

SEQUENCE LISTING

<110> Aeglea BioTherapeutics, Inc.

<120> METHODS FOR PRODUCTION OF HUMAN RECOMBINANT ARGINASE 1 AND USES THEREOF

<130> A0016

<160> 3

<170> PatentIn version 3.5

<210> 1

<211> 321

<212> PRT

<213> Homo sapiens

<400> 1

Ser Ala Lys Ser Arg Thr Ile Gly Ile Ile Gly Ala Pro Phe Ser Lys
1 5 10 15

Gly Gln Pro Arg Gly Gly Val Glu Glu Gly Pro Thr Val Leu Arg Lys
20 25 30

Ala Gly Leu Leu Glu Lys Leu Lys Glu Gln Glu Cys Asp Val Lys Asp
35 40 45

Tyr Gly Asp Leu Pro Phe Ala Asp Ile Pro Asn Asp Ser Pro Phe Gln
50 55 60

Ile Val Lys Asn Pro Arg Ser Val Gly Lys Ala Ser Glu Gln Leu Ala
65 70 75 80

Gly Lys Val Ala Glu Val Lys Lys Asn Gly Arg Ile Ser Leu Val Leu
85 90 95

Gly Gly Asp His Ser Leu Ala Ile Gly Ser Ile Ser Gly His Ala Arg
100 105 110

Val His Pro Asp Leu Gly Val Ile Trp Val Asp Ala His Thr Asp Ile
115 120 125

Asn Thr Pro Leu Thr Thr Thr Ser Gly Asn Leu His Gly Gln Pro Val
130 135 140

Ser Phe Leu Leu Lys Glu Leu Lys Gly Lys Ile Pro Asp Val Pro Gly
145 150 155 160

Phe Ser Trp Val Thr Pro Cys Ile Ser Ala Lys Asp Ile Val Tyr Ile
165 170 175

Gly Leu Arg Asp Val Asp Pro Gly Glu His Tyr Ile Leu Lys Thr Leu
180 185 190

Gly Ile Lys Tyr Phe Ser Met Thr Glu Val Asp Arg Leu Gly Ile Gly
195 200 205

Lys Val Met Glu Glu Thr Leu Ser Tyr Leu Leu Gly Arg Lys Lys Arg
210 215 220

Pro Ile His Leu Ser Phe Asp Val Asp Gly Leu Asp Pro Ser Phe Thr
225 230 235 240

Pro Ala Thr Gly Thr Pro Val Val Gly Gly Leu Thr Tyr Arg Glu Gly
245 250 255

Leu Tyr Ile Thr Glu Glu Ile Tyr Lys Thr Gly Leu Leu Ser Gly Leu
260 265 270

Asp Ile Met Glu Val Asn Pro Ser Leu Gly Lys Thr Pro Glu Glu Val
275 280 285

Thr Arg Thr Val Asn Thr Ala Val Ala Ile Thr Leu Ala Cys Phe Gly
290 295 300

Leu Ala Arg Glu Gly Asn His Lys Pro Ile Asp Tyr Leu Asn Pro Pro
305 310 315 320

Lys

<210> 2

<211> 969

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon Optimized DNA Sequence

<400> 2

```
atgtctgcga agagccgtac gatcggcatt attggtgcgc cgttctctaa aggtcagcca      60
cgcggtggtg tggagagagg tccgacggtt ctgcgtaagg ccggtttatt agaaaagctg     120
aaagagcagg agtgcgacgt taaggactac ggtgacttac cattcgcgga catcccgaat     180
gatagcccgt tccaaatcgt taagaatccg cgctctgtgg gtaaagcaag cgagcagtta     240
gcaggtaagg tggccgaggt caagaaaaac ggtcgtatta gcctggtttt aggcggtgat     300
catagcttag caattggctc tatctctggt catgcccgtg tgcaccaga tttaggtgtc     360
atttggggtg acgccatac ggatatcaat acgccattaa cgaccaccag cggcaatctg     420
catggccagc cggttagctt cttactgaag gagctgaagg gtaaaattcc agatgttccg     480
ggcttttagct gggtcacgcc atgtatttct gccaaaggata tcgtgtacat tggcttacgt     540
gacgtcgacc caggtgagca ctacatctta aagaccctgg gtatcaagta tttcagcatg     600
acggaagtgg accgcttagg catcggcaag gtgatggagg agacgtgag ctatctgctg     660
ggccgtaaga aacgtccaat ccatctgagc ttcgatgttg acggcttaga cccgagcttt     720
acgccagcca ccggcacgcc ggtcgttggg ggtttaacgt atcgcaagg cctgtatatc     780
acggaggaaa tctataagac gggtttactg agcgggtctgg acattatgga ggttaatcca     840
agcttaggta agacgccgga agaagttacc cgtaccgtta acacggcggg cgcgatcacg     900
ttagcatgtt tcggttttagc ccgcgagggc aaccataaac caattgatta tctgaatcca     960
ccgaagtga                                         969
```

<210> 3

<211> 353

<212> PRT

<213> Homo sapiens

<400> 3

```
Ser Leu Arg Gly Ser Leu Ser Arg Leu Leu Gln Thr Arg Val His Ser
1           5           10          15
```

```
Ile Leu Lys Lys Ser Val His Ser Val Ala Val Ile Gly Ala Pro Phe
          20          25          30
```

Ser Gln Gly Gln Lys Arg Lys Gly Val Glu His Gly Pro Ala Ala Ile
35 40 45

Arg Glu Ala Gly Leu Met Lys Arg Leu Ser Ser Leu Gly Cys His Leu
50 55 60

Lys Asp Phe Gly Asp Leu Ser Phe Thr Pro Val Pro Lys Asp Asp Leu
65 70 75 80

Tyr Asn Asn Leu Ile Val Asn Pro Arg Ser Val Gly Leu Ala Asn Gln
85 90 95

Glu Leu Ala Glu Val Val Ser Arg Ala Val Ser Asp Gly Tyr Ser Cys
100 105 110

Val Thr Leu Gly Gly Asp His Ser Leu Ala Ile Gly Thr Ile Ser Gly
115 120 125

His Ala Arg His Cys Pro Asp Leu Cys Val Val Trp Val Asp Ala His
130 135 140

Ala Asp Ile Asn Thr Pro Leu Thr Thr Ser Ser Gly Asn Leu His Gly
145 150 155 160

Gln Pro Val Ser Phe Leu Leu Arg Glu Leu Gln Asp Lys Val Pro Gln
165 170 175

Leu Pro Gly Phe Ser Trp Ile Lys Pro Cys Ile Ser Ser Ala Ser Ile
180 185 190

Val Tyr Ile Gly Leu Arg Asp Val Asp Pro Pro Glu His Phe Ile Leu
195 200 205

Lys Asn Tyr Asp Ile Gln Tyr Phe Ser Met Arg Asp Ile Asp Arg Leu
210 215 220

Gly Ile Gln Lys Val Met Glu Arg Thr Phe Asp Leu Leu Ile Gly Lys
225 230 235 240

Arg Gln Arg Pro Ile His Leu Ser Phe Asp Ile Asp Ala Phe Asp Pro

245

250

255

Thr Leu Ala Pro Ala Thr Gly Thr Pro Val Val Gly Gly Leu Thr Tyr
260 265 270

Arg Glu Gly Met Tyr Ile Ala Glu Glu Ile His Asn Thr Gly Leu Leu
275 280 285

Ser Ala Leu Asp Leu Val Glu Val Asn Pro Gln Leu Ala Thr Ser Glu
290 295 300

Glu Glu Ala Lys Thr Thr Ala Asn Leu Ala Val Asp Val Ile Ala Ser
305 310 315 320

Ser Phe Gly Gln Thr Arg Glu Gly Gly His Ile Val Tyr Asp Gln Leu
325 330 335

Pro Thr Pro Ser Ser Pro Asp Glu Ser Glu Asn Gln Ala Arg Val Arg
340 345 350

Ile