATCTGTTTGTTTGGCTCTAACAAACAGC    1500
LCMV-P52-2.1_LP     TTGAGGGGTTTACAGAGTTTGAGAAAACTGTCATCTGTTTGTTTGGCTCTAACAAACAGC    1500
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LCMV-WE_LP          ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA    1560
LCMV-P42_LP         ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA    1560
LCMV-P52_LP         ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA    1560
LCMV-P91_LP         ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA    1560
LCMV-P52-1_LP       ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA    1560
LCMV-P52-1.3_LP     ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA    1560
LCMV-P52-2.1_LP     ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA    1560
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LCMV-WE_LP          GTGGTGGAGTGCAAAGAGGTGTTTTGCCAGATAATAAAACTGGATTCCGAAGAGTATCAT    1620
LCMV-P42_LP         GTGGTGGAGTGCAAAGAGGTGTTTTGCCAGATAATAAAACTGGATTCCGAAGAGTATCAT    1620
LCMV-P52_LP         GTGGTGGAGTGCAAAGAGGTGTTTTGCCAGATAATAAAACTGGATTCCGAAGAGTATCAT    1620
LCMV-P91_LP         GTGGTGGAGTGCAAAGAGGTGTTTTGCCAGATAATAAAACTGGATTCCGAAGAGTATCAT    1620
LCMV-P52-1_LP       GTGGTGGAGTGCAAAGAGGTGTTTTGCCAGATAATAAAACTGGATTCCGAAGAGTATCAT    1620
LCMV-P52-1.3_LP     GTGGTGGAGTGCAAAGAGGTGTTTTGCCAGATAATAAAACTGGATTCCGAAGAGTATCAT    1620
LCMV-P52-2.1_LP     GTGGTGGAGTGCAAAGAGGTGTTTTGCCAGATAATAAAACTGGATTCCGAAGAGTATCAT    1620
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LCMV-WE_LP          CTACTATATCAGAAAACTGGAGAATCATCGAGGTGTTATTCCATACAAGGTCCGGATGGT    1680
LCMV-P42_LP         CTACTATATCAGAAAACTGGAGAATCATCGAGGTGTTATTCCATACAAGGTCCGGATGGT    1680
LCMV-P52_LP         CTACTATATCAGAAAACTGGAGAATCATCGAGGTGTTATTCCATACAAGGTCCGGATGGT    1680
LCMV-P91_LP         CTACTATATCAGAAAACTGGAGAATCATCGAGGTGTTATTCCATACAAGGTCCGGATGGT    1680
LCMV-P52-1_LP       CTACTATATCAGAAAACTGGAGAATCATCGAGGTGTTATTCCATACAAGGTCCGGATGGT    1680
LCMV-P52-1.3_LP     CTACTATATCAGAAAACTGGAGAATCATCGAGGTGTTATTCCATACAAGGTCCGGATGGT    1680
LCMV-P52-2.1_LP     CTACTATATCAGAAAACTGGAGAATCATCGAGGTGTTATTCCATACAAGGTCCGGATGGT    1680
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LCMV-WE_LP          CACTTGATTTCCTTTTACGCAGATCCAAAAAGGTTCTTTTTACCAATTTTTTCAGATGAG    1740
LCMV-P42_LP         CACTTGATTTCCTTTTACGCAGATCCAAAAAGGTTCTTTTTACCAATTTTTTCAGATGAG    1740
LCMV-P52_LP         CACTTGATTTCCTTTTACGCAGATCCAAAAAGGTTCTTTTTACCAATTTTTTCAGATGAG    1740
LCMV-P91_LP         CACTTGATTTCCTTTTACGCAGATCCAAAAAGGTTCTTTTTACCAATTTTTTCAGATGAG    1740
LCMV-P52-1_LP       CACTTGATTTCCTTTTACGCAGATCCAAAAAGGTTCTTTTTACCAATTTTTTCAGATGAG    1740
LCMV-P52-1.3_LP     CACTTGATTTCCTTTTACGCAGATCCAAAAAGGTTCTTTTTACCAATTTTTTCAGATGAG    1740
LCMV-P52-2.1_LP     CACTTGATTTCCTTTTACGCAGATCCAAAAAGGTTCTTTTTACCAATTTTTTCAGATGAG    1740
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LCMV-WE_LP          GTGTTGCACAACATGATAGACACAATGATTTCATGGATTAGGTCATGCCCTGACTTAAAA    1800
LCMV-P42_LP         GTGTTGCACAACATGATAGACACAATGATTTCATGGATTAGGTCATGCCCTGACTTAAAA    1800
LCMV-P52_LP         GTGTTGCACAACATGATAGACACAATGATTTCATGGATTAGGTCATGCCCTGACTTAAAA    1800
LCMV-P91_LP         GTGTTGCACAACATGATAGACACAATGATTTCATGGATTAGGTCATGCCCTGACTTAAAA    1800
LCMV-P52-1_LP       GTGTTGCACAACATGATAGACACAATGATTTCATGGATTAGGTCATGCCCTGACTTAAAA    1800
LCMV-P52-1.3_LP     GTGTTGCACAACATGATAGACACAATGATTTCATGGATTAGGTCATGCCCTGACTTAAAA    1800
LCMV-P52-2.1_LP     GTGTTGCACAACATGATAGACACAATGATTTCATGGATTAGGTCATGCCCTGACTTAAAA    1800
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LCMV-WE_LP          GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC    1860
LCMV-P42_LP         GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC    1860
LCMV-P52_LP         GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC    1860
LCMV-P91_LP         GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC    1860
LCMV-P52-1_LP       GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC    1860
LCMV-P52-1.3_LP     GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC    1860
LCMV-P52-2.1_LP     GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC    1860
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LCMV-WE_LP          CCAACAAAGAGAAATCAAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGTC    1920
LCMV-P42_LP         CCAACAAAGAGAAATCAAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGTC    1920
LCMV-P52_LP         CCAACAAAGAGAAATCAAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGTC    1920
LCMV-P91_LP         CCAACAAAGAGAAATCAAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGTC    1920
LCMV-P52-1_LP       CCAACAAAGAGAAATCAAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGTC    1920
LCMV-P52-1.3_LP     CCAACAAAGAGAAATCAAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGTC    1920
LCMV-P52-2.1_LP     CCAACAAAGAGAAATCAAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGTC    1920
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LCMV-WE_LP          TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC    1980
LCMV-P42_LP         TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC    1980
LCMV-P52_LP         TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC    1980
LCMV-P91_LP         TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC    1980
LCMV-P52-1_LP       TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC    1980
LCMV-P52-1.3_LP     TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC    1980
LCMV-P52-2.1_LP     TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC    1980
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LCMV-WE_LP          GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTGATTAGGACAATTTTTGGTACTGGTGAA    2040
LCMV-P42_LP         GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTGATTAGGACAATTTTTGGTACTGGTGAA    2040
LCMV-P52_LP         GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTGATTAGGACAATTTTTGGTACTGGTGAA    2040
LCMV-P91_LP         GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTGATTAGGACAATTTTTGGTACTGGTGAA    2040
LCMV-P52-1_LP       GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTGATTAGGACAATTTTTGGTACTGGTGAA    2040
LCMV-P52-1.3_LP     GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTGATTAGGACAATTTTTGGTACTGGTGAA    2040
LCMV-P52-2.1_LP     GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTGATTAGGACAATTTTTGGTACTGGTGAA    2040
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LCMV-WE_LP          AAGGTGTTATTGAGTGCAAAATTCAAGTTTATGTTGAATGTGTCATACCTGTGTCATTTG    2100
LCMV-P42_LP         AAGGTGTTATTGAGTGCAAAATTCAAGTTTATGTTGAATGTGTCATACCTGTGTCATTTG    2100
LCMV-P52_LP         AAGGTGTTATTGAGTGCAAAATTCAAGTTTATGTTGAATGTRTCATACCTGTGTCATTTG    2100
LCMV-P91_LP         AAGGTGTTATTGAGTGCAAAATTCAAGTTTATGTTGAATGTGTCATACCTGTGTCATTTG    2100
LCMV-P52-1_LP       AAGGTGTTATTGAGTGCAAAATTCAAGTTTATGTTGAATGTGTCATACCTGTGTCATTTG    2100
LCMV-P52-1.3_LP     AAGGTGTTATTGAGTGCAAAATTCAAGTTTATGTTGAATGTGTCATACCTGTGTCATTTG    2100
LCMV-P52-2.1_LP     AAGGTGTTATTGAGTGCAAAATTTAAGTTTATGTTGAATGTGTCATACCTGTGTCATTTG    2100
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LCMV-WE_LP          ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCTTT    2160
LCMV-P42_LP         ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCTTT    2160
LCMV-P52_LP         ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCTTT    2160
LCMV-P91_LP         ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCTTT    2160
LCMV-P52-1_LP       ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCTTT    2160
LCMV-P52-1.3_LP     ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCTTT    2160
LCMV-P52-2.1_LP     ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCTTT    2160
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LCMV-WE_LP          GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG    2220
LCMV-P42_LP         GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG    2220
LCMV-P52_LP         GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG    2220
LCMV-P91_LP         GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG    2220
LCMV-P52-1_LP       GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG    2220
LCMV-P52-1.3_LP     GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG    2220
LCMV-P52-2.1_LP     GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG    2220
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LCMV WE_LP          GAATGTGTTTTTTTATGAACAAATGAAGAAGTTCACCGGTAAAGATATTGATTGTCAGCAT    2280
LCMV-P42_LP         GAATGTGTTTTTTTATGAACAAATGAAGAAGTTCACCGGTAAAGATATTGATTGTCAGCAT    2280
LCMV-P52_LP         GAATGTGTTTTTTTATGAACAAATGAACAACTTCACCGGTAAAGATATTGATTGTCAGCAT    2280
LCMV-P91_LP         GAATGTGTTTTTTTATGAACAAATGAAGAAGTTCACCGGTAAAGATATTGATTGTCAGCAT    2280
LCMV-P52-1_LP       GAATGTGTTTTTTTATGAACAAATGAAGAAGTTCACCGGTAAAGATATTGATTGTCAGCAT    2280
LCMV-P52-1.3_LP     GAATGTGTTTTTTTATGAACAAATGAAGAAGTTCACCGGTAAAGATATTGATTGTCAGCAT    2280
LCMV-P52-2.1_LP     GAATGTGTTTTTTTATGAACAAATGAAGAAGTTCACCGGTAAAGATATTGATTGTCAGCAT    2280
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LCMV-WE_LP          TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC    2340
LCMV-P42_LP         TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC    2340
LCMV-P52_LP         TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC    2340
LCMV-P91_LP         TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC    2340
LCMV-P52-1_LP       TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC    2340
LCMV-P52-1.3_LP     TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC    2340
LCMV-P52-2.1_LP     TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC    2340
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LCMV-WE_LP          ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA    2400
LCMV-P42_LP         ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA    2400
LCMV-P52_LP         ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA    2400
LCMV-P91_LP         ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA    2400
LCMV-P52-1_LP       ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA    2400
LCMV-P52-1.3_LP     ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA    2400
LCMV-P52-2.1_LP     ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA    2400
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LCMV-WE_LP          TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT    2460
LCMV-P42_LP         TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT    2460
LCMV-P52_LP         TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT    2460
LCMV-P91_LP         TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT    2460
LCMV-P52-1_LP       TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT    2460
LCMV-P52-1.3_LP     TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT    2460
LCMV-P52-2.1_LP     TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT    2460
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LCMV-WE_LP          GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTTAGTGCTGTGAGCCAAATT    2520
LCMV-P42_LP         GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTTAGTGCTGTGAGCCAAATT    2520
LCMV-P52_LP         GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTTAGTGCTGTGAGCCAAATT    2520
LCMV-P91_LP         GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTTAGTGCTGTGAGCCAAATT    2520
LCMV-P52-1_LP       GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTTAGTGCTGTGAGCCAAATT    2520
LCMV-P52-1.3_LP     GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTTAGTGCTGTGAGCCAAATT    2520
LCMV-P52-2.1_LP     GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTTAGTGCTGTGAGCCAAATT    2520
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LCMV-WE_LP          ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG    2580
LCMV-P42_LP         ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG    2580
LCMV-P52_LP         ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG    2580
LCMV-P91_LP         ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG    2580
LCMV-P52-1_LP       ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG    2580
LCMV-P52-1.3_LP     ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG    2580
LCMV-P52-2.1_LP     ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG    2580
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LCMV-WE_LP          GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTG    2640
LCMV-P42_LP         GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTG    2640
LCMV-P52_LP         GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTG    2640
LCMV-P91_LP         GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTG    2640
LCMV-P52-1_LP       GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCTAGGAAAACAGAAGTAGACAAATTG    2640
LCMV-P52-1.3_LP     GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTA    2640
LCMV-P52-2.1_LP     GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTG    2640
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LCMV-WE_LP          GAAGATGATCCGGTAGATGTGTGTTTCGAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT    2700
LCMV-P42_LP         GAAGATGATCCGGTAGATGTGTGTTTCGAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT    2700
LCMV-P52_LP         GAAGATGATCCGGTAGATGTGTGTTTCGAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT    2700
LCMV-P91_LP         GAAGATGATCCGGTAGATGTGTGTTTCGAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT    2700
LCMV-P52-1_LP       GAAGATGATCCGGTAGATGTGTGTTTCGAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT    2700
LCMV-P52-1.3_LP     GAAGATGATCCGGTAGATGTGTGTTTCCAGCGCGCAGGAGGAGACAAGTTTTTTCAGGAGT    2700
LCMV-P52-2.1_LP     GAAGATGATCCGGTAGATGTGTGTTTCGAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT    2700
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LCMV-WE_LP          TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA    2760
LCMV-P42_LP         TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA    2760
LCMV-P52_LP         TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA    2760
LCMV-P91_LP         TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA    2760
LCMV-P52-1_LP       TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA    2760
LCMV-P52-1.3_LP     TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA    2760
LCMV-P52-2.1_LP     TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA    2760
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LCMV-WE_LP          GGGCAAGGGGAGGGAGAATTCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG    2820
LCMV-P42_LP         GGGCAAGGGGAGGGAGAATTCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG    2820
LCMV-P52_LP         GGGCAAGGGGAGGGAGAATTCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG    2820
LCMV-P91_LP         GGGCAAGGGGAGGGAGAATTCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG    2820
LCMV-P52-1_LP       GGGCAAGGGGAGGGAGAATTCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG    2820
LCMV-P52-1.3_LP     GGGCAAGGGGAGGGAGAATTCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG    2820
LCMV-P52-2.1_LP     GGGCAAGGGGAGGGAGAATTCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG    2820
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LCMV-WE_LP          TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTTCATTTCATCTAGTA    2880
LCMV-P42_LP         TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTTCATTTCATCTAGTA    2880
LCMV-P52_LP         TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTTCATTTCATCTAGTA    2880
LCMV-P91_LP         TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTTCATTTCATCTAGTA    2880
LCMV-P52-1_LP       TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTTCATTTCATCTAGTA    2880
LCMV-P52-1.3_LP     TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTTCATTTCATCTAGTA    2880
LCMV-P52-2.1_LP     TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTTCATTTCATCTAGTA    2880
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LCMV-WE_LP          GAGGACTTTGATCCATCCTGTCTCACCAATGACGACATGAGGTTTATTTGTGAGGCTGTT    2940
LCMV-P42_LP         GAGGACTTTGATCCATCCTGTCTCACCAATGACGACATGAGGTTTATTTGTGAGGCTGTT    2940
LCMV-P52_LP         GAGGACTTTGATCCATCCTGTCTCACCAATGACGACATGAGGTTTATTTGTGAGGCTGTT    2940
LCMV-P91_LP         GAGGACTTTGATCCATCCTGTCTCACCAATGACGACATGAGGTTTATTTGTGAGGCTGTT    2940
LCMV-P52-1_LP       GAGGACTTTGATCCATCCTGTCTCACCAATGACGACATGAGGTTTATTTGTGAGGCTGTT    2940
LCMV-P52-1.3_LP     GAGCACTTTGATCCATCCTCTCTCACCAATCACCACATGAGCTTTATTTCTCACCCTCTT    2940
LCMV-P52-2.1_LP     GAGGACTTTGATCCATCCTGTCTCACCAATGACGACATGAGGTTTATTTGTGAGGCTGTT    2940
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LCMV-WE_LP          GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT    3000
LCMV-P42_LP         GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT    3000
LCMV-P52_LP         GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT    3000
LCMV-P91_LP         GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT    3000
LCMV-P52-1_LP       GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT    3000
LCMV-P52-1.3_LP     GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT    3000
LCMV-P52-2.1_LP     GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT    3000
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LCMV-WE_LP          CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTTCTTCTCAGAGGGTGATTGGTTCTCA    3060
LCMV-P42_LP         CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTTCTTCTCAGAGGGTGATTGGTTCTCA    3060
LCMV-P52_LP         CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTTCTTCTCAGAGGGTGATTGGTTCTCA    3060
LCMV-P91_LP         CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTTCTTCTCAGAGGGTGATTGGTTCTCA    3060
LCMV-P52-1_LP       CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTTCTTCTCAGAGGGTGATTGGTTCTCA    3060
LCMV-P52-1.3_LP     CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTTCTTCTCAGAGGGTGATTGGTTCTCA    3060
LCMV-P52-2.1_LP     CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTTCTTCTCAGAGGGTGATTGGTTCTCA    3060
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LCMV-WE_LP          TGTATGAAGATGATCTTGTTACAGATGAATGCAAATGCGTATTCAGGGAAGTACAGACAC    3120
LCMV-P42_LP         TGTATGAAGATGATCTTGTTACAGATGAATGCAAATGCGTATTCAGGGAAGTACAGACAC    3120
LCMV-P52_LP         TGTATGAAGATGATCTTGTTACAGATGAATGCAAATGCGTATTCAGGGAAGTACAGACAC    3120
LCMV-P91_LP         TGTATGAAGATGATCTTGTTACAGATGAATGCAAATGCGTATTCAGGGAAGTACAGACAC    3120
LCMV-P52-1_LP       TGTATGAAGATGATCTTGTTACAGATGAATGCAAATGCGTATTCAGGGAAGTACAGACAC    3120
LCMV-P52-1.3_LP     TGTATGAAGATGATCTTGTTACAGATGAATGCAAATGCGTATTCAGGGAAGTACAGACAC    3120
LCMV-P52-2.1_LP     TGTATGAAGATGATCTTGTTACAGATGAATGCAAATGCGTATTCAGGGAAGTACAGACAC    3120
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LCMV-WE_LP          ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA    3180
LCMV-P42_LP         ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA    3180
LCMV-P52_LP         ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA    3180
LCMV-P91_LP         ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA    3180
LCMV-P52-1_LP       ATGCAGAGGCAGAGTTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA    3180
LCMV-P52-1.3_LP     ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA    3180
LCMV-P52-2.1_LP     ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA    3180
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LCMV-WE_LP          ATTAGTGAAAGGGAAAGCAATTCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC    3240
LCMV-P42_LP         ATTAGTGAAAGGGAAAGCAATTCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC    3240
LCMV-P52_LP         ATTAGTGAAAGGGAAAGCAATTCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC    3240
LCMV-P91_LP         ATTAGTGAAAGGGAAAGCAATTCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC    3240
LCMV-P52-1_LP       ATTAGTGAAAGGGAAAGCAATTCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC    3240
LCMV-P52-1.3_LP     ATTAGTGAAAGGGAAAGCAATTCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC    3240
LCMV-P52-2.1_LP     ATTAGTGAAAGGGAAAGCAATTCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC    3240
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LCMV-WE_LP          ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCAACATCATACACT    3300
LCMV-P42_LP         ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCAACATCATACACT    3300
LCMV-P52_LP         ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCAACATCATACACT    3300
LCMV-P91_LP         ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCAACATCATACACT    3300
LCMV-P52-1_LP       ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCAACATCATACACT    3300
LCMV-P52-1.3_LP     ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCAACATCATACACT    3300
LCMV-P52-2.1_LP     ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCAACATCATACACT    3300
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LCMV-WE_LP          TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG    3360
LCMV-P42_LP         TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG    3360
LCMV-P52_LP         TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG    3360
LCMV-P91_LP         TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG    3360
LCMV-P52-1_LP       TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG    3360
LCMV-P52-1.3_LP     TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG    3360
LCMV-P52-2.1_LP     TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG    3360
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LCMV-WE_LP          GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCACAAGATTGGTAGAA    3420
LCMV-P42_LP         GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCACAAGATTGGTAGAA    3420
LCMV-P52_LP         GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCACAAGATTGGTAGAA    3420
LCMV-P91_LP         GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCACAAGATTGGTAGAA    3420
LCMV-P52-1_LP       GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCACAAGATTGGTAGAA    3420
LCMV-P52-1.3_LP     GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCACAAGATTGGTAGAA    3420
LCMV-P52-2.1_LP     GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCACAAGATTGGTAGAA    3420
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LCMV-WE_LP          GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG    3480
LCMV-P42_LP         GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG    3480
LCMV-P52_LP         GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG    3480
LCMV-P91_LP         GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGATAAAGAG    3480
LCMV-P52-1_LP       GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG    3480
LCMV-P52-1.3_LP     GATTACTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG    3480
LCMV-P52-2.1_LP     GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG    3480
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LCMV-WE_LP          TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC    3540
LCMV-P42_LP         TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC    3540
LCMV-P52_LP         TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC    3540
LCMV-P91_LP         TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC    3540
LCMV-P52-1_LP       TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC    3540
LCMV-P52-1.3_LP     TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC    3540
LCMV-P52-2.1_LP     TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC    3540
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LCMV-WE_LP          ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA    3600
LCMV-P42_LP         ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTYCTCCAA    3600
LCMV-P52_LP         ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA    3600
LCMV-P91_LP         ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA    3600
LCMV-P52-1_LP       ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA    3600
LCMV-P52-1.3_LP     ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA    3600
LCMV-P52-2.1_LP     ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA    3600
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LCMV-WE_LP          AATCTCAAACTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG    3660
LCMV-P42_LP         AATCTCAAACTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG    3660
LCMV-P52_LP         AATCTCAAACTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG    3660
LCMV-P91_LP         AATCTCAAACTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG    3660
LCMV-P52-1_LP       AATCTCAAACTGGGTGATGATCAGTACGTGCGTTCTGGGAAAGATCATGTTAGCACCTTG    3660
LCMV-P52-1.3_LP     AATCTCAAACTGGGTGATGATCAGTACGTCCCTTCTGGAAAAGATCATGTTAGCACCTTG    3660
LCMV-P52-2.1_LP     AATCTCAAACTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG    3660
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LCMV-WE_LP          TTGACTTGGCATATGCATAAACTTGTTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG    3720
LCMV-P42_LP         TTGACTTGGCATATGCATAAACTTGTTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG    3720
LCMV-P52_LP         TTGACTTGGCATATGCATAAACTTGTTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG    3720
LCMV-P91_LP         TTGACTTGGCATATGCATAAACTTGTTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG    3720
LCMV-P52-1_LP       TTGACTTGGCATATGCATAAACTTGTTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG    3720
LCMV-P52-1.3_LP     TTGACTTGGCATATGCATAAACTTGTTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG    3720
LCMV-P52-2.1_LP     TTGACTTGGCATATGCATAAACTTGTTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG    3720
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LCMV-WE_LP          AAATCATATGTTAAATCAAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG    3780
LCMV-P42_LP         AAATCATATGTTAAATCAAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG    3780
LCMV-P52_LP         AAATCATATGTTAAATCAAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG    3780
LCMV-P91_LP         AAATCATATGTTAAATCAAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG    3780
LCMV-P52-1_LP       AAATCATATGTTAAATCAAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG    3780
LCMV-P52-1.3_LP     AAATCATATGTTAAATCAAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG    3780
LCMV-P52-2.1_LP     AAATCATATGTTAAATCAAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG    3780
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LCMV-WE_LP          AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT    3840
LCMV-P42_LP         AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT    3840
LCMV-P52_LP         AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT    3840
LCMV-P91_LP         AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT    3840
LCMV-P52-1_LP       AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT    3840
LCMV-P52-1.3_LP     AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT    3840
LCMV-P52-2.1_LP     AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT    3840
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LCMV-WE_LP          GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG    3900
LCMV-P42_LP         GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG    3900
LCMV-P52_LP         GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG    3900
LCMV-P91_LP         GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG    3900
LCMV-P52-1_LP       GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG    3900
LCMV-P52-1.3_LP     GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG    3900
LCMV-P52-2.1_LP     GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG    3900
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LCMV-WE_LP          TTTATCAATTATTGTATTGGTGTCATTTTTGGAGAGAGGCCAGAAGCCTATACATCAAGT    3960
LCMV-P42_LP         TTTATCAATTATTGTATTGGTGTCATTTTTGGAGAGAGGCCAGAAGCCTATACATCAAGT    3960
LCMV-P52_LP         TTTATCAATTATTGTATTGGTGTCATTTTTGGAGAGAGGCCAGAAGCCTATACATCAAGT    3960
LCMV-P91_LP         TTTATCAATTATTGTATTGGTGTCATTTTTGGAGAGAGGCCAGAAGCCTATACATCAAGT    3960
LCMV-P52-1_LP       TTTATCAATTATTGTATTGGTGTCATTTTTGGAGAGAGGCCAGAAGCCTATACATCAAGT    3960
LCMV-P52-1.3_LP     TTTATCAATTATTGTATTGGTGTCATTTTTGGAGAGAGGCCAGAAGCCTATACATCAAGT    3960
LCMV-P52-2.1_LP     TTTATCAATTATTGTATTGGTGTCATTTTTGGAGAGAGGCCAGAAGCCTATACATCAAGT    3960
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LCMV-WE_LP          GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA    4020
LCMV-P42_LP         GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA    4020
LCMV-P52_LP         GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA    4020
LCMV-P91_LP         GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA    4020
LCMV-P52-1_LP       GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA    4020
LCMV-P52-1.3_LP     GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA    4020
LCMV-P52-2.1_LP     GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA    4020
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LCMV-WE_LP          GAAGTCCTTGTCTTGCTGGAATTCCACTCTCACTTAAGTGGTTTGTTGAACAAGTTCATC    4080
LCMV-P42_LP         GAAGTCCTTGTCTTGCTGGAATTCCACTCTCACTTAAGTGGTTTGTTGAACAAGTTCATC    4080
LCMV-P52_LP         GAAGTCCTTGTCTTGCTGGAATTCCACTCTCACTTAAGTGGTTTGTTGAACAAGTTCATC    4080
LCMV-P91_LP         GAAGTCCTTGTCTTGCTGGAATTCCACTCTCACTTAAGTGGTTTGTTGAACAAGTTCATC    4080
LCMV-P52-1_LP       GAAGTCCTTGTCTTGCTGGAATTCCACTCTCACTTAAGTGGTTTGTTGAACAAGTTCATC    4080
LCMV-P52-1.3_LP     GAAGTCCTTGTCTTGCTGGAATTCCACTCTCACTTAAGTGGTTTGTTGAACAAGTTCATC    4080
LCMV-P52-2.1_LP     GAAGTCCTTGTCTTGCTGGAATTCCACTCTCACTTAAGTGGTTTGTTGAACAAGTTCATC    4080
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LCMV-WE_LP          AGTCCAAAAAGTGTGGTTGGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG    4140
LCMV-P42_LP         AGTCCAAAAAGTGTGGTTGGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG    4140
LCMV-P52_LP         AGTCCAAAAAGTGTGGTTGGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG    4140
LCMV-P91_LP         AGTCCAAAAAGTGTGGTTGGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG    4140
LCMV-P52-1_LP       AGTCCAAAAAGTGTGGTTGGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG    4140
LCMV-P52-1.3_LP     AGTCCAAAAAGTGTGGTTGGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG    4140
LCMV-P52-2.1_LP     AGTCCAAAAAGTGTGGTTGGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG    4140
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LCMV-WE_LP          GGGGAGGAGGTCCCTCTCCTCACGAAATTTGTGTCTGCGGCACTACACAATGTTAAGTGT    4200
LCMV-P42_LP         GGGGAGGAGGTCCCTCTCCTCACGAAATTTGTGTCTGCGGCACTACACAATGTTAAGTGT    4200
LCMV-P52_LP         GGGGAGGAGGTCCCTCTCCTCACGAAATTTGTGTCTGCGGCACTACACAATGTTAAGTGT    4200
LCMV-P91_LP         GGGGAGGAGGTCCCTCTCCTCACGAAATTTGTGTCTGCGGCACTACACAATGTTAAGTGT    4200
LCMV-P52-1_LP       GGGGAGGAGGTCCCTCTCCTCACGAAATTTGTGTCTGCGGCACTACACAATGTTAAGTGT    4200
LCMV-P52-1.3_LP     GGGGAGGAGGTCCCTCTCCTCACGAAATTTGTGTCTGCGGCACTACACAATGTTAAGTGT    4200
LCMV-P52-2.1_LP     GGGGAGGAGGTCCCTCTCCTCACGAAATTTGTGTCTGCGGCACTACACAATGTTAAGTGT    4200
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LCMV-WE_LP          AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAT    4260
LCMV-P42_LP         AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAT    4260
LCMV-P52_LP         AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAT    4260
LCMV-P91_LP         AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAT    4260
LCMV-P52-1_LP       AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAT    4260
LCMV-P52-1.3_LP     AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAT    4260
LCMV-P52-2.1_LP     AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAT    4260
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LCMV-WE_LP          GGAGTTCCAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAAATAT    4320
LCMV-P42_LP         GGAGTTCCAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAAATAT    4320
LCMV-P52_LP         GGAGTTCCAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAAATAT    4320
LCMV-P91_LP         GGAGTTCCAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAAATAT    4320
LCMV-P52-1_LP       GGAGTTCCAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAAATAT    4320
LCMV-P52-1.3_LP     GGAGTTCCAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAAATAT    4320
LCMV-P52-2.1_LP     GGAGTTCCAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAAATAT    4320
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LCMV-WE_LP          GCTAATTTCCCTTTAGATCCATTCTTGTTAAACACTCACACTGATGTAAAGGATTGGTTA    4380
LCMV-P42_LP         GCTAATTTCCCTTTAGATCCATTCTTGTTAAACACTCACACTGATGTAAAGGATTGGTTA    4380
LCMV-P52_LP         GCTAATTTCCCTTTAGATCCATTCTTGTTAAACACTCACACTGATGTAAAGGATTGGTTA    4380
LCMV-P91_LP         GCTAATTTCCCTTTAGATCCATTCTTGTTAAACACTCACACTGATGTAAAGGATTGGTTA    4380
LCMV-P52-1_LP       GCTAATTTCCCTTTAGATCCATTCTTGTTAAACACTCACACTGATGTAAAGGATTGGTTA    4380
LCMV-P52-1.3_LP     GCTAATTTCCCTTTAGATCCATTCTTGTTAAACACTCACACTGATGTAAAGGATTGGTTA    4380
LCMV-P52-2.1_LP     GCTAATTTCCCTTTAGATCCATTCTTGTTAAACACTCACACTGATGTAAAGGATTGGTTA    4380
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LCMV-WE_LP          GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA    4440
LCMV-P42_LP         GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA    4440
LCMV-P52_LP         GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA    4440
LCMV-P91_LP         GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA    4440
LCMV-P52-1_LP       GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA    4440
LCMV-P52-1.3_LP     GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA    4440
LCMV-P52-2.1_LP     GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA    4440
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LCMV-WE_LP          AAGATCATGAGAAAACTTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC    4500
LCMV-P42_LP         AAGATCATGAGAAAACTTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC    4500
LCMV-P52_LP         AAGATCATGAGAAAACTTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC    4500
LCMV-P91_LP         AAGATCATGAGAAAACTTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC    4500
LCMV-P52-1_LP       AAGATCATGAGAAAACTTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC    4500
LCMV-P52-1.3_LP     AAGATCATGAGAAAACTTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC    4500
LCMV-P52-2.1_LP     AAGATCATGAGAAAACTTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC    4500
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LCMV-WE_LP          GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA    4560
LCMV-P42_LP         GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA    4560
LCMV-P52_LP         GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA    4560
LCMV-P91_LP         GAGGAATTTTTTCTAGACCTCTTCAACACCCAAAACGAACACCCCATCCTTCAATTGGGA    4560
LCMV-P52-1_LP       GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAATGAAAGAGGCCATCCTTCAATTGGGA    4560
LCMV-P52-1.3_LP     GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA    4560
LCMV-P52-2.1_LP     GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA    4560
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LCMV-WE_LP          GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG    4620
LCMV-P42_LP         GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG    4620
LCMV-P52_LP         GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG    4620
LCMV-P91_LP         GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG    4620
LCMV-P52-1_LP       GAGATTCTTGGTCTTGAGGATGATCTGAATGAGTTGGCAAGCATCAATTGGTTGAATCTG    4620
LCMV-P52-1.3_LP     GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG    4620
LCMV-P52-2.1_LP     GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG    4620
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LCMV-WE_LP          AATGAAATGTTCCCATTGAGGATGGTTCTGAGACAAAAAGTGGTTTACCCATCAGTAATG    4680
LCMV-P42_LP         AATGAAATGTTCCCATTGAGGATGGTTCTGAGACAAAAAGTGGTTTACCCATCAGTRATG    4680
LCMV-P52_LP         AATGAAATGTTCCCATTGAGGATGGTTCTGAGACAAAAAGTGGTTTACCCATCAGTAATG    4680
LCMV-P91_LP         AATGAAATGTTCCCATTGAGGATGGTTCTGAGACAAAAAGTGGTTTACCCATCAGTAATG    4680
LCMV-P52-1_LP       AATGAAATGTTCCCATTGAGGATGGTTCTGAGACAAAAAGTGGTTTACCCATCAGTAATG    4680
LCMV-P52-1.3_LP     AATGAAATGTTCCCATTGAGGATGGTTCTGAGACAAAAAGTGGTTTACCCATCAGTAATG    4680
LCMV-P52-2.1_LP     AATGAAATGTTCCCATTGAGGATGGTTCTGAGACAAAAAGTGGTTTACCCATCAGTAATG    4680
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LCMV-WE_LP          ACCTTTCAAGAGGAAAAGATCCCCTCATTGATTAAAACACTCCAAAATAAGCTTTGTAGT    4740
LCMV-P42_LP         ACCTTTCAAGAGGAAAAGATCCCCTCATTGATTAAAACACTCCAAAATAAGCTTTGTAGT    4740
LCMV-P52_LP         ACCTTTCAAGAGGAAAAGATCCCCTCATTGATTAAAACACTCCAAAATAAGCTTTGTAGT    4740
LCMV-P91_LP         ACCTTTCAAGAGGAAAAGATCCCCTCATTGATTAAAACACTCCAAAATAAGCTTTGTAGT    4740
LCMV-P52-1_LP       ACCTTTCAAGAGGAAAAGATCCCCTCATTGATTAAAACACTCCAAAATAAGCTTTGTAGT    4740
LCMV-P52-1.3_LP     ACCTTTCAAGAGGAAAAGATCCCCTCATTGATTAAAACACTCCAAAATAAGCTTTGTAGT    4740
LCMV-P52-2.1_LP     ACCTTTCAAGAGGAAAAGATCCCCTCATTGATTAAAACACTCCAAAATAAGCTTTGTAGT    4740
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LCMV-WE_LP          AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG    4800
LCMV-P42_LP         AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG    4800
LCMV-P52_LP         AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG    4800
LCMV-P91_LP         AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG    4800
LCMV-P52-1_LP       AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG    4800
LCMV-P52-1.3_LP     AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG    4800
LCMV-P52-2.1_LP     AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG    4800
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LCMV-WE_LP          AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA    4860
LCMV-P42_LP         AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA    4860
LCMV-P52_LP         AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA    4860
LCMV-P91_LP         AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA    4860
LCMV-P52-1_LP       AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA    4860
LCMV-P52-1.3_LP     AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTACGTGTGTGACA    4860
LCMV-P52-2.1_LP     AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA    4860
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LCMV-WE_LP          AATAAAAACAGGGAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA    4920
LCMV-P42_LP         AATAAAAACAGGGAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA    4920
LCMV-P52_LP         AATAAAAACAGGGAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA    4920
LCMV-P91_LP         AATAAAAACAGGGAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA    4920
LCMV-P52-1_LP       AATAAAAACAGGGAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA    4920
LCMV-P52-1.3_LP     AATAAAAACAGGGAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA    4920
LCMV-P52-2.1_LP     AATAAAAACAGGGAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA    4920
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LCMV-WE_LP          CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA    4980
LCMV-P42_LP         CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA    4980
LCMV-P52_LP         CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA    4980
LCMV-P91_LP         CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA    4980
LCMV-P52-1_LP       CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA    4980
LCMV-P52-1.3_LP     CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA    4980
LCMV-P52-2.1_LP     CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA    4980
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LCMV-WE_LP          CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCCTTCTCTGGGACTACATT    5040
LCMV-P42_LP         CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCCTTCTCTGGGACTACATT    5040
LCMV-P52_LP         CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCCTTCTCTGGGACTACATT    5040
LCMV-P91_LP         CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCCTTCTCTGGGACTACATT    5040
LCMV-P52-1_LP       CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCCTTCTCTGGGACTACATT    5040
LCMV-P52-1.3_LP     CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCCTTCTCTGGGACTACATT    5040
LCMV-P52-2.1_LP     CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCCTTCTCTGGGACTACATT    5040
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LCMV-WE_LP          TGCATCTCATTGAGCAACTCTTTTGAGCTGGGTGTTTGGGTTTTAGCAGAACCTGTGAAA    5100
LCMV-P42_LP         TGCATCTCATTGAGCAACTCTTTTGAGCTGGGTGTTTGGGTTTTAGCAGAACCTGTGAAA    5100
LCMV-P52_LP         TGCATCTCATTGAGCAACTCTTTTGAGCTGGGTGTTTGGGTTTTAGCAGAACCTGTGAAA    5100
LCMV-P91_LP         TGCATCTCATTGAGCAACTCTTTTGAGCTGGGTGTTTGGGTTTTAGCAGAACCTGTGAAA    5100
LCMV-P52-1_LP       TGCATCTCATTGAGCAACTCTTTTGAGCTGGGTGTTTGGGTTTTAGCAGAACCTGTGAAA    5100
LCMV-P52-1.3_LP     TGCATCTCATTGAGCAACTCTTTTGAGCTGGGTGTTTGGGTTTTAGCAGAACCTGTGAAA    5100
LCMV-P52-2.1_LP     TGCATCTCATTGAGCAACTCTTTTGAGCTGGGTGTTTGGGTTTTAGCAGAACCTGTGAAA    5100
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LCMV-WE_LP          GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTGATTATGTAGCAAGA    5160
LCMV-P42_LP         GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTGATTATGTAGCAAGA    5160
LCMV-P52_LP         GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTGATTATGTAGCAAGA    5160
LCMV-P91_LP         GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTGATTATGTAGCAAGA    5160
LCMV-P52-1_LP       GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTGATTATGTAGCAAGA    5160
LCMV-P52-1.3_LP     GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTGATTATGTAGCAAGA    5160
LCMV-P52-2.1_LP     GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTGATTATGTAGCAAGA    5160
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LCMV-WE_LP          AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCAATCT    5220
LCMV-P42_LP         AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCAATCT    5220
LCMV-P52_LP         AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCAATCT    5220
LCMV-P91_LP         AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCAATCT    5220
LCMV-P52-1_LP       AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCAATCT    5220
LCMV-P52-1.3_LP     AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCAATCT    5220
LCMV-P52-2.1_LP     AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCAATCT    5220
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LCMV-WE_LP        GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTCTGATGTG    5280
LCMV-P42_LP       GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTTTGATGTG    5280
LCMV-P52_LP       GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTCTGATGTG    5280
LCMV-P91_LP       GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTCTGATGTG    5280
LCMV-P52-1_LP     GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTCTGATGTG    5280
LCMV-P52-1.3_LP   GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTCTGATGTG    5280
LCMV-P52-2.1_LP   GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTCTGATGTG    5280
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LCMV-WE_LP        AGCTCAAAAAATATGAGATGGAGTCCCAGCATTAAATTCCTTGACCTTTGTGTGCTGATT    5340
LCMV-P42_LP       AGCTCAAAAAATATGAGATGGAGTCCCAGCATTAAATTCCTTGACCTTTGTGTGCTGATT    5340
LCMV-P52_LP       AGCTCAAAAAATATGAGATGGAGTCCCAGCATTAAATTCCTTGACCTTTGTGTGCTGATT    5340
LCMV-P91_LP       AGCTCAAAAAATATGAGATGGAGTCCCAGCATTAAATTCCTTGACCTTTGTGTGCTGATT    5340
LCMV-P52-1_LP     AGCTCAAAAAATATGAGATGGAGTCCCAGCATTAAATTCCTTGACCTTTGTGTGCTGATT    5340
LCMV-P52-1.3_LP   AGCTCAAAAAATATGAGATGGAGTCCCAGCATTAAATTCCTTGACCTTTGTGTGCTGATT    5340
LCMV-P52-2.1_LP   AGCTCAAAAAATATGAGATGGAGTCCCAGCATTAAATTCCTTGACCTTTGTGTGCTGATT    5340
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LCMV-WE_LP        GACATCAACTCAGAGTCTTTGTCACTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA    5400
LCMV-P42_LP       GACATCAACTCAGAGTCTTTGTCACTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA    5400
LCMV-P52_LP       GACATCAACTCAGAGTCTTTGTCACTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA    5400
LCMV-P91_LP       GACATCAACTCAGAGTCTTTGTCACTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA    5400
LCMV-P52-1_LP     GACATCAACTCAGAGTCTTTGTCACTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA    5400
LCMV-P52-1.3_LP   GACATCAACTCAGAGTCTTTGTCACTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA    5400
LCMV-P52-2.1_LP   GACATCAACTCAGAGTCTTTGTCACTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA    5400
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LCMV-WE_LP        CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA    5460
LCMV-P42_LP       CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA    5460
LCMV-P52_LP       CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA    5460
LCMV-P91_LP       CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA    5460
LCMV-P52-1_LP     CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA    5460
LCMV-P52-1.3_LP   CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA    5460
LCMV-P52-2.1_LP   CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA    5460
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LCMV-WE_LP        GTTGATGAATTTGTTGTCAGCACAAGGGATGTCTGCAAGAACTTTTTGAAGCAAGTGTAT    5520
LCMV-P42_LP       GTTGATGAATTTGTTGTCAGCACAAGGGATGTCTGCAAGAACTTTTTGAAGCAAGTGTAT    5520
LCMV-P52_LP       GTTGATGAATTTGTTGTCAGCACAAGGGATGTCTGCAAGAACTTTTTGAAGCAAGTGTAT    5520
LCMV-P91_LP       GTTGATGAATTTGTTGTCAGCACAAGGGATGTCTGCAAGAACTTTTTGAAGCAAGTGTAT    5520
LCMV-P52-1_LP     GTTGATGAATTTGTTGTCAGCACAAGGGATGTCTGCAAGAACTTTTTGAAGCAAGTGTAT    5520
LCMV-P52-1.3_LP   GTTGATGAATTTGTTGTCAGCACAAGGGATGTCTGCAAGAACTTTTTGAAGCAAGTGTAT    5520
LCMV-P52-2.1_LP   GTTGATGAATTTGTTGTCAGCACAAGGGATGTCTGCAAGAACTTTTTGAAGCAAGTGTAT    5520
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LCMV-WE_LP        TTCGAATCATTTGTACGAGAGTTTGTTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG    5580
LCMV-P42_LP       TTCGAATCATTTGTACGAGAGTTTGTTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG    5580
LCMV-P52_LP       TTCGAATCATTTGTACGAGAGTTTGTTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG    5580
LCMV-P91_LP       TTCGAATCATTTGTACGAGAGTTTGTTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG    5580
LCMV-P52-1_LP     TTCGAATCATTTGTACGAGAGTTTGTTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG    5580
LCMV-P52-1.3_LP   TTCGAATCATTTGTACGAGAGTTTGTTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG    5580
LCMV-P52-2.1_LP   TTCGAATCATTTGTACGAGAGTTTGTTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG    5580
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LCMV-WE_LP        TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCCTTCCAA    5640
LCMV-P42_LP       TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCCTTCCAA    5640
LCMV-P52_LP       TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCCTTCCAA    5640
LCMV-P91_LP       TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCCTTCCAA    5640
LCMV-P52-1_LP     TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCCTTCCAA    5640
LCMV-P52-1.3_LP   TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCCTTCCAA    5640
LCMV-P52-2.1_LP   TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCCTTCCAA    5640
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LCMV-WE_LP        TCATTTATTTTGAAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG    5700
LCMV-P42_LP       TCATTTATTTTGAAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG    5700
LCMV-P52_LP       TCATTTATTTTGAAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG    5700
LCMV-P91_LP       TCATTTATTTTGAAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG    5700
LCMV-P52-1_LP     TCATTTATTTTGAAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG    5700
LCMV-P52-1.3_LP   TCATTTATTTTGAAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG    5700
LCMV-P52-2.1_LP   TCATTTATTTTGAAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG    5700
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LCMV-WE_LP          CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG    5760
LCMV-P42_LP         CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG    5760
LCMV-P52_LP         CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG    5760
LCMV-P91_LP         CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG    5760
LCMV-P52-1_LP       CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG    5760
LCMV-P52-1.3_LP     CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG    5760
LCMV-P52-2.1_LP     CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG    5760
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LCMV-WE_LP          TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTTGTGGGAT    5820
LCMV-P42_LP         TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTTGTGGGAT    5820
LCMV-P52_LP         TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTTGTGGGAT    5820
LCMV-P91_LP         TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTTGTGGGAT    5820
LCMV-P52-1_LP       TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTTGTGGGAT    5820
LCMV-P52-1.3_LP     TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTTGTGGGAT    5820
LCMV-P52-2.1_LP     TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTTGTGGGAT    5820
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LCMV-WE_LP          TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC    5880
LCMV-P42_LP         TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC    5880
LCMV-P52_LP         TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC    5880
LCMV-P91_LP         TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC    5880
LCMV-P52-1_LP       TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC    5880
LCMV-P52-1.3_LP     TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC    5880
LCMV-P52-2.1_LP     TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC    5880
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LCMV-WE_LP          AACCAGAACAACACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA    5940
LCMV-P42_LP         AACCAGAACAACACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA    5940
LCMV-P52_LP         AACCAGAACAACACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA    5940
LCMV-P91_LP         AACCAGAACAACACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA    5940
LCMV-P52-1_LP       AACCAGAACAACACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA    5940
LCMV-P52-1.3_LP     AACCAGAACAACACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA    5940
LCMV-P52-2.1_LP     AACCAGAACAACACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA    5940
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LCMV-WE_LP          TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTTCTTCAAAGGTGAGGTT    6000
LCMV-P42_LP         TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTTCTTCAAAGGTGAGGTT    6000
LCMV-P52_LP         TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTCCTTCAAAGGTGAGGTT    6000
LCMV-P91_LP         TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTCCTTCAAAGGTGAGGTT    6000
LCMV-P52-1_LP       TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTTCTTCAAAGGTGAGGTT    6000
LCMV-P52-1.3_LP     TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTCCTTCAAAGGTGAGGTT    6000
LCMV-P52-2.1_LP     TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTTCTTCAAAGGTGAGGTT    6000
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LCMV-WE_LP          GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG    6060
LCMV-P42_LP         GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG    6060
LCMV-P52_LP         GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG    6060
LCMV-P91_LP         GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG    6060
LCMV-P52-1_LP       GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG    6060
LCMV-P52-1.3_LP     GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG    6060
LCMV-P52-2.1_LP     GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG    6060
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LCMV-WE_LP          AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCTTTG    6120
LCMV-P42_LP         AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCTTTG    6120
LCMV-P52_LP         AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCTTTG    6120
LCMV-P91_LP         AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCTTTG    6120
LCMV-P52-1_LP       AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCTTTG    6120
LCMV-P52-1.3_LP     AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCTTTG    6120
LCMV-P52-2.1_LP     AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCTTTG    6120
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LCMV-WE_LP          ACACTTGGTGATTCACTAGAACTTGAACTAATAGGTTCTAGAAGGATTCTGAATGAGATC    6180
LCMV-P42_LP         ACACTTGGTGATTCACTAGAACTTGAACTAATAGGTTCTAGAAGGATTCTGAATGAGATC    6180
LCMV-P52_LP         ACACTTGGTGATTCACTAGAACTTGAACTAATAGGTTCTAGAAGGATTCTGAATGAGATC    6180
LCMV-P91_LP         ACACTTGGTGATTCACTAGAACTTGAACTAATAGGTTCTAGAAGGATTCTGAATGAGATC    6180
LCMV-P52-1_LP       ACACTTGGTGATTCACTAGAACTTGAACTAATAGGTTCTAGAAGGATTCTGAATGAGATC    6180
LCMV-P52-1.3_LP     ACACTTGGTGATTCACTAGAACTTGAACTAATAGGTTCTAGAAGGATTCTGAATGAGATC    6180
LCMV-P52-2.1_LP     ACACTTGGTGATTCACTAGAACTTGAACTAATAGGTTCTAGAAGGATTCTGAATGAGATC    6180
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LCMV-WE_LP          AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG    6240
LCMV-P42_LP         AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG    6240
LCMV-P52_LP         AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG    6240
LCMV-P91_LP         AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG    6240
LCMV-P52-1_LP       AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG    6240
LCMV-P52-1.3_LP     AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG    6240
LCMV-P52-2.1_LP     AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG    6240
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LCMV-WE_LP          AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAGAATATCTCTGTGAAATTGGAGACA    6300
LCMV-P42_LP         AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAGAATATCTCTGTGAAATTGGAGACA    6300
LCMV-P52_LP         AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAGAATRTCTCTGTGAAATTGGAGACA    6300
LCMV-P91_LP         AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAGAATATCTCTGTGAAATTGGAGACA    6300
LCMV-P52-1_LP       AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAGAATATCTCTGTGAAATTGGAGACA    6300
LCMV-P52-1.3_LP     AAGGGTGCCCTCTTTCAGGGGAGGAACTTTGTTCAGAATATCTCTGTGAAATTGGAGACA    6300
LCMV-P52-2.1_LP     AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAGAATATCTCTGTGAAATTGGAGACA    6300
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LCMV-WE_LP          AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATTGGTGATGTCCTC    6360
LCMV-P42_LP         AAGGACATGAGRGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATTGGTGATGTCCTC    6360
LCMV-P52_LP         AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATTGGTGATGTCCTC    6360
LCMV-P91_LP         AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATTGGTGATGTCCTC    6360
LCMV-P52-1_LP       AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAGAAATTGGTGATGTCCTC    6360
LCMV-P52-1.3_LP     AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATTGGTGATGTCCTC    6360
LCMV-P52-2.1_LP     AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAGAAATTGGTGATGTCCTC    6360
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LCMV-WE_LP          GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT    6420
LCMV-P42_LP         GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT    6420
LCMV-P52_LP         GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT    6420
LCMV-P91_LP         GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT    6420
LCMV-P52-1_LP       GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT    6420
LCMV-P52-1.3_LP     GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT    6420
LCMV-P52-2.1_LP     GGCAGCCTCCTCCTGCACCGATTCAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT    6420
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LCMV-WE_LP          ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG    6480
LCMV-P42_LP         ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG    6480
LCMV-P52_LP         RCAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG    6480
LCMV-P91_LP         ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG    6480
LCMV-P52-1_LP       RCAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG    6480
LCMV-P52-1.3_LP     ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG    6480
LCMV-P52-2.1_LP     ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG    6480
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LCMV-WE_LP          CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA    6540
LCMV-P42_LP         CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTR    6540
LCMV-P52_LP         CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA    6540
LCMV-P91_LP         CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCARGTCAAAGAACACTGTA    6540
LCMV-P52-1_LP       CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA    6540
LCMV-P52-1.3_LP     CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA    6540
LCMV-P52-2.1_LP     CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA    6540
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LCMV-WE_LP          ATGTATGAGACAACTGCGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG    6600
LCMV-P42_LP         ATGTATGAGACAACTGCGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG    6600
LCMV-P52_LP         ATGTATGAGACAACTGCGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG    6600
LCMV-P91_LP         ATGTATGAGACAACTGCGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG    6600
LCMV-P52-1_LP       ATGTATGAGACAGCTGCGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG    6600
LCMV-P52-1.3_LP     ATGTATGAGACAACTGCGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG    6600
LCMV-P52-2.1_LP     ATGTATGAGACAACTGCGGGGCAGGTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG    6600
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LCMV-WE_LP          GCGGAGCGGGTGGCCGAGGAGATCGACTAG  6630   LCMV-WE_LP:      SEQ ID NO: 15
LCMV-P42_LP         GCGGAGCGGGTGGCCGAGGAGATCGACTAG  6630   LCMV-P42_LP:     SEQ ID NO: 23
LCMV-P52_LP         GCGGAGCGGGTGGCCGAGGAGATCGACTAG  6630   LCMV-P52_LP:     SEQ ID NO: 31
LCMV-P91_LP         GCGGAGCGGGTGGCCGAGGAGATCGACTAG  6630   LCMV-P91_LP:     SEQ ID NO: 39
LCMV-P52-1_LP       GCGGAGCGGGTGGCCGAGGAGATCGACTAG  6630   LCMV-P52-1_LP:   SEQ ID NO: 47
LCMV-P52-1.3_LP     GCGGAGCGGGTGGCCGAGGAGATCGACTAG  6630   LCMV-P52-1.3_LP: SEQ ID NO: 55
LCMV-P52-2.1_LP     GCGGAGCGGGTGGCCGAGGAGATCGACTAG  6633   LCMV-P52-2.1_LP: SEQ ID NO: 63
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Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement
Sequence Alignment: Aminoacid

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LCMV-WE_LP        MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC    60
LCMV-P42_LP       MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC    60
LCMV-P52_LP       MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC    60
LCMV-P91_LP:      MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC    60
LCMV-P52-1_LP     MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC    60
LCMV-P52-1.3_LP   MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC    60
LCMV-P52-2.1_LP   MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC    60
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LCMV-WE_LP        IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT   120
LCMV-P42_LP       IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT   120
LCMV-P52_LP       IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT   120
LCMV-P91_LP:      IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT   120
LCMV-P52-1_LP     IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT   120
LCMV-P52-1.3_LP   IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT   120
LCMV-P52-2.1_LP   IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT   120
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LCMV-WE_LP        NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE   180
LCMV-P42_LP       NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE   180
LCMV-P52_LP       NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE   180
LCMV-P91_LP:      NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE   180
LCMV-P52-1_LP     NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE   180
LCMV-P52-1.3_LP   NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE   180
LCMV-P52-2.1_LP   NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE   180
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LCMV-WE_LP        SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS   240
LCMV-P42_LP       SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS   240
LCMV-P52_LP       SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS   240
LCMV-P91_LP:      SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS   240
LCMV-P52-1_LP     SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS   240
LCMV-P52-1.3_LP   SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS   240
LCMV-P52-2.1_LP   SEYFRLCESLKTTVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFGINS   240
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LCMV-WE_LP        FFGRFRRDLLNGKLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI   300
LCMV-P42_LP       FFGRFRRDLLNGKLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI   300
LCMV-P52_LP       FFGRFRRDLLNGKLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI   300
LCMV-P91_LP:      FFGRFRRDLLNGKLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI   300
LCMV-P52-1_LP     FFGRFRRDLLNGRLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI   300
LCMV-P52-1.3_LP   FFGRFRRDLLNGKLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI   300
LCMV-P52-2.1_LP   FFGRFRRDLLNGKLKRNFQKVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI   300
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LCMV-WE_LP        TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL   360
LCMV-P42_LP       TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL   360
LCMV-P52_LP       TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL   360
LCMV-P91_LP:      TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL   360
LCMV-P52-1_LP     TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL   360
LCMV-P52-1.3_LP   TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL   360
LCMV-P52-2.1_LP   TAETHGHERGSDANTEYERLLSMLNKVKSLKLLNTRRRQLLNLDVLCLSSLIKQSISKGL   360
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LCMV-WE_LP        ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK   420
LCMV-P42_LP       ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK   420
LCMV-P52_LP       ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK   420
LCMV-P91_LP:      ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK   420
LCMV-P52-1_LP     ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK   420
LCMV-P52-1.3_LP   ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK   420
LCMV-P52-2.1_LP   ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLKNRRKSRVHKKASLDELFRVSINEFIAK   420
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LCMV-WE_LP          IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ    480
LCMV-P42_LP         IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ    480
LCMV-P52_LP         IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ    480
LCMV-P91_LP:        IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ    480
LCMV-P52-1_LP       IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ    480
LCMV-P52-1.3_LP     IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ    480
LCMV-P52-2.1_LP     IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ    480
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LCMV-WE_LP          LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH    540
LCMV-P42_LP         LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH    540
LCMV-P52_LP         LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH    540
LCMV-P91_LP:        LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH    540
LCMV-P52-1_LP       LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH    540
LCMV-P52-1.3_LP     LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH    540
LCMV-P52-2.1_LP     LRGLQSLRKLSSVCLALTNSMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEYH    540
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LCMV-WE_LP          LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK    600
LCMV-P42_LP         LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK    600
LCMV-P52_LP         LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK    600
LCMV-P91_LP:        LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK    600
LCMV-P52-1_LP       LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK    600
LCMV-P52-1.3_LP     LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK    600
LCMV-P52-2.1_LP     LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK    600
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LCMV-WE_LP          DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA    660
LCMV-P42_LP         DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA    660
LCMV-P52_LP         DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA    660
LCMV-P91_LP:        DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA    660
LCMV-P52-1_LP       DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA    660
LCMV-P52-1.3_LP     DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA    660
LCMV-P52-2.1_LP     DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKLKEDLITPA    660
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LCMV-WE_LP          EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF    720
LCMV-P42_LP         EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF    720
LCMV-P52_LP         EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF    720
LCMV-P91_LP:        EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF    720
LCMV-P52-1_LP       EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF    720
LCMV-P52-1.3_LP     EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF    720
LCMV-P52-2.1_LP     EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKFF    720
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LCMV-WE_LP          EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG    780
LCMV-P42_LP         EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG    780
LCMV-P52_LP         EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG    780
LCMV-P91_LP:        EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG    780
LCMV-P52-1_LP       EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG    780
LCMV-P52-1.3_LP     EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG    780
LCMV-P52-2.1_LP     EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG    780
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LCMV-WE_LP          TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI    840
LCMV-P42_LP         TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI    840
LCMV-P52_LP         TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI    840
LCMV-P91_LP:        TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI    840
LCMV-P52-1_LP       TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI    840
LCMV-P52-1.3_LP     TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI    840
LCMV-P52-2.1_LP     TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLLVSAVSQI    840
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LCMV-WE_LP          TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS    900
LCMV-P42_LP         TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS    900
LCMV-P52_LP         TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS    900
LCMV-P91_LP:        TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS    900
LCMV-P52-1_LP       TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS    900
LCMV-P52-1.3_LP     TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS    900
LCMV-P52-2.1_LP     TEGFMRKQKYKLRHSDYEYKVSKLVSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS    900
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LCMV-WE_LP          LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV    960
LCMV-P42_LP         LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV    960
LCMV-P52_LP         LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV    960
LCMV-P91_LP:        LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV    960
LCMV-P52-1_LP       LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV    960
LCMV-P52-1.3_LP     LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV    960
LCMV-P52-2.1_LP     LEDKVSSTITRYNRGTRLNEGQGEGEFKNTKGLHHLQIILSGKRAYLRKVILSEISFHLV    960
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LCMV-WE_LP          EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS    1020
LCMV-P42_LP         EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS    1020
LCMV-P52_LP         EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS    1020
LCMV-P91_LP:        EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS    1020
LCMV-P52-1_LP       EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS    1020
LCMV-P52-1.3_LP     EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS    1020
LCMV-P52-2.1_LP     EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS    1020
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LCMV-WE_LP          CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC    1080
LCMV-P42_LP         CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC    1080
LCMV-P52_LP         CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC    1080
LCMV-P91_LP:        CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC    1080
LCMV-P52-1_LP       CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC    1080
LCMV-P52-1.3_LP     CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC    1080
LCMV-P52-2.1_LP     CMKMILLQMNANAYSGKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTKC    1080
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LCMV-WE_LP          MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE    1140
LCMV-P42_LP         MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE    1140
LCMV-P52_LP         MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE    1140
LCMV-P91_LP:        MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE    1140
LCMV-P52-1_LP       MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE    1140
LCMV-P52-1.3_LP     MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE    1140
LCMV-P52-2.1_LP     MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE    1140
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LCMV-WE_LP          DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ    1200
LCMV-P42_LP         DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ    1200
LCMV-P52_LP         DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ    1200
LCMV-P91_LP:        DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ    1200
LCMV-P52-1_LP       DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ    1200
LCMV-P52-1.3_LP     DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ    1200
LCMV-P52-2.1_LP     DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ    1200
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LCMV-WE_LP          NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE    1260
LCMV-P42_LP         NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE    1260
LCMV-P52_LP         NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE    1260
LCMV-P91_LP:        NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE    1260
LCMV-P52-1_LP       NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE    1260
LCMV-P52-1.3_LP     NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE    1260
LCMV-P52-2.1_LP     NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVPFPVVNAMMKSYVKSKLKLLKGSGTTVTE    1260
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LCMV-WE_LP          RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS    1320
LCMV-P42_LP         RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS    1320
LCMV-P52_LP         RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS    1320
LCMV-P91_LP:        RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS    1320
LCMV-P52-1_LP       RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS    1320
LCMV-P52-1.3_LP     RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS    1320
LCMV-P52-2.1_LP     RIFREYFEMGVVPSHISSLIDMGQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS    1320
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LCMV-WE_LP          DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW    1380
LCMV-P42_LP         DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW    1380
LCMV-P52_LP         DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW    1380
LCMV-P91_LP:        DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW    1380
LCMV-P52-1_LP       DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW    1380
LCMV-P52-1.3_LP     DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW    1380
LCMV-P52-2.1_LP     DDQITLFDKRLSDLVDSDPEEVLVLLEFHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW    1380
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LCMV-WE_LP          GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY    1440
LCMV-P42_LP         GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY    1440
LCMV-P52_LP         GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY    1440
LCMV-P91_LP:        GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY    1440
LCMV-P52-1_LP       GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY    1440
LCMV-P52-1.3_LP     GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY    1440
LCMV-P52-2.1_LP     GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY    1440
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LCMV-WE_LP          ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN    1500
LCMV-P42_LP         ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN    1500
LCMV-P52_LP         ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN    1500
LCMV-P91_LP:        ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN    1500
LCMV-P52-1_LP       ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN    1500
LCMV-P52-1.3_LP     ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN    1500
LCMV-P52-2.1_LP     ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN    1500
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LCMV-WE_LP          EEFFLDLFNREKKEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM    1560
LCMV-P42_LP         EEFFLDLFNREKKEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM    1560
LCMV-P52_LP         EEFFLDLFNREKKEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM    1560
LCMV-P91_LP:        EEFFLDLFNREKEEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM    1560
LCMV-P52-1_LP       EEFFLDLFNREMKEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM    1560
LCMV-P52-1.3_LP     EEFFLDLFNREKKEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM    1560
LCMV-P52-2.1_LP     EEFFLDLFNREKKEAILQLGEILGLEDDLNELASINWLNLNEMFPLRMVLRQKVVYPSVM    1560
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LCMV-WE_LP          TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR    1620
LCMV-P42_LP         TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR    1620
LCMV-P52_LP         TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR    1620
LCMV-P91_LP:        TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR    1620
LCMV-P52-1_LP       TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR    1620
LCMV-P52-1.3_LP     TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR    1620
LCMV-P52-2.1_LP     TFQEEKIPSLIKTLQNKLCSKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR    1620
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LCMV-WE_LP          NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI    1680
LCMV-P42_LP         NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI    1680
LCMV-P52_LP         NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI    1680
LCMV-P91_LP:        NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI    1680
LCMV-P52-1_LP       NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI    1680
LCMV-P52-1.3_LP     NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI    1680
LCMV-P52-2.1_LP     NKNRENMYIRKVLEDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI    1680
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LCMV-WE_LP          CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS    1740
LCMV-P42_LP         CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS    1740
LCMV-P52_LP         CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS    1740
LCMV-P91_LP:        CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS    1740
LCMV-P52-1_LP       CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS    1740
LCMV-P52-1.3_LP     CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS    1740
LCMV-P52-2.1_LP     CISLSNSFELGVWVLAEPVKGKNESNSAVRHLNPCDYVARKPESSRLLEDKVSLNHVIQS    1740
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LCMV-WE_LP          VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE    1800
LCMV-P42_LP         VRRLYPKIFEDQLLPFMEDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE    1800
LCMV-P52_LP         VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE    1800
LCMV-P91_LP:        VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE    1800
LCMV-P52-1_LP       VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE    1800
LCMV-P52-1.3_LP     VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE    1800
LCMV-P52-2.1_LP     VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLSLISHVVKWKRDE    1800
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LCMV-WE_LP          HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW    1860
LCMV-P42_LP         HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW    1860
LCMV-P52_LP         HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW    1860
LCMV-P91_LP:        HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW    1860
LCMV-P52-1_LP       HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW    1860
LCMV-P52-1.3_LP     HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW    1860
LCMV-P52-2.1_LP     HYTVLFSDLVNSHQRSDSSLVDEFVVSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW    1860
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LCMV-WE_LP          FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM    1920
LCMV-P42_LP         FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM    1920
LCMV-P52_LP         FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM    1920
LCMV-P91_LP:        FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM    1920
LCMV-P52-1_LP       FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM    1920
LCMV-P52-1.3_LP     FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM    1920
LCMV-P52-2.1_LP     FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM    1920
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LCMV-WE_LP          LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ    1980
LCMV-P42_LP         LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ    1980
LCMV-P52_LP         LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ    1980
LCMV-P91_LP:        LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ    1980
LCMV-P52-1_LP       LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ    1980
LCMV-P52-1.3_LP     LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ    1980
LCMV-P52-2.1_LP     LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ    1980
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LCMV-WE_LP          LQSPGVADYLSCSHFFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL    2040
LCMV-P42_LP         LQSPGVADYLSCSHFFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL    2040
LCMV-P52_LP         LQSPGVADYLSCSHSFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL    2040
LCMV-P91_LP:        LQSPGVADYLSCSHSFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL    2040
LCMV-P52-1_LP       LQSPGVADYLSCSHFFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL    2040
LCMV-P52-1.3_LP     LQSPGVADYLSCSHSFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL    2040
LCMV-P52-2.1_LP     LQSPGVADYLSCSHFFKGEVDRRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL    2040
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                                                                      X=I/V
LCMV-WE_LP          TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNISVKLET    2100
LCMV-P42_LP         TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNISVKLET    2100
LCMV-P52_LP         TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNXSVKLET    2100
LCMV-P91_LP:        TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNISVKLET    2100
LCMV-P52-1_LP       TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNISVKLET    2100
LCMV-P52-1.3_LP     TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNISVKLET    2100
LCMV-P52-2.1_LP     TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKGALFEGRNFVQNISVKLET    2100
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                                                        X=T/A
LCMV-WE_LP          KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMESEISTVLQELCMDRSVMLTPLSFV    2160
LCMV-P42_LP         KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMESEISTVLQELCMDRSVMLTPLSFV    2160
LCMV-P52_LP         KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMESEISXVLQELCMDRSVMLTPLSFV    2160
LCMV-P91_LP:        KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMESEISTVLQELCMDRSVMLTPLSFV    2160
LCMV-P52-1_LP       KDMRVFLAELEGCGEIGDVLGSLLLHRFRTGEHLMESEISTVLQELCMDRSVMLTPLSFV    2160
LCMV-P52-1.3_LP     KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMESEISTVLQELCMDRSVMLTPLSFV    2160
LCMV-P52-2.1_LP     KDMRVFLAELEGCGEIGDVLGSLLLHRFRTGEHLMESEISTVLQELCMDRSVMLTPLSFV    2160
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                                X=R/K
LCMV-WE_LP          PDWFTFRDCRLCFSRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID      2209
LCMV-P42_LP         PDWFTFRDCRLCFSRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID      2209
LCMV-P52_LP         PDWFTFRDCRLCFSRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID      2209
LCMV-P91_LP:        PDWFTFRDCRLCFSXSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID      2209
LCMV-P52-1_LP       PDWFTFRDCRLCFSRSKNTVMYETAGGRFRLKGKSCDDWLAERVAEEID      2209
LCMV-P52-1.3_LP     PDWFTFRDCRLCFSRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID      2209
LCMV-P52-2.1_LP     PDWFTFRDCRLCFSRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID      2209
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LCMV-WE_LP:      SEQ ID NO: 16
LCMV-P42_LP:     SEQ ID NO: 24
LCMV-P52_LP:     SEQ ID NO: 32
LCMV-P91_LP:     SEQ ID NO: 40
LCMV-P52-1_LP:   SEQ ID NO: 48
LCMV-P52-1.3_LP: SEQ ID NO: 56
LCMV-P52-2.1_LP: SEQ ID NO: 64
LCMV-P52-1.3_LP: SEQ ID NO: 56
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SEQUENCE LISTING

<110> Abalos Therapeutics GmbH

<120> Method for producing an antitumoral arenavirus as well as arenavirus mutants

<130> VIR16633PCT

<150> DE 10 2018 215 551.8

<151> 2018-09-12

<160> 64

<170> PatentIn version 3.5

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<213> Lymphocytic choriomeningitis virus

<220><221> MISC_FEATURE

<223> Lymphocytic choriomeningitis virus Mutant p52 Glycoprotein; ssrna ambisense-strand viruses; arenaviridae; arenavirus; old world

arenaviruses

<400> 1

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

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Trp Met Ile Leu Ala Ala Glu Leu Lys Cys Phe Gly Asn Thr Ala Val

290 295 300

Ala Lys Cys Asn Val Asn His Asp Glu Glu Phe Cys Asp Met Leu Arg

305 310 315 320

Leu Ile Asp Tyr Asn Lys Ala Ala Leu Ser Lys Phe Lys Gln Asp Val

325 330 335

Glu Ser Ala Leu His Val Phe Lys Thr Thr Val Asn Ser Leu Ile Ser

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Asp Gln Leu Leu Met Arg Asn His Leu Arg Asp Leu Met Gly Val Pro

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Asn Glu Thr His Phe Ser Asp Gln Ile Glu Gln Glu Ala Asp Asn Met

405 410 415

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

420 425 430

Pro Leu Ala Leu Met Asp Leu Leu Met Phe Ser Thr Ser Ala Tyr Leu

435 440 445

Ile Ser Ile Phe Leu His Leu Val Lys Ile Pro Thr His Arg His Ile

450 455 460

Lys Gly Gly Ser Cys Pro Lys Pro His Arg Leu Thr Asn Lys Gly Ile
465 470 475 480
Cys Ser Cys Gly Ala Phe Lys Val Pro Gly Val Lys Thr Ile Trp Lys
485 490 495
Arg Arg

<210> 2
<211> 1497
<212> DNA
<213> Lymphocytic choriomeningitis virus
<220><221> MISC_FEATURE

<223> Lymphocytic choriomeningitis virus Mutant p52 Glycoprotein; ssrna ambisense-strand viruses; arenaviridae; arenavirus; old world arenaviruses
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tgtgggatat tagcactggt cagcttcctt tttttggctg gtaggtcctg tggcatgtac 180
ggccttaatg gtcccgacat ctataaaggg gtttaccagt tcaaatcagt ggagtttgat 240
atgtctcact taaatctgac gatgcccaat gcgtgctcag ccaacaactc tcatcactac 300

atcagtatgg gaagctctgg actggagcta actttcacta acgactccat ccttaatcac 360
aatttttgca acttaacctc cgctttcaac aaaaagactt ttgaccatac actcatgagt 420
atagtctcga gtctgcacct cagtattaga gggaattcca accacaaagc agtgtcttgt 480
gattttaaca atggcatcac cattcaatac aacttgtcat tttcggaccc acagagcgct 540
atgagccagt gttggacttt cagaggtaga gtcttggaca tgtttagaac tgcctttgga 600
ggaaaataca tgagaagtgg ctggggctgg gcaggttcag atggcaagac cacttggtgc 660
agccaaacaa gctatcagta cctaatcata caaaacagga cttgggaaaa ccactgtaga 720

tatgcaggcc cttttgggat gtctagaatc ctctttgctc aggaaaagac aaagtttctc 780
actaggagac ttgcaggcac attcacctgg accctgtcag actcctcagg agtagaaaat 840
ccaggtggtt attgcctgac caaatggatg atccttgctg cagagctcaa atgttttggg 900
aatacagctg ttgcaaaatg taatgtcaat catgatgaag agttctgtga catgctacga 960
ctaattgatt acaacaaggc cgccctgagt aagttcaagc aagatgtaga gtctgccttg 1020

catgtattca aaacaacagt aaattctctg atttccgatc agctgttgat gaggaatcat 1080

ctaagagatc taatgggggt accatactgt aattactcaa agttctggta tctggaacat 1140

gctaagactg gtgagactag tgtacccaag tgctggcttg tcactaatgg ctcctacttg 1200

aatgagaccc actttagtga tcaaatcgaa caagaagcag ataacatgat cacagagatg 1260

ttgaggaagg actacataaa aagacaaggg agtactcctt tagccttaat ggatcttttg 1320

atgttttcaa catcagcata tctaatcagc atctttctgc atcttgtgaa gataccaaca 1380

catagacaca taaagggcgg ttcatgtcca aagccacacc gcttgaccaa caaggggatc 1440

tgtagttgtg gtgcattcaa ggtgcctggt gtaaaaacta tctggaaaag acgctga 1497

<210> 3

<211> 498

<212> PRT

<213> Lymphocytic choriomeningitis virus

<220><221> MISC_FEATURE

<223> Lymphocytic choriomeningitis virus Mutant p42 Glycoprotein; ssrna ambisense-strand viruses; arenaviridae; arenavirus; old world arenaviruses

<400> 3

Met Gly Gln Ile Val Thr Met Phe Glu Ala Leu Pro His Ile Ile Asp

1 5 10 15

Glu Val Ile Asn Ile Val Ile Ile Val Leu Ile Ile Ile Thr Ser Ile

20 25 30

Lys Ala Val Tyr Asn Phe Ala Thr Cys Gly Ile Leu Ala Leu Val Ser

35 40 45

Phe Leu Phe Leu Ala Gly Arg Ser Cys Gly Met Tyr Gly Leu Asn Gly

50 55 60

Pro Asp Ile Tyr Lys Gly Val Tyr Gln Phe Lys Ser Val Glu Phe Asp

65 70 75 80

Met Ser His Leu Asn Leu Thr Met Pro Asn Ala Cys Ser Ala Asn Asn

85 90 95

Ser His His Tyr Ile Ser Met Gly Ser Ser Gly Leu Glu Leu Thr Phe

100 105 110

Thr Asn Asp Ser Ile Leu Asn His Asn Phe Cys Asn Leu Thr Ser Ala
115 120 125
Phe Asn Lys Lys Thr Phe Asp His Thr Leu Met Ser Ile Val Ser Ser
130 135 140
Leu His Leu Ser Ile Arg Gly Asn Ser Asn His Lys Ala Val Ser Cys
145 150 155 160
Asp Phe Asn Asn Gly Ile Thr Ile Gln Tyr Asn Leu Ser Phe Ser Asp

165 170 175
Pro Gln Ser Ala Met Ser Gln Cys Arg Thr Phe Arg Gly Arg Val Leu
180 185 190
Asp Met Phe Arg Thr Ala Phe Gly Gly Lys Tyr Met Arg Ser Gly Trp
195 200 205
Gly Trp Ala Gly Ser Asp Gly Lys Thr Thr Trp Cys Ser Gln Thr Ser
210 215 220
Tyr Gln Tyr Leu Ile Ile Gln Asn Arg Thr Trp Glu Asn His Cys Arg

225 230 235 240
Tyr Ala Gly Pro Phe Gly Met Ser Arg Ile Leu Phe Ala Gln Glu Lys
245 250 255
Thr Lys Phe Leu Thr Arg Arg Leu Ala Gly Thr Phe Thr Trp Thr Leu
260 265 270
Ser Asp Ser Ser Gly Val Glu Asn Pro Gly Gly Tyr Cys Leu Thr Lys
275 280 285
Trp Met Ile Leu Ala Ala Glu Leu Lys Cys Phe Gly Asn Thr Ala Val

290 295 300
Ala Lys Cys Asn Val Asn His Asp Glu Glu Phe Cys Asp Met Leu Arg
305 310 315 320
Leu Ile Asp Tyr Asn Lys Ala Ala Leu Ser Lys Phe Lys Gln Asp Val
325 330 335
Glu Ser Ala Leu His Val Phe Lys Thr Thr Val Asn Ser Leu Ile Ser
340 345 350
Asp Gln Leu Leu Met Arg Asn His Leu Arg Asp Leu Met Gly Val Pro

355 360 365

Tyr Cys Asn Tyr Ser Lys Phe Trp Tyr Leu Glu His Ala Lys Thr Gly

370 375 380

Glu Thr Ser Val Pro Lys Cys Trp Leu Val Thr Asn Gly Ser Tyr Leu

385 390 395 400

Asn Glu Thr His Phe Ser Asp Gln Ile Glu Gln Glu Ala Asp Asn Met

405 410 415

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

420 425 430

Pro Leu Ala Leu Met Asp Leu Leu Met Phe Ser Thr Ser Ala Tyr Leu

435 440 445

Ile Ser Ile Phe Leu His Leu Val Lys Ile Pro Thr His Arg His Ile

450 455 460

Lys Gly Gly Ser Cys Pro Lys Pro His Arg Leu Thr Asn Lys Gly Ile

465 470 475 480

Cys Ser Cys Gly Ala Phe Lys Val Pro Gly Val Lys Thr Ile Trp Lys

485 490 495

Arg Arg

<210> 4

<211> 1497

<212> DNA

<213> Lymphocytic choriomeningitis virus

<220><221> MISC_FEATURE

<223> Lymphocytic choriomeningitis virus Mutant p42 Glycoprotein; ssrna ambisense-strand viruses; arenaviridae; arenavirus; old world arenaviruses

<400> 4

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attgtcatta ttgtgctcat tataatcacg agcatcaaag ctgtgtacaa tttcgccacc 120

tgtgggatat tagcactggt cagcttcctt tttttggctg gtaggtcctg tggcatgtac 180

ggccttaatg gtcccgacat ctataaaggg gtttaccagt tcaaatcagt ggagtttgat 240

atgtctcact taaatctgac gatgcccaat gcgtgctcag ccaacaactc tcatcactac 300

atcagtatgg gaagctctgg actggagcta actttcacta acgactccat ccttaatcac 360

aatttttgca acttaacctc cgctttcaac aaaaagactt ttgaccatac actcatgagt 420

atagtctcga gtctgcacct cagtattaga gggaattcca accacaaagc agtgtcttgt 480

gattttaaca atggcatcac cattcaatac aacttgtcat tttcggaccc acagagcgct 540

atgagccagt gtaggacttt cagaggtaga gtcttggaca tgtttagaac tgcctttgga 600

ggaaaataca tgagaagtgg ctggggctgg gcaggttcag atggcaagac cacttggtgc 660

agccaaacaa gctatcagta cctaatcata caaaacagga cttgggaaaa ccactgtaga 720

tatgcaggcc cttttgggat gtctagaatc ctctttgctc aggaaaagac aaagtttctc 780

actaggagac ttgcaggcac attcacctgg accctgtcag actcctcagg agtagaaaat 840

ccaggtggtt attgcctgac caaatggatg atccttgctg cagagctcaa atgttttggg 900

aatacagctg ttgcaaaatg taatgtcaat catgatgaag agttctgtga catgctacga 960

ctaattgatt acaacaaggc cgccctgagt aagttcaagc aagatgtaga gtctgccttg 1020

catgtattca aaacaacagt aaattctctg atttccgatc agctgttgat gaggaatcat 1080

ctaagagatc taatgggggt accatactgt aattactcaa agttctggta tctggaacat 1140

gctaagactg gtgagactag tgtacccaag tgctggcttg tcactaatgg ctcctacttg 1200

aatgagaccc actttagtga tcaaatcgaa caagaagcag ataacatgat cacagagatg 1260

ttgaggaagg actacataaa aagacaaggg agtactcctt tagccttaat ggatcttttg 1320

atgttttcaa catcagcata tctaatcagc atctttctgc atcttgtgaa gataccaaca 1380

catagacaca taaagggcgg ttcatgtcca aagccacacc gcttgaccaa caaggggatc 1440

tgtagttgtg gtgcattcaa ggtgcctggt gtaaaaacta tctggaaaag acgctga 1497

<210> 5

<211> 2209

<212> PRT

<213> Lymphocytic choriomeningitis virus

<220><221> MISC_FEATURE

<223> Lymphocytic choriomeningitis virus Mutant L-Protein; ssrna ambisense-strand viruses; arenaviridae; arenavirus; old world arenaviruses

<400> 5

Met Asp Glu Thr Ile Ala Asp Leu Arg Glu Leu Cys Leu Asn Tyr Ile

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Glu Gln Asp Glu Arg Leu Ser Arg Gln Lys Leu Asn Phe Leu Gly Gln
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Arg Glu Pro Arg Met Val Leu Ile Glu Gly Leu Lys Leu Leu Ser Arg
35 40 45
Cys Ile Glu Ile Asp Ser Ala Asp Lys Ser Gly Cys Ile His Asn His
50 55 60
Asp Asp Lys Ser Val Glu Thr Ile Leu Ile Asp Ser Gly Ile Val Cys
65 70 75 80

Pro Gly Leu Pro Leu Ile Ile Pro Asp Gly Tyr Lys Leu Ile Asp Asn
85 90 95
Ser Leu Ile Leu Leu Glu Cys Phe Val Arg Ser Thr Pro Ala Ser Phe
100 105 110
Glu Lys Lys Phe Ile Glu Asp Thr Asn Lys Leu Ala Cys Ile Lys Glu
115 120 125
Asp Leu Ala Val Ala Gly Ile Thr Leu Val Pro Ile Val Asp Gly Arg
130 135 140

Cys Asp Tyr Asp Asn Ser Phe Met Pro Glu Trp Val Asn Phe Lys Phe
145 150 155 160
Arg Asp Leu Leu Phe Lys Leu Leu Glu Tyr Ser Ser Gln Asp Glu Lys
165 170 175
Val Phe Glu Glu Ser Glu Tyr Phe Arg Leu Cys Glu Ser Leu Lys Thr
180 185 190
Thr Val Asp Lys Arg Ser Gly Met Asp Ser Met Lys Ile Leu Lys Asp
195 200 205

Ala Arg Ser Phe His Asn Asp Glu Ile Met Lys Met Cys His Asp Gly
210 215 220
Val Asn Pro Asn Met Ser Cys Asp Asp Val Val Phe Gly Ile Asn Ser
225 230 235 240
Phe Phe Gly Arg Phe Arg Arg Asp Leu Leu Asn Gly Lys Leu Lys Arg
245 250 255

Asn Phe Gln Lys Val Ser Pro Gly Gly Leu Ile Lys Glu Phe Ser Glu
260 265 270

Leu Tyr Glu Thr Leu Thr Asp Asn Asp Asp Ile Leu Met Leu Ser Lys
275 280 285
Glu Ala Val Glu Ser Cys Pro Leu Met Arg Phe Ile Thr Ala Glu Thr
290 295 300
His Gly His Glu Arg Gly Ser Asp Ala Asn Thr Glu Tyr Glu Arg Leu
305 310 315 320
Leu Ser Met Leu Asn Lys Val Lys Ser Leu Lys Leu Leu Asn Thr Arg
325 330 335

Arg Arg Gln Leu Leu Asn Leu Asp Val Leu Cys Leu Ser Ser Leu Ile
340 345 350
Lys Gln Ser Ile Ser Lys Gly Leu Glu Asn Asp Lys His Trp Val Gly
355 360 365
Cys Cys Tyr Ser Ser Val Asn Asp Arg Leu Val Ser Leu Gln Ser Thr
370 375 380
Lys Glu Glu Phe Met Arg Leu Leu Lys Asn Arg Arg Lys Ser Arg Val
385 390 395 400

His Lys Lys Ala Ser Leu Asp Glu Leu Phe Arg Val Ser Ile Asn Glu
405 410 415
Phe Ile Ala Lys Ile Gln Lys Cys Leu Ser Thr Val Gly Leu Ser Phe
420 425 430
Glu His Tyr Gly Leu Ser Glu Cys Leu Val Gln Glu Cys His Ile Pro
435 440 445
Phe Ala Glu Phe Glu Asn Phe Met Arg Ala Gly Thr His Pro Val Met
450 455 460

His Tyr Thr Lys Phe Glu Asp Tyr Thr Phe Gln Pro Asn Ile Glu Gln
465 470 475 480
Leu Arg Gly Leu Gln Ser Leu Arg Lys Leu Ser Ser Val Cys Leu Ala
485 490 495
Leu Thr Asn Ser Met Lys Thr Ser Ser Val Ala Arg Leu Arg Gln Asn

500 505 510

Gln Leu Gly Ser Val Arg Tyr Gln Val Val Glu Cys Lys Glu Val Phe

515 520 525

Cys Gln Ile Ile Lys Leu Asp Ser Glu Glu Tyr His Leu Leu Tyr Gln

530 535 540

Lys Thr Gly Glu Ser Ser Arg Cys Tyr Ser Ile Gln Gly Pro Asp Gly

545 550 555 560

His Leu Ile Ser Phe Tyr Ala Asp Pro Lys Arg Phe Phe Leu Pro Ile

565 570 575

Phe Ser Asp Glu Val Leu His Asn Met Ile Asp Thr Met Ile Ser Trp

580 585 590

Ile Arg Ser Cys Pro Asp Leu Lys Asp Ser Leu Ile Asp Ile Glu Thr

595 600 605

Ala Leu Arg Thr Leu Ile Leu Leu Met Leu Thr Asn Pro Thr Lys Arg

610 615 620

Asn Gln Lys Gln Val Gln Asn Ile Arg Tyr Leu Val Met Ala Ile Val

625 630 635 640

Ser Asp Phe Ser Ser Thr Ser Leu Met Asp Lys Leu Lys Glu Asp Leu

645 650 655

Ile Thr Pro Ala Glu Lys Val Val Tyr Arg Leu Leu Arg Phe Leu Ile

660 665 670

Arg Thr Ile Phe Gly Thr Gly Glu Lys Val Leu Leu Ser Ala Lys Phe

675 680 685

Lys Phe Met Leu Asn Val Ser Tyr Leu Cys His Leu Ile Thr Lys Glu

690 695 700

Thr Pro Asp Arg Leu Thr Asp Gln Ile Lys Cys Phe Glu Lys Phe Phe

705 710 715 720

Glu Pro Lys Ser Glu Phe Gly Phe Phe Val Asn Pro Lys Glu Thr Ile

725 730 735

Thr Pro Glu Glu Glu Cys Val Phe Tyr Glu Gln Met Lys Lys Phe Thr

740 745 750

Gly Lys Asp Ile Asp Cys Gln His Ser Thr Pro Gly Val Asn Leu Glu
755 760 765
Ile Phe Ser Met Met Val Ser Ser Phe Asn Asn Gly Thr Leu Ile Leu
770 775 780

Lys Gly Glu Lys Arg Leu Asn Asn Leu Asp Pro Met Thr Asn Ser Gly
785 790 795 800
Cys Ala Thr Ala Leu Asp Leu Ala Ser Asn Lys Ser Val Val Val Asn
805 810 815
Lys His Leu Asn Gly Glu Arg Leu Leu Glu Tyr Asp Phe Asn Lys Leu
820 825 830
Leu Val Ser Ala Val Ser Gln Ile Thr Glu Gly Phe Met Arg Lys Gln
835 840 845

Lys Tyr Lys Leu Arg His Ser Asp Tyr Glu Tyr Lys Val Ser Lys Leu
850 855 860
Val Ser Arg Leu Val Ile Gly Ser Arg Lys Thr Glu Val Asp Lys Leu
865 870 875 880
Glu Asp Asp Pro Val Asp Val Cys Phe Glu Gly Glu Glu Glu Thr Ser
885 890 895
Phe Phe Arg Ser Leu Glu Asp Lys Val Ser Ser Thr Ile Thr Arg Tyr
900 905 910

Asn Arg Gly Thr Arg Leu Asn Glu Gly Gln Gly Glu Gly Glu Phe Lys
915 920 925
Asn Thr Lys Gly Leu His His Leu Gln Ile Ile Leu Ser Gly Lys Arg
930 935 940
Ala Tyr Leu Arg Lys Val Ile Leu Ser Glu Ile Ser Phe His Leu Val
945 950 955 960
Glu Asp Phe Asp Pro Ser Cys Leu Thr Asn Asp Asp Met Arg Phe Ile
965 970 975

Cys Glu Ala Val Glu Gly Ser Thr Glu Leu Ser Pro Leu Tyr Phe Thr
980 985 990
Ser Ala Val Lys Glu Gln Cys Gly Leu Asp Glu Met Ala Arg Asn Leu

995 1000 1005

Cys Arg Lys Phe Phe Ser Glu Gly Asp Trp Phe Ser Cys Met Lys

1010 1015 1020

Met Ile Leu Leu Gln Met Asn Ala Asn Ala Tyr Ser Gly Lys Tyr

1025 1030 1035

Arg His Met Gln Arg Gln Ser Leu Asn Phe Lys Phe Asp Trp Asp

1040 1045 1050

Lys Leu Glu Glu Asp Val Arg Ile Ser Glu Arg Glu Ser Asn Ser

1055 1060 1065

Glu Ser Leu Ser Lys Ala Leu Ser Leu Thr Lys Cys Met Ser Ala

1070 1075 1080

Ala Leu Lys Asn Leu Cys Phe Tyr Ser Glu Glu Ser Pro Thr Ser

1085 1090 1095

Tyr Thr Ser Val Gly Pro Asp Ser Gly Arg Leu Lys Phe Ala Leu

1100 1105 1110

Ser Tyr Lys Glu Gln Val Gly Gly Asn Arg Glu Leu Tyr Ile Gly

1115 1120 1125

Asp Leu Arg Thr Lys Met Phe Thr Arg Leu Val Glu Asp Tyr Phe

1130 1135 1140

Glu Ser Phe Ser Ser Phe Phe Ser Gly Ser Cys Leu Asn Asn Asp

1145 1150 1155

Lys Glu Phe Glu Asn Ala Ile Leu Ser Met Thr Ile Asn Val Arg

1160 1165 1170

Glu Gly Leu Leu Asn Tyr Ser Met Asp His Ser Lys Trp Gly Pro

1175 1180 1185

Met Met Cys Pro Phe Leu Phe Leu Met Leu Leu Gln Asn Leu Lys

1190 1195 1200

Leu Gly Asp Asp Gln Tyr Val Arg Ser Gly Lys Asp His Val Ser

1205 1210 1215

Thr Leu Leu Thr Trp His Met His Lys Leu Val Glu Val Pro Phe

1220 1225 1230

Pro Val Val Asn Ala Met Met Lys Ser Tyr Val Lys Ser Lys Leu
1235 1240 1245
Lys Leu Leu Lys Gly Ser Gly Thr Thr Val Thr Glu Arg Ile Phe
1250 1255 1260
Arg Glu Tyr Phe Glu Met Gly Val Val Pro Ser His Ile Ser Ser
1265 1270 1275

Leu Ile Asp Met Gly Gln Gly Ile Leu His Asn Ala Ser Asp Phe
1280 1285 1290
Tyr Gly Leu Ile Ser Glu Arg Phe Ile Asn Tyr Cys Ile Gly Val
1295 1300 1305
Ile Phe Gly Glu Arg Pro Glu Ala Tyr Thr Ser Ser Asp Asp Gln
1310 1315 1320
Ile Thr Leu Phe Asp Lys Arg Leu Ser Asp Leu Val Asp Ser Asp
1325 1330 1335

Pro Glu Glu Val Leu Val Leu Leu Glu Phe His Ser His Leu Ser
1340 1345 1350
Gly Leu Leu Asn Lys Phe Ile Ser Pro Lys Ser Val Val Gly Arg
1355 1360 1365
Phe Ala Ala Glu Phe Lys Ser Arg Phe Tyr Val Trp Gly Glu Glu
1370 1375 1380
Val Pro Leu Leu Thr Lys Phe Val Ser Ala Ala Leu His Asn Val
1385 1390 1395

Lys Cys Lys Glu Pro His Gln Leu Cys Glu Thr Ile Asp Thr Ile
1400 1405 1410
Ala Asp Gln Ala Ile Ala Asn Gly Val Pro Val Phe Leu Val Asn
1415 1420 1425
Cys Ile Gln Arg Arg Thr Leu Asp Leu Leu Lys Tyr Ala Asn Phe
1430 1435 1440
Pro Leu Asp Pro Phe Leu Leu Asn Thr His Thr Asp Val Lys Asp
1445 1450 1455

Trp Leu Asp Gly Ser Arg Gly Tyr Arg Ile Gln Arg Leu Ile Glu

1460 1465 1470

Glu Leu Cys Pro Ser Glu Thr Lys Ile Met Arg Lys Leu Val Arg

1475 1480 1485

Arg Leu His His Lys Leu Lys Asn Gly Glu Cys Asn Glu Glu Phe

1490 1495 1500

Phe Leu Asp Leu Phe Asn Arg Glu Lys Glu Glu Ala Ile Leu Gln

1505 1510 1515

Leu Gly Glu Ile Leu Gly Leu Glu Asp Asp Leu Asn Glu Leu Ala

1520 1525 1530

Ser Ile Asn Trp Leu Asn Leu Asn Glu Met Phe Pro Leu Arg Met

1535 1540 1545

Val Leu Arg Gln Lys Val Val Tyr Pro Ser Val Met Thr Phe Gln

1550 1555 1560

Glu Glu Lys Ile Pro Ser Leu Ile Lys Thr Leu Gln Asn Lys Leu

1565 1570 1575

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

1580 1585 1590

Ile Asn Lys Ser Ala Phe Gln Ser Cys Val Ser Ser Gly Phe Ile

1595 1600 1605

Gly Leu Cys Lys Thr Leu Gly Ser Arg Cys Val Arg Asn Lys Asn

1610 1615 1620

Arg Glu Asn Met Tyr Ile Arg Lys Val Leu Glu Asp Leu Thr Met

1625 1630 1635

Asp Glu His Val Thr Arg Val His Lys Gln Asp Gly Val Met Leu

1640 1645 1650

Tyr Ile Cys Asp Lys Gln Arg His Pro Glu Ala His Arg Asp His

1655 1660 1665

Ile Asn Leu Leu Arg Pro Leu Leu Trp Asp Tyr Ile Cys Ile Ser

1670 1675 1680

Leu Ser Asn Ser Phe Glu Leu Gly Val Trp Val Leu Ala Glu Pro

1685 1690 1695

Val Lys Gly Lys Asn Glu Ser Asn Ser Ala Val Arg His Leu Asn
1700 1705 1710
Pro Cys Asp Tyr Val Ala Arg Lys Pro Glu Ser Ser Arg Leu Leu
1715 1720 1725
Glu Asp Lys Val Ser Leu Asn His Val Ile Gln Ser Val Arg Arg
1730 1735 1740
Leu Tyr Pro Lys Ile Phe Glu Asp Gln Leu Leu Pro Phe Met Ser
1745 1750 1755

Asp Val Ser Ser Lys Asn Met Arg Trp Ser Pro Arg Ile Lys Phe
1760 1765 1770
Leu Asp Leu Cys Val Leu Ile Asp Ile Asn Ser Glu Ser Leu Ser
1775 1780 1785
Leu Ile Ser His Val Val Lys Trp Lys Arg Asp Glu His Tyr Thr
1790 1795 1800
Val Leu Phe Ser Asp Leu Val Asn Ser His Gln Arg Ser Asp Ser
1805 1810 1815

Ser Leu Val Asp Glu Phe Val Val Ser Thr Arg Asp Val Cys Lys
1820 1825 1830
Asn Phe Leu Lys Gln Val Tyr Phe Glu Ser Phe Val Arg Glu Phe
1835 1840 1845
Val Ala Thr Ala Arg Thr Leu Gly Asn Phe Ser Trp Phe Pro His
1850 1855 1860
Lys Asp Met Met Pro Ser Glu Asp Gly Ala Glu Ala Leu Gly Pro
1865 1870 1875

Phe Gln Ser Phe Ile Leu Lys Val Val Asn Lys Lys Ile Glu Arg
1880 1885 1890
Pro Met Phe Arg Asn Asp Leu Gln Phe Gly Phe Gly Trp Phe Ser
1895 1900 1905
Tyr Arg Val Gly Asp Val Val Cys Asn Ala Ala Met Leu Ile Lys
1910 1915 1920
Gln Gly Leu Thr Asp Pro Lys Ala Phe Lys Ser Leu Arg Asp Leu

1925 1930 1935

Trp Asp Tyr Met Leu Ser Ser Thr Glu Gly Ile Leu Glu Phe Ser
1940 1945 1950
Ile Thr Val Asp Phe Thr His Asn Gln Asn Asn Thr Asp Cys Leu
1955 1960 1965
Arg Lys Phe Ser Leu Ile Phe Val Val Lys Cys Gln Leu Gln Ser
1970 1975 1980
Pro Gly Val Ala Asp Tyr Leu Ser Cys Ser His Ser Phe Lys Gly
1985 1990 1995

Glu Val Asp Arg Arg Leu Leu Asp Glu Cys Leu Asn Leu Leu Arg
2000 2005 2010
Thr Asp Pro Ile Phe Lys Ala Asn Asp Gly Val Phe Asp Ile Arg
2015 2020 2025
Ser Glu Glu Phe Glu Asp Tyr Met Glu Asp Pro Leu Thr Leu Gly
2030 2035 2040
Asp Ser Leu Glu Leu Glu Leu Ile Gly Ser Arg Arg Ile Leu Asn
2045 2050 2055

Glu Ile Lys Ser Thr Asp Phe Glu Arg Ile Gly Pro Glu Trp Glu
2060 2065 2070
Pro Val Pro Leu Thr Ile Arg Lys Gly Ala Leu Phe Glu Gly Arg
2075 2080 2085
Asn Phe Val Gln Asn Ile Ser Val Lys Leu Glu Thr Lys Asp Met
2090 2095 2100
Arg Val Phe Leu Ala Glu Leu Glu Gly Cys Gly Lys Ile Gly Asp
2105 2110 2115

Val Leu Gly Ser Leu Leu Leu His Arg Phe Arg Thr Gly Glu His
2120 2125 2130
Leu Met Glu Ser Glu Ile Ser Thr Val Leu Gln Glu Leu Cys Met
2135 2140 2145
Asp Arg Ser Val Met Leu Thr Pro Leu Ser Phe Val Pro Asp Trp
2150 2155 2160

Phe Thr Phe Arg Asp Cys Arg Leu Cys Phe Ser Lys Ser Lys Asn
    2165 2170 2175

Thr Val Met Tyr Glu Thr Thr Gly Gly Arg Phe Arg Leu Lys Gly
    2180 2185 2190
Lys Ser Cys Asp Asp Trp Leu Ala Glu Arg Val Ala Glu Glu Ile
    2195 2200 2205
Asp

<210> 6
<211> 6630
<212> DNA
<213> Lymphocytic choriomeningitis virus
<220><221> MISC_FEATURE
<223> Lymphocytic choriomeningitis virus Mutant L-Protein; ssrna
       ambisense-strand viruses; arenaviridae; arenavirus; old world

       arenaviruses
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gagggactca aattgttatc acgctgtata gagatagaca gtgcagacaa aagtggttgc 180
atacacaacc acgatgacaa atctgttgaa acaatcctaa tagactctgg gattgtgtgt 240
ccaggactgc cactcatcat ccctgatggt tataagttga ttgacaattc ccttattctt 300
cttgaatgtt ttgttagaag cacaccagct agttttgaaa agaagttcat tgaggacacc 360
aacaaactag catgcatcaa agaagatctt gctgttgcag gcatcacact ggttccaata 420

gtggatggtc gttgtgatta tgataacagt ttcatgccag aatgggtgaa ttttaagttc 480
agagacctcc tatttaaact cctggagtat tctagtcaag atgagaaagt ttttgaggag 540
tctgaatact tcaggctctg tgagtctctt aagaccactg ttgacaaacg ttccggcatg 600
gactcaatga aaattttgaa agacgcaaga tcatttcata acgatgagat tatgaaaatg 660
tgccacgatg gtgtcaaccc caacatgagt tgcgatgatg tggtctttgg cataaattcc 720
ttttttggca ggtttaggag ggacctgtta aatgggaaac tcaaaaggaa tttccaaaag 780
gtcagccctg ggggcttaat caaggaattc tctgaacttt atgaaaccct tactgataat 840

gatgacatat taatgttgag caaagaggca gttgaatcct gccccttaat gaggttcatt 900

acagcagaga cccatgggca tgagagagga agcgatgcta acactgagta tgaaaggcta 960

ctctctatgt tgaacaaggt gaaaagttta aaattattaa acactagaag gagacagctg 1020

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<223> Lymphocytic choriomeningitis virus Wildtype L-Protein; ssrna ambisense-strand viruses; arenaviridae; arenavirus; old world arenaviruses

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Cys Ile Glu Ile Asp Ser Ala Asp Lys Ser Gly Cys Ile His Asn His

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Asp Asp Lys Ser Val Glu Thr Ile Leu Ile Asp Ser Gly Ile Val Cys

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Pro Gly Leu Pro Leu Ile Ile Pro Asp Gly Tyr Lys Leu Ile Asp Asn

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Ser Leu Ile Leu Leu Glu Cys Phe Val Arg Ser Thr Pro Ala Ser Phe

100 105 110

Glu Lys Lys Phe Ile Glu Asp Thr Asn Lys Leu Ala Cys Ile Lys Glu

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Val Asn Pro Asn Met Ser Cys Asp Asp Val Val Phe Gly Ile Asn Ser

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Phe Phe Gly Arg Phe Arg Arg Asp Leu Leu Asn Gly Lys Leu Lys Arg

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260 265 270

Leu Tyr Glu Thr Leu Thr Asp Asn Asp Asp Ile Leu Met Leu Ser Lys

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Glu Ala Val Glu Ser Cys Pro Leu Met Arg Phe Ile Thr Ala Glu Thr

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His Gly His Glu Arg Gly Ser Asp Ala Asn Thr Glu Tyr Glu Arg Leu

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Arg Arg Gln Leu Leu Asn Leu Asp Val Leu Cys Leu Ser Ser Leu Ile

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Lys Gln Ser Ile Ser Lys Gly Leu Glu Asn Asp Lys His Trp Val Gly

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Cys Cys Tyr Ser Ser Val Asn Asp Arg Leu Val Ser Leu Gln Ser Thr

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Lys Thr Gly Glu Ser Ser Arg Cys Tyr Ser Ile Gln Gly Pro Asp Gly

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675 680 685

Lys Phe Met Leu Asn Val Ser Tyr Leu Cys His Leu Ile Thr Lys Glu

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725 730 735

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755 760 765

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785 790 795 800

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Lys His Leu Asn Gly Glu Arg Leu Leu Glu Tyr Asp Phe Asn Lys Leu

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Lys Tyr Lys Leu Arg His Ser Asp Tyr Glu Tyr Lys Val Ser Lys Leu

850 855 860

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1820 1825 1830

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1985 1990 1995

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<223> Lymphocytic choriomeningitis virus Wildtype L-Protein; ssrna ambisense-strand viruses; arenaviridae; arenavirus; old world arenaviruses

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<210> 9

<211> 1497

<212> DNA

<213> Lymphocytic choriomeningitis virus (strain WE)

<400> 9

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tgtgggatat tagcactggt cagcttcctt tttttggctg gtaggtcctg tggcatgtac 180

ggccttaatg gtcccgacat ctataaaggg gtttaccagt tcaaatcagt ggagtttgat 240

atgtctcact taaatctgac gatgcccaat gcgtgctcag ccaacaactc tcatcactac 300

atcagtatgg gaagctctgg actggagcta actttcacta acgactccat ccttaatcac 360

aatttttgca acttaacctc cgctttcaac aaaaagactt ttgaccatac actcatgagt 420

atagtctcga gtctgcacct cagtattaga gggaattcca accacaaagc agtgtcttgt 480

gattttaaca atggcatcac cattcaatac aacttgtcat tttcggaccc acagagcgct 540

ataagccagt gtaggacttt cagaggtaga gtcttggaca tgtttagaac tgcctttgga 600

ggaaaataca tgagaagtgg ctggggctgg gcaggttcag atggcaagac cacttggtgc 660

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tgtagttgtg gtgcattcaa ggtgcctggt gtaaaaacta tctggaaaag acgctga 1497

<210> 10

<211> 498

<212> PRT

<213> Lymphocytic choriomeningitis virus (strain WE)

<400> 10

Met Gly Gln Ile Val Thr Met Phe Glu Ala Leu Pro His Ile Ile Asp

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Glu Val Ile Asn Ile Val Ile Ile Val Leu Ile Ile Ile Thr Ser Ile

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Lys Ala Val Tyr Asn Phe Ala Thr Cys Gly Ile Leu Ala Leu Val Ser

35 40 45

Phe Leu Phe Leu Ala Gly Arg Ser Cys Gly Met Tyr Gly Leu Asn Gly

50 55 60

Pro Asp Ile Tyr Lys Gly Val Tyr Gln Phe Lys Ser Val Glu Phe Asp

65 70 75 80

Met Ser His Leu Asn Leu Thr Met Pro Asn Ala Cys Ser Ala Asn Asn

85 90 95

Ser His His Tyr Ile Ser Met Gly Ser Ser Gly Leu Glu Leu Thr Phe

100 105 110

Thr Asn Asp Ser Ile Leu Asn His Asn Phe Cys Asn Leu Thr Ser Ala

115 120 125

Phe Asn Lys Lys Thr Phe Asp His Thr Leu Met Ser Ile Val Ser Ser

130 135 140

Leu His Leu Ser Ile Arg Gly Asn Ser Asn His Lys Ala Val Ser Cys

145 150 155 160

Asp Phe Asn Asn Gly Ile Thr Ile Gln Tyr Asn Leu Ser Phe Ser Asp

165 170 175

Pro Gln Ser Ala Ile Ser Gln Cys Arg Thr Phe Arg Gly Arg Val Leu

180 185 190

Asp Met Phe Arg Thr Ala Phe Gly Gly Lys Tyr Met Arg Ser Gly Trp

195 200 205

Gly Trp Ala Gly Ser Asp Gly Lys Thr Thr Trp Cys Ser Gln Thr Ser

210 215 220

Tyr Gln Tyr Leu Ile Ile Gln Asn Arg Thr Trp Glu Asn His Cys Arg

225 230 235 240

Tyr Ala Gly Pro Phe Gly Met Ser Arg Ile Leu Phe Ala Gln Glu Lys

245 250 255

Thr Lys Phe Leu Thr Arg Arg Leu Ala Gly Thr Phe Thr Trp Thr Leu

260 265 270

Ser Asp Ser Ser Gly Val Glu Asn Pro Gly Gly Tyr Cys Leu Thr Lys

275 280 285

Trp Met Ile Leu Ala Ala Glu Leu Lys Cys Phe Gly Asn Thr Ala Val
290 295 300
Ala Lys Cys Asn Val Asn His Asp Glu Glu Phe Cys Asp Met Leu Arg
305 310 315 320
Leu Ile Asp Tyr Asn Lys Ala Ala Leu Ser Lys Phe Lys Gln Asp Val
325 330 335
Glu Ser Ala Leu His Val Phe Lys Thr Thr Val Asn Ser Leu Ile Ser
340 345 350

Asp Gln Leu Leu Met Arg Asn His Leu Arg Asp Leu Met Gly Val Pro
355 360 365
Tyr Cys Asn Tyr Ser Lys Phe Trp Tyr Leu Glu His Ala Lys Thr Gly
370 375 380
Glu Thr Ser Val Pro Lys Cys Trp Leu Val Thr Asn Gly Ser Tyr Leu
385 390 395 400
Asn Glu Thr His Phe Ser Asp Gln Ile Glu Gln Glu Ala Asp Asn Met
405 410 415

Ile Thr Glu Met Leu Arg Lys Asp Tyr Ile Lys Arg Gln Gly Ser Thr
420 425 430
Pro Leu Ala Leu Met Asp Leu Leu Met Phe Ser Thr Ser Ala Tyr Leu
435 440 445
Ile Ser Ile Phe Leu His Leu Val Lys Ile Pro Thr His Arg His Ile
450 455 460
Lys Gly Gly Ser Cys Pro Lys Pro His Arg Leu Thr Asn Lys Gly Ile
465 470 475 480

Cys Ser Cys Gly Ala Phe Lys Val Pro Gly Val Lys Thr Ile Trp Lys
485 490 495
Arg Arg

<210> 11
<211> 1677
<212> DNA
<213> Lymphocytic choriomeningitis virus (strain WE)

<400> 11

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gggttggact tttctgaagt cagcaacgtt cagaggatca tgagaaagga aaggagggat 180

gataaagact tgcagagact caggagtctt aaccagactg tgcattctct tgttgatctg 240

aagtctacat caaagaaaaa tgttctgaaa gtgggaagac ttagtgcaga ggaattgatg 300

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gcttctggag tctacatggg aaatttgaca gcacaacaac ttgatcaaag atcccaaata 420

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cacaacatcc tgccacatga tttaatcttc agaggaccca atgttgtgac actctaa 1677

<210> 12

<211> 558

<212> PRT

<213> Lymphocytic choriomeningitis virus (strain WE)

<400> 12

Met Ser Leu Ser Lys Glu Val Lys Ser Phe Gln Trp Thr Gln Ala Leu

1 5 10 15

Arg Arg Glu Leu Gln Ser Phe Thr Ser Asp Val Lys Ala Ala Val Ile

20 25 30

Lys Asp Ala Thr Ser Leu Leu Asn Gly Leu Asp Phe Ser Glu Val Ser

35 40 45

Asn Val Gln Arg Ile Met Arg Lys Glu Arg Arg Asp Asp Lys Asp Leu

50 55 60

Gln Arg Leu Arg Ser Leu Asn Gln Thr Val His Ser Leu Val Asp Leu

65 70 75 80

Lys Ser Thr Ser Lys Lys Asn Val Leu Lys Val Gly Arg Leu Ser Ala

85 90 95

Glu Glu Leu Met Thr Leu Ala Ala Asp Leu Glu Lys Leu Lys Ala Lys

100 105 110

Ile Met Arg Thr Glu Arg Pro Gln Ala Ser Gly Val Tyr Met Gly Asn

115 120 125

Leu Thr Ala Gln Gln Leu Asp Gln Arg Ser Gln Ile Leu Gln Met Val

130 135 140

Gly Met Arg Arg Pro Gln Gln Gly Ala Ser Gly Val Val Arg Val Trp

145 150 155 160

Asp Val Lys Asp Ser Ser Leu Leu Asn Asn Gln Phe Gly Thr Met Pro

165 170 175

Ser Leu Thr Met Ala Cys Met Ala Lys Gln Ser Gln Thr Pro Leu Asn

180 185 190

Asp Val Val Gln Ala Leu Thr Asp Leu Gly Leu Leu Tyr Thr Val Lys

195 200 205

Tyr Pro Asn Leu Ser Asp Leu Glu Arg Leu Lys Asp Lys His Pro Val

210 215 220

Leu Gly Val Ile Thr Glu Gln Gln Ser Ser Ile Asn Ile Ser Gly Tyr
225 230 235 240
Asn Phe Ser Leu Gly Ala Ala Val Lys Ala Gly Ala Ala Leu Leu Asp
245 250 255
Gly Gly Asn Met Leu Glu Ser Ile Leu Ile Lys Pro Ser Asn Ser Glu
260 265 270
Asp Leu Leu Lys Ala Val Leu Gly Ala Lys Lys Lys Leu Asn Met Phe

275 280 285
Val Ser Asp Gln Val Gly Asp Arg Asn Pro Tyr Glu Asn Ile Leu Tyr
290 295 300
Lys Val Cys Leu Ser Gly Glu Gly Trp Pro Tyr Ile Ala Cys Arg Thr
305 310 315 320
Ser Val Val Gly Arg Ala Trp Glu Asn Thr Thr Ile Asp Leu Thr Asn
325 330 335
Glu Lys Leu Val Ala Asn Ser Ser Arg Pro Val Pro Gly Ala Ala Gly

340 345 350
Pro Pro Gln Val Gly Leu Ser Tyr Ser Gln Thr Met Leu Leu Lys Asp
355 360 365
Leu Met Gly Gly Ile Asp Pro Asn Ala Pro Thr Trp Ile Asp Ile Glu
370 375 380
Gly Arg Phe Asn Asp Pro Val Glu Ile Ala Ile Phe Gln Pro Gln Asn
385 390 395 400
Gly Gln Phe Ile His Phe Tyr Arg Glu Pro Thr Asp Gln Lys Gln Phe

405 410 415
Lys Gln Asp Ser Lys Tyr Ser His Gly Met Asp Leu Ala Asp Leu Phe
420 425 430
Asn Ala Gln Pro Gly Leu Thr Ser Ser Val Ile Gly Ala Leu Pro Gln
435 440 445
Gly Met Val Leu Ser Cys Gln Gly Ser Asp Asp Ile Arg Lys Leu Leu
450 455 460
Asp Ser Gln Asn Arg Arg Asp Ile Lys Leu Ile Asp Val Glu Met Thr

465 470 475 480

Lys Glu Ala Ser Arg Glu Tyr Glu Asp Lys Val Trp Asp Lys Tyr Gly

485 490 495

Trp Leu Cys Lys Met His Thr Gly Val Val Arg Asp Lys Lys Lys Lys

500 505 510

Glu Ile Thr Pro His Cys Ala Leu Met Asp Cys Ile Ile Phe Glu Ser

515 520 525

Ala Ser Lys Ala Arg Leu Pro Asp Leu Lys Thr Val His Asn Ile Leu

530 535 540

Pro His Asp Leu Ile Phe Arg Gly Pro Asn Val Val Thr Leu

545 550 555

<210> 13

<211> 273

<212> DNA

<213> Lymphocytic choriomeningitis virus (strain WE)

<400> 13

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agcttggtta gatgccatga ccactatctt tgcagacact gtctgaatct cctgctgtca 180

gtttccgaca gatgtcctct ctgtaagtat ccactgccaa ccaaactgaa ggtgtcaaca 240

gtcccaagct ccccacctcc ctatgaggag tga 273

<210> 14

<211> 90

<212> PRT

<213> Lymphocytic choriomeningitis virus (strain WE)

<400> 14

Met Gly Gln Gly Lys Ser Lys Glu Glu Arg Asp Thr Ser Asn Thr Gly

1 5 10 15

Arg Ala Glu Leu Leu Pro Asp Thr Thr Tyr Leu Gly Pro Leu Asn Cys

20 25 30

Lys Ser Cys Trp Gln Lys Phe Asp Ser Leu Val Arg Cys His Asp His

35 40 45

Tyr Leu Cys Arg His Cys Leu Asn Leu Leu Leu Ser Val Ser Asp Arg

50 55 60

Cys Pro Leu Cys Lys Tyr Pro Leu Pro Thr Lys Leu Lys Val Ser Thr

65 70 75 80

Val Pro Ser Ser Pro Pro Pro Tyr Glu Glu

85 90

<210> 15

<211> 6630

<212

> DNA

<213> Lymphocytic choriomeningitis virus (strain WE)

<400> 15

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gagggactca aattgttatc acgctgtata gagatagaca gtgcagacaa aagtggttgc 180

atacacaacc acgatgacaa atctgttgaa acaatcctaa tagactctgg gattgtgtgt 240

ccaggactgc cactcatcat ccctgatggt tataagttga ttgacaattc ccttattctt 300

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<211> 2209

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<400> 16

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Arg Glu Pro Arg Met Val Leu Ile Glu Gly Leu Lys Leu Leu Ser Arg
35 40 45

Cys Ile Glu Ile Asp Ser Ala Asp Lys Ser Gly Cys Ile His Asn His

50 55 60

Asp Asp Lys Ser Val Glu Thr Ile Leu Ile Asp Ser Gly Ile Val Cys
65 70 75 80

Pro Gly Leu Pro Leu Ile Ile Pro Asp Gly Tyr Lys Leu Ile Asp Asn
85 90 95

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

Glu Lys Lys Phe Ile Glu Asp Thr Asn Lys Leu Ala Cys Ile Lys Glu

115 120 125

Asp Leu Ala Val Ala Gly Ile Thr Leu Val Pro Ile Val Asp Gly Arg
130 135 140

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

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

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Val Asn Pro Asn Met Ser Cys Asp Asp Val Val Phe Gly Ile Asn Ser

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Phe Phe Gly Arg Phe Arg Arg Asp Leu Leu Asn Gly Lys Leu Lys Arg

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Asn Phe Gln Lys Val Ser Pro Gly Gly Leu Ile Lys Glu Phe Ser Glu

260 265 270

Leu Tyr Glu Thr Leu Thr Asp Asn Asp Asp Ile Leu Met Leu Ser Lys

275 280 285

Glu Ala Val Glu Ser Cys Pro Leu Met Arg Phe Ile Thr Ala Glu Thr

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His Gly His Glu Arg Gly Ser Asp Ala Asn Thr Glu Tyr Glu Arg Leu

305 310 315 320

Leu Ser Met Leu Asn Lys Val Lys Ser Leu Lys Leu Leu Asn Thr Arg

325 330 335

Arg Arg Gln Leu Leu Asn Leu Asp Val Leu Cys Leu Ser Ser Leu Ile

340 345 350

Lys Gln Ser Ile Ser Lys Gly Leu Glu Asn Asp Lys His Trp Val Gly

355 360 365

Cys Cys Tyr Ser Ser Val Asn Asp Arg Leu Val Ser Leu Gln Ser Thr

370 375 380

Lys Glu Glu Phe Met Arg Leu Leu Lys Asn Arg Arg Lys Ser Arg Val

385 390 395 400

His Lys Lys Ala Ser Leu Asp Glu Leu Phe Arg Val Ser Ile Asn Glu

405 410 415

Phe Ile Ala Lys Ile Gln Lys Cys Leu Ser Thr Val Gly Leu Ser Phe

420 425 430

Glu His Tyr Gly Leu Ser Glu Cys Leu Val Gln Glu Cys His Ile Pro

435 440 445

Phe Ala Glu Phe Glu Asn Phe Met Arg Ala Gly Thr His Pro Val Met

450 455 460

His Tyr Thr Lys Phe Glu Asp Tyr Thr Phe Gln Pro Asn Ile Glu Gln

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Leu Thr Asn Ser Met Lys Thr Ser Ser Val Ala Arg Leu Arg Gln Asn

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Gln Leu Gly Ser Val Arg Tyr Gln Val Val Glu Cys Lys Glu Val Phe

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Cys Gln Ile Ile Lys Leu Asp Ser Glu Glu Tyr His Leu Leu Tyr Gln

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Lys Thr Gly Glu Ser Ser Arg Cys Tyr Ser Ile Gln Gly Pro Asp Gly

545 550 555 560

His Leu Ile Ser Phe Tyr Ala Asp Pro Lys Arg Phe Phe Leu Pro Ile

565 570 575

Phe Ser Asp Glu Val Leu His Asn Met Ile Asp Thr Met Ile Ser Trp

580 585 590

Ile Arg Ser Cys Pro Asp Leu Lys Asp Ser Leu Ile Asp Ile Glu Thr

595 600 605

Ala Leu Arg Thr Leu Ile Leu Leu Met Leu Thr Asn Pro Thr Lys Arg

610 615 620

Asn Gln Lys Gln Val Gln Asn Ile Arg Tyr Leu Val Met Ala Ile Val

625 630 635 640

Ser Asp Phe Ser Ser Thr Ser Leu Met Asp Lys Leu Lys Glu Asp Leu

645 650 655

Ile Thr Pro Ala Glu Lys Val Val Tyr Arg Leu Leu Arg Phe Leu Ile

660 665 670

Arg Thr Ile Phe Gly Thr Gly Glu Lys Val Leu Leu Ser Ala Lys Phe

675 680 685

Lys Phe Met Leu Asn Val Ser Tyr Leu Cys His Leu Ile Thr Lys Glu

690 695 700

Thr Pro Asp Arg Leu Thr Asp Gln Ile Lys Cys Phe Glu Lys Phe Phe

705 710 715 720

Glu Pro Lys Ser Glu Phe Gly Phe Phe Val Asn Pro Lys Glu Thr Ile

725 730 735

Thr Pro Glu Glu Glu Cys Val Phe Tyr Glu Gln Met Lys Lys Phe Thr

740 745 750

Gly Lys Asp Ile Asp Cys Gln His Ser Thr Pro Gly Val Asn Leu Glu

755 760 765

Ile Phe Ser Met Met Val Ser Ser Phe Asn Asn Gly Thr Leu Ile Leu

770 775 780

Lys Gly Glu Lys Arg Leu Asn Asn Leu Asp Pro Met Thr Asn Ser Gly

785 790 795 800

Cys Ala Thr Ala Leu Asp Leu Ala Ser Asn Lys Ser Val Val Val Asn

805 810 815

Lys His Leu Asn Gly Glu Arg Leu Leu Glu Tyr Asp Phe Asn Lys Leu

820 825 830

Leu Val Ser Ala Val Ser Gln Ile Thr Glu Gly Phe Met Arg Lys Gln

835 840 845

Lys Tyr Lys Leu Arg His Ser Asp Tyr Glu Tyr Lys Val Ser Lys Leu

850 855 860

Val Ser Arg Leu Val Ile Gly Ser Arg Lys Thr Glu Val Asp Lys Leu

865 870 875 880

Glu Asp Asp Pro Val Asp Val Cys Phe Glu Gly Glu Glu Glu Thr Ser

885 890 895

Phe Phe Arg Ser Leu Glu Asp Lys Val Ser Ser Thr Ile Thr Arg Tyr

900 905 910

Asn Arg Gly Thr Arg Leu Asn Glu Gly Gln Gly Glu Gly Glu Phe Lys

915 920 925

Asn Thr Lys Gly Leu His His Leu Gln Ile Ile Leu Ser Gly Lys Arg

930 935 940

Ala Tyr Leu Arg Lys Val Ile Leu Ser Glu Ile Ser Phe His Leu Val

945 950 955 960

Glu Asp Phe Asp Pro Ser Cys Leu Thr Asn Asp Asp Met Arg Phe Ile

965 970 975

Cys Glu Ala Val Glu Gly Ser Thr Glu Leu Ser Pro Leu Tyr Phe Thr

980 985 990

Ser Ala Val Lys Glu Gln Cys Gly Leu Asp Glu Met Ala Arg Asn Leu

995 1000 1005

Cys Arg Lys Phe Phe Ser Glu Gly Asp Trp Phe Ser Cys Met Lys

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Met Ile Leu Leu Gln Met Asn Ala Asn Ala Tyr Ser Gly Lys Tyr

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Ala Leu Lys Asn Leu Cys Phe Tyr Ser Glu Glu Ser Pro Thr Ser

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Tyr Thr Ser Val Gly Pro Asp Ser Gly Arg Leu Lys Phe Ala Leu

1100 1105 1110

Ser Tyr Lys Glu Gln Val Gly Gly Asn Arg Glu Leu Tyr Ile Gly

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Asp Leu Arg Thr Lys Met Phe Thr Arg Leu Val Glu Asp Tyr Phe

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Glu Gly Leu Leu Asn Tyr Ser Met Asp His Ser Lys Trp Gly Pro

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Met Met Cys Pro Phe Leu Phe Leu Met Leu Leu Gln Asn Leu Lys

1190 1195 1200

Leu Gly Asp Asp Gln Tyr Val Arg Ser Gly Lys Asp His Val Ser

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Thr Leu Leu Thr Trp His Met His Lys Leu Val Glu Val Pro Phe

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Pro Val Val Asn Ala Met Met Lys Ser Tyr Val Lys Ser Lys Leu

1235 1240 1245

Lys Leu Leu Lys Gly Ser Gly Thr Thr Val Thr Glu Arg Ile Phe

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Arg Glu Tyr Phe Glu Met Gly Val Val Pro Ser His Ile Ser Ser

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Leu Ile Asp Met Gly Gln Gly Ile Leu His Asn Ala Ser Asp Phe

1280 1285 1290

Tyr Gly Leu Ile Ser Glu Arg Phe Ile Asn Tyr Cys Ile Gly Val

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

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1325 1330 1335

Pro Glu Glu Val Leu Val Leu Leu Glu Phe His Ser His Leu Ser

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Gly Leu Leu Asn Lys Phe Ile Ser Pro Lys Ser Val Val Gly Arg

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Phe Ala Ala Glu Phe Lys Ser Arg Phe Tyr Val Trp Gly Glu Glu

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Val Pro Leu Leu Thr Lys Phe Val Ser Ala Ala Leu His Asn Val

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Lys Cys Lys Glu Pro His Gln Leu Cys Glu Thr Ile Asp Thr Ile

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Ala Asp Gln Ala Ile Ala Asn Gly Val Pro Val Phe Leu Val Asn

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Pro Leu Asp Pro Phe Leu Leu Asn Thr His Thr Asp Val Lys Asp

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Trp Leu Asp Gly Ser Arg Gly Tyr Arg Ile Gln Arg Leu Ile Glu

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Arg Leu His His Lys Leu Lys Asn Gly Glu Cys Asn Glu Glu Phe

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Phe Leu Asp Leu Phe Asn Arg Glu Lys Lys Glu Ala Ile Leu Gln

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Val Leu Arg Gln Lys Val Val Tyr Pro Ser Val Met Thr Phe Gln

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

1580 1585 1590

Ile Asn Lys Ser Ala Phe Gln Ser Cys Val Ser Ser Gly Phe Ile

1595 1600 1605

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1685 1690 1695

Val Lys Gly Lys Asn Glu Ser Asn Ser Ala Val Arg His Leu Asn

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Pro Cys Asp Tyr Val Ala Arg Lys Pro Glu Ser Ser Arg Leu Leu

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Glu Asp Lys Val Ser Leu Asn His Val Ile Gln Ser Val Arg Arg

1730 1735 1740

Leu Tyr Pro Lys Ile Phe Glu Asp Gln Leu Leu Pro Phe Met Ser

1745 1750 1755

Asp Val Ser Ser Lys Asn Met Arg Trp Ser Pro Arg Ile Lys Phe

1760 1765 1770

Leu Asp Leu Cys Val Leu Ile Asp Ile Asn Ser Glu Ser Leu Ser

1775 1780 1785

Leu Ile Ser His Val Val Lys Trp Lys Arg Asp Glu His Tyr Thr

1790 1795 1800

Val Leu Phe Ser Asp Leu Val Asn Ser His Gln Arg Ser Asp Ser

1805 1810 1815

Ser Leu Val Asp Glu Phe Val Val Ser Thr Arg Asp Val Cys Lys

1820 1825 1830

Asn Phe Leu Lys Gln Val Tyr Phe Glu Ser Phe Val Arg Glu Phe

1835 1840 1845

Val Ala Thr Ala Arg Thr Leu Gly Asn Phe Ser Trp Phe Pro His

1850 1855 1860

Lys Asp Met Met Pro Ser Glu Asp Gly Ala Glu Ala Leu Gly Pro

1865 1870 1875

Phe Gln Ser Phe Ile Leu Lys Val Val Asn Lys Lys Ile Glu Arg

1880 1885 1890

Pro Met Phe Arg Asn Asp Leu Gln Phe Gly Phe Gly Trp Phe Ser

1895 1900 1905

Tyr Arg Val Gly Asp Val Val Cys Asn Ala Ala Met Leu Ile Lys

1910 1915 1920

Gln Gly Leu Thr Asp Pro Lys Ala Phe Lys Ser Leu Arg Asp Leu

1925 1930 1935

Trp Asp Tyr Met Leu Ser Ser Thr Glu Gly Ile Leu Glu Phe Ser

1940 1945 1950

Ile Thr Val Asp Phe Thr His Asn Gln Asn Asn Thr Asp Cys Leu

1955 1960 1965

Arg Lys Phe Ser Leu Ile Phe Val Val Lys Cys Gln Leu Gln Ser

1970 1975 1980

Pro Gly Val Ala Asp Tyr Leu Ser Cys Ser His Phe Phe Lys Gly

1985 1990 1995

Glu Val Asp Arg Arg Leu Leu Asp Glu Cys Leu Asn Leu Leu Arg

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Asp Arg Ser Val Met Leu Thr Pro Leu Ser Phe Val Pro Asp Trp

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Phe Thr Phe Arg Asp Cys Arg Leu Cys Phe Ser Arg Ser Lys Asn

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Lys Ser Cys Asp Asp Trp Leu Ala Glu Arg Val Ala Glu Glu Ile

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Asp

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<212> DNA

<213

> Lymphocytic choriomeningitis virus (mutant P42)

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<210> 18

<211> 498

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P42)

<400> 18

Met Gly Gln Ile Val Thr Met Phe Glu Ala Leu Pro His Ile Ile Asp

1 5 10 15

Glu Val Ile Asn Ile Val Ile Ile Val Leu Ile Ile Ile Thr Ser Ile

20 25 30

Lys Ala Val Tyr Asn Phe Ala Thr Cys Gly Ile Leu Ala Leu Val Ser

35 40 45

Phe Leu Phe Leu Ala Gly Arg Ser Cys Gly Met Tyr Gly Leu Asn Gly

50 55 60

Pro Asp Ile Tyr Lys Gly Val Tyr Gln Phe Lys Ser Val Glu Phe Asp

65 70 75 80

Met Ser His Leu Asn Leu Thr Met Pro Asn Ala Cys Ser Ala Asn Asn

85 90 95

Ser His His Tyr Ile Ser Met Gly Ser Ser Gly Leu Glu Leu Thr Phe

100 105 110

Thr Asn Asp Ser Ile Leu Asn His Asn Phe Cys Asn Leu Thr Ser Ala

115 120 125

Phe Asn Lys Lys Thr Phe Asp His Thr Leu Met Ser Ile Val Ser Ser

130 135 140

Leu His Leu Ser Ile Arg Gly Asn Ser Asn His Lys Ala Val Ser Cys

145 150 155 160

Asp Phe Asn Asn Gly Ile Thr Ile Gln Tyr Asn Leu Ser Phe Ser Asp

165 170 175

Pro Gln Ser Ala Met Ser Gln Cys Arg Thr Phe Arg Gly Arg Val Leu

180 185 190

Asp Met Phe Arg Thr Ala Phe Gly Gly Lys Tyr Met Arg Ser Gly Trp

195 200 205

Gly Trp Ala Gly Ser Asp Gly Lys Thr Thr Trp Cys Ser Gln Thr Ser

210 215 220

Tyr Gln Tyr Leu Ile Ile Gln Asn Arg Thr Trp Glu Asn His Cys Arg

225 230 235 240

Tyr Ala Gly Pro Phe Gly Met Ser Arg Ile Leu Phe Ala Gln Glu Lys

245 250 255

Thr Lys Phe Leu Thr Arg Arg Leu Ala Gly Thr Phe Thr Trp Thr Leu

260 265 270

Ser Asp Ser Ser Gly Val Glu Asn Pro Gly Gly Tyr Cys Leu Thr Lys

275 280 285

Trp Met Ile Leu Ala Ala Glu Leu Lys Cys Phe Gly Asn Thr Ala Val

290 295 300

Ala Lys Cys Asn Val Asn His Asp Glu Glu Phe Cys Asp Met Leu Arg

305 310 315 320

Leu Ile Asp Tyr Asn Lys Ala Ala Leu Ser Lys Phe Lys Gln Asp Val

325 330 335

Glu Ser Ala Leu His Val Phe Lys Thr Thr Val Asn Ser Leu Ile Ser

340 345 350

Asp Gln Leu Leu Met Arg Asn His Leu Arg Asp Leu Met Gly Val Pro

355 360 365

Tyr Cys Asn Tyr Ser Lys Phe Trp Tyr Leu Glu His Ala Lys Thr Gly

370 375 380

Glu Thr Ser Val Pro Lys Cys Trp Leu Val Thr Asn Gly Ser Tyr Leu

385 390 395 400

Asn Glu Thr His Phe Ser Asp Gln Ile Glu Gln Glu Ala Asp Asn Met

405 410 415

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

420 425 430

Pro Leu Ala Leu Met Asp Leu Leu Met Phe Ser Thr Ser Ala Tyr Leu

435 440 445

Ile Ser Ile Phe Leu His Leu Val Lys Ile Pro Thr His Arg His Ile

450 455 460

Lys Gly Gly Ser Cys Pro Lys Pro His Arg Leu Thr Asn Lys Gly Ile

465 470 475 480

Cys Ser Cys Gly Ala Phe Lys Val Pro Gly Val Lys Thr Ile Trp Lys

485 490 495

Arg Arg

<210> 19

<211> 1677

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P42)

<400> 19

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gggttggact tttctgaagt cagcaacgtt cagaggatca tgagaaagga aaggagggat 180

gataaagact tgcagagact caggagtctt aaccagactg tgcattctct tgttgatctg 240

aagtctacat caaagaaaaa tgttctgaaa gtgggaagac ttagtgcaga ggaattgatg 300

acccttgcag ctgatcttga gaagctgaag gccaaaatta tgagaactga gaggcctcaa 360

gcttctggag tctacatggg aaatttgaca gcacaacaac ttgatcaaag atcccaaata 420

ctgcaaatgg ttgggatgag aagacctcag cagggtgcaa gtggtgtagt aagggtttgg 480

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aaacacccag ttctgggggt cattactgaa cagcaatcta gtatcaatat ctctggttat 720

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cacaacatcc tgccacatga tttaatcttc agaggaccca atgttgtgac actctaa 1677

<210> 20

<211> 558

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P42)

<400> 20

Met Ser Leu Ser Lys Glu Val Lys Ser Phe Gln Trp Thr Gln Ala Leu

1 5 10 15

Arg Arg Glu Leu Gln Ser Phe Thr Ser Asp Val Lys Ala Ala Val Ile

20 25 30

Lys Asp Ala Thr Ser Leu Leu Asn Gly Leu Asp Phe Ser Glu Val Ser

35 40 45

Asn Val Gln Arg Ile Met Arg Lys Glu Arg Arg Asp Asp Lys Asp Leu

50 55 60

Gln Arg Leu Arg Ser Leu Asn Gln Thr Val His Ser Leu Val Asp Leu
65 70 75 80
Lys Ser Thr Ser Lys Lys Asn Val Leu Lys Val Gly Arg Leu Ser Ala
85 90 95
Glu Glu Leu Met Thr Leu Ala Ala Asp Leu Glu Lys Leu Lys Ala Lys
100 105 110
Ile Met Arg Thr Glu Arg Pro Gln Ala Ser Gly Val Tyr Met Gly Asn
115 120 125

Leu Thr Ala Gln Gln Leu Asp Gln Arg Ser Gln Ile Leu Gln Met Val
130 135 140
Gly Met Arg Arg Pro Gln Gln Gly Ala Ser Gly Val Val Arg Val Trp
145 150 155 160
Asp Val Lys Asp Ser Ser Leu Leu Asn Asn Gln Phe Gly Thr Met Pro
165 170 175
Ser Leu Thr Met Ala Cys Met Ala Lys Gln Ser Gln Thr Pro Leu Asn
180 185 190

Asp Val Val Gln Ala Leu Thr Asp Leu Gly Leu Leu Tyr Thr Val Lys
195 200 205
Tyr Pro Asn Leu Ser Asp Leu Glu Arg Leu Lys Asp Lys His Pro Val
210 215 220
Leu Gly Val Ile Thr Glu Gln Gln Ser Ser Ile Asn Ile Ser Gly Tyr
225 230 235 240
Asn Phe Ser Leu Gly Ala Ala Val Lys Ala Gly Ala Ala Leu Leu Asp
245 250 255

Gly Gly Asn Met Leu Glu Ser Ile Leu Ile Lys Pro Ser Asn Ser Glu
260 265 270
Asp Leu Leu Lys Ala Val Leu Gly Ala Lys Lys Lys Leu Asn Met Phe
275 280 285
Val Ser Asp Gln Val Gly Asp Arg Asn Pro Tyr Glu Asn Ile Leu Tyr
290 295 300

Lys Val Cys Leu Ser Gly Glu Gly Trp Pro Tyr Ile Ala Cys Arg Thr
305 310 315 320

Ser Val Val Gly Arg Ala Trp Glu Asn Thr Thr Ile Asp Leu Thr Asn
325 330 335
Glu Lys Leu Val Ala Asn Ser Ser Arg Pro Val Pro Gly Ala Ala Gly
340 345 350
Pro Pro Gln Val Gly Leu Ser Tyr Ser Gln Thr Met Leu Leu Lys Asp
355 360 365
Leu Met Gly Gly Ile Asp Pro Asn Ala Pro Thr Trp Ile Asp Ile Glu
370 375 380

Gly Arg Phe Asn Asp Pro Val Glu Ile Ala Ile Phe Gln Pro Gln Asn
385 390 395 400
Gly Gln Phe Ile His Phe Tyr Arg Glu Pro Thr Asp Gln Lys Gln Phe
405 410 415
Lys Gln Asp Ser Lys Tyr Ser His Gly Met Asp Leu Ala Asp Leu Phe
420 425 430
Asn Ala Gln Pro Gly Leu Thr Ser Ser Val Ile Gly Ala Leu Pro Gln
435 440 445

Gly Met Val Leu Ser Cys Gln Gly Ser Asp Asp Ile Arg Lys Leu Leu
450 455 460
Asp Ser Gln Asn Arg Arg Asp Ile Lys Leu Ile Asp Val Glu Met Thr
465 470 475 480
Lys Glu Ala Ser Arg Glu Tyr Glu Asp Lys Val Trp Asp Lys Tyr Gly
485 490 495
Trp Leu Cys Lys Met His Thr Gly Val Val Arg Asp Lys Lys Lys Lys
500 505 510

Glu Ile Thr Pro His Cys Ala Leu Met Asp Cys Ile Ile Phe Glu Ser
515 520 525
Ala Ser Lys Ala Arg Leu Pro Asp Leu Lys Thr Val His Asn Ile Leu
530 535 540
Pro His Asp Leu Ile Phe Arg Gly Pro Asn Val Val Thr Leu

545 550 555

<210> 21

<211> 273

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P42)

<400> 21

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agcttggtta gatgccatga ccactatctt tgcagacact gtctgaatct cctgctgtca 180

gtttccgaca gatgtcctct ctgtaagtat ccactgccaa ccaaactgaa ggtgtcaaca 240

gtcccaagct ccccacctcc ctatgaggag tga 273

<210> 22

<211> 90

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P42)

<400> 22

Met Gly Gln Gly Lys Ser Lys Glu Glu Arg Asp Thr Ser Asn Thr Gly

1 5 10 15

Arg Ala Glu Leu Leu Pro Asp Thr Thr Tyr Leu Gly Pro Leu Asn Cys

20 25 30

Lys Ser Cys Trp Gln Lys Phe Asp Ser Leu Val Arg Cys His Asp His

35 40 45

Tyr Leu Cys Arg His Cys Leu Asn Leu Leu Leu Ser Val Ser Asp Arg

50 55 60

Cys Pro Leu Cys Lys Tyr Pro Leu Pro Thr Lys Leu Lys Val Ser Thr

65 70 75 80

Val Pro Ser Ser Pro Pro Pro Tyr Glu Glu

85 90

<210> 23

<211> 6630

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P42)

<400> 23

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gagggactca aattgttatc acgctgtata gagatagaca gtgcagacaa aagtggttgc 180

atacacaacc acgatgacaa atctgttgaa acaatcctaa tagactctgg gattgtgtgt 240

ccaggactgc cactcatcat ccctgatggt tataagttga ttgacaattc ccttattctt 300

cttgaatgtt ttgttagaag cacaccagct agttttgaaa agaagttcat tgaggacacc 360

aacaaactag catgcatcaa agaagatctt gctgttgcag gcatcacact ggttccaata 420

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tgccacgatg gtgtcaaccc caacatgagt tgcgatgatg tggtctttgg cataaattcc 720

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<210> 24

<211> 2209

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P42)

<400> 24

Met Asp Glu Thr Ile Ala Asp Leu Arg Glu Leu Cys Leu Asn Tyr Ile

1 5 10 15

Glu Gln Asp Glu Arg Leu Ser Arg Gln Lys Leu Asn Phe Leu Gly Gln

20 25 30

Arg Glu Pro Arg Met Val Leu Ile Glu Gly Leu Lys Leu Leu Ser Arg

35 40 45

Cys Ile Glu Ile Asp Ser Ala Asp Lys Ser Gly Cys Ile His Asn His

50 55 60

Asp Asp Lys Ser Val Glu Thr Ile Leu Ile Asp Ser Gly Ile Val Cys

65 70 75 80

Pro Gly Leu Pro Leu Ile Ile Pro Asp Gly Tyr Lys Leu Ile Asp Asn

85 90 95

Ser Leu Ile Leu Leu Glu Cys Phe Val Arg Ser Thr Pro Ala Ser Phe

100 105 110

Glu Lys Lys Phe Ile Glu Asp Thr Asn Lys Leu Ala Cys Ile Lys Glu

115 120 125

Asp Leu Ala Val Ala Gly Ile Thr Leu Val Pro Ile Val Asp Gly Arg

130 135 140

Cys Asp Tyr Asp Asn Ser Phe Met Pro Glu Trp Val Asn Phe Lys Phe

145 150 155 160

Arg Asp Leu Leu Phe Lys Leu Leu Glu Tyr Ser Ser Gln Asp Glu Lys

165 170 175

Val Phe Glu Glu Ser Glu Tyr Phe Arg Leu Cys Glu Ser Leu Lys Thr

180 185 190

Thr Val Asp Lys Arg Ser Gly Met Asp Ser Met Lys Ile Leu Lys Asp

195 200 205

Ala Arg Ser Phe His Asn Asp Glu Ile Met Lys Met Cys His Asp Gly

210 215 220

Val Asn Pro Asn Met Ser Cys Asp Asp Val Val Phe Gly Ile Asn Ser

225 230 235 240

Phe Phe Gly Arg Phe Arg Arg Asp Leu Leu Asn Gly Lys Leu Lys Arg

245 250 255

Asn Phe Gln Lys Val Ser Pro Gly Gly Leu Ile Lys Glu Phe Ser Glu

260 265 270

Leu Tyr Glu Thr Leu Thr Asp Asn Asp Asp Ile Leu Met Leu Ser Lys

275 280 285

Glu Ala Val Glu Ser Cys Pro Leu Met Arg Phe Ile Thr Ala Glu Thr

290 295 300

His Gly His Glu Arg Gly Ser Asp Ala Asn Thr Glu Tyr Glu Arg Leu

305 310 315 320

Leu Ser Met Leu Asn Lys Val Lys Ser Leu Lys Leu Leu Asn Thr Arg

325 330 335

Arg Arg Gln Leu Leu Asn Leu Asp Val Leu Cys Leu Ser Ser Leu Ile

340 345 350

Lys Gln Ser Ile Ser Lys Gly Leu Glu Asn Asp Lys His Trp Val Gly

355 360 365

Cys Cys Tyr Ser Ser Val Asn Asp Arg Leu Val Ser Leu Gln Ser Thr

370 375 380

Lys Glu Glu Phe Met Arg Leu Leu Lys Asn Arg Arg Lys Ser Arg Val

385 390 395 400

His Lys Lys Ala Ser Leu Asp Glu Leu Phe Arg Val Ser Ile Asn Glu

405 410 415

Phe Ile Ala Lys Ile Gln Lys Cys Leu Ser Thr Val Gly Leu Ser Phe

420 425 430

Glu His Tyr Gly Leu Ser Glu Cys Leu Val Gln Glu Cys His Ile Pro

435 440 445

Phe Ala Glu Phe Glu Asn Phe Met Arg Ala Gly Thr His Pro Val Met

450 455 460

His Tyr Thr Lys Phe Glu Asp Tyr Thr Phe Gln Pro Asn Ile Glu Gln

465 470 475 480

Leu Arg Gly Leu Gln Ser Leu Arg Lys Leu Ser Ser Val Cys Leu Ala

485 490 495

Leu Thr Asn Ser Met Lys Thr Ser Ser Val Ala Arg Leu Arg Gln Asn

500 505 510

Gln Leu Gly Ser Val Arg Tyr Gln Val Val Glu Cys Lys Glu Val Phe

515 520 525

Cys Gln Ile Ile Lys Leu Asp Ser Glu Glu Tyr His Leu Leu Tyr Gln
530 535 540
Lys Thr Gly Glu Ser Ser Arg Cys Tyr Ser Ile Gln Gly Pro Asp Gly

545 550 555 560
His Leu Ile Ser Phe Tyr Ala Asp Pro Lys Arg Phe Phe Leu Pro Ile
565 570 575
Phe Ser Asp Glu Val Leu His Asn Met Ile Asp Thr Met Ile Ser Trp
580 585 590
Ile Arg Ser Cys Pro Asp Leu Lys Asp Ser Leu Ile Asp Ile Glu Thr
595 600 605
Ala Leu Arg Thr Leu Ile Leu Leu Met Leu Thr Asn Pro Thr Lys Arg

610 615 620
Asn Gln Lys Gln Val Gln Asn Ile Arg Tyr Leu Val Met Ala Ile Val
625 630 635 640
Ser Asp Phe Ser Ser Thr Ser Leu Met Asp Lys Leu Lys Glu Asp Leu
645 650 655
Ile Thr Pro Ala Glu Lys Val Val Tyr Arg Leu Leu Arg Phe Leu Ile
660 665 670
Arg Thr Ile Phe Gly Thr Gly Glu Lys Val Leu Leu Ser Ala Lys Phe

675 680 685
Lys Phe Met Leu Asn Val Ser Tyr Leu Cys His Leu Ile Thr Lys Glu
690 695 700
Thr Pro Asp Arg Leu Thr Asp Gln Ile Lys Cys Phe Glu Lys Phe Phe
705 710 715 720
Glu Pro Lys Ser Glu Phe Gly Phe Phe Val Asn Pro Lys Glu Thr Ile
725 730 735
Thr Pro Glu Glu Glu Cys Val Phe Tyr Glu Gln Met Lys Lys Phe Thr

740 745 750
Gly Lys Asp Ile Asp Cys Gln His Ser Thr Pro Gly Val Asn Leu Glu
755 760 765
Ile Phe Ser Met Met Val Ser Ser Phe Asn Asn Gly Thr Leu Ile Leu

770 775 780

Lys Gly Glu Lys Arg Leu Asn Asn Leu Asp Pro Met Thr Asn Ser Gly

785 790 795 800

Cys Ala Thr Ala Leu Asp Leu Ala Ser Asn Lys Ser Val Val Val Asn

805 810 815

Lys His Leu Asn Gly Glu Arg Leu Leu Glu Tyr Asp Phe Asn Lys Leu

820 825 830

Leu Val Ser Ala Val Ser Gln Ile Thr Glu Gly Phe Met Arg Lys Gln

835 840 845

Lys Tyr Lys Leu Arg His Ser Asp Tyr Glu Tyr Lys Val Ser Lys Leu

850 855 860

Val Ser Arg Leu Val Ile Gly Ser Arg Lys Thr Glu Val Asp Lys Leu

865 870 875 880

Glu Asp Asp Pro Val Asp Val Cys Phe Glu Gly Glu Glu Glu Thr Ser

885 890 895

Phe Phe Arg Ser Leu Glu Asp Lys Val Ser Ser Thr Ile Thr Arg Tyr

900 905 910

Asn Arg Gly Thr Arg Leu Asn Glu Gly Gln Gly Glu Gly Glu Phe Lys

915 920 925

Asn Thr Lys Gly Leu His His Leu Gln Ile Ile Leu Ser Gly Lys Arg

930 935 940

Ala Tyr Leu Arg Lys Val Ile Leu Ser Glu Ile Ser Phe His Leu Val

945 950 955 960

Glu Asp Phe Asp Pro Ser Cys Leu Thr Asn Asp Asp Met Arg Phe Ile

965 970 975

Cys Glu Ala Val Glu Gly Ser Thr Glu Leu Ser Pro Leu Tyr Phe Thr

980 985 990

Ser Ala Val Lys Glu Gln Cys Gly Leu Asp Glu Met Ala Arg Asn Leu

995 1000 1005

Cys Arg Lys Phe Phe Ser Glu Gly Asp Trp Phe Ser Cys Met Lys

1010 1015 1020

Met Ile Leu Leu Gln Met Asn Ala Asn Ala Tyr Ser Gly Lys Tyr

1025 1030 1035

Arg His Met Gln Arg Gln Ser Leu Asn Phe Lys Phe Asp Trp Asp

1040 1045 1050

Lys Leu Glu Glu Asp Val Arg Ile Ser Glu Arg Glu Ser Asn Ser

1055 1060 1065

Glu Ser Leu Ser Lys Ala Leu Ser Leu Thr Lys Cys Met Ser Ala

1070 1075 1080

Ala Leu Lys Asn Leu Cys Phe Tyr Ser Glu Glu Ser Pro Thr Ser

1085 1090 1095

Tyr Thr Ser Val Gly Pro Asp Ser Gly Arg Leu Lys Phe Ala Leu

1100 1105 1110

Ser Tyr Lys Glu Gln Val Gly Gly Asn Arg Glu Leu Tyr Ile Gly

1115 1120 1125

Asp Leu Arg Thr Lys Met Phe Thr Arg Leu Val Glu Asp Tyr Phe

1130 1135 1140

Glu Ser Phe Ser Ser Phe Phe Ser Gly Ser Cys Leu Asn Asn Asp

1145 1150 1155

Lys Glu Phe Glu Asn Ala Ile Leu Ser Met Thr Ile Asn Val Arg

1160 1165 1170

Glu Gly Leu Leu Asn Tyr Ser Met Asp His Ser Lys Trp Gly Pro

1175 1180 1185

Met Met Cys Pro Phe Leu Phe Leu Met Leu Leu Gln Asn Leu Lys

1190 1195 1200

Leu Gly Asp Asp Gln Tyr Val Arg Ser Gly Lys Asp His Val Ser

1205 1210 1215

Thr Leu Leu Thr Trp His Met His Lys Leu Val Glu Val Pro Phe

1220 1225 1230

Pro Val Val Asn Ala Met Met Lys Ser Tyr Val Lys Ser Lys Leu

1235 1240 1245

Lys Leu Leu Lys Gly Ser Gly Thr Thr Val Thr Glu Arg Ile Phe

1250 1255 1260

Arg Glu Tyr Phe Glu Met Gly Val Val Pro Ser His Ile Ser Ser

1265 1270 1275

Leu Ile Asp Met Gly Gln Gly Ile Leu His Asn Ala Ser Asp Phe

1280 1285 1290

Tyr Gly Leu Ile Ser Glu Arg Phe Ile Asn Tyr Cys Ile Gly Val

1295 1300 1305

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

1310 1315 1320

Ile Thr Leu Phe Asp Lys Arg Leu Ser Asp Leu Val Asp Ser Asp

1325 1330 1335

Pro Glu Glu Val Leu Val Leu Leu Glu Phe His Ser His Leu Ser

1340 1345 1350

Gly Leu Leu Asn Lys Phe Ile Ser Pro Lys Ser Val Val Gly Arg

1355 1360 1365

Phe Ala Ala Glu Phe Lys Ser Arg Phe Tyr Val Trp Gly Glu Glu

1370 1375 1380

Val Pro Leu Leu Thr Lys Phe Val Ser Ala Ala Leu His Asn Val

1385 1390 1395

Lys Cys Lys Glu Pro His Gln Leu Cys Glu Thr Ile Asp Thr Ile

1400 1405 1410

Ala Asp Gln Ala Ile Ala Asn Gly Val Pro Val Phe Leu Val Asn

1415 1420 1425

Cys Ile Gln Arg Arg Thr Leu Asp Leu Leu Lys Tyr Ala Asn Phe

1430 1435 1440

Pro Leu Asp Pro Phe Leu Leu Asn Thr His Thr Asp Val Lys Asp

1445 1450 1455

Trp Leu Asp Gly Ser Arg Gly Tyr Arg Ile Gln Arg Leu Ile Glu

1460 1465 1470

Glu Leu Cys Pro Ser Glu Thr Lys Ile Met Arg Lys Leu Val Arg

1475 1480 1485

Arg Leu His His Lys Leu Lys Asn Gly Glu Cys Asn Glu Glu Phe

1490 1495 1500

Phe Leu Asp Leu Phe Asn Arg Glu Lys Lys Glu Ala Ile Leu Gln

1505 1510 1515

Leu Gly Glu Ile Leu Gly Leu Glu Asp Asp Leu Asn Glu Leu Ala

1520 1525 1530

Ser Ile Asn Trp Leu Asn Leu Asn Glu Met Phe Pro Leu Arg Met

1535 1540 1545

Val Leu Arg Gln Lys Val Val Tyr Pro Ser Val Met Thr Phe Gln

1550 1555 1560

Glu Glu Lys Ile Pro Ser Leu Ile Lys Thr Leu Gln Asn Lys Leu

1565 1570 1575

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

1580 1585 1590

Ile Asn Lys Ser Ala Phe Gln Ser Cys Val Ser Ser Gly Phe Ile

1595 1600 1605

Gly Leu Cys Lys Thr Leu Gly Ser Arg Cys Val Arg Asn Lys Asn

1610 1615 1620

Arg Glu Asn Met Tyr Ile Arg Lys Val Leu Glu Asp Leu Thr Met

1625 1630 1635

Asp Glu His Val Thr Arg Val His Lys Gln Asp Gly Val Met Leu

1640 1645 1650

Tyr Ile Cys Asp Lys Gln Arg His Pro Glu Ala His Arg Asp His

1655 1660 1665

Ile Asn Leu Leu Arg Pro Leu Leu Trp Asp Tyr Ile Cys Ile Ser

1670 1675 1680

Leu Ser Asn Ser Phe Glu Leu Gly Val Trp Val Leu Ala Glu Pro

1685 1690 1695

Val Lys Gly Lys Asn Glu Ser Asn Ser Ala Val Arg His Leu Asn

1700 1705 1710

Pro Cys Asp Tyr Val Ala Arg Lys Pro Glu Ser Ser Arg Leu Leu

1715 1720 1725

Glu Asp Lys Val Ser Leu Asn His Val Ile Gln Ser Val Arg Arg

1730 1735 1740

Leu Tyr Pro Lys Ile Phe Glu Asp Gln Leu Leu Pro Phe Met Phe

1745 1750 1755

Asp Val Ser Ser Lys Asn Met Arg Trp Ser Pro Arg Ile Lys Phe

1760 1765 1770

Leu Asp Leu Cys Val Leu Ile Asp Ile Asn Ser Glu Ser Leu Ser

1775 1780 1785

Leu Ile Ser His Val Val Lys Trp Lys Arg Asp Glu His Tyr Thr

1790 1795 1800

Val Leu Phe Ser Asp Leu Val Asn Ser His Gln Arg Ser Asp Ser

1805 1810 1815

Ser Leu Val Asp Glu Phe Val Val Ser Thr Arg Asp Val Cys Lys

1820 1825 1830

Asn Phe Leu Lys Gln Val Tyr Phe Glu Ser Phe Val Arg Glu Phe

1835 1840 1845

Val Ala Thr Ala Arg Thr Leu Gly Asn Phe Ser Trp Phe Pro His

1850 1855 1860

Lys Asp Met Met Pro Ser Glu Asp Gly Ala Glu Ala Leu Gly Pro

1865 1870 1875

Phe Gln Ser Phe Ile Leu Lys Val Val Asn Lys Lys Ile Glu Arg

1880 1885 1890

Pro Met Phe Arg Asn Asp Leu Gln Phe Gly Phe Gly Trp Phe Ser

1895 1900 1905

Tyr Arg Val Gly Asp Val Val Cys Asn Ala Ala Met Leu Ile Lys

1910 1915 1920

Gln Gly Leu Thr Asp Pro Lys Ala Phe Lys Ser Leu Arg Asp Leu

1925 1930 1935

Trp Asp Tyr Met Leu Ser Ser Thr Glu Gly Ile Leu Glu Phe Ser

1940 1945 1950

Ile Thr Val Asp Phe Thr His Asn Gln Asn Asn Thr Asp Cys Leu

1955 1960 1965

Arg Lys Phe Ser Leu Ile Phe Val Val Lys Cys Gln Leu Gln Ser

1970 1975 1980

Pro Gly Val Ala Asp Tyr Leu Ser Cys Ser His Phe Phe Lys Gly

1985 1990 1995

Glu Val Asp Arg Arg Leu Leu Asp Glu Cys Leu Asn Leu Leu Arg

2000 2005 2010

Thr Asp Pro Ile Phe Lys Ala Asn Asp Gly Val Phe Asp Ile Arg

2015 2020 2025

Ser Glu Glu Phe Glu Asp Tyr Met Glu Asp Pro Leu Thr Leu Gly

2030 2035 2040

Asp Ser Leu Glu Leu Glu Leu Ile Gly Ser Arg Arg Ile Leu Asn

2045 2050 2055

Glu Ile Lys Ser Thr Asp Phe Glu Arg Ile Gly Pro Glu Trp Glu

2060 2065 2070

Pro Val Pro Leu Thr Ile Arg Lys Gly Ala Leu Phe Glu Gly Arg

2075 2080 2085

Asn Phe Val Gln Asn Ile Ser Val Lys Leu Glu Thr Lys Asp Met

2090 2095 2100

Arg Val Phe Leu Ala Glu Leu Glu Gly Cys Gly Lys Ile Gly Asp

2105 2110 2115

Val Leu Gly Ser Leu Leu Leu His Arg Phe Arg Thr Gly Glu His

2120 2125 2130

Leu Met Glu Ser Glu Ile Ser Thr Val Leu Gln Glu Leu Cys Met

2135 2140 2145

Asp Arg Ser Val Met Leu Thr Pro Leu Ser Phe Val Pro Asp Trp

2150 2155 2160

Phe Thr Phe Arg Asp Cys Arg Leu Cys Phe Ser Arg Ser Lys Asn

2165 2170 2175

Thr Val Met Tyr Glu Thr Thr Gly Gly Arg Phe Arg Leu Lys Gly

2180 2185 2190

Lys Ser Cys Asp Asp Trp Leu Ala Glu Arg Val Ala Glu Glu Ile

2195 2200 2205

Asp

<210> 25

<211> 1497

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P52)

<400> 25

atgggtcaga ttgtgacaat gtttgaggct ttgcctcaca tcattgatga ggtcatcaac 60

attgtcatta ttgtgctcat tataatcacg agcatcaaag ctgtgtacaa tttcgccacc 120

tgtgggatat tagcactggt cagcttcctt tttttggctg gtaggtcctg tggcatgtac 180

ggccttaatg gtcccgacat ctataaaggg gtttaccagt tcaaatcagt ggagtttgat 240

atgtctcact taaatctgac gatgcccaat gcgtgctcag ccaacaactc tcatcactac 300

atcagtatgg gaagctctgg actggagcta actttcacta acgactccat ccttaatcac 360

aatttttgca acttaacctc cgctttcaac aaaaagactt ttgaccatac actcatgagt 420

atagtctcga gtctgcacct cagtattaga gggaattcca accacaaagc agtgtcttgt 480

gattttaaca atggcatcac cattcaatac aacttgtcat tttcggaccc acagagcgct 540

atgagccagt gttggacttt cagaggtaga gtcttggaca tgtttagaac tgcctttgga 600

ggaaaataca tgagaagtgg ctggggctgg gcaggttcag atggcaagac cacttggtgc 660

agccaaacaa gctatcagta cctaatcata caaaacagga cttgggaaaa ccactgtaga 720

tatgcaggcc cttttgggat gtctagaatc ctctttgctc aggaaaagac aaagtttctc 780

actaggagac ttgcaggcac attcacctgg accctgtcag actcctcagg agtagaaaat 840

ccaggtggtt attgcctgac caaatggatg atccttgctg cagagctcaa atgttttggg 900

aatacagctg ttgcaaaatg taatgtcaat catgatgaag agttctgtga catgctacga 960

ctaattgatt acaacaaggc cgccctgagt aagttcaagc aagatgtaga gtctgccttg 1020

catgtattca aaacaacagt aaattctctg atttccgatc agctgttgat gaggaatcat 1080

ctaagagatc taatgggggt accatactgt aattactcaa agttctggta tctggaacat 1140

gctaagactg gtgagactag tgtacccaag tgctggcttg tcactaatgg ctcctacttg 1200

aatgagaccc actttagtga tcaaatcgaa caagaagcag ataacatgat cacagagatg 1260

ttgaggaagg actacataaa aagacaaggg agtactcctt tagccttaat ggatcttttg 1320

atgttttcaa catcagcata tctaatcagc atctttctgc atcttgtgaa gataccaaca 1380

catagacaca taaagggcgg ttcatgtcca aagccacacc gcttgaccaa caaggggatc 1440

tgtagttgtg gtgcattcaa ggtgcctggt gtaaaaacta tctggaaaag acgctga 1497

<210> 26

<211> 498

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52)

<400> 26

Met Gly Gln Ile Val Thr Met Phe Glu Ala Leu Pro His Ile Ile Asp

1 5 10 15

Glu Val Ile Asn Ile Val Ile Ile Val Leu Ile Ile Ile Thr Ser Ile

20 25 30

Lys Ala Val Tyr Asn Phe Ala Thr Cys Gly Ile Leu Ala Leu Val Ser

35 40 45

Phe Leu Phe Leu Ala Gly Arg Ser Cys Gly Met Tyr Gly Leu Asn Gly

50 55 60

Pro Asp Ile Tyr Lys Gly Val Tyr Gln Phe Lys Ser Val Glu Phe Asp

65 70 75 80

Met Ser His Leu Asn Leu Thr Met Pro Asn Ala Cys Ser Ala Asn Asn

85 90 95

Ser His His Tyr Ile Ser Met Gly Ser Ser Gly Leu Glu Leu Thr Phe

100 105 110

Thr Asn Asp Ser Ile Leu Asn His Asn Phe Cys Asn Leu Thr Ser Ala

115 120 125

Phe Asn Lys Lys Thr Phe Asp His Thr Leu Met Ser Ile Val Ser Ser

130 135 140

Leu His Leu Ser Ile Arg Gly Asn Ser Asn His Lys Ala Val Ser Cys

145 150 155 160

Asp Phe Asn Asn Gly Ile Thr Ile Gln Tyr Asn Leu Ser Phe Ser Asp

165 170 175

Pro Gln Ser Ala Met Ser Gln Cys Trp Thr Phe Arg Gly Arg Val Leu

180 185 190

Asp Met Phe Arg Thr Ala Phe Gly Gly Lys Tyr Met Arg Ser Gly Trp
195 200 205
Gly Trp Ala Gly Ser Asp Gly Lys Thr Thr Trp Cys Ser Gln Thr Ser
210 215 220
Tyr Gln Tyr Leu Ile Ile Gln Asn Arg Thr Trp Glu Asn His Cys Arg
225 230 235 240
Tyr Ala Gly Pro Phe Gly Met Ser Arg Ile Leu Phe Ala Gln Glu Lys
245 250 255

Thr Lys Phe Leu Thr Arg Arg Leu Ala Gly Thr Phe Thr Trp Thr Leu
260 265 270
Ser Asp Ser Ser Gly Val Glu Asn Pro Gly Gly Tyr Cys Leu Thr Lys
275 280 285
Trp Met Ile Leu Ala Ala Glu Leu Lys Cys Phe Gly Asn Thr Ala Val
290 295 300
Ala Lys Cys Asn Val Asn His Asp Glu Glu Phe Cys Asp Met Leu Arg
305 310 315 320

Leu Ile Asp Tyr Asn Lys Ala Ala Leu Ser Lys Phe Lys Gln Asp Val
325 330 335
Glu Ser Ala Leu His Val Phe Lys Thr Thr Val Asn Ser Leu Ile Ser
340 345 350
Asp Gln Leu Leu Met Arg Asn His Leu Arg Asp Leu Met Gly Val Pro
355 360 365
Tyr Cys Asn Tyr Ser Lys Phe Trp Tyr Leu Glu His Ala Lys Thr Gly
370 375 380

Glu Thr Ser Val Pro Lys Cys Trp Leu Val Thr Asn Gly Ser Tyr Leu
385 390 395 400
Asn Glu Thr His Phe Ser Asp Gln Ile Glu Gln Glu Ala Asp Asn Met
405 410 415
Ile Thr Glu Met Leu Arg Lys Asp Tyr Ile Lys Arg Gln Gly Ser Thr
420 425 430

Pro Leu Ala Leu Met Asp Leu Leu Met Phe Ser Thr Ser Ala Tyr Leu
435 440 445

Ile Ser Ile Phe Leu His Leu Val Lys Ile Pro Thr His Arg His Ile
450 455 460
Lys Gly Gly Ser Cys Pro Lys Pro His Arg Leu Thr Asn Lys Gly Ile
465 470 475 480
Cys Ser Cys Gly Ala Phe Lys Val Pro Gly Val Lys Thr Ile Trp Lys
485 490 495
Arg Arg

<210> 27
<211> 1677
<212> DNA
<213> Lymphocytic choriomeningitis virus (mutant P52)

<400> 27
atgtctttgt ccaaagaagt caaaagcttt cagtggacac aggcgttgag gagggagttg 60
cagagtttta catcagatgt aaaggctgcc gtcatcaagg acgcaaccag tcttctaaat 120
gggttggact tttctgaagt cagcaacgtt cagaggatca tgagaaagga aaggagggat 180
gataaagact tgcagagact caggagtctt aaccagactg tgcattctct tgttgatctg 240
aagtctacat caaagaaaaa tgttctgaaa gtgggaagac ttagtgcaga ggaattgatg 300
acccttgcag ctgatcttga gaagctgaag gccaaaatta tgagaactga gaggcctcaa 360
gcttctggag tctacatggg aaatttgaca gcacaacaac ttgatcaaag atcccaaata 420

ctgcaaatgg ttgggatgag aagacctcag cagggtgcaa gtggtgtagt aagggtttgg 480
gatgtgaagg actcatcact tctgaacaat cagttcggca caatgccaag cctgacaatg 540
gcttgcatgg caaaacagtc acagacccca ctcaatgatg ttgtgcaggc actcacagac 600
cttggcttac tttacacagt caaatacccg aatctcagtg atcttgaaag gctaaaggat 660
aaacacccag ttctgggggt cattactgaa cagcaatcta gtatcaatat ctctggttat 720
aatttcagtc ttggtgcagc tgtgaaagcg ggggcagctc tgctagatgg agggaacatg 780
ctggaatcta tcttgatcaa accgagcaac agtgaggatc tcctaaaagc agtcctcggg 840

gccaagaaga aactcaacat gtttgtctca gatcaagttg gagatagaaa tccctatgaa 900
aacatccttt ataaagtctg tctttcaggt gaaggatggc catacatagc ctgtagaacg 960

tcagttgtgg ggagagcatg ggagaacaca acaattgatc tcacaaatga aaaacttgtt 1020

gccaactcat ctaggccagt gcctggagca gcaggcccac ctcaggtggg cttgagttac 1080

agtcagacaa tgctgttgaa agacttgatg ggagggattg atcccaatgc tcccacatgg 1140

attgacattg agggcaggtt caatgatcca gtggagatag caatattcca accacaaaat 1200

gggcaattca tacattttta cagggaacct acggaccaga agcaattcaa gcaggactca 1260

aagtattcac acggcatgga tcttgctgat ctcttcaatg cacagcctgg gctgacctca 1320

tcagttatag gtgctctccc acaagggatg gttttgagct gtcaaggttc tgatgacatc 1380

agaaagcttc tggactcaca aaayagaagg gacataaaac tcattgatgt tgagatgacc 1440

aaggaggcct caagagaata tgaagataaa gtgtgggaca aatatggctg gctatgcaaa 1500

atgcacactg gggtagtgag agacaaaaag aagaaagaga tcaccccaca ctgtgcactc 1560

atggactgca tcatttttga gagtgcttcc aaggcaagac tccctgatct aaaaaccgtt 1620

cacaacatcc tgccacatga tttaatcttc agaggaccca atgttgtgac actctaa 1677

<210> 28

<211> 558

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52)

<400> 28

Met Ser Leu Ser Lys Glu Val Lys Ser Phe Gln Trp Thr Gln Ala Leu

1 5 10 15

Arg Arg Glu Leu Gln Ser Phe Thr Ser Asp Val Lys Ala Ala Val Ile

20 25 30

Lys Asp Ala Thr Ser Leu Leu Asn Gly Leu Asp Phe Ser Glu Val Ser

35 40 45

Asn Val Gln Arg Ile Met Arg Lys Glu Arg Arg Asp Asp Lys Asp Leu

50 55 60

Gln Arg Leu Arg Ser Leu Asn Gln Thr Val His Ser Leu Val Asp Leu

65 70 75 80

Lys Ser Thr Ser Lys Lys Asn Val Leu Lys Val Gly Arg Leu Ser Ala

85 90 95

Glu Glu Leu Met Thr Leu Ala Ala Asp Leu Glu Lys Leu Lys Ala Lys

100 105 110

Ile Met Arg Thr Glu Arg Pro Gln Ala Ser Gly Val Tyr Met Gly Asn

115 120 125

Leu Thr Ala Gln Gln Leu Asp Gln Arg Ser Gln Ile Leu Gln Met Val

130 135 140

Gly Met Arg Arg Pro Gln Gln Gly Ala Ser Gly Val Val Arg Val Trp

145 150 155 160

Asp Val Lys Asp Ser Ser Leu Leu Asn Asn Gln Phe Gly Thr Met Pro

165 170 175

Ser Leu Thr Met Ala Cys Met Ala Lys Gln Ser Gln Thr Pro Leu Asn

180 185 190

Asp Val Val Gln Ala Leu Thr Asp Leu Gly Leu Leu Tyr Thr Val Lys

195 200 205

Tyr Pro Asn Leu Ser Asp Leu Glu Arg Leu Lys Asp Lys His Pro Val

210 215 220

Leu Gly Val Ile Thr Glu Gln Gln Ser Ser Ile Asn Ile Ser Gly Tyr

225 230 235 240

Asn Phe Ser Leu Gly Ala Ala Val Lys Ala Gly Ala Ala Leu Leu Asp

245 250 255

Gly Gly Asn Met Leu Glu Ser Ile Leu Ile Lys Pro Ser Asn Ser Glu

260 265 270

Asp Leu Leu Lys Ala Val Leu Gly Ala Lys Lys Lys Leu Asn Met Phe

275 280 285

Val Ser Asp Gln Val Gly Asp Arg Asn Pro Tyr Glu Asn Ile Leu Tyr

290 295 300

Lys Val Cys Leu Ser Gly Glu Gly Trp Pro Tyr Ile Ala Cys Arg Thr

305 310 315 320

Ser Val Val Gly Arg Ala Trp Glu Asn Thr Thr Ile Asp Leu Thr Asn

325 330 335

Glu Lys Leu Val Ala Asn Ser Ser Arg Pro Val Pro Gly Ala Ala Gly

340 345 350

Pro Pro Gln Val Gly Leu Ser Tyr Ser Gln Thr Met Leu Leu Lys Asp

355 360 365

Leu Met Gly Gly Ile Asp Pro Asn Ala Pro Thr Trp Ile Asp Ile Glu

370 375 380

Gly Arg Phe Asn Asp Pro Val Glu Ile Ala Ile Phe Gln Pro Gln Asn

385 390 395 400

Gly Gln Phe Ile His Phe Tyr Arg Glu Pro Thr Asp Gln Lys Gln Phe

405 410 415

Lys Gln Asp Ser Lys Tyr Ser His Gly Met Asp Leu Ala Asp Leu Phe

420 425 430

Asn Ala Gln Pro Gly Leu Thr Ser Ser Val Ile Gly Ala Leu Pro Gln

435 440 445

Gly Met Val Leu Ser Cys Gln Gly Ser Asp Asp Ile Arg Lys Leu Leu

450 455 460

Asp Ser Gln Asn Arg Arg Asp Ile Lys Leu Ile Asp Val Glu Met Thr

465 470 475 480

Lys Glu Ala Ser Arg Glu Tyr Glu Asp Lys Val Trp Asp Lys Tyr Gly

485 490 495

Trp Leu Cys Lys Met His Thr Gly Val Val Arg Asp Lys Lys Lys Lys

500 505 510

Glu Ile Thr Pro His Cys Ala Leu Met Asp Cys Ile Ile Phe Glu Ser

515 520 525

Ala Ser Lys Ala Arg Leu Pro Asp Leu Lys Thr Val His Asn Ile Leu

530 535 540

Pro His Asp Leu Ile Phe Arg Gly Pro Asn Val Val Thr Leu

545 550 555

<210> 29

<211> 273

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P52)

<400> 29

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<211> 90

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52)

<400> 30

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20 25 30

Lys Ser Cys Trp Gln Lys Phe Asp Ser Leu Val Arg Cys His Asp His

35 40 45

Tyr Leu Cys Arg His Cys Leu Asn Leu Leu Leu Ser Val Ser Asp Arg

50 55 60

Cys Pro Leu Cys Lys Tyr Pro Leu Pro Thr Lys Leu Lys Val Ser Thr

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Val Pro Ser Ser Pro Pro Pro Tyr Glu Glu

85 90

<210> 31

<211> 6630

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P52)

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cttgaatgtt ttgttagaag cacaccagct agttttgaaa agaagttcat tgaggacacc 360

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<210> 32

<211> 2209

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52)

<220><221> MISC_FEATURE

<222> (2094)..(2094)

<223> Xaa can be Ile or Val

<220><221> MISC_FEATURE

<222> (2141)..(2141)

<223> Xaa can be Thr or Ala

<400> 32

Met Asp Glu Thr Ile Ala Asp Leu Arg Glu Leu Cys Leu Asn Tyr Ile

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Glu Gln Asp Glu Arg Leu Ser Arg Gln Lys Leu Asn Phe Leu Gly Gln

20 25 30

Arg Glu Pro Arg Met Val Leu Ile Glu Gly Leu Lys Leu Leu Ser Arg

35 40 45

Cys Ile Glu Ile Asp Ser Ala Asp Lys Ser Gly Cys Ile His Asn His

50 55 60

Asp Asp Lys Ser Val Glu Thr Ile Leu Ile Asp Ser Gly Ile Val Cys

65 70 75 80

Pro Gly Leu Pro Leu Ile Ile Pro Asp Gly Tyr Lys Leu Ile Asp Asn

85 90 95

Ser Leu Ile Leu Leu Glu Cys Phe Val Arg Ser Thr Pro Ala Ser Phe

100 105 110

Glu Lys Lys Phe Ile Glu Asp Thr Asn Lys Leu Ala Cys Ile Lys Glu

115 120 125

Asp Leu Ala Val Ala Gly Ile Thr Leu Val Pro Ile Val Asp Gly Arg

130 135 140

Cys Asp Tyr Asp Asn Ser Phe Met Pro Glu Trp Val Asn Phe Lys Phe

145 150 155 160

Arg Asp Leu Leu Phe Lys Leu Leu Glu Tyr Ser Ser Gln Asp Glu Lys

165 170 175

Val Phe Glu Glu Ser Glu Tyr Phe Arg Leu Cys Glu Ser Leu Lys Thr

180 185 190

Thr Val Asp Lys Arg Ser Gly Met Asp Ser Met Lys Ile Leu Lys Asp

195 200 205

Ala Arg Ser Phe His Asn Asp Glu Ile Met Lys Met Cys His Asp Gly

210 215 220

Val Asn Pro Asn Met Ser Cys Asp Asp Val Val Phe Gly Ile Asn Ser

225 230 235 240

Phe Phe Gly Arg Phe Arg Arg Asp Leu Leu Asn Gly Lys Leu Lys Arg

245 250 255

Asn Phe Gln Lys Val Ser Pro Gly Gly Leu Ile Lys Glu Phe Ser Glu

260 265 270

Leu Tyr Glu Thr Leu Thr Asp Asn Asp Asp Ile Leu Met Leu Ser Lys

275 280 285

Glu Ala Val Glu Ser Cys Pro Leu Met Arg Phe Ile Thr Ala Glu Thr
290 295 300
His Gly His Glu Arg Gly Ser Asp Ala Asn Thr Glu Tyr Glu Arg Leu
305 310 315 320
Leu Ser Met Leu Asn Lys Val Lys Ser Leu Lys Leu Leu Asn Thr Arg
325 330 335

Arg Arg Gln Leu Leu Asn Leu Asp Val Leu Cys Leu Ser Ser Leu Ile
340 345 350
Lys Gln Ser Ile Ser Lys Gly Leu Glu Asn Asp Lys His Trp Val Gly
355 360 365
Cys Cys Tyr Ser Ser Val Asn Asp Arg Leu Val Ser Leu Gln Ser Thr
370 375 380
Lys Glu Glu Phe Met Arg Leu Leu Lys Asn Arg Arg Lys Ser Arg Val
385 390 395 400

His Lys Lys Ala Ser Leu Asp Glu Leu Phe Arg Val Ser Ile Asn Glu
405 410 415
Phe Ile Ala Lys Ile Gln Lys Cys Leu Ser Thr Val Gly Leu Ser Phe
420 425 430
Glu His Tyr Gly Leu Ser Glu Cys Leu Val Gln Glu Cys His Ile Pro
435 440 445
Phe Ala Glu Phe Glu Asn Phe Met Arg Ala Gly Thr His Pro Val Met
450 455 460

His Tyr Thr Lys Phe Glu Asp Tyr Thr Phe Gln Pro Asn Ile Glu Gln
465 470 475 480
Leu Arg Gly Leu Gln Ser Leu Arg Lys Leu Ser Ser Val Cys Leu Ala
485 490 495
Leu Thr Asn Ser Met Lys Thr Ser Ser Val Ala Arg Leu Arg Gln Asn
500 505 510
Gln Leu Gly Ser Val Arg Tyr Gln Val Val Glu Cys Lys Glu Val Phe
515 520 525

Cys Gln Ile Ile Lys Leu Asp Ser Glu Glu Tyr His Leu Leu Tyr Gln

530 535 540

Lys Thr Gly Glu Ser Ser Arg Cys Tyr Ser Ile Gln Gly Pro Asp Gly

545 550 555 560

His Leu Ile Ser Phe Tyr Ala Asp Pro Lys Arg Phe Phe Leu Pro Ile

565 570 575

Phe Ser Asp Glu Val Leu His Asn Met Ile Asp Thr Met Ile Ser Trp

580 585 590

Ile Arg Ser Cys Pro Asp Leu Lys Asp Ser Leu Ile Asp Ile Glu Thr

595 600 605

Ala Leu Arg Thr Leu Ile Leu Leu Met Leu Thr Asn Pro Thr Lys Arg

610 615 620

Asn Gln Lys Gln Val Gln Asn Ile Arg Tyr Leu Val Met Ala Ile Val

625 630 635 640

Ser Asp Phe Ser Ser Thr Ser Leu Met Asp Lys Leu Lys Glu Asp Leu

645 650 655

Ile Thr Pro Ala Glu Lys Val Val Tyr Arg Leu Leu Arg Phe Leu Ile

660 665 670

Arg Thr Ile Phe Gly Thr Gly Glu Lys Val Leu Leu Ser Ala Lys Phe

675 680 685

Lys Phe Met Leu Asn Val Ser Tyr Leu Cys His Leu Ile Thr Lys Glu

690 695 700

Thr Pro Asp Arg Leu Thr Asp Gln Ile Lys Cys Phe Glu Lys Phe Phe

705 710 715 720

Glu Pro Lys Ser Glu Phe Gly Phe Phe Val Asn Pro Lys Glu Thr Ile

725 730 735

Thr Pro Glu Glu Glu Cys Val Phe Tyr Glu Gln Met Lys Lys Phe Thr

740 745 750

Gly Lys Asp Ile Asp Cys Gln His Ser Thr Pro Gly Val Asn Leu Glu

755 760 765

Ile Phe Ser Met Met Val Ser Ser Phe Asn Asn Gly Thr Leu Ile Leu

770 775 780

Lys Gly Glu Lys Arg Leu Asn Asn Leu Asp Pro Met Thr Asn Ser Gly
785 790 795 800
Cys Ala Thr Ala Leu Asp Leu Ala Ser Asn Lys Ser Val Val Val Asn
805 810 815
Lys His Leu Asn Gly Glu Arg Leu Leu Glu Tyr Asp Phe Asn Lys Leu
820 825 830
Leu Val Ser Ala Val Ser Gln Ile Thr Glu Gly Phe Met Arg Lys Gln
835 840 845

Lys Tyr Lys Leu Arg His Ser Asp Tyr Glu Tyr Lys Val Ser Lys Leu
850 855 860
Val Ser Arg Leu Val Ile Gly Ser Arg Lys Thr Glu Val Asp Lys Leu
865 870 875 880
Glu Asp Asp Pro Val Asp Val Cys Phe Glu Gly Glu Glu Glu Thr Ser
885 890 895
Phe Phe Arg Ser Leu Glu Asp Lys Val Ser Ser Thr Ile Thr Arg Tyr
900 905 910

Asn Arg Gly Thr Arg Leu Asn Glu Gly Gln Gly Glu Gly Glu Phe Lys
915 920 925
Asn Thr Lys Gly Leu His His Leu Gln Ile Ile Leu Ser Gly Lys Arg
930 935 940
Ala Tyr Leu Arg Lys Val Ile Leu Ser Glu Ile Ser Phe His Leu Val
945 950 955 960
Glu Asp Phe Asp Pro Ser Cys Leu Thr Asn Asp Asp Met Arg Phe Ile
965 970 975

Cys Glu Ala Val Glu Gly Ser Thr Glu Leu Ser Pro Leu Tyr Phe Thr
980 985 990
Ser Ala Val Lys Glu Gln Cys Gly Leu Asp Glu Met Ala Arg Asn Leu
995 1000 1005
Cys Arg Lys Phe Phe Ser Glu Gly Asp Trp Phe Ser Cys Met Lys
1010 1015 1020
Met Ile Leu Leu Gln Met Asn Ala Asn Ala Tyr Ser Gly Lys Tyr

1025 1030 1035

Arg His Met Gln Arg Gln Ser Leu Asn Phe Lys Phe Asp Trp Asp
1040 1045 1050
Lys Leu Glu Glu Asp Val Arg Ile Ser Glu Arg Glu Ser Asn Ser
1055 1060 1065
Glu Ser Leu Ser Lys Ala Leu Ser Leu Thr Lys Cys Met Ser Ala
1070 1075 1080
Ala Leu Lys Asn Leu Cys Phe Tyr Ser Glu Glu Ser Pro Thr Ser
1085 1090 1095

Tyr Thr Ser Val Gly Pro Asp Ser Gly Arg Leu Lys Phe Ala Leu
1100 1105 1110
Ser Tyr Lys Glu Gln Val Gly Gly Asn Arg Glu Leu Tyr Ile Gly
1115 1120 1125
Asp Leu Arg Thr Lys Met Phe Thr Arg Leu Val Glu Asp Tyr Phe
1130 1135 1140
Glu Ser Phe Ser Ser Phe Phe Ser Gly Ser Cys Leu Asn Asn Asp
1145 1150 1155

Lys Glu Phe Glu Asn Ala Ile Leu Ser Met Thr Ile Asn Val Arg
1160 1165 1170
Glu Gly Leu Leu Asn Tyr Ser Met Asp His Ser Lys Trp Gly Pro
1175 1180 1185
Met Met Cys Pro Phe Leu Phe Leu Met Leu Leu Gln Asn Leu Lys
1190 1195 1200
Leu Gly Asp Asp Gln Tyr Val Arg Ser Gly Lys Asp His Val Ser
1205 1210 1215

Thr Leu Leu Thr Trp His Met His Lys Leu Val Glu Val Pro Phe
1220 1225 1230
Pro Val Val Asn Ala Met Met Lys Ser Tyr Val Lys Ser Lys Leu
1235 1240 1245
Lys Leu Leu Lys Gly Ser Gly Thr Thr Val Thr Glu Arg Ile Phe
1250 1255 1260

Arg Glu Tyr Phe Glu Met Gly Val Val Pro Ser His Ile Ser Ser
1265 1270 1275

Leu Ile Asp Met Gly Gln Gly Ile Leu His Asn Ala Ser Asp Phe
1280 1285 1290
Tyr Gly Leu Ile Ser Glu Arg Phe Ile Asn Tyr Cys Ile Gly Val
1295 1300 1305
Ile Phe Gly Glu Arg Pro Glu Ala Tyr Thr Ser Ser Asp Asp Gln
1310 1315 1320
Ile Thr Leu Phe Asp Lys Arg Leu Ser Asp Leu Val Asp Ser Asp
1325 1330 1335

Pro Glu Glu Val Leu Val Leu Leu Glu Phe His Ser His Leu Ser
1340 1345 1350
Gly Leu Leu Asn Lys Phe Ile Ser Pro Lys Ser Val Val Gly Arg
1355 1360 1365
Phe Ala Ala Glu Phe Lys Ser Arg Phe Tyr Val Trp Gly Glu Glu
1370 1375 1380
Val Pro Leu Leu Thr Lys Phe Val Ser Ala Ala Leu His Asn Val
1385 1390 1395

Lys Cys Lys Glu Pro His Gln Leu Cys Glu Thr Ile Asp Thr Ile
1400 1405 1410
Ala Asp Gln Ala Ile Ala Asn Gly Val Pro Val Phe Leu Val Asn
1415 1420 1425
Cys Ile Gln Arg Arg Thr Leu Asp Leu Leu Lys Tyr Ala Asn Phe
1430 1435 1440
Pro Leu Asp Pro Phe Leu Leu Asn Thr His Thr Asp Val Lys Asp
1445 1450 1455

Trp Leu Asp Gly Ser Arg Gly Tyr Arg Ile Gln Arg Leu Ile Glu
1460 1465 1470
Glu Leu Cys Pro Ser Glu Thr Lys Ile Met Arg Lys Leu Val Arg
1475 1480 1485
Arg Leu His His Lys Leu Lys Asn Gly Glu Cys Asn Glu Glu Phe

1490 1495 1500

Phe Leu Asp Leu Phe Asn Arg Glu Lys Lys Glu Ala Ile Leu Gln

1505 1510 1515

Leu Gly Glu Ile Leu Gly Leu Glu Asp Asp Leu Asn Glu Leu Ala

1520 1525 1530

Ser Ile Asn Trp Leu Asn Leu Asn Glu Met Phe Pro Leu Arg Met

1535 1540 1545

Val Leu Arg Gln Lys Val Val Tyr Pro Ser Val Met Thr Phe Gln

1550 1555 1560

Glu Glu Lys Ile Pro Ser Leu Ile Lys Thr Leu Gln Asn Lys Leu

1565 1570 1575

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

1580 1585 1590

Ile Asn Lys Ser Ala Phe Gln Ser Cys Val Ser Ser Gly Phe Ile

1595 1600 1605

Gly Leu Cys Lys Thr Leu Gly Ser Arg Cys Val Arg Asn Lys Asn

1610 1615 1620

Arg Glu Asn Met Tyr Ile Arg Lys Val Leu Glu Asp Leu Thr Met

1625 1630 1635

Asp Glu His Val Thr Arg Val His Lys Gln Asp Gly Val Met Leu

1640 1645 1650

Tyr Ile Cys Asp Lys Gln Arg His Pro Glu Ala His Arg Asp His

1655 1660 1665

Ile Asn Leu Leu Arg Pro Leu Leu Trp Asp Tyr Ile Cys Ile Ser

1670 1675 1680

Leu Ser Asn Ser Phe Glu Leu Gly Val Trp Val Leu Ala Glu Pro

1685 1690 1695

Val Lys Gly Lys Asn Glu Ser Asn Ser Ala Val Arg His Leu Asn

1700 1705 1710

Pro Cys Asp Tyr Val Ala Arg Lys Pro Glu Ser Ser Arg Leu Leu

1715 1720 1725

Glu Asp Lys Val Ser Leu Asn His Val Ile Gln Ser Val Arg Arg
1730 1735 1740
Leu Tyr Pro Lys Ile Phe Glu Asp Gln Leu Leu Pro Phe Met Ser
1745 1750 1755

Asp Val Ser Ser Lys Asn Met Arg Trp Ser Pro Arg Ile Lys Phe
1760 1765 1770
Leu Asp Leu Cys Val Leu Ile Asp Ile Asn Ser Glu Ser Leu Ser
1775 1780 1785
Leu Ile Ser His Val Val Lys Trp Lys Arg Asp Glu His Tyr Thr
1790 1795 1800
Val Leu Phe Ser Asp Leu Val Asn Ser His Gln Arg Ser Asp Ser
1805 1810 1815

Ser Leu Val Asp Glu Phe Val Val Ser Thr Arg Asp Val Cys Lys
1820 1825 1830
Asn Phe Leu Lys Gln Val Tyr Phe Glu Ser Phe Val Arg Glu Phe
1835 1840 1845
Val Ala Thr Ala Arg Thr Leu Gly Asn Phe Ser Trp Phe Pro His
1850 1855 1860
Lys Asp Met Met Pro Ser Glu Asp Gly Ala Glu Ala Leu Gly Pro
1865 1870 1875

Phe Gln Ser Phe Ile Leu Lys Val Val Asn Lys Lys Ile Glu Arg
1880 1885 1890
Pro Met Phe Arg Asn Asp Leu Gln Phe Gly Phe Gly Trp Phe Ser
1895 1900 1905
Tyr Arg Val Gly Asp Val Val Cys Asn Ala Ala Met Leu Ile Lys
1910 1915 1920
Gln Gly Leu Thr Asp Pro Lys Ala Phe Lys Ser Leu Arg Asp Leu
1925 1930 1935

Trp Asp Tyr Met Leu Ser Ser Thr Glu Gly Ile Leu Glu Phe Ser
1940 1945 1950
Ile Thr Val Asp Phe Thr His Asn Gln Asn Asn Thr Asp Cys Leu

1955 1960 1965

Arg Lys Phe Ser Leu Ile Phe Val Val Lys Cys Gln Leu Gln Ser

1970 1975 1980

Pro Gly Val Ala Asp Tyr Leu Ser Cys Ser His Ser Phe Lys Gly

1985 1990 1995

Glu Val Asp Arg Arg Leu Leu Asp Glu Cys Leu Asn Leu Leu Arg

2000 2005 2010

Thr Asp Pro Ile Phe Lys Ala Asn Asp Gly Val Phe Asp Ile Arg

2015 2020 2025

Ser Glu Glu Phe Glu Asp Tyr Met Glu Asp Pro Leu Thr Leu Gly

2030 2035 2040

Asp Ser Leu Glu Leu Glu Leu Ile Gly Ser Arg Arg Ile Leu Asn

2045 2050 2055

Glu Ile Lys Ser Thr Asp Phe Glu Arg Ile Gly Pro Glu Trp Glu

2060 2065 2070

Pro Val Pro Leu Thr Ile Arg Lys Gly Ala Leu Phe Glu Gly Arg

2075 2080 2085

Asn Phe Val Gln Asn Xaa Ser Val Lys Leu Glu Thr Lys Asp Met

2090 2095 2100

Arg Val Phe Leu Ala Glu Leu Glu Gly Cys Gly Lys Ile Gly Asp

2105 2110 2115

Val Leu Gly Ser Leu Leu Leu His Arg Phe Arg Thr Gly Glu His

2120 2125 2130

Leu Met Glu Ser Glu Ile Ser Xaa Val Leu Gln Glu Leu Cys Met

2135 2140 2145

Asp Arg Ser Val Met Leu Thr Pro Leu Ser Phe Val Pro Asp Trp

2150 2155 2160

Phe Thr Phe Arg Asp Cys Arg Leu Cys Phe Ser Arg Ser Lys Asn

2165 2170 2175

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2180 2185 2190

Lys Ser Cys Asp Asp Trp Leu Ala Glu Arg Val Ala Glu Glu Ile

2195 2200 2205

Asp

<210> 33

<211> 1497

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P91)

<400> 33

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gattttaaca atggcatcac cattcaatac aacttgtcat tttcggaccc acagagcgct 540

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<210> 34

<211> 498

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P91)

<400> 34

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Glu Val Ile Asn Ile Val Ile Ile Val Leu Ile Ile Ile Thr Ser Ile

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Lys Ala Val Tyr Asn Phe Ala Thr Cys Gly Ile Leu Ala Leu Val Ser

35 40 45

Phe Leu Phe Leu Ala Gly Arg Ser Cys Gly Met Tyr Gly Leu Asn Gly

50 55 60

Pro Asp Ile Tyr Lys Gly Val Tyr Gln Phe Lys Ser Val Glu Phe Asp

65 70 75 80

Met Ser His Leu Asn Leu Thr Met Pro Asn Ala Cys Ser Ala Asn Asn

85 90 95

Ser His His Tyr Ile Ser Met Gly Ser Ser Gly Leu Glu Leu Thr Phe

100 105 110

Thr Asn Asp Ser Ile Leu Asn His Asn Phe Cys Asn Leu Thr Ser Ala

115 120 125

Phe Asn Lys Lys Thr Phe Asp His Thr Leu Met Ser Ile Val Ser Ser

130 135 140

Leu His Leu Ser Ile Arg Gly Asn Ser Asn His Lys Ala Val Ser Cys

145 150 155 160

Asp Phe Asn Asn Gly Ile Thr Ile Gln Tyr Asn Leu Ser Phe Ser Asp

165 170 175

Pro Gln Ser Ala Met Ser Gln Cys Trp Thr Phe Arg Gly Arg Val Leu

180 185 190

Asp Met Phe Arg Thr Ala Phe Gly Gly Lys Tyr Met Arg Ser Gly Trp

195 200 205

Gly Trp Ala Gly Ser Asp Gly Lys Thr Thr Trp Cys Ser Gln Thr Ser

210 215 220

Tyr Gln Tyr Leu Ile Ile Gln Asn Arg Thr Trp Glu Asn His Cys Arg

225 230 235 240

Tyr Ala Gly Pro Phe Gly Met Ser Arg Ile Leu Phe Ala Gln Glu Lys

245 250 255

Thr Lys Phe Leu Thr Arg Arg Leu Ala Gly Thr Phe Thr Trp Thr Leu

260 265 270

Ser Asp Ser Ser Gly Val Glu Asn Pro Gly Gly Tyr Cys Leu Thr Lys

275 280 285

Trp Met Ile Leu Ala Ala Glu Leu Lys Cys Phe Gly Asn Thr Ala Val

290 295 300

Ala Lys Cys Asn Val Asn His Asp Glu Glu Phe Cys Asp Met Leu Arg

305 310 315 320

Leu Ile Asp Tyr Asn Lys Ala Ala Leu Ser Lys Phe Lys Gln Asp Val

325 330 335

Glu Ser Ala Leu His Val Phe Lys Thr Thr Val Asn Ser Leu Ile Ser

340 345 350

Asp Gln Leu Leu Met Arg Asn His Leu Arg Asp Leu Met Gly Val Pro

355 360 365

Tyr Cys Asn Tyr Ser Lys Phe Trp Tyr Leu Glu His Ala Lys Thr Gly

370 375 380

Glu Thr Ser Val Pro Lys Cys Trp Leu Val Thr Asn Gly Ser Tyr Leu

385 390 395 400

Asn Glu Thr His Phe Ser Asp Gln Ile Glu Gln Glu Ala Asp Asn Met

405 410 415

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

420 425 430

Pro Leu Ala Leu Met Asp Leu Leu Met Phe Ser Thr Ser Ala Tyr Leu
435 440 445
Ile Ser Ile Phe Leu His Leu Val Lys Ile Pro Thr His Arg His Ile
450 455 460
Lys Gly Gly Ser Cys Pro Lys Pro His Arg Leu Thr Asn Lys Gly Ile
465 470 475 480

Cys Ser Cys Gly Ala Phe Lys Val Pro Gly Val Lys Thr Ile Trp Lys
485 490 495
Arg Arg

<210> 35
<211> 1677
<212> DNA
<213> Lymphocytic choriomeningitis virus (mutant P91)
<400> 35
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atggactgca tcatttttga gagtgcttcc aaggcaagac tccctgatct aaaaaccgtt 1620

cacaacatcc tgccacatga tttaatcttc agaggaccca atgttgtgac actctaa 1677

<210> 36

<211> 558

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P91)

<400> 36

Met Ser Leu Ser Lys Glu Val Lys Ser Phe Gln Trp Thr Gln Ala Leu

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Arg Arg Glu Leu Gln Ser Phe Thr Ser Asp Val Lys Ala Ala Val Ile

20 25 30

Lys Asp Ala Thr Ser Leu Leu Asn Gly Leu Asp Phe Ser Glu Val Ser

35 40 45

Asn Val Gln Arg Ile Met Arg Lys Glu Arg Arg Asp Asp Lys Asp Leu

50 55 60

Gln Arg Leu Arg Ser Leu Asn Gln Thr Val His Ser Leu Val Asp Leu

65 70 75 80

Lys Ser Thr Ser Lys Lys Asn Val Leu Lys Val Gly Arg Leu Ser Ala

85 90 95

Glu Glu Leu Met Thr Leu Ala Ala Asp Leu Glu Lys Leu Lys Ala Lys

100 105 110

Ile Met Arg Thr Glu Arg Pro Gln Ala Ser Gly Val Tyr Met Gly Asn

115 120 125

Leu Thr Ala Gln Gln Leu Asp Gln Arg Ser Gln Ile Leu Gln Met Val

130 135 140

Gly Met Arg Arg Pro Gln Gln Gly Ala Ser Gly Val Val Arg Val Trp

145 150 155 160

Asp Val Lys Asp Ser Ser Leu Leu Asn Asn Gln Phe Gly Thr Met Pro

165 170 175

Ser Leu Thr Met Ala Cys Met Ala Lys Gln Ser Gln Thr Pro Leu Asn

180 185 190

Asp Val Val Gln Ala Leu Thr Asp Leu Gly Leu Leu Tyr Thr Val Lys

195 200 205

Tyr Pro Asn Leu Ser Asp Leu Glu Arg Leu Lys Asp Lys His Pro Val

210 215 220

Leu Gly Val Ile Thr Glu Gln Gln Ser Ser Ile Asn Ile Ser Gly Tyr

225 230 235 240

Asn Phe Ser Leu Gly Ala Ala Val Lys Ala Gly Ala Ala Leu Leu Asp

245 250 255

Gly Gly Asn Met Leu Glu Ser Ile Leu Ile Lys Pro Ser Asn Ser Glu

260 265 270

Asp Leu Leu Lys Ala Val Leu Gly Ala Lys Lys Lys Leu Asn Met Phe

275 280 285

Val Ser Asp Gln Val Gly Asp Arg Asn Pro Tyr Glu Asn Ile Leu Tyr

290 295 300

Lys Val Cys Leu Ser Gly Glu Gly Trp Pro Tyr Ile Ala Cys Arg Thr

305 310 315 320

Ser Val Val Gly Arg Ala Trp Glu Asn Thr Thr Ile Asp Leu Thr Asn

325 330 335

Glu Lys Leu Val Ala Asn Ser Ser Arg Pro Val Pro Gly Ala Ala Gly

340 345 350

Pro Pro Gln Val Gly Leu Ser Tyr Ser Gln Thr Met Leu Leu Lys Asp

355 360 365

Leu Met Gly Gly Ile Asp Pro Asn Ala Pro Thr Trp Ile Asp Ile Glu

370 375 380

Gly Arg Phe Asn Asp Pro Val Glu Ile Ala Ile Phe Gln Pro Gln Asn

385 390 395 400

Gly Gln Phe Ile His Phe Tyr Arg Glu Pro Thr Asp Gln Lys Gln Phe

405 410 415

Lys Gln Asp Ser Lys Tyr Ser His Gly Met Asp Leu Ala Asp Leu Phe

420 425 430

Asn Ala Gln Pro Gly Leu Thr Ser Ser Val Ile Gly Ala Leu Pro Gln

435 440 445

Gly Met Val Leu Ser Cys Gln Gly Ser Asp Asp Ile Arg Lys Leu Leu

450 455 460

Asp Ser Gln Asn Arg Arg Asp Ile Lys Leu Ile Asp Val Glu Met Thr

465 470 475 480

Lys Glu Ala Ser Arg Glu Tyr Glu Asp Lys Val Trp Asp Lys Tyr Gly

485 490 495

Trp Leu Cys Lys Met His Thr Gly Val Val Arg Asp Lys Lys Lys Lys

500 505 510

Glu Ile Thr Pro His Cys Ala Leu Met Asp Cys Ile Ile Phe Glu Ser

515 520 525

Ala Ser Lys Ala Arg Leu Pro Asp Leu Lys Thr Val His Asn Ile Leu

530 535 540

Pro His Asp Leu Ile Phe Arg Gly Pro Asn Val Val Thr Leu

545 550 555

<210> 37

<211> 273

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P91)

<400> 37

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agcttggtta gatgccatga ccactatctt tgcagacact gtctgaatct cctgctgtca 180

gtttccgaca gatgtcctct ctgtaagtat ccactgccaa ccaaactgaa ggtgtcaaca 240

gtcccaagct ccccacctcc ctatgaggag tga 273

<210> 38

<211> 90

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P91)

<400> 38

Met Gly Gln Gly Lys Ser Lys Glu Glu Arg Asp Thr Ser Asn Thr Gly

1 5 10 15

Arg Ala Glu Leu Leu Pro Asp Thr Thr Tyr Leu Gly Pro Leu Asn Cys

20 25 30

Lys Ser Cys Trp Gln Lys Phe Asp Ser Leu Val Arg Cys His Asp His

35 40 45

Tyr Leu Cys Arg His Cys Leu Asn Leu Leu Leu Ser Val Ser Asp Arg

50 55 60

Cys Pro Leu Cys Lys Tyr Pro Leu Pro Thr Lys Leu Lys Val Ser Thr

65 70 75 80

Val Pro Ser Ser Pro Pro Pro Tyr Glu Glu

85 90

<210> 39

<211> 6630

<212

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<213> Lymphocytic choriomeningitis virus (mutant P91)

<400> 39

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gagggactca aattgttatc acgctgtata gagatagaca gtgcagacaa aagtggttgc 180

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tcatttattt tgaaagtggt gaacaagaaa atagagaggc ccatgtttag gaatgacttg 5700
cagtttggtt ttggttggtt ctcttatcgt gtgggggatg ttgtgtgtaa tgccgctatg 5760
ttaattaagc agggtttgac agatccaaaa gcatttaaat ctttaagaga tttgtgggat 5820

tacatgctca gcagcacaga ggggatattg gagttctcaa tcacagtgga tttcacacac 5880

aaccagaaca acactgactg cttgaggaaa ttttcattga tctttgtggt taaatgccaa 5940

ttacagagtc caggtgtagc tgattactta tcgtgctctc attccttcaa aggtgaggtt 6000

gacaggagat tattagatga gtgtctcaat ctgttgagga cagaccccat ctttaaagcg 6060

aatgatggag tctttgacat taggtctgaa gagtttgaag attacatgga agaccctttg 6120

acacttggtg attcactaga acttgaacta ataggttcta gaaggattct gaatgagatc 6180

aaatctactg actttgagag gatagggcct gagtgggaac ctgtgcctct gaccataagg 6240

aagggtgccc tctttgaggg gaggaacttt gttcagaata tctctgtgaa attggagaca 6300

aaggacatga gggtctttct ggcagagctc gagggctgtg gaaaaattgg tgatgtcctc 6360

ggcagcctcc tcctgcaccg attcagaact ggtgagcact tgatggagtc agaaataagt 6420

acagttcttc aggagctctg catggacaga tccgtcatgc tgacaccatt atcttttgtg 6480

ccagattggt tcaccttcag agattgtagg ctctgcttca gcargtcaaa gaacactgta 6540

atgtatgaga caactggggg caggttcaga ctcaagggga aatcctgtga cgattggctg 6600

gcggagcggg tggccgagga gatcgactag 6630

<210> 40

<211> 2209

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P91)

<220><221> MISC_FEATURE

<222> (2175)..(2175)

<223> Xaa can be Arg or Lys

<400> 40

Met Asp Glu Thr Ile Ala Asp Leu Arg Glu Leu Cys Leu Asn Tyr Ile

1 5 10 15

Glu Gln Asp Glu Arg Leu Ser Arg Gln Lys Leu Asn Phe Leu Gly Gln

20 25 30

Arg Glu Pro Arg Met Val Leu Ile Glu Gly Leu Lys Leu Leu Ser Arg

35 40 45

Cys Ile Glu Ile Asp Ser Ala Asp Lys Ser Gly Cys Ile His Asn His

50 55 60

Asp Asp Lys Ser Val Glu Thr Ile Leu Ile Asp Ser Gly Ile Val Cys

65 70 75 80

Pro Gly Leu Pro Leu Ile Ile Pro Asp Gly Tyr Lys Leu Ile Asp Asn
85 90 95
Ser Leu Ile Leu Leu Glu Cys Phe Val Arg Ser Thr Pro Ala Ser Phe

100 105 110
Glu Lys Lys Phe Ile Glu Asp Thr Asn Lys Leu Ala Cys Ile Lys Glu
115 120 125
Asp Leu Ala Val Ala Gly Ile Thr Leu Val Pro Ile Val Asp Gly Arg
130 135 140
Cys Asp Tyr Asp Asn Ser Phe Met Pro Glu Trp Val Asn Phe Lys Phe
145 150 155 160
Arg Asp Leu Leu Phe Lys Leu Leu Glu Tyr Ser Ser Gln Asp Glu Lys

165 170 175
Val Phe Glu Glu Ser Glu Tyr Phe Arg Leu Cys Glu Ser Leu Lys Thr
180 185 190
Thr Val Asp Lys Arg Ser Gly Met Asp Ser Met Lys Ile Leu Lys Asp
195 200 205
Ala Arg Ser Phe His Asn Asp Glu Ile Met Lys Met Cys His Asp Gly
210 215 220
Val Asn Pro Asn Met Ser Cys Asp Asp Val Val Phe Gly Ile Asn Ser

225 230 235 240
Phe Phe Gly Arg Phe Arg Arg Asp Leu Leu Asn Gly Lys Leu Lys Arg
245 250 255
Asn Phe Gln Lys Val Ser Pro Gly Gly Leu Ile Lys Glu Phe Ser Glu
260 265 270
Leu Tyr Glu Thr Leu Thr Asp Asn Asp Asp Ile Leu Met Leu Ser Lys
275 280 285
Glu Ala Val Glu Ser Cys Pro Leu Met Arg Phe Ile Thr Ala Glu Thr

290 295 300
His Gly His Glu Arg Gly Ser Asp Ala Asn Thr Glu Tyr Glu Arg Leu
305 310 315 320
Leu Ser Met Leu Asn Lys Val Lys Ser Leu Lys Leu Leu Asn Thr Arg

325 330 335

Arg Arg Gln Leu Leu Asn Leu Asp Val Leu Cys Leu Ser Ser Leu Ile

340 345 350

Lys Gln Ser Ile Ser Lys Gly Leu Glu Asn Asp Lys His Trp Val Gly

355 360 365

Cys Cys Tyr Ser Ser Val Asn Asp Arg Leu Val Ser Leu Gln Ser Thr

370 375 380

Lys Glu Glu Phe Met Arg Leu Leu Lys Asn Arg Arg Lys Ser Arg Val

385 390 395 400

His Lys Lys Ala Ser Leu Asp Glu Leu Phe Arg Val Ser Ile Asn Glu

405 410 415

Phe Ile Ala Lys Ile Gln Lys Cys Leu Ser Thr Val Gly Leu Ser Phe

420 425 430

Glu His Tyr Gly Leu Ser Glu Cys Leu Val Gln Glu Cys His Ile Pro

435 440 445

Phe Ala Glu Phe Glu Asn Phe Met Arg Ala Gly Thr His Pro Val Met

450 455 460

His Tyr Thr Lys Phe Glu Asp Tyr Thr Phe Gln Pro Asn Ile Glu Gln

465 470 475 480

Leu Arg Gly Leu Gln Ser Leu Arg Lys Leu Ser Ser Val Cys Leu Ala

485 490 495

Leu Thr Asn Ser Met Lys Thr Ser Ser Val Ala Arg Leu Arg Gln Asn

500 505 510

Gln Leu Gly Ser Val Arg Tyr Gln Val Val Glu Cys Lys Glu Val Phe

515 520 525

Cys Gln Ile Ile Lys Leu Asp Ser Glu Glu Tyr His Leu Leu Tyr Gln

530 535 540

Lys Thr Gly Glu Ser Ser Arg Cys Tyr Ser Ile Gln Gly Pro Asp Gly

545 550 555 560

His Leu Ile Ser Phe Tyr Ala Asp Pro Lys Arg Phe Phe Leu Pro Ile

565 570 575

Phe Ser Asp Glu Val Leu His Asn Met Ile Asp Thr Met Ile Ser Trp

580 585 590

Ile Arg Ser Cys Pro Asp Leu Lys Asp Ser Leu Ile Asp Ile Glu Thr

595 600 605

Ala Leu Arg Thr Leu Ile Leu Leu Met Leu Thr Asn Pro Thr Lys Arg

610 615 620

Asn Gln Lys Gln Val Gln Asn Ile Arg Tyr Leu Val Met Ala Ile Val

625 630 635 640

Ser Asp Phe Ser Ser Thr Ser Leu Met Asp Lys Leu Lys Glu Asp Leu

645 650 655

Ile Thr Pro Ala Glu Lys Val Val Tyr Arg Leu Leu Arg Phe Leu Ile

660 665 670

Arg Thr Ile Phe Gly Thr Gly Glu Lys Val Leu Leu Ser Ala Lys Phe

675 680 685

Lys Phe Met Leu Asn Val Ser Tyr Leu Cys His Leu Ile Thr Lys Glu

690 695 700

Thr Pro Asp Arg Leu Thr Asp Gln Ile Lys Cys Phe Glu Lys Phe Phe

705 710 715 720

Glu Pro Lys Ser Glu Phe Gly Phe Phe Val Asn Pro Lys Glu Thr Ile

725 730 735

Thr Pro Glu Glu Glu Cys Val Phe Tyr Glu Gln Met Lys Lys Phe Thr

740 745 750

Gly Lys Asp Ile Asp Cys Gln His Ser Thr Pro Gly Val Asn Leu Glu

755 760 765

Ile Phe Ser Met Met Val Ser Ser Phe Asn Asn Gly Thr Leu Ile Leu

770 775 780

Lys Gly Glu Lys Arg Leu Asn Asn Leu Asp Pro Met Thr Asn Ser Gly

785 790 795 800

Cys Ala Thr Ala Leu Asp Leu Ala Ser Asn Lys Ser Val Val Val Asn

805 810 815

Lys His Leu Asn Gly Glu Arg Leu Leu Glu Tyr Asp Phe Asn Lys Leu

820 825 830

Leu Val Ser Ala Val Ser Gln Ile Thr Glu Gly Phe Met Arg Lys Gln

835 840 845

Lys Tyr Lys Leu Arg His Ser Asp Tyr Glu Tyr Lys Val Ser Lys Leu

850 855 860

Val Ser Arg Leu Val Ile Gly Ser Arg Lys Thr Glu Val Asp Lys Leu

865 870 875 880

Glu Asp Asp Pro Val Asp Val Cys Phe Glu Gly Glu Glu Glu Thr Ser

885 890 895

Phe Phe Arg Ser Leu Glu Asp Lys Val Ser Ser Thr Ile Thr Arg Tyr

900 905 910

Asn Arg Gly Thr Arg Leu Asn Glu Gly Gln Gly Glu Gly Glu Phe Lys

915 920 925

Asn Thr Lys Gly Leu His His Leu Gln Ile Ile Leu Ser Gly Lys Arg

930 935 940

Ala Tyr Leu Arg Lys Val Ile Leu Ser Glu Ile Ser Phe His Leu Val

945 950 955 960

Glu Asp Phe Asp Pro Ser Cys Leu Thr Asn Asp Asp Met Arg Phe Ile

965 970 975

Cys Glu Ala Val Glu Gly Ser Thr Glu Leu Ser Pro Leu Tyr Phe Thr

980 985 990

Ser Ala Val Lys Glu Gln Cys Gly Leu Asp Glu Met Ala Arg Asn Leu

995 1000 1005

Cys Arg Lys Phe Phe Ser Glu Gly Asp Trp Phe Ser Cys Met Lys

1010 1015 1020

Met Ile Leu Leu Gln Met Asn Ala Asn Ala Tyr Ser Gly Lys Tyr

1025 1030 1035

Arg His Met Gln Arg Gln Ser Leu Asn Phe Lys Phe Asp Trp Asp

1040 1045 1050

Lys Leu Glu Glu Asp Val Arg Ile Ser Glu Arg Glu Ser Asn Ser

1055 1060 1065

Glu Ser Leu Ser Lys Ala Leu Ser Leu Thr Lys Cys Met Ser Ala

1070 1075 1080

Ala Leu Lys Asn Leu Cys Phe Tyr Ser Glu Glu Ser Pro Thr Ser

1085 1090 1095

Tyr Thr Ser Val Gly Pro Asp Ser Gly Arg Leu Lys Phe Ala Leu

1100 1105 1110

Ser Tyr Lys Glu Gln Val Gly Gly Asn Arg Glu Leu Tyr Ile Gly

1115 1120 1125

Asp Leu Arg Thr Lys Met Phe Thr Arg Leu Val Glu Asp Tyr Phe

1130 1135 1140

Glu Ser Phe Ser Ser Phe Phe Ser Gly Ser Cys Leu Asn Asn Asp

1145 1150 1155

Lys Glu Phe Glu Asn Ala Ile Leu Ser Met Thr Ile Asn Val Arg

1160 1165 1170

Glu Gly Leu Leu Asn Tyr Ser Met Asp His Ser Lys Trp Gly Pro

1175 1180 1185

Met Met Cys Pro Phe Leu Phe Leu Met Leu Leu Gln Asn Leu Lys

1190 1195 1200

Leu Gly Asp Asp Gln Tyr Val Arg Ser Gly Lys Asp His Val Ser

1205 1210 1215

Thr Leu Leu Thr Trp His Met His Lys Leu Val Glu Val Pro Phe

1220 1225 1230

Pro Val Val Asn Ala Met Met Lys Ser Tyr Val Lys Ser Lys Leu

1235 1240 1245

Lys Leu Leu Lys Gly Ser Gly Thr Thr Val Thr Glu Arg Ile Phe

1250 1255 1260

Arg Glu Tyr Phe Glu Met Gly Val Val Pro Ser His Ile Ser Ser

1265 1270 1275

Leu Ile Asp Met Gly Gln Gly Ile Leu His Asn Ala Ser Asp Phe

1280 1285 1290

Tyr Gly Leu Ile Ser Glu Arg Phe Ile Asn Tyr Cys Ile Gly Val

1295 1300 1305

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

1310 1315 1320

Ile Thr Leu Phe Asp Lys Arg Leu Ser Asp Leu Val Asp Ser Asp

1325 1330 1335

Pro Glu Glu Val Leu Val Leu Leu Glu Phe His Ser His Leu Ser

1340 1345 1350

Gly Leu Leu Asn Lys Phe Ile Ser Pro Lys Ser Val Val Gly Arg

1355 1360 1365

Phe Ala Ala Glu Phe Lys Ser Arg Phe Tyr Val Trp Gly Glu Glu

1370 1375 1380

Val Pro Leu Leu Thr Lys Phe Val Ser Ala Ala Leu His Asn Val

1385 1390 1395

Lys Cys Lys Glu Pro His Gln Leu Cys Glu Thr Ile Asp Thr Ile

1400 1405 1410

Ala Asp Gln Ala Ile Ala Asn Gly Val Pro Val Phe Leu Val Asn

1415 1420 1425

Cys Ile Gln Arg Arg Thr Leu Asp Leu Leu Lys Tyr Ala Asn Phe

1430 1435 1440

Pro Leu Asp Pro Phe Leu Leu Asn Thr His Thr Asp Val Lys Asp

1445 1450 1455

Trp Leu Asp Gly Ser Arg Gly Tyr Arg Ile Gln Arg Leu Ile Glu

1460 1465 1470

Glu Leu Cys Pro Ser Glu Thr Lys Ile Met Arg Lys Leu Val Arg

1475 1480 1485

Arg Leu His His Lys Leu Lys Asn Gly Glu Cys Asn Glu Glu Phe

1490 1495 1500

Phe Leu Asp Leu Phe Asn Arg Glu Lys Glu Glu Ala Ile Leu Gln

1505 1510 1515

Leu Gly Glu Ile Leu Gly Leu Glu Asp Asp Leu Asn Glu Leu Ala

1520 1525 1530

Ser Ile Asn Trp Leu Asn Leu Asn Glu Met Phe Pro Leu Arg Met

1535 1540 1545

Val Leu Arg Gln Lys Val Val Tyr Pro Ser Val Met Thr Phe Gln

1550 1555 1560

Glu Glu Lys Ile Pro Ser Leu Ile Lys Thr Leu Gln Asn Lys Leu

1565 1570 1575

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

1580 1585 1590

Ile Asn Lys Ser Ala Phe Gln Ser Cys Val Ser Ser Gly Phe Ile

1595 1600 1605

Gly Leu Cys Lys Thr Leu Gly Ser Arg Cys Val Arg Asn Lys Asn

1610 1615 1620

Arg Glu Asn Met Tyr Ile Arg Lys Val Leu Glu Asp Leu Thr Met

1625 1630 1635

Asp Glu His Val Thr Arg Val His Lys Gln Asp Gly Val Met Leu

1640 1645 1650

Tyr Ile Cys Asp Lys Gln Arg His Pro Glu Ala His Arg Asp His

1655 1660 1665

Ile Asn Leu Leu Arg Pro Leu Leu Trp Asp Tyr Ile Cys Ile Ser

1670 1675 1680

Leu Ser Asn Ser Phe Glu Leu Gly Val Trp Val Leu Ala Glu Pro

1685 1690 1695

Val Lys Gly Lys Asn Glu Ser Asn Ser Ala Val Arg His Leu Asn

1700 1705 1710

Pro Cys Asp Tyr Val Ala Arg Lys Pro Glu Ser Ser Arg Leu Leu

1715 1720 1725

Glu Asp Lys Val Ser Leu Asn His Val Ile Gln Ser Val Arg Arg

1730 1735 1740

Leu Tyr Pro Lys Ile Phe Glu Asp Gln Leu Leu Pro Phe Met Ser

1745 1750 1755

Asp Val Ser Ser Lys Asn Met Arg Trp Ser Pro Arg Ile Lys Phe

1760 1765 1770

Leu Asp Leu Cys Val Leu Ile Asp Ile Asn Ser Glu Ser Leu Ser

1775 1780 1785

Leu Ile Ser His Val Val Lys Trp Lys Arg Asp Glu His Tyr Thr

1790 1795 1800

Val Leu Phe Ser Asp Leu Val Asn Ser His Gln Arg Ser Asp Ser

1805 1810 1815

Ser Leu Val Asp Glu Phe Val Val Ser Thr Arg Asp Val Cys Lys

1820 1825 1830

Asn Phe Leu Lys Gln Val Tyr Phe Glu Ser Phe Val Arg Glu Phe

1835 1840 1845

Val Ala Thr Ala Arg Thr Leu Gly Asn Phe Ser Trp Phe Pro His

1850 1855 1860

Lys Asp Met Met Pro Ser Glu Asp Gly Ala Glu Ala Leu Gly Pro

1865 1870 1875

Phe Gln Ser Phe Ile Leu Lys Val Val Asn Lys Lys Ile Glu Arg

1880 1885 1890

Pro Met Phe Arg Asn Asp Leu Gln Phe Gly Phe Gly Trp Phe Ser

1895 1900 1905

Tyr Arg Val Gly Asp Val Val Cys Asn Ala Ala Met Leu Ile Lys

1910 1915 1920

Gln Gly Leu Thr Asp Pro Lys Ala Phe Lys Ser Leu Arg Asp Leu

1925 1930 1935

Trp Asp Tyr Met Leu Ser Ser Thr Glu Gly Ile Leu Glu Phe Ser

1940 1945 1950

Ile Thr Val Asp Phe Thr His Asn Gln Asn Asn Thr Asp Cys Leu

1955 1960 1965

Arg Lys Phe Ser Leu Ile Phe Val Val Lys Cys Gln Leu Gln Ser

1970 1975 1980

Pro Gly Val Ala Asp Tyr Leu Ser Cys Ser His Ser Phe Lys Gly

1985 1990 1995

Glu Val Asp Arg Arg Leu Leu Asp Glu Cys Leu Asn Leu Leu Arg

2000 2005 2010

Thr Asp Pro Ile Phe Lys Ala Asn Asp Gly Val Phe Asp Ile Arg

2015 2020 2025

Ser Glu Glu Phe Glu Asp Tyr Met Glu Asp Pro Leu Thr Leu Gly

2030 2035 2040

Asp Ser Leu Glu Leu Glu Leu Ile Gly Ser Arg Arg Ile Leu Asn

2045 2050 2055

Glu Ile Lys Ser Thr Asp Phe Glu Arg Ile Gly Pro Glu Trp Glu

2060 2065 2070

Pro Val Pro Leu Thr Ile Arg Lys Gly Ala Leu Phe Glu Gly Arg

2075 2080 2085

Asn Phe Val Gln Asn Ile Ser Val Lys Leu Glu Thr Lys Asp Met

2090 2095 2100

Arg Val Phe Leu Ala Glu Leu Glu Gly Cys Gly Lys Ile Gly Asp

2105 2110 2115

Val Leu Gly Ser Leu Leu Leu His Arg Phe Arg Thr Gly Glu His

2120 2125 2130

Leu Met Glu Ser Glu Ile Ser Thr Val Leu Gln Glu Leu Cys Met

2135 2140 2145

Asp Arg Ser Val Met Leu Thr Pro Leu Ser Phe Val Pro Asp Trp

2150 2155 2160

Phe Thr Phe Arg Asp Cys Arg Leu Cys Phe Ser Xaa Ser Lys Asn

2165 2170 2175

Thr Val Met Tyr Glu Thr Thr Gly Gly Arg Phe Arg Leu Lys Gly

2180 2185 2190

Lys Ser Cys Asp Asp Trp Leu Ala Glu Arg Val Ala Glu Glu Ile

2195 2200 2205

Asp

<210> 41

<211> 1497

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P52-1)

<400> 41

atgggtcaga ttgtgacaat gtttgaggct ttgcctcaca tcattgatga ggtcatcaac 60

attgtcatta ttgtgctcat tataatcacg agcatcaaag ctgtgtacaa tttcgccacc 120

tgtgggatat tagcactggt cagcttcctt tttttggctg gtaggtcctg tggcatgtac 180

ggcctcaatg gtcccgacat ctataaaggg gtttaccagt tcaaatcagt ggagtttgat 240

atgtctcact taaatctgac gatgcccaat gcgtgctcag ccaacaactc tcatcactac 300

atcagtatgg gaagctctgg actggagcta actttcacta acgactccat ccttaatcac 360

aatttttgca acttaacctc cgctttcaac aaaaagactt ttgaccatac actcatgagt 420

atagtctcga gtctgcacct cagtattaga gggaattcca accacaaagc agtgtcttgt 480

gattttaaca atggcatcac cattcaatac aacttgtcat tttcggaccc acagagcgct 540

atgagccagt gttggacttt cagaggtaga gtcttggaca tgtttagaac tgcctttgga 600

ggaaaataca tgagaagtgg ctggggctgg gcaggttcag atggcaagac cacttggtgc 660

agccaaacaa gctatcagta cctaatcata caaaacagga cttgggaaaa ccactgtaga 720

tatgcaggcc cttttgggat gtctagaatc ctctttgctc aggaaaagac aaagtttctc 780

actaggagac ttgcaggcac attcacctgg accctgtcag actcctcagg agtagaaaat 840

ccaggtggtt attgcctgac caaatggatg atccttgctg cagagctcaa atgttttggg 900

aatacagctg ttgcaaaatg taatgtcaat catgatgaag agttctgtga catgctacga 960

ctaattgatt acaacaaggc cgccctgagt aagttcaagc aagatgtaga gtctgccttg 1020

catgtattca aaacaacagt aaattctctg atttccgatc agctgttgat gaggaatcat 1080

ctaagagatc taatgggggt accatactgt aattactcaa agttctggta tctggaacat 1140

gctaagactg gtgagactag tgtacccaag tgctggcttg tcactaatgg ctcctacttg 1200

aatgagaccc actttagtga tcaaatcgaa caagaagcag ataacatgat cacagagatg 1260

ttgaggaagg actacataaa aagacaaggg agtactcctt tagccttaat ggatcttttg 1320

atgttttcaa catcagcata tctaatcagc atctttctgc atcttgtgaa gataccaaca 1380

catagacaca taaagggcgg ttcatgtcca aagccacacc gcttgaccaa caaggggatc 1440

tgtagttgtg gtgcattcaa ggtgcctggt gtaaaaacta tctggaaaag acgctga 1497

<210> 42

<211> 498

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52-1)

<400> 42

Met Gly Gln Ile Val Thr Met Phe Glu Ala Leu Pro His Ile Ile Asp
1 5 10 15

Glu Val Ile Asn Ile Val Ile Ile Val Leu Ile Ile Ile Thr Ser Ile
20 25 30

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

Phe Leu Phe Leu Ala Gly Arg Ser Cys Gly Met Tyr Gly Leu Asn Gly
50 55 60

Pro Asp Ile Tyr Lys Gly Val Tyr Gln Phe Lys Ser Val Glu Phe Asp
65 70 75 80

Met Ser His Leu Asn Leu Thr Met Pro Asn Ala Cys Ser Ala Asn Asn
85 90 95

Ser His His Tyr Ile Ser Met Gly Ser Ser Gly Leu Glu Leu Thr Phe
100 105 110

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

Phe Asn Lys Lys Thr Phe Asp His Thr Leu Met Ser Ile Val Ser Ser
130 135 140

Leu His Leu Ser Ile Arg Gly Asn Ser Asn His Lys Ala Val Ser Cys
145 150 155 160

Asp Phe Asn Asn Gly Ile Thr Ile Gln Tyr Asn Leu Ser Phe Ser Asp
165 170 175

Pro Gln Ser Ala Met Ser Gln Cys Trp Thr Phe Arg Gly Arg Val Leu
180 185 190

Asp Met Phe Arg Thr Ala Phe Gly Gly Lys Tyr Met Arg Ser Gly Trp
195 200 205

Gly Trp Ala Gly Ser Asp Gly Lys Thr Thr Trp Cys Ser Gln Thr Ser
210 215 220

Tyr Gln Tyr Leu Ile Ile Gln Asn Arg Thr Trp Glu Asn His Cys Arg

225 230 235 240

Tyr Ala Gly Pro Phe Gly Met Ser Arg Ile Leu Phe Ala Gln Glu Lys

245 250 255

Thr Lys Phe Leu Thr Arg Arg Leu Ala Gly Thr Phe Thr Trp Thr Leu

260 265 270

Ser Asp Ser Ser Gly Val Glu Asn Pro Gly Gly Tyr Cys Leu Thr Lys

275 280 285

Trp Met Ile Leu Ala Ala Glu Leu Lys Cys Phe Gly Asn Thr Ala Val

290 295 300

Ala Lys Cys Asn Val Asn His Asp Glu Glu Phe Cys Asp Met Leu Arg

305 310 315 320

Leu Ile Asp Tyr Asn Lys Ala Ala Leu Ser Lys Phe Lys Gln Asp Val

325 330 335

Glu Ser Ala Leu His Val Phe Lys Thr Thr Val Asn Ser Leu Ile Ser

340 345 350

Asp Gln Leu Leu Met Arg Asn His Leu Arg Asp Leu Met Gly Val Pro

355 360 365

Tyr Cys Asn Tyr Ser Lys Phe Trp Tyr Leu Glu His Ala Lys Thr Gly

370 375 380

Glu Thr Ser Val Pro Lys Cys Trp Leu Val Thr Asn Gly Ser Tyr Leu

385 390 395 400

Asn Glu Thr His Phe Ser Asp Gln Ile Glu Gln Glu Ala Asp Asn Met

405 410 415

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

420 425 430

Pro Leu Ala Leu Met Asp Leu Leu Met Phe Ser Thr Ser Ala Tyr Leu

435 440 445

Ile Ser Ile Phe Leu His Leu Val Lys Ile Pro Thr His Arg His Ile

450 455 460

Lys Gly Gly Ser Cys Pro Lys Pro His Arg Leu Thr Asn Lys Gly Ile

465 470 475 480

Cys Ser Cys Gly Ala Phe Lys Val Pro Gly Val Lys Thr Ile Trp Lys

485 490 495

Arg Arg

<210> 43

<211> 1677

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P52-1)

<400> 43

atgtctttgt ccaaagaagt caaaagcttt cagtggacac aggcgttgag gagggagttg 60

cagagtttta catcagatgt aaaggctgcc gtcatcaagg acgcaaccag tcttctaaat 120

gggttggact tttctgaagt cagcaacgtt cagaggatca tgagaaagga aaggagggat 180

gataaagact tgcagagact caggagtctt aaccagactg tgcattctct tgttgatctg 240

aagtctacat caaagaaaaa tgttctgaaa gtgggaagac ttagtgcaga ggaattgatg 300

acccttgcag ctgatcttga gaagctgaag gccaaaatta tgagaactga gaggcctcaa 360

gcttctggag tctacatggg aaatttgaca gcacaacaac ttgatcaaag atcccaaata 420

ctgcaaatgg ttgggatgag aagacctcag cagggtgcaa gtggtgtagt aagggtttgg 480

gatgtgaagg actcatcact tctgaacaat cagttcggca caatgccaag cctgacaatg 540

gcttgcatgg caaaacagtc acagacccca ctcaatgatg ttgtgcaggc actcacagac 600

cttggcttac tttacacagt caaatacccg aatctcagtg atcttgaaag gctaaaggat 660

aaacacccag ttctgggggt cattactgaa cagcaatcta gtatcaatat ctctggttat 720

aatttcagtc ttggtgcagc tgtgaaagcg ggggcagctc tgctagatgg agggaacatg 780

ctggaatcta tcttgatcaa accgagcaac agtgaggatc tcctaaaagc agtcctcggg 840

gccaagaaga aactcaacat gtttgtctca gatcaagttg gagatagaaa tccctatgaa 900

aacatccttt ataaagtctg tctttcaggt gaaggatggc catacatagc ctgtagaacg 960

tcagttgtgg ggagagcatg ggagaacaca acaattgatc tcacaaatga aaaacttgtt 1020

gccaactcat ctaggccagt gcctggagca gcaggcccac ctcaggtggg cttgagttac 1080

agtcagacaa tgctgttgaa agacttgatg ggagggattg atcccaatgc tcccacatgg 1140

attgacattg agggcaggtt caatgatcca gtggagatag caatattcca accacaaaat 1200

gggcaattca tacattttta cagggaacct acggaccaga agcaattcaa gcaggactca 1260

aagtattcac acggcatgga tcttgctgat ctcttcaatg cacagcctgg gctgacctca 1320

tcagttatag gtgctctccc acaagggatg gttttgagct gtcaaggttc tgatgacatc 1380

agaaagcttc tggactcaca aaatagaagg gacataaaac tcattgatgt tgagatgacc 1440

aaggaggcct caagagaata tgaagataaa gtgtgggaca aatatggctg gctatgcaaa 1500

atgcacactg gggtagtgag agacaaaaag aagaaagaga tcaccccaca ctgtgcactc 1560

atggactgca tcatttttga gagtgcttcc aaggcaagac tccctgatct aaaaaccgtt 1620

cacaacatcc tgccacatga tttaatcttc agaggaccca atgttgtgac actctaa 1677

<210> 44

<211> 558

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52-1)

<400> 44

Met Ser Leu Ser Lys Glu Val Lys Ser Phe Gln Trp Thr Gln Ala Leu

1 5 10 15

Arg Arg Glu Leu Gln Ser Phe Thr Ser Asp Val Lys Ala Ala Val Ile

20 25 30

Lys Asp Ala Thr Ser Leu Leu Asn Gly Leu Asp Phe Ser Glu Val Ser

35 40 45

Asn Val Gln Arg Ile Met Arg Lys Glu Arg Arg Asp Asp Lys Asp Leu

50 55 60

Gln Arg Leu Arg Ser Leu Asn Gln Thr Val His Ser Leu Val Asp Leu

65 70 75 80

Lys Ser Thr Ser Lys Lys Asn Val Leu Lys Val Gly Arg Leu Ser Ala

85 90 95

Glu Glu Leu Met Thr Leu Ala Ala Asp Leu Glu Lys Leu Lys Ala Lys

100 105 110

Ile Met Arg Thr Glu Arg Pro Gln Ala Ser Gly Val Tyr Met Gly Asn

115 120 125

Leu Thr Ala Gln Gln Leu Asp Gln Arg Ser Gln Ile Leu Gln Met Val

130 135 140

Gly Met Arg Arg Pro Gln Gln Gly Ala Ser Gly Val Val Arg Val Trp

145 150 155 160

Asp Val Lys Asp Ser Ser Leu Leu Asn Asn Gln Phe Gly Thr Met Pro

165 170 175

Ser Leu Thr Met Ala Cys Met Ala Lys Gln Ser Gln Thr Pro Leu Asn

180 185 190

Asp Val Val Gln Ala Leu Thr Asp Leu Gly Leu Leu Tyr Thr Val Lys

195 200 205

Tyr Pro Asn Leu Ser Asp Leu Glu Arg Leu Lys Asp Lys His Pro Val

210 215 220

Leu Gly Val Ile Thr Glu Gln Gln Ser Ser Ile Asn Ile Ser Gly Tyr

225 230 235 240

Asn Phe Ser Leu Gly Ala Ala Val Lys Ala Gly Ala Ala Leu Leu Asp

245 250 255

Gly Gly Asn Met Leu Glu Ser Ile Leu Ile Lys Pro Ser Asn Ser Glu

260 265 270

Asp Leu Leu Lys Ala Val Leu Gly Ala Lys Lys Lys Leu Asn Met Phe

275 280 285

Val Ser Asp Gln Val Gly Asp Arg Asn Pro Tyr Glu Asn Ile Leu Tyr

290 295 300

Lys Val Cys Leu Ser Gly Glu Gly Trp Pro Tyr Ile Ala Cys Arg Thr

305 310 315 320

Ser Val Val Gly Arg Ala Trp Glu Asn Thr Thr Ile Asp Leu Thr Asn

325 330 335

Glu Lys Leu Val Ala Asn Ser Ser Arg Pro Val Pro Gly Ala Ala Gly

340 345 350

Pro Pro Gln Val Gly Leu Ser Tyr Ser Gln Thr Met Leu Leu Lys Asp

355 360 365

Leu Met Gly Gly Ile Asp Pro Asn Ala Pro Thr Trp Ile Asp Ile Glu

370 375 380

Gly Arg Phe Asn Asp Pro Val Glu Ile Ala Ile Phe Gln Pro Gln Asn

385 390 395 400

Gly Gln Phe Ile His Phe Tyr Arg Glu Pro Thr Asp Gln Lys Gln Phe

405 410 415

Lys Gln Asp Ser Lys Tyr Ser His Gly Met Asp Leu Ala Asp Leu Phe

420 425 430

Asn Ala Gln Pro Gly Leu Thr Ser Ser Val Ile Gly Ala Leu Pro Gln

435 440 445

Gly Met Val Leu Ser Cys Gln Gly Ser Asp Asp Ile Arg Lys Leu Leu

450 455 460

Asp Ser Gln Asn Arg Arg Asp Ile Lys Leu Ile Asp Val Glu Met Thr

465 470 475 480

Lys Glu Ala Ser Arg Glu Tyr Glu Asp Lys Val Trp Asp Lys Tyr Gly

485 490 495

Trp Leu Cys Lys Met His Thr Gly Val Val Arg Asp Lys Lys Lys Lys

500 505 510

Glu Ile Thr Pro His Cys Ala Leu Met Asp Cys Ile Ile Phe Glu Ser

515 520 525

Ala Ser Lys Ala Arg Leu Pro Asp Leu Lys Thr Val His Asn Ile Leu

530 535 540

Pro His Asp Leu Ile Phe Arg Gly Pro Asn Val Val Thr Leu

545 550 555

<210> 45

<211> 273

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P52-1)

<400> 45

atgggccaag gcaagtccaa agaagaaagg gacaccagca atacaggcag agcagagctt 60

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agcttggtta gatgccatga ccactatctt tgcagacact gtctgaatct cctgctgtca 180

gtttccgaca gatgtcctct ctgtaagtat ccactgccaa ccaaactgaa ggtgtcaaca 240

gtcccaagct ccccacctcc ctatgaggag tga 273

<210> 46

<211> 90

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52-1)

<400> 46

Met Gly Gln Gly Lys Ser Lys Glu Glu Arg Asp Thr Ser Asn Thr Gly

1 5 10 15

Arg Ala Glu Leu Leu Pro Asp Thr Thr Tyr Leu Gly Pro Leu Asn Cys

20 25 30

Lys Ser Cys Trp Gln Lys Phe Asp Ser Leu Val Arg Cys His Asp His

35 40 45

Tyr Leu Cys Arg His Cys Leu Asn Leu Leu Leu Ser Val Ser Asp Arg

50 55 60

Cys Pro Leu Cys Lys Tyr Pro Leu Pro Thr Lys Leu Lys Val Ser Thr

65 70 75 80

Val Pro Ser Ser Pro Pro Pro Tyr Glu Glu

85 90

<210> 47

<211> 6630

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P52-1)

<400> 47

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gagggactca aattgttatc acgctgtata gagatagaca gtgcagacaa aagtggttgc 180

atacacaacc acgatgacaa atctgttgaa acaatcctaa tagactctgg gattgtgtgt 240

ccaggactgc cactcatcat ccctgatggt tataagttga ttgacaattc ccttattctt 300

cttgaatgtt ttgttagaag cacaccagct agttttgaaa agaagttcat tgaggacacc 360

aacaaactag catgcatcaa agaagatctt gctgttgcag gcatcacact ggttccaata 420

gtggatggtc gttgtgatta tgataacagt ttcatgccag aatgggtgaa ttttaagttc 480

agagacctcc tatttaaact cctggagtat tctagtcaag atgagaaagt ttttgaggag 540

tctgaatact tcaggctctg tgagtctctt aagaccactg ttgacaaacg ttccggcatg 600

gactcaatga aaattttgaa agacgcaaga tcatttcata acgatgagat tatgaaaatg 660

tgccacgatg gtgtcaaccc caacatgagt tgcgatgatg tggtctttgg cataaattcc 720

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gcggagcggg tggccgagga gatcgactag 6630

<210> 48

<211> 2209

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52-1)

<400> 48

Met Asp Glu Thr Ile Ala Asp Leu Arg Glu Leu Cys Leu Asn Tyr Ile

1 5 10 15

Glu Gln Asp Glu Arg Leu Ser Arg Gln Lys Leu Asn Phe Leu Gly Gln

20 25 30

Arg Glu Pro Arg Met Val Leu Ile Glu Gly Leu Lys Leu Leu Ser Arg

35 40 45

Cys Ile Glu Ile Asp Ser Ala Asp Lys Ser Gly Cys Ile His Asn His

50 55 60

Asp Asp Lys Ser Val Glu Thr Ile Leu Ile Asp Ser Gly Ile Val Cys

65 70 75 80

Pro Gly Leu Pro Leu Ile Ile Pro Asp Gly Tyr Lys Leu Ile Asp Asn

85 90 95

Ser Leu Ile Leu Leu Glu Cys Phe Val Arg Ser Thr Pro Ala Ser Phe

100 105 110

Glu Lys Lys Phe Ile Glu Asp Thr Asn Lys Leu Ala Cys Ile Lys Glu

115 120 125

Asp Leu Ala Val Ala Gly Ile Thr Leu Val Pro Ile Val Asp Gly Arg

130 135 140

Cys Asp Tyr Asp Asn Ser Phe Met Pro Glu Trp Val Asn Phe Lys Phe
145 150 155 160

Arg Asp Leu Leu Phe Lys Leu Leu Glu Tyr Ser Ser Gln Asp Glu Lys
165 170 175
Val Phe Glu Glu Ser Glu Tyr Phe Arg Leu Cys Glu Ser Leu Lys Thr
180 185 190
Thr Val Asp Lys Arg Ser Gly Met Asp Ser Met Lys Ile Leu Lys Asp
195 200 205
Ala Arg Ser Phe His Asn Asp Glu Ile Met Lys Met Cys His Asp Gly
210 215 220

Val Asn Pro Asn Met Ser Cys Asp Asp Val Val Phe Gly Ile Asn Ser
225 230 235 240
Phe Phe Gly Arg Phe Arg Arg Asp Leu Leu Asn Gly Arg Leu Lys Arg
245 250 255
Asn Phe Gln Lys Val Ser Pro Gly Gly Leu Ile Lys Glu Phe Ser Glu
260 265 270
Leu Tyr Glu Thr Leu Thr Asp Asn Asp Asp Ile Leu Met Leu Ser Lys
275 280 285

Glu Ala Val Glu Ser Cys Pro Leu Met Arg Phe Ile Thr Ala Glu Thr
290 295 300
His Gly His Glu Arg Gly Ser Asp Ala Asn Thr Glu Tyr Glu Arg Leu
305 310 315 320
Leu Ser Met Leu Asn Lys Val Lys Ser Leu Lys Leu Leu Asn Thr Arg
325 330 335
Arg Arg Gln Leu Leu Asn Leu Asp Val Leu Cys Leu Ser Ser Leu Ile
340 345 350

Lys Gln Ser Ile Ser Lys Gly Leu Glu Asn Asp Lys His Trp Val Gly
355 360 365
Cys Cys Tyr Ser Ser Val Asn Asp Arg Leu Val Ser Leu Gln Ser Thr
370 375 380
Lys Glu Glu Phe Met Arg Leu Leu Lys Asn Arg Arg Lys Ser Arg Val

385 390 395 400

His Lys Lys Ala Ser Leu Asp Glu Leu Phe Arg Val Ser Ile Asn Glu

405 410 415

Phe Ile Ala Lys Ile Gln Lys Cys Leu Ser Thr Val Gly Leu Ser Phe

420 425 430

Glu His Tyr Gly Leu Ser Glu Cys Leu Val Gln Glu Cys His Ile Pro

435 440 445

Phe Ala Glu Phe Glu Asn Phe Met Arg Ala Gly Thr His Pro Val Met

450 455 460

His Tyr Thr Lys Phe Glu Asp Tyr Thr Phe Gln Pro Asn Ile Glu Gln

465 470 475 480

Leu Arg Gly Leu Gln Ser Leu Arg Lys Leu Ser Ser Val Cys Leu Ala

485 490 495

Leu Thr Asn Ser Met Lys Thr Ser Ser Val Ala Arg Leu Arg Gln Asn

500 505 510

Gln Leu Gly Ser Val Arg Tyr Gln Val Val Glu Cys Lys Glu Val Phe

515 520 525

Cys Gln Ile Ile Lys Leu Asp Ser Glu Glu Tyr His Leu Leu Tyr Gln

530 535 540

Lys Thr Gly Glu Ser Ser Arg Cys Tyr Ser Ile Gln Gly Pro Asp Gly

545 550 555 560

His Leu Ile Ser Phe Tyr Ala Asp Pro Lys Arg Phe Phe Leu Pro Ile

565 570 575

Phe Ser Asp Glu Val Leu His Asn Met Ile Asp Thr Met Ile Ser Trp

580 585 590

Ile Arg Ser Cys Pro Asp Leu Lys Asp Ser Leu Ile Asp Ile Glu Thr

595 600 605

Ala Leu Arg Thr Leu Ile Leu Leu Met Leu Thr Asn Pro Thr Lys Arg

610 615 620

Asn Gln Lys Gln Val Gln Asn Ile Arg Tyr Leu Val Met Ala Ile Val

625 630 635 640

Ser Asp Phe Ser Ser Thr Ser Leu Met Asp Lys Leu Lys Glu Asp Leu
645 650 655
Ile Thr Pro Ala Glu Lys Val Val Tyr Arg Leu Leu Arg Phe Leu Ile
660 665 670

Arg Thr Ile Phe Gly Thr Gly Glu Lys Val Leu Leu Ser Ala Lys Phe
675 680 685
Lys Phe Met Leu Asn Val Ser Tyr Leu Cys His Leu Ile Thr Lys Glu
690 695 700
Thr Pro Asp Arg Leu Thr Asp Gln Ile Lys Cys Phe Glu Lys Phe Phe
705 710 715 720
Glu Pro Lys Ser Glu Phe Gly Phe Phe Val Asn Pro Lys Glu Thr Ile
725 730 735

Thr Pro Glu Glu Glu Cys Val Phe Tyr Glu Gln Met Lys Lys Phe Thr
740 745 750
Gly Lys Asp Ile Asp Cys Gln His Ser Thr Pro Gly Val Asn Leu Glu
755 760 765
Ile Phe Ser Met Met Val Ser Ser Phe Asn Asn Gly Thr Leu Ile Leu
770 775 780
Lys Gly Glu Lys Arg Leu Asn Asn Leu Asp Pro Met Thr Asn Ser Gly
785 790 795 800

Cys Ala Thr Ala Leu Asp Leu Ala Ser Asn Lys Ser Val Val Val Asn
805 810 815
Lys His Leu Asn Gly Glu Arg Leu Leu Glu Tyr Asp Phe Asn Lys Leu
820 825 830
Leu Val Ser Ala Val Ser Gln Ile Thr Glu Gly Phe Met Arg Lys Gln
835 840 845
Lys Tyr Lys Leu Arg His Ser Asp Tyr Glu Tyr Lys Val Ser Lys Leu
850 855 860

Val Ser Arg Leu Val Ile Gly Ser Arg Lys Thr Glu Val Asp Lys Leu
865 870 875 880
Glu Asp Asp Pro Val Asp Val Cys Phe Glu Gly Glu Glu Glu Thr Ser

885 890 895

Phe Phe Arg Ser Leu Glu Asp Lys Val Ser Ser Thr Ile Thr Arg Tyr

900 905 910

Asn Arg Gly Thr Arg Leu Asn Glu Gly Gln Gly Glu Gly Glu Phe Lys

915 920 925

Asn Thr Lys Gly Leu His His Leu Gln Ile Ile Leu Ser Gly Lys Arg

930 935 940

Ala Tyr Leu Arg Lys Val Ile Leu Ser Glu Ile Ser Phe His Leu Val

945 950 955 960

Glu Asp Phe Asp Pro Ser Cys Leu Thr Asn Asp Asp Met Arg Phe Ile

965 970 975

Cys Glu Ala Val Glu Gly Ser Thr Glu Leu Ser Pro Leu Tyr Phe Thr

980 985 990

Ser Ala Val Lys Glu Gln Cys Gly Leu Asp Glu Met Ala Arg Asn Leu

995 1000 1005

Cys Arg Lys Phe Phe Ser Glu Gly Asp Trp Phe Ser Cys Met Lys

1010 1015 1020

Met Ile Leu Leu Gln Met Asn Ala Asn Ala Tyr Ser Gly Lys Tyr

1025 1030 1035

Arg His Met Gln Arg Gln Ser Leu Asn Phe Lys Phe Asp Trp Asp

1040 1045 1050

Lys Leu Glu Glu Asp Val Arg Ile Ser Glu Arg Glu Ser Asn Ser

1055 1060 1065

Glu Ser Leu Ser Lys Ala Leu Ser Leu Thr Lys Cys Met Ser Ala

1070 1075 1080

Ala Leu Lys Asn Leu Cys Phe Tyr Ser Glu Glu Ser Pro Thr Ser

1085 1090 1095

Tyr Thr Ser Val Gly Pro Asp Ser Gly Arg Leu Lys Phe Ala Leu

1100 1105 1110

Ser Tyr Lys Glu Gln Val Gly Gly Asn Arg Glu Leu Tyr Ile Gly

1115 1120 1125

Asp Leu Arg Thr Lys Met Phe Thr Arg Leu Val Glu Asp Tyr Phe
1130 1135 1140
Glu Ser Phe Ser Ser Phe Phe Ser Gly Ser Cys Leu Asn Asn Asp
1145 1150 1155
Lys Glu Phe Glu Asn Ala Ile Leu Ser Met Thr Ile Asn Val Arg
1160 1165 1170

Glu Gly Leu Leu Asn Tyr Ser Met Asp His Ser Lys Trp Gly Pro
1175 1180 1185
Met Met Cys Pro Phe Leu Phe Leu Met Leu Leu Gln Asn Leu Lys
1190 1195 1200
Leu Gly Asp Asp Gln Tyr Val Arg Ser Gly Lys Asp His Val Ser
1205 1210 1215
Thr Leu Leu Thr Trp His Met His Lys Leu Val Glu Val Pro Phe
1220 1225 1230

Pro Val Val Asn Ala Met Met Lys Ser Tyr Val Lys Ser Lys Leu
1235 1240 1245
Lys Leu Leu Lys Gly Ser Gly Thr Thr Val Thr Glu Arg Ile Phe
1250 1255 1260
Arg Glu Tyr Phe Glu Met Gly Val Val Pro Ser His Ile Ser Ser
1265 1270 1275
Leu Ile Asp Met Gly Gln Gly Ile Leu His Asn Ala Ser Asp Phe
1280 1285 1290

Tyr Gly Leu Ile Ser Glu Arg Phe Ile Asn Tyr Cys Ile Gly Val
1295 1300 1305
Ile Phe Gly Glu Arg Pro Glu Ala Tyr Thr Ser Ser Asp Asp Gln
1310 1315 1320
Ile Thr Leu Phe Asp Lys Arg Leu Ser Asp Leu Val Asp Ser Asp
1325 1330 1335
Pro Glu Glu Val Leu Val Leu Leu Glu Phe His Ser His Leu Ser
1340 1345 1350

Gly Leu Leu Asn Lys Phe Ile Ser Pro Lys Ser Val Val Gly Arg

1355 1360 1365

Phe Ala Ala Glu Phe Lys Ser Arg Phe Tyr Val Trp Gly Glu Glu

1370 1375 1380

Val Pro Leu Leu Thr Lys Phe Val Ser Ala Ala Leu His Asn Val

1385 1390 1395

Lys Cys Lys Glu Pro His Gln Leu Cys Glu Thr Ile Asp Thr Ile

1400 1405 1410

Ala Asp Gln Ala Ile Ala Asn Gly Val Pro Val Phe Leu Val Asn

1415 1420 1425

Cys Ile Gln Arg Arg Thr Leu Asp Leu Leu Lys Tyr Ala Asn Phe

1430 1435 1440

Pro Leu Asp Pro Phe Leu Leu Asn Thr His Thr Asp Val Lys Asp

1445 1450 1455

Trp Leu Asp Gly Ser Arg Gly Tyr Arg Ile Gln Arg Leu Ile Glu

1460 1465 1470

Glu Leu Cys Pro Ser Glu Thr Lys Ile Met Arg Lys Leu Val Arg

1475 1480 1485

Arg Leu His His Lys Leu Lys Asn Gly Glu Cys Asn Glu Glu Phe

1490 1495 1500

Phe Leu Asp Leu Phe Asn Arg Glu Met Lys Glu Ala Ile Leu Gln

1505 1510 1515

Leu Gly Glu Ile Leu Gly Leu Glu Asp Asp Leu Asn Glu Leu Ala

1520 1525 1530

Ser Ile Asn Trp Leu Asn Leu Asn Glu Met Phe Pro Leu Arg Met

1535 1540 1545

Val Leu Arg Gln Lys Val Val Tyr Pro Ser Val Met Thr Phe Gln

1550 1555 1560

Glu Glu Lys Ile Pro Ser Leu Ile Lys Thr Leu Gln Asn Lys Leu

1565 1570 1575

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

1580 1585 1590

Ile Asn Lys Ser Ala Phe Gln Ser Cys Val Ser Ser Gly Phe Ile
1595 1600 1605
Gly Leu Cys Lys Thr Leu Gly Ser Arg Cys Val Arg Asn Lys Asn
1610 1615 1620
Arg Glu Asn Met Tyr Ile Arg Lys Val Leu Glu Asp Leu Thr Met
1625 1630 1635
Asp Glu His Val Thr Arg Val His Lys Gln Asp Gly Val Met Leu
1640 1645 1650

Tyr Ile Cys Asp Lys Gln Arg His Pro Glu Ala His Arg Asp His
1655 1660 1665
Ile Asn Leu Leu Arg Pro Leu Leu Trp Asp Tyr Ile Cys Ile Ser
1670 1675 1680
Leu Ser Asn Ser Phe Glu Leu Gly Val Trp Val Leu Ala Glu Pro
1685 1690 1695
Val Lys Gly Lys Asn Glu Ser Asn Ser Ala Val Arg His Leu Asn
1700 1705 1710

Pro Cys Asp Tyr Val Ala Arg Lys Pro Glu Ser Ser Arg Leu Leu
1715 1720 1725
Glu Asp Lys Val Ser Leu Asn His Val Ile Gln Ser Val Arg Arg
1730 1735 1740
Leu Tyr Pro Lys Ile Phe Glu Asp Gln Leu Leu Pro Phe Met Ser
1745 1750 1755
Asp Val Ser Ser Lys Asn Met Arg Trp Ser Pro Arg Ile Lys Phe
1760 1765 1770

Leu Asp Leu Cys Val Leu Ile Asp Ile Asn Ser Glu Ser Leu Ser
1775 1780 1785
Leu Ile Ser His Val Val Lys Trp Lys Arg Asp Glu His Tyr Thr
1790 1795 1800
Val Leu Phe Ser Asp Leu Val Asn Ser His Gln Arg Ser Asp Ser
1805 1810 1815
Ser Leu Val Asp Glu Phe Val Val Ser Thr Arg Asp Val Cys Lys

1820 1825 1830

Asn Phe Leu Lys Gln Val Tyr Phe Glu Ser Phe Val Arg Glu Phe
1835 1840 1845
Val Ala Thr Ala Arg Thr Leu Gly Asn Phe Ser Trp Phe Pro His
1850 1855 1860
Lys Asp Met Met Pro Ser Glu Asp Gly Ala Glu Ala Leu Gly Pro
1865 1870 1875
Phe Gln Ser Phe Ile Leu Lys Val Val Asn Lys Lys Ile Glu Arg
1880 1885 1890

Pro Met Phe Arg Asn Asp Leu Gln Phe Gly Phe Gly Trp Phe Ser
1895 1900 1905
Tyr Arg Val Gly Asp Val Val Cys Asn Ala Ala Met Leu Ile Lys
1910 1915 1920
Gln Gly Leu Thr Asp Pro Lys Ala Phe Lys Ser Leu Arg Asp Leu
1925 1930 1935
Trp Asp Tyr Met Leu Ser Ser Thr Glu Gly Ile Leu Glu Phe Ser
1940 1945 1950

Ile Thr Val Asp Phe Thr His Asn Gln Asn Asn Thr Asp Cys Leu
1955 1960 1965
Arg Lys Phe Ser Leu Ile Phe Val Val Lys Cys Gln Leu Gln Ser
1970 1975 1980
Pro Gly Val Ala Asp Tyr Leu Ser Cys Ser His Phe Phe Lys Gly
1985 1990 1995
Glu Val Asp Arg Arg Leu Leu Asp Glu Cys Leu Asn Leu Leu Arg
2000 2005 2010

Thr Asp Pro Ile Phe Lys Ala Asn Asp Gly Val Phe Asp Ile Arg
2015 2020 2025
Ser Glu Glu Phe Glu Asp Tyr Met Glu Asp Pro Leu Thr Leu Gly
2030 2035 2040
Asp Ser Leu Glu Leu Glu Leu Ile Gly Ser Arg Arg Ile Leu Asn
2045 2050 2055

Glu Ile Lys Ser Thr Asp Phe Glu Arg Ile Gly Pro Glu Trp Glu
2060 2065 2070

Pro Val Pro Leu Thr Ile Arg Lys Gly Ala Leu Phe Glu Gly Arg
2075 2080 2085
Asn Phe Val Gln Asn Ile Ser Val Lys Leu Glu Thr Lys Asp Met
2090 2095 2100
Arg Val Phe Leu Ala Glu Leu Glu Gly Cys Gly Glu Ile Gly Asp
2105 2110 2115
Val Leu Gly Ser Leu Leu Leu His Arg Phe Arg Thr Gly Glu His
2120 2125 2130

Leu Met Glu Ser Glu Ile Ser Thr Val Leu Gln Glu Leu Cys Met
2135 2140 2145
Asp Arg Ser Val Met Leu Thr Pro Leu Ser Phe Val Pro Asp Trp
2150 2155 2160
Phe Thr Phe Arg Asp Cys Arg Leu Cys Phe Ser Arg Ser Lys Asn
2165 2170 2175
Thr Val Met Tyr Glu Thr Ala Gly Gly Arg Phe Arg Leu Lys Gly
2180 2185 2190

Lys Ser Cys Asp Asp Trp Leu Ala Glu Arg Val Ala Glu Glu Ile
2195 2200 2205
Asp

<210> 49
<211> 1497
<212> DNA
<213> Lymphocytic choriomeningitis virus (mutant P52-1.3)
<400> 49
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tgtgggatat tagcactggt cagcttcctt tttttggctg gtaggtcctg tggcatgtac 180
ggccttaatg gtcccgacat ctataaaggg gtttaccagt tcaaatcagt ggagtttgat 240

atgtctcact taaatctgac gatgcccaat gcgtgctcag ccaacaactc tcatcactac 300

atcagtatgg gaagctctgg actggagcta actttcacta acgactccat ccttaatcac 360

aatttttgca acttaacctc cgctttcaac aaaaagactt ttgaccatac actcatgagt 420

atagtctcga gtctgcacct cagtattaga gggaattcca accacaaagc agtgtcttgt 480

gattttaaca atggcatcac cattcaatac aacttgtcat tttcggaccc acagagcgct 540

ataagccagt gttggacttt cagaggtaga gtcttggaca tgtttagaac tgcctttgga 600

ggaaaataca tgagaagtgg ctggggctgg gcaggttcag atggcaagac cacttggtgc 660

agccaaacaa gctatcagta cctaatcata caaaacagga cttgggaaaa ccactgtaga 720

tatgcaggcc cttttgggat gtctagaatc ctctttgctc aggaaaagac aaagtttctc 780

actaggagac ttgcaggcac attcacctgg accctgtcag actcctcagg agtagaaaat 840

ccaggtggtt attgcctgac caaatggatg atccttgctg cagagctcaa atgttttggg 900

aacacagctg ttgcaaaatg taatgtcaat catgatgaag agttctgtga catgctacga 960

ctaattgatt acaacaaggc cgccctgagt aagttcaagc aagatgtaga gtctgccttg 1020

catgtattca aaacaacagt aaattctctg atttccgatc agctgttgat gaggaatcat 1080

ctaagagatc taatgggggt accatactgt aattactcaa agttctggta tctggaacat 1140

gctaagactg gtgagactag tgtacccaag tgctggcttg tcactaatgg ctcctacttg 1200

aatgagaccc actttagtga tcaaatcgaa caagaagcag ataacatgat cacagagatg 1260

ttgaggaagg actacataaa aagacaaggg agtactcctt tagccttaat ggatcttttg 1320

atgttttcaa catcagcata tctaatcagc atctttctgc atcttgtgaa gataccaaca 1380

catagacaca taaagggcgg ttcatgtcca aagccacacc gcttgaccaa caaggggatc 1440

tgtagttgtg gtgcattcaa ggtgcctggt gtaaaaacta tctggaaaag acgctga 1497

<210> 50

<211> 498

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52-1.3)

<400> 50

Met Gly Gln Ile Val Thr Met Phe Glu Ala Leu Pro His Ile Ile Asp

1 5 10 15

Glu Val Ile Asn Ile Val Ile Ile Val Leu Ile Ile Ile Thr Ser Ile

20 25 30

Lys Ala Val Tyr Asn Phe Ala Thr Cys Gly Ile Leu Ala Leu Val Ser

35 40 45

Phe Leu Phe Leu Ala Gly Arg Ser Cys Gly Met Tyr Gly Leu Asn Gly

50 55 60

Pro Asp Ile Tyr Lys Gly Val Tyr Gln Phe Lys Ser Val Glu Phe Asp

65 70 75 80

Met Ser His Leu Asn Leu Thr Met Pro Asn Ala Cys Ser Ala Asn Asn

85 90 95

Ser His His Tyr Ile Ser Met Gly Ser Ser Gly Leu Glu Leu Thr Phe

100 105 110

Thr Asn Asp Ser Ile Leu Asn His Asn Phe Cys Asn Leu Thr Ser Ala

115 120 125

Phe Asn Lys Lys Thr Phe Asp His Thr Leu Met Ser Ile Val Ser Ser

130 135 140

Leu His Leu Ser Ile Arg Gly Asn Ser Asn His Lys Ala Val Ser Cys

145 150 155 160

Asp Phe Asn Asn Gly Ile Thr Ile Gln Tyr Asn Leu Ser Phe Ser Asp

165 170 175

Pro Gln Ser Ala Ile Ser Gln Cys Trp Thr Phe Arg Gly Arg Val Leu

180 185 190

Asp Met Phe Arg Thr Ala Phe Gly Gly Lys Tyr Met Arg Ser Gly Trp

195 200 205

Gly Trp Ala Gly Ser Asp Gly Lys Thr Thr Trp Cys Ser Gln Thr Ser

210 215 220

Tyr Gln Tyr Leu Ile Ile Gln Asn Arg Thr Trp Glu Asn His Cys Arg

225 230 235 240

Tyr Ala Gly Pro Phe Gly Met Ser Arg Ile Leu Phe Ala Gln Glu Lys

245 250 255

Thr Lys Phe Leu Thr Arg Arg Leu Ala Gly Thr Phe Thr Trp Thr Leu

260 265 270

Ser Asp Ser Ser Gly Val Glu Asn Pro Gly Gly Tyr Cys Leu Thr Lys

275 280 285

Trp Met Ile Leu Ala Ala Glu Leu Lys Cys Phe Gly Asn Thr Ala Val

290 295 300

Ala Lys Cys Asn Val Asn His Asp Glu Glu Phe Cys Asp Met Leu Arg

305 310 315 320

Leu Ile Asp Tyr Asn Lys Ala Ala Leu Ser Lys Phe Lys Gln Asp Val

325 330 335

Glu Ser Ala Leu His Val Phe Lys Thr Thr Val Asn Ser Leu Ile Ser

340 345 350

Asp Gln Leu Leu Met Arg Asn His Leu Arg Asp Leu Met Gly Val Pro

355 360 365

Tyr Cys Asn Tyr Ser Lys Phe Trp Tyr Leu Glu His Ala Lys Thr Gly

370 375 380

Glu Thr Ser Val Pro Lys Cys Trp Leu Val Thr Asn Gly Ser Tyr Leu

385 390 395 400

Asn Glu Thr His Phe Ser Asp Gln Ile Glu Gln Glu Ala Asp Asn Met

405 410 415

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

420 425 430

Pro Leu Ala Leu Met Asp Leu Leu Met Phe Ser Thr Ser Ala Tyr Leu

435 440 445

Ile Ser Ile Phe Leu His Leu Val Lys Ile Pro Thr His Arg His Ile

450 455 460

Lys Gly Gly Ser Cys Pro Lys Pro His Arg Leu Thr Asn Lys Gly Ile

465 470 475 480

Cys Ser Cys Gly Ala Phe Lys Val Pro Gly Val Lys Thr Ile Trp Lys

485 490 495

Arg Arg

<210> 51

<211> 1677

<

212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P52-1.3)

<400> 51

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cagagtttta catcagatgt aaaggctgcc gtcatcaagg acgcaaccag tcttctaaat 120

gggttggact tttctgaagt cagcaacgtt cagaggatca tgagaaagga aaggagggat 180

gataaagact tgcagagact caggagtctt aaccagactg tgcattctct tgttgatctg 240

aagtctacat caaagaaaaa tgttctgaaa gtgggaagac ttagtgcaga ggaattgatg 300

acccttgcag ctgatctcga gaagctgaag gccaaaatta tgagaactga gaggcctcaa 360

gcttctggag tctacatggg aaatttgaca gcacaacaac ttgatcaaag atcccaaata 420

ctgcaaatgg ttgggatgag aagacctcag cagggtgcaa gtggtgtagt aagggtttgg 480

gatgtgaagg actcatcact tctgaacaat cagttcggca caatgccaag cctgacaatg 540

gcttgcatgg caaaacagtc acagacccca ctcaatgatg ttgtgcaggc actcacagac 600

cttggcttac tttacacagt caaatacccg aatctcagtg atcttgaaag gctaaaggat 660

aaacacccag ttctgggggt cattactgaa cagcaatcta gtatcaatat ctctggttat 720

aatttcagtc ttggtgcagc tgtgaaagcg ggggcagctc tgctagatgg agggaacatg 780

ctggaatcta tcttgatcaa accgagcaac agtgaggatc tcctaaaagc agtcctcggg 840

gccaagaaga aactcaacat gtttgtctca gatcaagttg gagatagaaa tccctatgaa 900

aacatccttt ataaagtctg tctttcaggt gaaggatggc catacatagc ctgtagaacg 960

tcagttgtgg ggagagcatg ggagaacaca acaattgatc tcacaaatga aaaacttgtt 1020

gccaactcat ctaggccagt gcctggagca gcaggcccac ctcaggtggg cttgagttac 1080

agtcagacaa tgctgttgaa agacttgatg ggagggattg atcccaatgc tcccacatgg 1140

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agaaagcttc tggactcaca aaatagaagg gacataaaac tcattgatgt tgagatgacc 1440

aaggaggcct caagagaata tgaagataaa gtgtgggaca aatatggctg gctatgcaaa 1500

atgcacactg gggtagtgag agacaaaaag aagaaagaga tcaccccaca ctgtgcactc 1560

atggactgca tcatttttga gagtgcttcc aaggcaagac tccctgatct aaaaaccgtt 1620

cacaacatcc tgccacatga tttaatcttc agaggaccca atgttgtgac actctaa 1677

<210> 52

<211> 558

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52-1.3)

<400> 52

Met Ser Leu Ser Lys Glu Val Lys Ser Phe Gln Trp Thr Gln Ala Leu

1 5 10 15

Arg Arg Glu Leu Gln Ser Phe Thr Ser Asp Val Lys Ala Ala Val Ile

20 25 30

Lys Asp Ala Thr Ser Leu Leu Asn Gly Leu Asp Phe Ser Glu Val Ser

35 40 45

Asn Val Gln Arg Ile Met Arg Lys Glu Arg Arg Asp Asp Lys Asp Leu

50 55 60

Gln Arg Leu Arg Ser Leu Asn Gln Thr Val His Ser Leu Val Asp Leu

65 70 75 80

Lys Ser Thr Ser Lys Lys Asn Val Leu Lys Val Gly Arg Leu Ser Ala

85 90 95

Glu Glu Leu Met Thr Leu Ala Ala Asp Leu Glu Lys Leu Lys Ala Lys

100 105 110

Ile Met Arg Thr Glu Arg Pro Gln Ala Ser Gly Val Tyr Met Gly Asn

115 120 125

Leu Thr Ala Gln Gln Leu Asp Gln Arg Ser Gln Ile Leu Gln Met Val

130 135 140

Gly Met Arg Arg Pro Gln Gln Gly Ala Ser Gly Val Val Arg Val Trp

145 150 155 160

Asp Val Lys Asp Ser Ser Leu Leu Asn Asn Gln Phe Gly Thr Met Pro

165 170 175

Ser Leu Thr Met Ala Cys Met Ala Lys Gln Ser Gln Thr Pro Leu Asn

180 185 190

Asp Val Val Gln Ala Leu Thr Asp Leu Gly Leu Leu Tyr Thr Val Lys

195 200 205

Tyr Pro Asn Leu Ser Asp Leu Glu Arg Leu Lys Asp Lys His Pro Val

210 215 220

Leu Gly Val Ile Thr Glu Gln Gln Ser Ser Ile Asn Ile Ser Gly Tyr

225 230 235 240

Asn Phe Ser Leu Gly Ala Ala Val Lys Ala Gly Ala Ala Leu Leu Asp

245 250 255

Gly Gly Asn Met Leu Glu Ser Ile Leu Ile Lys Pro Ser Asn Ser Glu

260 265 270

Asp Leu Leu Lys Ala Val Leu Gly Ala Lys Lys Lys Leu Asn Met Phe

275 280 285

Val Ser Asp Gln Val Gly Asp Arg Asn Pro Tyr Glu Asn Ile Leu Tyr

290 295 300

Lys Val Cys Leu Ser Gly Glu Gly Trp Pro Tyr Ile Ala Cys Arg Thr

305 310 315 320

Ser Val Val Gly Arg Ala Trp Glu Asn Thr Thr Ile Asp Leu Thr Asn

325 330 335

Glu Lys Leu Val Ala Asn Ser Ser Arg Pro Val Pro Gly Ala Ala Gly

340 345 350

Pro Pro Gln Val Gly Leu Ser Tyr Ser Gln Thr Met Leu Leu Lys Asp

355 360 365

Leu Met Gly Gly Ile Asp Pro Asn Ala Pro Thr Trp Ile Asp Ile Glu

370 375 380

Gly Arg Phe Asn Asp Pro Val Glu Ile Ala Ile Phe Gln Pro Gln Asn

385 390 395 400

Gly Gln Phe Ile His Phe Tyr Arg Glu Pro Thr Asp Gln Lys Gln Phe

405 410 415

Lys Gln Asp Ser Lys Tyr Ser His Gly Met Asp Leu Ala Asp Leu Phe

420 425 430

Asn Ala Gln Pro Gly Leu Thr Ser Ser Val Ile Gly Ala Leu Pro Gln

435 440 445

Gly Met Val Leu Ser Cys Gln Gly Ser Asp Asp Ile Arg Lys Leu Leu

450 455 460

Asp Ser Gln Asn Arg Arg Asp Ile Lys Leu Ile Asp Val Glu Met Thr

465 470 475 480

Lys Glu Ala Ser Arg Glu Tyr Glu Asp Lys Val Trp Asp Lys Tyr Gly

485 490 495

Trp Leu Cys Lys Met His Thr Gly Val Val Arg Asp Lys Lys Lys Lys

500 505 510

Glu Ile Thr Pro His Cys Ala Leu Met Asp Cys Ile Ile Phe Glu Ser

515 520 525

Ala Ser Lys Ala Arg Leu Pro Asp Leu Lys Thr Val His Asn Ile Leu

530 535 540

Pro His Asp Leu Ile Phe Arg Gly Pro Asn Val Val Thr Leu

545 550 555

<210> 53

<211> 273

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P52-1.3)

<400> 53

atgggccaag gcaagtccaa agaagaaagg gacaccagca atacaggcag agcagagctt 60

ttgccagaca ccacctatct tggtcctcta aattgtaaat catgttggca gaaatttgac 120

agcttggtta gatgccatga ccactatctt tgcagacact gtctgaatct cctgctgtca 180

gtttccgaca gatgtcctct ctgtaagtat ccactgccaa ccaaactgaa ggtgtcaaca 240

gtcccaagct ccccacctcc ctatgaggag tga 273

<210> 54

<211> 90

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52-1.3)

<400> 54

Met Gly Gln Gly Lys Ser Lys Glu Glu Arg Asp Thr Ser Asn Thr Gly

1 5 10 15

Arg Ala Glu Leu Leu Pro Asp Thr Thr Tyr Leu Gly Pro Leu Asn Cys

20 25 30

Lys Ser Cys Trp Gln Lys Phe Asp Ser Leu Val Arg Cys His Asp His

35 40 45

Tyr Leu Cys Arg His Cys Leu Asn Leu Leu Leu Ser Val Ser Asp Arg

50 55 60

Cys Pro Leu Cys Lys Tyr Pro Leu Pro Thr Lys Leu Lys Val Ser Thr

65 70 75 80

Val Pro Ser Ser Pro Pro Pro Tyr Glu Glu

85 90

<210> 55

<211> 6630

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P52-1.3)

<400> 55

atggatgaaa ctattgcaga tttgagagag ttgtgtctaa attacataga acaggacgag 60

aggctgtcaa ggcaaaaact caacttcctg ggacaaagag aacccagaat ggtgctaatt 120

gagggactca aattgttatc acgctgtata gagatagaca gtgcagacaa aagtggttgc 180

atacacaacc acgatgacaa atctgttgaa acaatcctaa tagactctgg gattgtgtgt 240

ccaggactgc cactcatcat ccctgatggt tataagttga ttgacaattc ccttattctt 300

cttgaatgtt ttgttagaag cacaccagct agttttgaaa agaagttcat tgaggacacc 360

aacaaactag catgcatcaa agaagatctt gctgttgcag gcatcacact ggttccaata 420

gtggatggtc gttgtgatta tgataacagt ttcatgccag aatgggtgaa ttttaagttc 480

agagacctcc tatttaaact cctggagtat tctagtcaag atgagaaagt ttttgaggag 540

tctgaatact tcaggctctg tgagtctctt aagaccactg ttgacaaacg ttccggcatg 600

gactcaatga aaattttgaa agacgcaaga tcatttcata acgatgagat tatgaaaatg 660

tgccacgatg gtgtcaaccc caacatgagt tgcgatgatg tggtctttgg cataaattcc 720

ttttttggca ggtttaggag ggacctgtta aatgggaaac tcaaaaggaa tttccaaaag 780

gtcagccctg ggggcttaat caaggaattc tctgaacttt atgaaaccct tactgataat 840

gatgacatat taatgttgag caaagaggca gttgaatcct gccccttaat gaggttcatt 900

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gaaaatgata aacattgggt tggttgttgc tacagtagtg tgaatgatag gcttgtgagc 1140

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gaggaatttt ttctagacct cttcaacagg gaaaagaaag aggccatcct tcaattggga 4560
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cacccagagg ctcaccgtga ccacatcaac cttttgaggc cccttctctg ggactacatt 5040
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aaacctgaga gttcgagact actagaggat aaagtgagtt tgaatcatgt aattcaatct 5220
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acagttcttc aggagctctg catggacaga tccgtcatgc tgacaccatt atcttttgtg 6480
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gcggagcggg tggccgagga gatcgactag 6630

<210> 56

<211> 2209

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52-1.3)

<400> 56

Met Asp Glu Thr Ile Ala Asp Leu Arg Glu Leu Cys Leu Asn Tyr Ile
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Glu Gln Asp Glu Arg Leu Ser Arg Gln Lys Leu Asn Phe Leu Gly Gln
20 25 30

Arg Glu Pro Arg Met Val Leu Ile Glu Gly Leu Lys Leu Leu Ser Arg
35 40 45

Cys Ile Glu Ile Asp Ser Ala Asp Lys Ser Gly Cys Ile His Asn His
50 55 60

Asp Asp Lys Ser Val Glu Thr Ile Leu Ile Asp Ser Gly Ile Val Cys
65 70 75 80

Pro Gly Leu Pro Leu Ile Ile Pro Asp Gly Tyr Lys Leu Ile Asp Asn
85 90 95

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

Glu Lys Lys Phe Ile Glu Asp Thr Asn Lys Leu Ala Cys Ile Lys Glu
115 120 125

Asp Leu Ala Val Ala Gly Ile Thr Leu Val Pro Ile Val Asp Gly Arg
130 135 140

Cys Asp Tyr Asp Asn Ser Phe Met Pro Glu Trp Val Asn Phe Lys Phe
145 150 155 160

Arg Asp Leu Leu Phe Lys Leu Leu Glu Tyr Ser Ser Gln Asp Glu Lys
165 170 175

Val Phe Glu Glu Ser Glu Tyr Phe Arg Leu Cys Glu Ser Leu Lys Thr
180 185 190

Thr Val Asp Lys Arg Ser Gly Met Asp Ser Met Lys Ile Leu Lys Asp

195 200 205

Ala Arg Ser Phe His Asn Asp Glu Ile Met Lys Met Cys His Asp Gly
210 215 220
Val Asn Pro Asn Met Ser Cys Asp Asp Val Val Phe Gly Ile Asn Ser
225 230 235 240
Phe Phe Gly Arg Phe Arg Arg Asp Leu Leu Asn Gly Lys Leu Lys Arg
245 250 255
Asn Phe Gln Lys Val Ser Pro Gly Gly Leu Ile Lys Glu Phe Ser Glu
260 265 270

Leu Tyr Glu Thr Leu Thr Asp Asn Asp Asp Ile Leu Met Leu Ser Lys
275 280 285
Glu Ala Val Glu Ser Cys Pro Leu Met Arg Phe Ile Thr Ala Glu Thr
290 295 300
His Gly His Glu Arg Gly Ser Asp Ala Asn Thr Glu Tyr Glu Arg Leu
305 310 315 320
Leu Ser Met Leu Asn Lys Val Lys Ser Leu Lys Leu Leu Asn Thr Arg
325 330 335

Arg Arg Gln Leu Leu Asn Leu Asp Val Leu Cys Leu Ser Ser Leu Ile
340 345 350
Lys Gln Ser Ile Ser Lys Gly Leu Glu Asn Asp Lys His Trp Val Gly
355 360 365
Cys Cys Tyr Ser Ser Val Asn Asp Arg Leu Val Ser Leu Gln Ser Thr
370 375 380
Lys Glu Glu Phe Met Arg Leu Leu Lys Asn Arg Arg Lys Ser Arg Val
385 390 395 400

His Lys Lys Ala Ser Leu Asp Glu Leu Phe Arg Val Ser Ile Asn Glu
405 410 415
Phe Ile Ala Lys Ile Gln Lys Cys Leu Ser Thr Val Gly Leu Ser Phe
420 425 430
Glu His Tyr Gly Leu Ser Glu Cys Leu Val Gln Glu Cys His Ile Pro
435 440 445

Phe Ala Glu Phe Glu Asn Phe Met Arg Ala Gly Thr His Pro Val Met
450 455 460

His Tyr Thr Lys Phe Glu Asp Tyr Thr Phe Gln Pro Asn Ile Glu Gln
465 470 475 480
Leu Arg Gly Leu Gln Ser Leu Arg Lys Leu Ser Ser Val Cys Leu Ala
485 490 495
Leu Thr Asn Ser Met Lys Thr Ser Ser Val Ala Arg Leu Arg Gln Asn
500 505 510
Gln Leu Gly Ser Val Arg Tyr Gln Val Val Glu Cys Lys Glu Val Phe
515 520 525

Cys Gln Ile Ile Lys Leu Asp Ser Glu Glu Tyr His Leu Leu Tyr Gln
530 535 540
Lys Thr Gly Glu Ser Ser Arg Cys Tyr Ser Ile Gln Gly Pro Asp Gly
545 550 555 560
His Leu Ile Ser Phe Tyr Ala Asp Pro Lys Arg Phe Phe Leu Pro Ile
565 570 575
Phe Ser Asp Glu Val Leu His Asn Met Ile Asp Thr Met Ile Ser Trp
580 585 590

Ile Arg Ser Cys Pro Asp Leu Lys Asp Ser Leu Ile Asp Ile Glu Thr
595 600 605
Ala Leu Arg Thr Leu Ile Leu Leu Met Leu Thr Asn Pro Thr Lys Arg
610 615 620
Asn Gln Lys Gln Val Gln Asn Ile Arg Tyr Leu Val Met Ala Ile Val
625 630 635 640
Ser Asp Phe Ser Ser Thr Ser Leu Met Asp Lys Leu Lys Glu Asp Leu
645 650 655

Ile Thr Pro Ala Glu Lys Val Val Tyr Arg Leu Leu Arg Phe Leu Ile
660 665 670
Arg Thr Ile Phe Gly Thr Gly Glu Lys Val Leu Leu Ser Ala Lys Phe
675 680 685
Lys Phe Met Leu Asn Val Ser Tyr Leu Cys His Leu Ile Thr Lys Glu

690 695 700

Thr Pro Asp Arg Leu Thr Asp Gln Ile Lys Cys Phe Glu Lys Phe Phe

705 710 715 720

Glu Pro Lys Ser Glu Phe Gly Phe Phe Val Asn Pro Lys Glu Thr Ile

725 730 735

Thr Pro Glu Glu Glu Cys Val Phe Tyr Glu Gln Met Lys Lys Phe Thr

740 745 750

Gly Lys Asp Ile Asp Cys Gln His Ser Thr Pro Gly Val Asn Leu Glu

755 760 765

Ile Phe Ser Met Met Val Ser Ser Phe Asn Asn Gly Thr Leu Ile Leu

770 775 780

Lys Gly Glu Lys Arg Leu Asn Asn Leu Asp Pro Met Thr Asn Ser Gly

785 790 795 800

Cys Ala Thr Ala Leu Asp Leu Ala Ser Asn Lys Ser Val Val Val Asn

805 810 815

Lys His Leu Asn Gly Glu Arg Leu Leu Glu Tyr Asp Phe Asn Lys Leu

820 825 830

Leu Val Ser Ala Val Ser Gln Ile Thr Glu Gly Phe Met Arg Lys Gln

835 840 845

Lys Tyr Lys Leu Arg His Ser Asp Tyr Glu Tyr Lys Val Ser Lys Leu

850 855 860

Val Ser Arg Leu Val Ile Gly Ser Arg Lys Thr Glu Val Asp Lys Leu

865 870 875 880

Glu Asp Asp Pro Val Asp Val Cys Phe Glu Gly Glu Glu Glu Thr Ser

885 890 895

Phe Phe Arg Ser Leu Glu Asp Lys Val Ser Ser Thr Ile Thr Arg Tyr

900 905 910

Asn Arg Gly Thr Arg Leu Asn Glu Gly Gln Gly Glu Gly Glu Phe Lys

915 920 925

Asn Thr Lys Gly Leu His His Leu Gln Ile Ile Leu Ser Gly Lys Arg

930 935 940

Ala Tyr Leu Arg Lys Val Ile Leu Ser Glu Ile Ser Phe His Leu Val
945 950 955 960
Glu Asp Phe Asp Pro Ser Cys Leu Thr Asn Asp Asp Met Arg Phe Ile
965 970 975

Cys Glu Ala Val Glu Gly Ser Thr Glu Leu Ser Pro Leu Tyr Phe Thr
980 985 990
Ser Ala Val Lys Glu Gln Cys Gly Leu Asp Glu Met Ala Arg Asn Leu
995 1000 1005
Cys Arg Lys Phe Phe Ser Glu Gly Asp Trp Phe Ser Cys Met Lys
1010 1015 1020
Met Ile Leu Leu Gln Met Asn Ala Asn Ala Tyr Ser Gly Lys Tyr
1025 1030 1035

Arg His Met Gln Arg Gln Ser Leu Asn Phe Lys Phe Asp Trp Asp
1040 1045 1050
Lys Leu Glu Glu Asp Val Arg Ile Ser Glu Arg Glu Ser Asn Ser
1055 1060 1065
Glu Ser Leu Ser Lys Ala Leu Ser Leu Thr Lys Cys Met Ser Ala
1070 1075 1080
Ala Leu Lys Asn Leu Cys Phe Tyr Ser Glu Glu Ser Pro Thr Ser
1085 1090 1095

Tyr Thr Ser Val Gly Pro Asp Ser Gly Arg Leu Lys Phe Ala Leu
1100 1105 1110
Ser Tyr Lys Glu Gln Val Gly Gly Asn Arg Glu Leu Tyr Ile Gly
1115 1120 1125
Asp Leu Arg Thr Lys Met Phe Thr Arg Leu Val Glu Asp Tyr Phe
1130 1135 1140
Glu Ser Phe Ser Ser Phe Phe Ser Gly Ser Cys Leu Asn Asn Asp
1145 1150 1155

Lys Glu Phe Glu Asn Ala Ile Leu Ser Met Thr Ile Asn Val Arg
1160 1165 1170
Glu Gly Leu Leu Asn Tyr Ser Met Asp His Ser Lys Trp Gly Pro

1175 1180 1185

Met Met Cys Pro Phe Leu Phe Leu Met Leu Leu Gln Asn Leu Lys

1190 1195 1200

Leu Gly Asp Asp Gln Tyr Val Arg Ser Gly Lys Asp His Val Ser

1205 1210 1215

Thr Leu Leu Thr Trp His Met His Lys Leu Val Glu Val Pro Phe

1220 1225 1230

Pro Val Val Asn Ala Met Met Lys Ser Tyr Val Lys Ser Lys Leu

1235 1240 1245

Lys Leu Leu Lys Gly Ser Gly Thr Thr Val Thr Glu Arg Ile Phe

1250 1255 1260

Arg Glu Tyr Phe Glu Met Gly Val Val Pro Ser His Ile Ser Ser

1265 1270 1275

Leu Ile Asp Met Gly Gln Gly Ile Leu His Asn Ala Ser Asp Phe

1280 1285 1290

Tyr Gly Leu Ile Ser Glu Arg Phe Ile Asn Tyr Cys Ile Gly Val

1295 1300 1305

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

1310 1315 1320

Ile Thr Leu Phe Asp Lys Arg Leu Ser Asp Leu Val Asp Ser Asp

1325 1330 1335

Pro Glu Glu Val Leu Val Leu Leu Glu Phe His Ser His Leu Ser

1340 1345 1350

Gly Leu Leu Asn Lys Phe Ile Ser Pro Lys Ser Val Val Gly Arg

1355 1360 1365

Phe Ala Ala Glu Phe Lys Ser Arg Phe Tyr Val Trp Gly Glu Glu

1370 1375 1380

Val Pro Leu Leu Thr Lys Phe Val Ser Ala Ala Leu His Asn Val

1385 1390 1395

Lys Cys Lys Glu Pro His Gln Leu Cys Glu Thr Ile Asp Thr Ile

1400 1405 1410

Ala Asp Gln Ala Ile Ala Asn Gly Val Pro Val Phe Leu Val Asn
1415 1420 1425
Cys Ile Gln Arg Arg Thr Leu Asp Leu Leu Lys Tyr Ala Asn Phe
1430 1435 1440
Pro Leu Asp Pro Phe Leu Leu Asn Thr His Thr Asp Val Lys Asp
1445 1450 1455

Trp Leu Asp Gly Ser Arg Gly Tyr Arg Ile Gln Arg Leu Ile Glu
1460 1465 1470
Glu Leu Cys Pro Ser Glu Thr Lys Ile Met Arg Lys Leu Val Arg
1475 1480 1485
Arg Leu His His Lys Leu Lys Asn Gly Glu Cys Asn Glu Glu Phe
1490 1495 1500
Phe Leu Asp Leu Phe Asn Arg Glu Lys Lys Glu Ala Ile Leu Gln
1505 1510 1515

Leu Gly Glu Ile Leu Gly Leu Glu Asp Asp Leu Asn Glu Leu Ala
1520 1525 1530
Ser Ile Asn Trp Leu Asn Leu Asn Glu Met Phe Pro Leu Arg Met
1535 1540 1545
Val Leu Arg Gln Lys Val Val Tyr Pro Ser Val Met Thr Phe Gln
1550 1555 1560
Glu Glu Lys Ile Pro Ser Leu Ile Lys Thr Leu Gln Asn Lys Leu
1565 1570 1575

Cys Ser Lys Phe Thr Arg Gly Ala Gln Lys Leu Leu Ser Glu Ala
1580 1585 1590
Ile Asn Lys Ser Ala Phe Gln Ser Cys Val Ser Ser Gly Phe Ile
1595 1600 1605
Gly Leu Cys Lys Thr Leu Gly Ser Arg Cys Val Arg Asn Lys Asn
1610 1615 1620
Arg Glu Asn Met Tyr Ile Arg Lys Val Leu Glu Asp Leu Thr Met
1625 1630 1635

Asp Glu His Val Thr Arg Val His Lys Gln Asp Gly Val Met Leu

1640 1645 1650

Tyr Ile Cys Asp Lys Gln Arg His Pro Glu Ala His Arg Asp His

1655 1660 1665

Ile Asn Leu Leu Arg Pro Leu Leu Trp Asp Tyr Ile Cys Ile Ser

1670 1675 1680

Leu Ser Asn Ser Phe Glu Leu Gly Val Trp Val Leu Ala Glu Pro

1685 1690 1695

Val Lys Gly Lys Asn Glu Ser Asn Ser Ala Val Arg His Leu Asn

1700 1705 1710

Pro Cys Asp Tyr Val Ala Arg Lys Pro Glu Ser Ser Arg Leu Leu

1715 1720 1725

Glu Asp Lys Val Ser Leu Asn His Val Ile Gln Ser Val Arg Arg

1730 1735 1740

Leu Tyr Pro Lys Ile Phe Glu Asp Gln Leu Leu Pro Phe Met Ser

1745 1750 1755

Asp Val Ser Ser Lys Asn Met Arg Trp Ser Pro Arg Ile Lys Phe

1760 1765 1770

Leu Asp Leu Cys Val Leu Ile Asp Ile Asn Ser Glu Ser Leu Ser

1775 1780 1785

Leu Ile Ser His Val Val Lys Trp Lys Arg Asp Glu His Tyr Thr

1790 1795 1800

Val Leu Phe Ser Asp Leu Val Asn Ser His Gln Arg Ser Asp Ser

1805 1810 1815

Ser Leu Val Asp Glu Phe Val Val Ser Thr Arg Asp Val Cys Lys

1820 1825 1830

Asn Phe Leu Lys Gln Val Tyr Phe Glu Ser Phe Val Arg Glu Phe

1835 1840 1845

Val Ala Thr Ala Arg Thr Leu Gly Asn Phe Ser Trp Phe Pro His

1850 1855 1860

Lys Asp Met Met Pro Ser Glu Asp Gly Ala Glu Ala Leu Gly Pro

1865 1870 1875

Phe Gln Ser Phe Ile Leu Lys Val Val Asn Lys Lys Ile Glu Arg
1880 1885 1890
Pro Met Phe Arg Asn Asp Leu Gln Phe Gly Phe Gly Trp Phe Ser
1895 1900 1905
Tyr Arg Val Gly Asp Val Val Cys Asn Ala Ala Met Leu Ile Lys
1910 1915 1920
Gln Gly Leu Thr Asp Pro Lys Ala Phe Lys Ser Leu Arg Asp Leu
1925 1930 1935

Trp Asp Tyr Met Leu Ser Ser Thr Glu Gly Ile Leu Glu Phe Ser
1940 1945 1950
Ile Thr Val Asp Phe Thr His Asn Gln Asn Asn Thr Asp Cys Leu
1955 1960 1965
Arg Lys Phe Ser Leu Ile Phe Val Val Lys Cys Gln Leu Gln Ser
1970 1975 1980
Pro Gly Val Ala Asp Tyr Leu Ser Cys Ser His Ser Phe Lys Gly
1985 1990 1995

Glu Val Asp Arg Arg Leu Leu Asp Glu Cys Leu Asn Leu Leu Arg
2000 2005 2010
Thr Asp Pro Ile Phe Lys Ala Asn Asp Gly Val Phe Asp Ile Arg
2015 2020 2025
Ser Glu Glu Phe Glu Asp Tyr Met Glu Asp Pro Leu Thr Leu Gly
2030 2035 2040
Asp Ser Leu Glu Leu Glu Leu Ile Gly Ser Arg Arg Ile Leu Asn
2045 2050 2055

Glu Ile Lys Ser Thr Asp Phe Glu Arg Ile Gly Pro Glu Trp Glu
2060 2065 2070
Pro Val Pro Leu Thr Ile Arg Lys Gly Ala Leu Phe Glu Gly Arg
2075 2080 2085
Asn Phe Val Gln Asn Ile Ser Val Lys Leu Glu Thr Lys Asp Met
2090 2095 2100
Arg Val Phe Leu Ala Glu Leu Glu Gly Cys Gly Lys Ile Gly Asp

2105 2110 2115

Val Leu Gly Ser Leu Leu Leu His Arg Phe Arg Thr Gly Glu His
2120 2125 2130
Leu Met Glu Ser Glu Ile Ser Thr Val Leu Gln Glu Leu Cys Met
2135 2140 2145
Asp Arg Ser Val Met Leu Thr Pro Leu Ser Phe Val Pro Asp Trp
2150 2155 2160
Phe Thr Phe Arg Asp Cys Arg Leu Cys Phe Ser Arg Ser Lys Asn
2165 2170 2175

Thr Val Met Tyr Glu Thr Thr Gly Gly Arg Phe Arg Leu Lys Gly
2180 2185 2190
Lys Ser Cys Asp Asp Trp Leu Ala Glu Arg Val Ala Glu Glu Ile
2195 2200 2205
Asp

<210> 57
<211> 1497
<212> DNA
<213> Lymphocytic choriomeningitis virus (mutant P52-2.1)
<400> 57
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attgttatta ttgtgctcat tataatcacg agcatcaaag ctgtgtacaa tttcgccacc 120

tgtgggatat tagcactggt cagcttcctt tttttggctg gtaggtcctg tggcatgtac 180
ggccttaatg gtcccgacat ctataaaggg gtttaccagt tcaaatcagt ggagtttgat 240
atgtctcact taaatctgac gatgcccaat gcgtgctcag ccaacaactc tcatcactac 300
atcagtatgg gaagctctgg actggagcta actttcacta acgactccat ccttaatcac 360
aatttttgca acttaacctc cgctttcaac aaaaagactt ttgaccatac actcatgagt 420
atagtctcga gtctgcacct cagtattaga gggaattcca accacaaagc agtgtcttgt 480
gattttaaca atggcatcac cattcaatac aacttgtcat tttcggaccc acagagcgct 540

atgagccagt gtaggacttt cagaggtaga gtcttggaca tgtttagaac tgcctttgga 600
ggaaaataca tgagaagtgg ctggggctgg gcaggttcag atggcaagac cacttggtgc 660

agccaaacaa gctatcagta cctaatcata caaaacagga cttgggaaaa ccactgtaga 720

tatgcaggcc cttttgggat gtctagaatc ctctttgctc aggaaaagac aaagtttctc 780

actaggagac ttgcaggcac attcacctgg accctgtcag actcctcagg agtagaaaat 840

ccaggtggtt attgcctgac caaatggatg atccttgctg cagagctcaa atgttttggg 900

aatacagctg ttgcaaaatg taatgtcaat catgatgaag agttctgtga catgctacga 960

ctaattgatt acaacaaggc cgccctgagt aagttcaagc aagatgtaga gtctgccttg 1020

catgtattca aaacaacagt aaattctctg atttccgatc agctgttgat gaggaatcat 1080

ctaagagatc taatgggggt accatactgt aattactcaa agttctggta tctggaacat 1140

gctaagactg gtgagactag tgtacccaag tgctggcttg tcactaatgg ctcctacttg 1200

aatgagaccc actttagtga tcaaatcgaa caagaagcag ataacatgat cacagagatg 1260

ttgaggaagg actacataaa aagacaaggg agtactcctt tagccttaat ggatcttttg 1320

atgttttcaa catcagcata tctaatcagc atctttctgc atcttgtgaa gataccaaca 1380

catagacaca taaagggcgg ttcatgtcca aagccacacc gcttgaccaa caaggggatc 1440

tgtagttgtg gtgcattcaa ggtgcctggt gtaaaaacta tctggaaaag acgctga 1497

<210> 58

<211> 498

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52-2.1)

<400> 58

Met Gly Gln Ile Val Thr Met Phe Glu Ala Leu Pro His Ile Ile Asp

1 5 10 15

Glu Val Ile Asn Ile Val Ile Ile Val Leu Ile Ile Ile Thr Ser Ile

20 25 30

Lys Ala Val Tyr Asn Phe Ala Thr Cys Gly Ile Leu Ala Leu Val Ser

35 40 45

Phe Leu Phe Leu Ala Gly Arg Ser Cys Gly Met Tyr Gly Leu Asn Gly

50 55 60

Pro Asp Ile Tyr Lys Gly Val Tyr Gln Phe Lys Ser Val Glu Phe Asp

65 70 75 80

Met Ser His Leu Asn Leu Thr Met Pro Asn Ala Cys Ser Ala Asn Asn

85 90 95

Ser His His Tyr Ile Ser Met Gly Ser Ser Gly Leu Glu Leu Thr Phe
100 105 110
Thr Asn Asp Ser Ile Leu Asn His Asn Phe Cys Asn Leu Thr Ser Ala
115 120 125
Phe Asn Lys Lys Thr Phe Asp His Thr Leu Met Ser Ile Val Ser Ser
130 135 140
Leu His Leu Ser Ile Arg Gly Asn Ser Asn His Lys Ala Val Ser Cys
145 150 155 160

Asp Phe Asn Asn Gly Ile Thr Ile Gln Tyr Asn Leu Ser Phe Ser Asp
165 170 175
Pro Gln Ser Ala Met Ser Gln Cys Arg Thr Phe Arg Gly Arg Val Leu
180 185 190
Asp Met Phe Arg Thr Ala Phe Gly Gly Lys Tyr Met Arg Ser Gly Trp
195 200 205
Gly Trp Ala Gly Ser Asp Gly Lys Thr Thr Trp Cys Ser Gln Thr Ser
210 215 220

Tyr Gln Tyr Leu Ile Ile Gln Asn Arg Thr Trp Glu Asn His Cys Arg
225 230 235 240
Tyr Ala Gly Pro Phe Gly Met Ser Arg Ile Leu Phe Ala Gln Glu Lys
245 250 255
Thr Lys Phe Leu Thr Arg Arg Leu Ala Gly Thr Phe Thr Trp Thr Leu
260 265 270
Ser Asp Ser Ser Gly Val Glu Asn Pro Gly Gly Tyr Cys Leu Thr Lys
275 280 285

Trp Met Ile Leu Ala Ala Glu Leu Lys Cys Phe Gly Asn Thr Ala Val
290 295 300
Ala Lys Cys Asn Val Asn His Asp Glu Glu Phe Cys Asp Met Leu Arg
305 310 315 320
Leu Ile Asp Tyr Asn Lys Ala Ala Leu Ser Lys Phe Lys Gln Asp Val
325 330 335
Glu Ser Ala Leu His Val Phe Lys Thr Thr Val Asn Ser Leu Ile Ser

340 345 350

Asp Gln Leu Leu Met Arg Asn His Leu Arg Asp Leu Met Gly Val Pro
355 360 365
Tyr Cys Asn Tyr Ser Lys Phe Trp Tyr Leu Glu His Ala Lys Thr Gly
370 375 380
Glu Thr Ser Val Pro Lys Cys Trp Leu Val Thr Asn Gly Ser Tyr Leu
385 390 395 400
Asn Glu Thr His Phe Ser Asp Gln Ile Glu Gln Glu Ala Asp Asn Met
405 410 415

Ile Thr Glu Met Leu Arg Lys Asp Tyr Ile Lys Arg Gln Gly Ser Thr
420 425 430
Pro Leu Ala Leu Met Asp Leu Leu Met Phe Ser Thr Ser Ala Tyr Leu
435 440 445
Ile Ser Ile Phe Leu His Leu Val Lys Ile Pro Thr His Arg His Ile
450 455 460
Lys Gly Gly Ser Cys Pro Lys Pro His Arg Leu Thr Asn Lys Gly Ile
465 470 475 480

Cys Ser Cys Gly Ala Phe Lys Val Pro Gly Val Lys Thr Ile Trp Lys
485 490 495
Arg Arg

<210> 59
<211> 1677
<212> DNA
<213> Lymphocytic choriomeningitis virus (mutant P52-2.1)
<400> 59
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gggttggact tttctgaagt cagcaacgtt cagaggatca tgagaaagga aaggagggat 180
gataaagact tgcagagact caggagtctt aaccagactg tgcattctct tgttgatctg 240

aagtctacat caaagaaaaa tgttctgaaa gtgggaagac ttagtgcaga ggaattgatg 300

acccttgcag ctgatcttga gaagctgaag gccaaaatta tgagaactga gaggcctcaa 360

gcttctggag tctacatggg aaatttgaca gcacaacaac ttgatcaaag atcccaaata 420

ctgcaaatgg ttgggatgag aagacctcag cagggtgcaa gtggtgtagt aagggtttgg 480

gatgtgaagg actcatcact tctgaacaat cagttcggca caatgccaag cctgacaatg 540

gcttgcatgg caaaacagtc acagacccca ctcaatgatg ttgtgcaggc actcacagac 600

cttggcttac tttacacagt caaatacccg aatctcagtg atcttgaaag gctaaaggat 660

aaacacccag ttctgggggt cattactgaa cagcaatcta gtatcaatat ctctggttat 720

aatttcagtc ttggtgcagc tgtgaaagcg ggggcagctc tgctagatgg agggaacatg 780

ctggaatcta tcttgatcaa accgagcaac agtgaggatc tcctaaaagc agtcctcggg 840

gccaaaaaga aactcaacat gtttgtctca gatcaagttg gagatagaaa tccctatgaa 900

aacatccttt ataaagtctg tctttcaggt gaaggatggc catacatagc ctgtagaacg 960

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gccaactcat ctaggccagt gcctggagca gcaggcccac ctcaggtggg cttgagttac 1080

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<210> 60

<211> 558

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52-2.1)

<400> 60

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Arg Arg Glu Leu Gln Ser Phe Thr Ser Asp Val Lys Ala Ala Val Ile

20 25 30

Lys Asp Ala Thr Ser Leu Leu Asn Gly Leu Asp Phe Ser Glu Val Ser

35 40 45

Asn Val Gln Arg Ile Met Arg Lys Glu Arg Arg Asp Asp Lys Asp Leu

50 55 60

Gln Arg Leu Arg Ser Leu Asn Gln Thr Val His Ser Leu Val Asp Leu

65 70 75 80

Lys Ser Thr Ser Lys Lys Asn Val Leu Lys Val Gly Arg Leu Ser Ala

85 90 95

Glu Glu Leu Met Thr Leu Ala Ala Asp Leu Glu Lys Leu Lys Ala Lys

100 105 110

Ile Met Arg Thr Glu Arg Pro Gln Ala Ser Gly Val Tyr Met Gly Asn

115 120 125

Leu Thr Ala Gln Gln Leu Asp Gln Arg Ser Gln Ile Leu Gln Met Val

130 135 140

Gly Met Arg Arg Pro Gln Gln Gly Ala Ser Gly Val Val Arg Val Trp

145 150 155 160

Asp Val Lys Asp Ser Ser Leu Leu Asn Asn Gln Phe Gly Thr Met Pro

165 170 175

Ser Leu Thr Met Ala Cys Met Ala Lys Gln Ser Gln Thr Pro Leu Asn

180 185 190

Asp Val Val Gln Ala Leu Thr Asp Leu Gly Leu Leu Tyr Thr Val Lys

195 200 205

Tyr Pro Asn Leu Ser Asp Leu Glu Arg Leu Lys Asp Lys His Pro Val

210 215 220

Leu Gly Val Ile Thr Glu Gln Gln Ser Ser Ile Asn Ile Ser Gly Tyr

225 230 235 240

Asn Phe Ser Leu Gly Ala Ala Val Lys Ala Gly Ala Ala Leu Leu Asp

245 250 255

Gly Gly Asn Met Leu Glu Ser Ile Leu Ile Lys Pro Ser Asn Ser Glu

260 265 270

Asp Leu Leu Lys Ala Val Leu Gly Ala Lys Lys Lys Leu Asn Met Phe

275 280 285

Val Ser Asp Gln Val Gly Asp Arg Asn Pro Tyr Glu Asn Ile Leu Tyr

290 295 300

Lys Val Cys Leu Ser Gly Glu Gly Trp Pro Tyr Ile Ala Cys Arg Thr

305 310 315 320

Ser Val Val Gly Arg Ala Trp Glu Asn Thr Thr Ile Asp Leu Thr Asn

325 330 335

Glu Lys Leu Val Ala Asn Ser Ser Arg Pro Val Pro Gly Ala Ala Gly

340 345 350

Pro Pro Gln Val Gly Leu Ser Tyr Ser Gln Thr Met Leu Leu Lys Asp

355 360 365

Leu Met Gly Gly Ile Asp Pro Asn Ala Pro Thr Trp Ile Asp Ile Glu

370 375 380

Gly Arg Phe Asn Asp Pro Val Glu Ile Ala Ile Phe Gln Pro Gln Asn

385 390 395 400

Gly Gln Phe Ile His Phe Tyr Arg Glu Pro Thr Asp Gln Lys Gln Phe

405 410 415

Lys Gln Asp Ser Lys Tyr Ser His Gly Met Asp Leu Ala Asp Leu Phe

420 425 430

Asn Ala Gln Pro Gly Leu Thr Ser Ser Val Ile Gly Ala Leu Pro Gln

435 440 445

Gly Met Val Leu Ser Cys Gln Gly Ser Asp Asp Ile Arg Lys Leu Leu

450 455 460

Asp Ser Gln Asn Arg Arg Asp Ile Lys Leu Ile Asp Val Glu Met Thr

465 470 475 480

Lys Glu Ala Ser Arg Glu Tyr Glu Asp Lys Val Trp Asp Lys Tyr Gly

485 490 495

Trp Leu Cys Lys Met His Thr Gly Val Val Arg Asp Lys Lys Lys Lys

500 505 510

Glu Ile Thr Pro His Cys Ala Leu Met Asp Cys Ile Ile Phe Glu Ser

515 520 525

Ala Ser Lys Ala Arg Leu Pro Asp Leu Lys Thr Val His Asn Ile Leu

530 535 540

Pro His Asp Leu Ile Phe Arg Gly Pro Asn Val Val Thr Leu

545 550 555

<210> 61

<211> 273

<212> DNA

<213> Lymphocytic choriomeningitis virus (mutant P52-2.1)

<400> 61

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gtttccgaca gatgtcctct ctgtaagtat ccactgccaa ccaaactgaa ggtgtcaaca 240

gtcccaagct ccccacctcc ctatgaggag tga 273

<210> 62

<211> 90

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52-2.1)

<400> 62

Met Gly Gln Gly Lys Ser Lys Glu Glu Arg Asp Thr Ser Asn Thr Gly

1 5 10 15

Arg Ala Glu Leu Leu Pro Asp Thr Thr Tyr Leu Gly Pro Leu Asn Cys

20 25 30

Lys Ser Cys Trp Gln Lys Phe Asp Ser Leu Val Arg Cys His Asp His

35 40 45

Tyr Leu Cys Arg His Cys Leu Asn Leu Leu Leu Ser Val Ser Asp Arg

50 55 60

Cys Pro Leu Cys Lys Tyr Pro Leu Pro Thr Lys Leu Lys Val Ser Thr

65 70 75 80

Val Pro Ser Ser Pro Pro Pro Tyr Glu Glu

85 90

<210> 63

<211> 6630

<212

> DNA

<213> Lymphocytic choriomeningitis virus (mutant P52-2.1)

<400> 63

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cttgaatgtt ttgttagaag cacaccagct agttttgaaa agaagttcat tgaggacacc 360

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<210> 64

<211> 2209

<212> PRT

<213> Lymphocytic choriomeningitis virus (mutant P52-2.1)

<400> 64

Met Asp Glu Thr Ile Ala Asp Leu Arg Glu Leu Cys Leu Asn Tyr Ile

1 5 10 15

Glu Gln Asp Glu Arg Leu Ser Arg Gln Lys Leu Asn Phe Leu Gly Gln

20 25 30

Arg Glu Pro Arg Met Val Leu Ile Glu Gly Leu Lys Leu Leu Ser Arg

35 40 45

Cys Ile Glu Ile Asp Ser Ala Asp Lys Ser Gly Cys Ile His Asn His

50 55 60

Asp Asp Lys Ser Val Glu Thr Ile Leu Ile Asp Ser Gly Ile Val Cys

65 70 75 80

Pro Gly Leu Pro Leu Ile Ile Pro Asp Gly Tyr Lys Leu Ile Asp Asn

85 90 95

Ser Leu Ile Leu Leu Glu Cys Phe Val Arg Ser Thr Pro Ala Ser Phe

100 105 110

Glu Lys Lys Phe Ile Glu Asp Thr Asn Lys Leu Ala Cys Ile Lys Glu

115 120 125

Asp Leu Ala Val Ala Gly Ile Thr Leu Val Pro Ile Val Asp Gly Arg

130 135 140

Cys Asp Tyr Asp Asn Ser Phe Met Pro Glu Trp Val Asn Phe Lys Phe

145 150 155 160

Arg Asp Leu Leu Phe Lys Leu Leu Glu Tyr Ser Ser Gln Asp Glu Lys

165 170 175

Val Phe Glu Glu Ser Glu Tyr Phe Arg Leu Cys Glu Ser Leu Lys Thr

180 185 190

Thr Val Asp Lys Arg Ser Gly Met Asp Ser Met Lys Ile Leu Lys Asp

195 200 205

Ala Arg Ser Phe His Asn Asp Glu Ile Met Lys Met Cys His Asp Gly

210 215 220

Val Asn Pro Asn Met Ser Cys Asp Asp Val Val Phe Gly Ile Asn Ser

225 230 235 240

Phe Phe Gly Arg Phe Arg Arg Asp Leu Leu Asn Gly Lys Leu Lys Arg

245 250 255

Asn Phe Gln Lys Val Ser Pro Gly Gly Leu Ile Lys Glu Phe Ser Glu

260 265 270

Leu Tyr Glu Thr Leu Thr Asp Asn Asp Asp Ile Leu Met Leu Ser Lys

275 280 285

Glu Ala Val Glu Ser Cys Pro Leu Met Arg Phe Ile Thr Ala Glu Thr

290 295 300

His Gly His Glu Arg Gly Ser Asp Ala Asn Thr Glu Tyr Glu Arg Leu

305 310 315 320

Leu Ser Met Leu Asn Lys Val Lys Ser Leu Lys Leu Leu Asn Thr Arg

325 330 335

Arg Arg Gln Leu Leu Asn Leu Asp Val Leu Cys Leu Ser Ser Leu Ile

340 345 350

Lys Gln Ser Ile Ser Lys Gly Leu Glu Asn Asp Lys His Trp Val Gly

355 360 365

Cys Cys Tyr Ser Ser Val Asn Asp Arg Leu Val Ser Leu Gln Ser Thr

370 375 380

Lys Glu Glu Phe Met Arg Leu Leu Lys Asn Arg Arg Lys Ser Arg Val

385 390 395 400

His Lys Lys Ala Ser Leu Asp Glu Leu Phe Arg Val Ser Ile Asn Glu

405 410 415

Phe Ile Ala Lys Ile Gln Lys Cys Leu Ser Thr Val Gly Leu Ser Phe

420 425 430

Glu His Tyr Gly Leu Ser Glu Cys Leu Val Gln Glu Cys His Ile Pro

435 440 445

Phe Ala Glu Phe Glu Asn Phe Met Arg Ala Gly Thr His Pro Val Met

450 455 460

His Tyr Thr Lys Phe Glu Asp Tyr Thr Phe Gln Pro Asn Ile Glu Gln

465 470 475 480

Leu Arg Gly Leu Gln Ser Leu Arg Lys Leu Ser Ser Val Cys Leu Ala

485 490 495

Leu Thr Asn Ser Met Lys Thr Ser Ser Val Ala Arg Leu Arg Gln Asn

500 505 510

Gln Leu Gly Ser Val Arg Tyr Gln Val Val Glu Cys Lys Glu Val Phe

515 520 525

Cys Gln Ile Ile Lys Leu Asp Ser Glu Glu Tyr His Leu Leu Tyr Gln

530 535 540

Lys Thr Gly Glu Ser Ser Arg Cys Tyr Ser Ile Gln Gly Pro Asp Gly

545 550 555 560

His Leu Ile Ser Phe Tyr Ala Asp Pro Lys Arg Phe Phe Leu Pro Ile

565 570 575

Phe Ser Asp Glu Val Leu His Asn Met Ile Asp Thr Met Ile Ser Trp

580 585 590

Ile Arg Ser Cys Pro Asp Leu Lys Asp Ser Leu Ile Asp Ile Glu Thr

595 600 605

Ala Leu Arg Thr Leu Ile Leu Leu Met Leu Thr Asn Pro Thr Lys Arg

610 615 620

Asn Gln Lys Gln Val Gln Asn Ile Arg Tyr Leu Val Met Ala Ile Val

625 630 635 640

Ser Asp Phe Ser Ser Thr Ser Leu Met Asp Lys Leu Lys Glu Asp Leu

645 650 655

Ile Thr Pro Ala Glu Lys Val Val Tyr Arg Leu Leu Arg Phe Leu Ile

660 665 670

Arg Thr Ile Phe Gly Thr Gly Glu Lys Val Leu Leu Ser Ala Lys Phe

675 680 685

Lys Phe Met Leu Asn Val Ser Tyr Leu Cys His Leu Ile Thr Lys Glu

690 695 700

Thr Pro Asp Arg Leu Thr Asp Gln Ile Lys Cys Phe Glu Lys Phe Phe

705 710 715 720

Glu Pro Lys Ser Glu Phe Gly Phe Phe Val Asn Pro Lys Glu Thr Ile

725 730 735

Thr Pro Glu Glu Glu Cys Val Phe Tyr Glu Gln Met Lys Lys Phe Thr

740 745 750

Gly Lys Asp Ile Asp Cys Gln His Ser Thr Pro Gly Val Asn Leu Glu

755 760 765

Ile Phe Ser Met Met Val Ser Ser Phe Asn Asn Gly Thr Leu Ile Leu

770 775 780

Lys Gly Glu Lys Arg Leu Asn Asn Leu Asp Pro Met Thr Asn Ser Gly

785 790 795 800

Cys Ala Thr Ala Leu Asp Leu Ala Ser Asn Lys Ser Val Val Val Asn

805 810 815

Lys His Leu Asn Gly Glu Arg Leu Leu Glu Tyr Asp Phe Asn Lys Leu

820 825 830

Leu Val Ser Ala Val Ser Gln Ile Thr Glu Gly Phe Met Arg Lys Gln

835 840 845

Lys Tyr Lys Leu Arg His Ser Asp Tyr Glu Tyr Lys Val Ser Lys Leu

850 855 860

Val Ser Arg Leu Val Ile Gly Ser Arg Lys Thr Glu Val Asp Lys Leu

865 870 875 880

Glu Asp Asp Pro Val Asp Val Cys Phe Glu Gly Glu Glu Glu Thr Ser

885 890 895

Phe Phe Arg Ser Leu Glu Asp Lys Val Ser Ser Thr Ile Thr Arg Tyr

900 905 910

Asn Arg Gly Thr Arg Leu Asn Glu Gly Gln Gly Glu Gly Glu Phe Lys

915 920 925

Asn Thr Lys Gly Leu His His Leu Gln Ile Ile Leu Ser Gly Lys Arg

930 935 940

Ala Tyr Leu Arg Lys Val Ile Leu Ser Glu Ile Ser Phe His Leu Val

945 950 955 960

Glu Asp Phe Asp Pro Ser Cys Leu Thr Asn Asp Asp Met Arg Phe Ile

965 970 975

Cys Glu Ala Val Glu Gly Ser Thr Glu Leu Ser Pro Leu Tyr Phe Thr

980 985 990

Ser Ala Val Lys Glu Gln Cys Gly Leu Asp Glu Met Ala Arg Asn Leu

995 1000 1005

Cys Arg Lys Phe Phe Ser Glu Gly Asp Trp Phe Ser Cys Met Lys

1010 1015 1020

Met Ile Leu Leu Gln Met Asn Ala Asn Ala Tyr Ser Gly Lys Tyr

1025 1030 1035

Arg His Met Gln Arg Gln Ser Leu Asn Phe Lys Phe Asp Trp Asp

1040 1045 1050

Lys Leu Glu Glu Asp Val Arg Ile Ser Glu Arg Glu Ser Asn Ser

1055 1060 1065

Glu Ser Leu Ser Lys Ala Leu Ser Leu Thr Lys Cys Met Ser Ala

1070 1075 1080

Ala Leu Lys Asn Leu Cys Phe Tyr Ser Glu Glu Ser Pro Thr Ser

1085 1090 1095

Tyr Thr Ser Val Gly Pro Asp Ser Gly Arg Leu Lys Phe Ala Leu

1100 1105 1110

Ser Tyr Lys Glu Gln Val Gly Gly Asn Arg Glu Leu Tyr Ile Gly

1115 1120 1125

Asp Leu Arg Thr Lys Met Phe Thr Arg Leu Val Glu Asp Tyr Phe

1130 1135 1140

Glu Ser Phe Ser Ser Phe Phe Ser Gly Ser Cys Leu Asn Asn Asp

1145 1150 1155

Lys Glu Phe Glu Asn Ala Ile Leu Ser Met Thr Ile Asn Val Arg

1160 1165 1170

Glu Gly Leu Leu Asn Tyr Ser Met Asp His Ser Lys Trp Gly Pro

1175 1180 1185

Met Met Cys Pro Phe Leu Phe Leu Met Leu Leu Gln Asn Leu Lys

1190 1195 1200

Leu Gly Asp Asp Gln Tyr Val Arg Ser Gly Lys Asp His Val Ser

1205 1210 1215

Thr Leu Leu Thr Trp His Met His Lys Leu Val Glu Val Pro Phe

1220 1225 1230

Pro Val Val Asn Ala Met Met Lys Ser Tyr Val Lys Ser Lys Leu

1235 1240 1245

Lys Leu Leu Lys Gly Ser Gly Thr Thr Val Thr Glu Arg Ile Phe

1250 1255 1260

Arg Glu Tyr Phe Glu Met Gly Val Val Pro Ser His Ile Ser Ser

1265 1270 1275

Leu Ile Asp Met Gly Gln Gly Ile Leu His Asn Ala Ser Asp Phe

1280 1285 1290

Tyr Gly Leu Ile Ser Glu Arg Phe Ile Asn Tyr Cys Ile Gly Val

1295 1300 1305

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

1310 1315 1320

Ile Thr Leu Phe Asp Lys Arg Leu Ser Asp Leu Val Asp Ser Asp

1325 1330 1335

Pro Glu Glu Val Leu Val Leu Leu Glu Phe His Ser His Leu Ser

1340 1345 1350

Gly Leu Leu Asn Lys Phe Ile Ser Pro Lys Ser Val Val Gly Arg

1355 1360 1365

Phe Ala Ala Glu Phe Lys Ser Arg Phe Tyr Val Trp Gly Glu Glu

1370 1375 1380

Val Pro Leu Leu Thr Lys Phe Val Ser Ala Ala Leu His Asn Val

1385 1390 1395

Lys Cys Lys Glu Pro His Gln Leu Cys Glu Thr Ile Asp Thr Ile

1400 1405 1410

Ala Asp Gln Ala Ile Ala Asn Gly Val Pro Val Phe Leu Val Asn

1415 1420 1425

Cys Ile Gln Arg Arg Thr Leu Asp Leu Leu Lys Tyr Ala Asn Phe

1430 1435 1440

Pro Leu Asp Pro Phe Leu Leu Asn Thr His Thr Asp Val Lys Asp

1445 1450 1455

Trp Leu Asp Gly Ser Arg Gly Tyr Arg Ile Gln Arg Leu Ile Glu

1460 1465 1470

Glu Leu Cys Pro Ser Glu Thr Lys Ile Met Arg Lys Leu Val Arg

1475 1480 1485

Arg Leu His His Lys Leu Lys Asn Gly Glu Cys Asn Glu Glu Phe

1490 1495 1500

Phe Leu Asp Leu Phe Asn Arg Glu Lys Lys Glu Ala Ile Leu Gln

1505 1510 1515

Leu Gly Glu Ile Leu Gly Leu Glu Asp Asp Leu Asn Glu Leu Ala

1520 1525 1530

Ser Ile Asn Trp Leu Asn Leu Asn Glu Met Phe Pro Leu Arg Met

1535 1540 1545

Val Leu Arg Gln Lys Val Val Tyr Pro Ser Val Met Thr Phe Gln

1550 1555 1560

Glu Glu Lys Ile Pro Ser Leu Ile Lys Thr Leu Gln Asn Lys Leu

1565 1570 1575

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

1580 1585 1590

Ile Asn Lys Ser Ala Phe Gln Ser Cys Val Ser Ser Gly Phe Ile

1595 1600 1605

Gly Leu Cys Lys Thr Leu Gly Ser Arg Cys Val Arg Asn Lys Asn

1610 1615 1620

Arg Glu Asn Met Tyr Ile Arg Lys Val Leu Glu Asp Leu Thr Met

1625 1630 1635

Asp Glu His Val Thr Arg Val His Lys Gln Asp Gly Val Met Leu

1640 1645 1650

Tyr Ile Cys Asp Lys Gln Arg His Pro Glu Ala His Arg Asp His

1655 1660 1665

Ile Asn Leu Leu Arg Pro Leu Leu Trp Asp Tyr Ile Cys Ile Ser

1670 1675 1680

Leu Ser Asn Ser Phe Glu Leu Gly Val Trp Val Leu Ala Glu Pro

1685 1690 1695

Val Lys Gly Lys Asn Glu Ser Asn Ser Ala Val Arg His Leu Asn

1700 1705 1710

Pro Cys Asp Tyr Val Ala Arg Lys Pro Glu Ser Ser Arg Leu Leu

1715 1720 1725

Glu Asp Lys Val Ser Leu Asn His Val Ile Gln Ser Val Arg Arg

1730 1735 1740

Leu Tyr Pro Lys Ile Phe Glu Asp Gln Leu Leu Pro Phe Met Ser

1745 1750 1755

Asp Val Ser Ser Lys Asn Met Arg Trp Ser Pro Arg Ile Lys Phe

1760 1765 1770

Leu Asp Leu Cys Val Leu Ile Asp Ile Asn Ser Glu Ser Leu Ser

1775 1780 1785

Leu Ile Ser His Val Val Lys Trp Lys Arg Asp Glu His Tyr Thr

1790 1795 1800

Val Leu Phe Ser Asp Leu Val Asn Ser His Gln Arg Ser Asp Ser

1805 1810 1815

Ser Leu Val Asp Glu Phe Val Val Ser Thr Arg Asp Val Cys Lys

1820 1825 1830

Asn Phe Leu Lys Gln Val Tyr Phe Glu Ser Phe Val Arg Glu Phe

1835 1840 1845

Val Ala Thr Ala Arg Thr Leu Gly Asn Phe Ser Trp Phe Pro His

1850 1855 1860

Lys Asp Met Met Pro Ser Glu Asp Gly Ala Glu Ala Leu Gly Pro

1865 1870 1875

Phe Gln Ser Phe Ile Leu Lys Val Val Asn Lys Lys Ile Glu Arg

1880 1885 1890

Pro Met Phe Arg Asn Asp Leu Gln Phe Gly Phe Gly Trp Phe Ser

1895 1900 1905

Tyr Arg Val Gly Asp Val Val Cys Asn Ala Ala Met Leu Ile Lys

1910 1915 1920

Gln Gly Leu Thr Asp Pro Lys Ala Phe Lys Ser Leu Arg Asp Leu

1925 1930 1935

Trp Asp Tyr Met Leu Ser Ser Thr Glu Gly Ile Leu Glu Phe Ser

1940 1945 1950

Ile Thr Val Asp Phe Thr His Asn Gln Asn Asn Thr Asp Cys Leu

1955 1960 1965

Arg Lys Phe Ser Leu Ile Phe Val Val Lys Cys Gln Leu Gln Ser

1970 1975 1980

Pro Gly Val Ala Asp Tyr Leu Ser Cys Ser His Phe Phe Lys Gly

1985 1990 1995

Glu Val Asp Arg Arg Leu Leu Asp Glu Cys Leu Asn Leu Leu Arg

2000 2005 2010

Thr Asp Pro Ile Phe Lys Ala Asn Asp Gly Val Phe Asp Ile Arg

2015 2020 2025

Ser Glu Glu Phe Glu Asp Tyr Met Glu Asp Pro Leu Thr Leu Gly

2030 2035 2040

Asp Ser Leu Glu Leu Glu Leu Ile Gly Ser Arg Arg Ile Leu Asn

2045 2050 2055

Glu Ile Lys Ser Thr Asp Phe Glu Arg Ile Gly Pro Glu Trp Glu

2060 2065 2070

Pro Val Pro Leu Thr Ile Arg Lys Gly Ala Leu Phe Glu Gly Arg

2075 2080 2085

Asn Phe Val Gln Asn Ile Ser Val Lys Leu Glu Thr Lys Asp Met

2090 2095 2100

Arg Val Phe Leu Ala Glu Leu Glu Gly Cys Gly Glu Ile Gly Asp

2105 2110 2115

Val Leu Gly Ser Leu Leu Leu His Arg Phe Arg Thr Gly Glu His

2120 2125 2130

Leu Met Glu Ser Glu Ile Ser Thr Val Leu Gln Glu Leu Cys Met

2135 2140 2145

Asp Arg Ser Val Met Leu Thr Pro Leu Ser Phe Val Pro Asp Trp

2150 2155 2160

Phe Thr Phe Arg Asp Cys Arg Leu Cys Phe Ser Arg Ser Lys Asn

2165 2170 2175

Thr Val Met Tyr Glu Thr Thr Gly Gly Arg Phe Arg Leu Lys Gly

2180 2185 2190

Lys Ser Cys Asp Asp Trp Leu Ala Glu Arg Val Ala Glu Glu Ile

2195 2200 2205

Asp