

SEQUENCE LISTING

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<120> IMMUNOTHERAPY METHODS AND COMPOSITIONS INVOLVING TRYPTOPHAN
 METABOLIC PATHWAY MODULATORS

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<150> US 62/407,776

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<160> 73

<170> PatentIn version 3.5

<210> 1

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> spacer derived from homo sapiens igG4 hinge

<400> 1

Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro
1				5						10	

<210> 2

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> spacer derived from IgG4 hinge of Homo sapiens

<400> 2

gaatctaagt acggaccgcc ctgccccct tgccct

36

<210> 3

<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge-CH3 spacer derived from

Homo sapiens

<400> 3

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Gly Gln Pro Arg
1 5 10 15

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
20 25 30

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
35 40 45

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
50 55 60

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

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
85 90 95

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
100 105 110

Leu Ser Leu Ser Leu Gly Lys
115

<210> 4
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> spacer derived from Hinge-CH2-CH3 Homo sapiens

<400> 4

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 5
<211> 282
<212> PRT
<213> Artificial Sequence

<220>
<223> IgD-hinge-Fc Homo sapiens

<400> 5

Arg Trp Pro Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro Thr Ala
1 5 10 15

Gln Pro Gln Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro Ala
20 25 30

Thr Thr Arg Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys
35 40 45

Glu Lys Glu Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro Glu Cys Pro
50 55 60

Ser His Thr Gln Pro Leu Gly Val Tyr Leu Leu Thr Pro Ala Val Gln
65 70 75 80

Asp Leu Trp Leu Arg Asp Lys Ala Thr Phe Thr Cys Phe Val Val Gly
85 90 95

Ser Asp Leu Lys Asp Ala His Leu Thr Trp Glu Val Ala Gly Lys Val
100 105 110

Pro Thr Gly Gly Val Glu Glu Gly Leu Leu Glu Arg His Ser Asn Gly
115 120 125

Ser Gln Ser Gln His Ser Arg Leu Thr Leu Pro Arg Ser Leu Trp Asn
130 135 140

Ala Gly Thr Ser Val Thr Cys Thr Leu Asn His Pro Ser Leu Pro Pro
145 150 155 160

Gln Arg Leu Met Ala Leu Arg Glu Pro Ala Ala Gln Ala Pro Val Lys
165 170 175

Leu Ser Leu Asn Leu Leu Ala Ser Ser Asp Pro Pro Glu Ala Ala Ser
180 185 190

Trp Leu Leu Cys Glu Val Ser Gly Phe Ser Pro Pro Asn Ile Leu Leu
195 200 205

Met Trp Leu Glu Asp Gln Arg Glu Val Asn Thr Ser Gly Phe Ala Pro
210 215 220

Ala Arg Pro Pro Pro Gln Pro Gly Ser Thr Thr Phe Trp Ala Trp Ser
225 230 235 240

Val Leu Arg Val Pro Ala Pro Pro Ser Pro Gln Pro Ala Thr Tyr Thr
245 250 255

Cys Val Val Ser His Glu Asp Ser Arg Thr Leu Leu Asn Ala Ser Arg
260 265 270

Ser Leu Glu Val Ser Tyr Val Thr Asp His
275 280

<210> 6

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> T2A sequence artificial

<400> 6

Leu Glu Gly Gly Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
1 5 10 15

Val Glu Glu Asn Pro Gly Pro Arg
20

<210> 7

<211> 335

<212> PRT

<213> Artificial Sequence

<220>

<223> tEGFR artificial

<400> 7

Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
245 250 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
260 265 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His
275 280 285

Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro
290 295 300

Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala
305 310 315 320

Leu Leu Leu Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met
325 330 335

<210> 8
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD28 (amino acids 153-179 of Accession No. P10747)

Homo sapiens

<400> 8

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 9
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD28 (amino acids 114-179 of Accession No. P10747)

Homo sapiens

<400> 9

Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn
1 5 10 15

Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu
20 25 30

Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly
35 40 45

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
50 55 60

Trp Val
65

<210> 10
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD28 (amino acids 180-220 of P10747)

Homo sapiens

<400> 10

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 11
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 (LL to GG) Homo sapiens

<400> 11

Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 12
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> 4-1BB (amino acids 214-255 of Q07011.1) Homo sapiens

<400> 12

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 13
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD3 zeta Homo sapiens

<400> 13

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 14
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD3 zeta Homo sapiens

<400> 14

Arg Val Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 15
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD3 zeta Homo sapiens

<400> 15

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 16
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence

<400> 16

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Pro
20 25 30

<210> 17
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 17

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Gly Lys
1 5 10 15

Ser

<210> 18
<211> 1368
<212> PRT
<213> Streptococcus pyogenes

<220>
<221> MISC_FEATURE
<223> S. Pyogenes Cas9 Q99ZW2

<400> 18

Met Asp Lys Lys Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val
1 5 10 15

Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
20 25 30

Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
35 40 45

Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
50 55 60

Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
65 70 75 80

Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
85 90 95

Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
100 105 110

His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
115 120 125

His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
130 135 140

Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145 150 155 160

Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
165 170 175

Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
180 185 190

Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
195 200 205

Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
210 215 220

Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225 230 235 240

Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
245 250 255

Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
260 265 270

Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
275 280 285

Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
290 295 300

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

Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
325 330 335

Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
340 345 350

Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365

Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
370 375 380

Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385 390 395 400

Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
405 410 415

Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
420 425 430

Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
435 440 445

Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
450 455 460

Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465 470 475 480

Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
485 490 495

Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
500 505 510

Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
515 520 525

Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
530 535 540

Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545 550 555 560

Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
565 570 575

Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
580 585 590

Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
595 600 605

Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
610 615 620

Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625 630 635 640

His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
645 650 655

Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670

Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685

Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
690 695 700

Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720

His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735

Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750

Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765

Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780

Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800

Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815

Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830

Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
835 840 845

Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860

Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865 870 875 880

Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895

Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
900 905 910

Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
915 920 925

Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940

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

Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975

Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990

Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005

Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
1010 1015 1020

Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
1025 1030 1035

Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
1040 1045 1050

Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
1055 1060 1065

Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
1070 1075 1080

Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
1085 1090 1095

Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
1100 1105 1110

Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
1115 1120 1125

Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
1130 1135 1140

Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
1145 1150 1155

Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
1160 1165 1170

Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys
1175 1180 1185

Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu
1190 1195 1200

Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly
1205 1210 1215

Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val
1220 1225 1230

Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser
1235 1240 1245

Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys
1250 1255 1260

His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys
1265 1270 1275

Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala
1280 1285 1290

Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn
1295 1300 1305

Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala
1310 1315 1320

Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser
1325 1330 1335

Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr
1340 1345 1350

Gly Leu Tyr Glu Thr Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp
1355 1360 1365

<210> 19
<211> 1368
<212> PRT
<213> Streptococcus pyogenes

<220>
<221> MISC_FEATURE
<223> S. Pyogenes Cas9 D10A

<400> 19

Met Asp Lys Lys Tyr Ser Ile Gly Leu Ala Ile Gly Thr Asn Ser Val
1 5 10 15

Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
20 25 30

Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
35 40 45

Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
50 55 60

Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
65 70 75 80

Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
85 90 95

Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
100 105 110

His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
115 120 125

His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
130 135 140

Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145 150 155 160

Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
165 170 175

Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
180 185 190

Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
195 200 205

Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
210 215 220

Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225 230 235 240

Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
245 250 255

Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
260 265 270

Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
275 280 285

Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
290 295 300

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

Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
325 330 335

Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
340 345 350

Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365

Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
370 375 380

Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385 390 395 400

Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
405 410 415

Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
420 425 430

Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
435 440 445

Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
450 455 460

Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465 470 475 480

Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
485 490 495

Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
500 505 510

Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
515 520 525

Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
530 535 540

Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545 550 555 560

Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
565 570 575

Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
580 585 590

Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
595 600 605

Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
610 615 620

Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625 630 635 640

His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
645 650 655

Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670

Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685

Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
690 695 700

Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720

His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735

Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750

Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765

Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780

Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800

Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815

Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830

Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
835 840 845

Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860

Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
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Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895

Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
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Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
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Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940

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

Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975

Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990

Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005

Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
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Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
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Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
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Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
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Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
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Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
1085 1090 1095

Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
1100 1105 1110

Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
1115 1120 1125

Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
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Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
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Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
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Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys
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Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu
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Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly
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Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val
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Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser
1235 1240 1245

Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys
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His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys
1265 1270 1275

Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala
1280 1285 1290

Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn
1295 1300 1305

Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala
1310 1315 1320

Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser
1325 1330 1335

Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr
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Thr Met Glu Leu Arg Glu Met Ser Gln Glu Glu Ser Thr Arg Phe Tyr
50 55 60

Asp Gln Leu Asn His His Ile Phe Glu Leu Val Ser Ser Ser Asp Ala
65 70 75 80

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

Glu Gly Gly Asn Ala Thr Arg Ile Gly Arg Phe Ala Asn Tyr Leu Arg
100 105 110

Asn Leu Leu Pro Ser Asn Asp Pro Val Val Met Glu Met Ala Ser Lys
115 120 125

Ala Ile Gly Arg Leu Ala Met Ala Gly Asp Thr Phe Thr Ala Glu Tyr
130 135 140

Val Glu Phe Glu Val Lys Arg Ala Leu Glu Trp Leu Gly Ala Asp Arg
145 150 155 160

Asn Glu Gly Arg Arg His Ala Ala Val Leu Val Leu Arg Glu Leu Ala
165 170 175

Ile Ser Val Pro Thr Phe Phe Phe Gln Gln Val Gln Pro Phe Phe Asp
180 185 190

Asn Ile Phe Val Ala Val Trp Asp Pro Lys Gln Ala Ile Arg Glu Gly
195 200 205

Ala Val Ala Ala Leu Arg Ala Cys Leu Ile Leu Thr Thr Gln Arg Glu
210 215 220

Pro Lys Glu Met Gln Lys Pro Gln Trp Tyr Arg His Thr Phe Glu Glu
225 230 235 240

Ala Glu Lys Gly Phe Asp Glu Thr Leu Ala Lys Glu Lys Gly Met Asn
245 250 255

Arg Asp Asp Arg Ile His Gly Ala Leu Leu Ile Leu Asn Glu Leu Val
260 265 270

Arg Ile Ser Ser Met Glu Gly Glu Arg Leu Arg Glu Glu Met Glu Glu
275 280 285

Ile Thr Gln Gln Gln Leu Val His Asp Lys Tyr Cys Lys Asp Leu Met
290 295 300

Gly Phe Gly Thr Lys Pro Arg His Ile Thr Pro Phe Thr Ser Phe Gln

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Ala Val Gln Pro Gln Gln Ser Asn Ala Leu Val Gly Leu Leu Gly Tyr						
		325		330		335
Ser Ser His Gln Gly Leu Met Gly Phe Gly Thr Ser Pro Ser Pro Ala						
		340		345		350
Lys Ser Thr Leu Val Glu Ser Arg Cys Cys Arg Asp Leu Met Glu Glu						
		355		360		365
Lys Phe Asp Gln Val Cys Gln Trp Val Leu Lys Cys Arg Asn Ser Lys						
		370		375		380
Asn Ser Leu Ile Gln Met Thr Ile Leu Asn Leu Leu Pro Arg Leu Ala						
385		390		395		400
Ala Phe Arg Pro Ser Ala Phe Thr Asp Thr Gln Tyr Leu Gln Asp Thr						
		405		410		415
Met Asn His Val Leu Ser Cys Val Lys Lys Glu Lys Glu Arg Thr Ala						
		420		425		430
Ala Phe Gln Ala Leu Gly Leu Leu Ser Val Ala Val Arg Ser Glu Phe						
		435		440		445
Lys Val Tyr Leu Pro Arg Val Leu Asp Ile Ile Arg Ala Ala Leu Pro						
		450		455		460
Pro Lys Asp Phe Ala His Lys Arg Gln Lys Ala Met Gln Val Asp Ala						
465		470		475		480
Thr Val Phe Thr Cys Ile Ser Met Leu Ala Arg Ala Met Gly Pro Gly						
		485		490		495
Ile Gln Gln Asp Ile Lys Glu Leu Leu Glu Pro Met Leu Ala Val Gly						
		500		505		510

Leu Ser Pro Ala Leu Thr Ala Val Leu Tyr Asp Leu Ser Arg Gln Ile
515 520 525

Pro Gln Leu Lys Lys Asp Ile Gln Asp Gly Leu Leu Lys Met Leu Ser
530 535 540

Leu Val Leu Met His Lys Pro Leu Arg His Pro Gly Met Pro Lys Gly
545 550 555 560

Leu Ala His Gln Leu Ala Ser Pro Gly Leu Thr Thr Leu Pro Glu Ala
565 570 575

Ser Asp Val Gly Ser Ile Thr Leu Ala Leu Arg Thr Leu Gly Ser Phe
580 585 590

Glu Phe Glu Gly His Ser Leu Thr Gln Phe Val Arg His Cys Ala Asp
595 600 605

His Phe Leu Asn Ser Glu His Lys Glu Ile Arg Met Glu Ala Ala Arg
610 615 620

Thr Cys Ser Arg Leu Leu Thr Pro Ser Ile His Leu Ile Ser Gly His
625 630 635 640

Ala His Val Val Ser Gln Thr Ala Val Gln Val Val Ala Asp Val Leu
645 650 655

Ser Lys Leu Leu Val Val Gly Ile Thr Asp Pro Asp Pro Asp Ile Arg
660 665 670

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

Gln Ala Glu Asn Leu Gln Ala Leu Phe Val Ala Leu Asn Asp Gln Val
690 695 700

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

705		710		715		720
Met Asn Pro Ala Phe Val Met Pro Phe Leu Arg Lys Met Leu Ile Gln						
		725		730		735
Ile Leu Thr Glu Leu Glu His Ser Gly Ile Gly Arg Ile Lys Glu Gln						
		740		745		750
Ser Ala Arg Met Leu Gly His Leu Val Ser Asn Ala Pro Arg Leu Ile						
		755		760		765
Arg Pro Tyr Met Glu Pro Ile Leu Lys Ala Leu Ile Leu Lys Leu Lys						
		770		775		780
Asp Pro Asp Pro Asp Pro Asn Pro Gly Val Ile Asn Asn Val Leu Ala						
		785		790		800
Thr Ile Gly Glu Leu Ala Gln Val Ser Gly Leu Glu Met Arg Lys Trp						
		805		810		815
Val Asp Glu Leu Phe Ile Ile Ile Met Asp Met Leu Gln Asp Ser Ser						
		820		825		830
Leu Leu Ala Lys Arg Gln Val Ala Leu Trp Thr Leu Gly Gln Leu Val						
		835		840		845
Ala Ser Thr Gly Tyr Val Val Glu Pro Tyr Arg Lys Tyr Pro Thr Leu						
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Leu Glu Val Leu Leu Asn Phe Leu Lys Thr Glu Gln Asn Gln Gly Thr						
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Arg Arg Glu Ala Ile Arg Val Leu Gly Leu Leu Gly Ala Leu Asp Pro						
		885		890		895
Tyr Lys His Lys Val Asn Ile Gly Met Ile Asp Gln Ser Arg Asp Ala						
		900		905		910

Ser Ala Val Ser Leu Ser Glu Ser Lys Ser Ser Gln Asp Ser Ser Asp
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Tyr Ser Thr Ser Glu Met Leu Val Asn Met Gly Asn Leu Pro Leu Asp
930 935 940

Glu Phe Tyr Pro Ala Val Ser Met Val Ala Leu Met Arg Ile Phe Arg
945 950 955 960

Asp Gln Ser Leu Ser His His His Thr Met Val Val Gln Ala Ile Thr
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Phe Ile Phe Lys Ser Leu Gly Leu Lys Cys Val Gln Phe Leu Pro Gln
980 985 990

Val Met Pro Thr Phe Leu Asn Val Ile Arg Val Cys Asp Gly Ala Ile
995 1000 1005

Arg Glu Phe Leu Phe Gln Gln Leu Gly Met Leu Val Ser Phe Val
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Lys Ser His Ile Arg Pro Tyr Met Asp Glu Ile Val Thr Leu Met
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Arg Glu Phe Trp Val Met Asn Thr Ser Ile Gln Ser Thr Ile Ile
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Leu Leu Ile Glu Gln Ile Val Val Ala Leu Gly Gly Glu Phe Lys
1055 1060 1065

Leu Tyr Leu Pro Gln Leu Ile Pro His Met Leu Arg Val Phe Met
1070 1075 1080

His Asp Asn Ser Pro Gly Arg Ile Val Ser Ile Lys Leu Leu Ala
1085 1090 1095

Ala Ile Gln Leu Phe Gly Ala Asn Leu Asp Asp Tyr Leu His Leu

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Leu	Leu	Pro	Pro	Ile	Val	Lys	Leu	Phe	Asp	Ala	Pro	Glu
1115						1120					1125	Ala
												Pro
Leu	Pro	Ser	Arg	Lys	Ala	Ala	Leu	Glu	Thr	Val	Asp	Arg
1130						1135					1140	Leu
												Thr
Glu	Ser	Leu	Asp	Phe	Thr	Asp	Tyr	Ala	Ser	Arg	Ile	Ile
1145						1150					1155	His
												Pro
Ile	Val	Arg	Thr	Leu	Asp	Gln	Ser	Pro	Glu	Leu	Arg	Ser
1160						1165					1170	Thr
												Ala
Met	Asp	Thr	Leu	Ser	Ser	Leu	Val	Phe	Gln	Leu	Gly	Lys
1175						1180					1185	Lys
												Tyr
Gln	Ile	Phe	Ile	Pro	Met	Val	Asn	Lys	Val	Leu	Val	Arg
1190						1195					1200	His
												Arg
Ile	Asn	His	Gln	Arg	Tyr	Asp	Val	Leu	Ile	Cys	Arg	Ile
1205						1210					1215	Val
												Lys
Gly	Tyr	Thr	Leu	Ala	Asp	Glu	Glu	Glu	Asp	Pro	Leu	Ile
1220						1225					1230	Tyr
												Gln
His	Arg	Met	Leu	Arg	Ser	Gly	Gln	Gly	Asp	Ala	Leu	Ala
1235						1240					1245	Ser
												Gly
Pro	Val	Glu	Thr	Gly	Pro	Met	Lys	Lys	Leu	His	Val	Ser
1250						1255					1260	Thr
												Ile
Asn	Leu	Gln	Lys	Ala	Trp	Gly	Ala	Ala	Arg	Arg	Val	Ser
1265						1270					1275	Lys
												Asp
Asp	Trp	Leu	Glu	Trp	Leu	Arg	Arg	Leu	Ser	Leu	Glu	Leu
1280						1285					1290	Lys

Asp Ser Ser Ser Pro Ser Leu Arg Ser Cys Trp Ala Leu Ala Gln
1295 1300 1305

Ala Tyr Asn Pro Met Ala Arg Asp Leu Phe Asn Ala Ala Phe Val
1310 1315 1320

Ser Cys Trp Ser Glu Leu Asn Glu Asp Gln Gln Asp Glu Leu Ile
1325 1330 1335

Arg Ser Ile Glu Leu Ala Leu Thr Ser Gln Asp Ile Ala Glu Val
1340 1345 1350

Thr Gln Thr Leu Leu Asn Leu Ala Glu Phe Met Glu His Ser Asp
1355 1360 1365

Lys Gly Pro Leu Pro Leu Arg Asp Asp Asn Gly Ile Val Leu Leu
1370 1375 1380

Gly Glu Arg Ala Ala Lys Cys Arg Ala Tyr Ala Lys Ala Leu His
1385 1390 1395

Tyr Lys Glu Leu Glu Phe Gln Lys Gly Pro Thr Pro Ala Ile Leu
1400 1405 1410

Glu Ser Leu Ile Ser Ile Asn Asn Lys Leu Gln Gln Pro Glu Ala
1415 1420 1425

Ala Ala Gly Val Leu Glu Tyr Ala Met Lys His Phe Gly Glu Leu
1430 1435 1440

Glu Ile Gln Ala Thr Trp Tyr Glu Lys Leu His Glu Trp Glu Asp
1445 1450 1455

Ala Leu Val Ala Tyr Asp Lys Lys Met Asp Thr Asn Lys Asp Asp
1460 1465 1470

Pro Glu Leu Met Leu Gly Arg Met Arg Cys Leu Glu Ala Leu Gly

1475

1480

1485

Glu Trp Gly Gln Leu His Gln Gln Cys Cys Glu Lys Trp Thr Leu
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Val Asn Asp Glu Thr Gln Ala Lys Met Ala Arg Met Ala Ala Ala
 1505 1510 1515

Ala Ala Trp Gly Leu Gly Gln Trp Asp Ser Met Glu Glu Tyr Thr
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Cys Met Ile Pro Arg Asp Thr His Asp Gly Ala Phe Tyr Arg Ala
 1535 1540 1545

Val Leu Ala Leu His Gln Asp Leu Phe Ser Leu Ala Gln Gln Cys
 1550 1555 1560

Ile Asp Lys Ala Arg Asp Leu Leu Asp Ala Glu Leu Thr Ala Met
 1565 1570 1575

Ala Gly Glu Ser Tyr Ser Arg Ala Tyr Gly Ala Met Val Ser Cys
 1580 1585 1590

His Met Leu Ser Glu Leu Glu Glu Val Ile Gln Tyr Lys Leu Val
 1595 1600 1605

Pro Glu Arg Arg Glu Ile Ile Arg Gln Ile Trp Trp Glu Arg Leu
 1610 1615 1620

Gln Gly Cys Gln Arg Ile Val Glu Asp Trp Gln Lys Ile Leu Met
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Val Arg Ser Leu Val Val Ser Pro His Glu Asp Met Arg Thr Trp
 1640 1645 1650

Leu Lys Tyr Ala Ser Leu Cys Gly Lys Ser Gly Arg Leu Ala Leu
 1655 1660 1665

Ala His Lys Thr Leu Val Leu Leu Leu Gly Val Asp Pro Ser Arg
1670 1675 1680

Gln Leu Asp His Pro Leu Pro Thr Val His Pro Gln Val Thr Tyr
1685 1690 1695

Ala Tyr Met Lys Asn Met Trp Lys Ser Ala Arg Lys Ile Asp Ala
1700 1705 1710

Phe Gln His Met Gln His Phe Val Gln Thr Met Gln Gln Gln Ala
1715 1720 1725

Gln His Ala Ile Ala Thr Glu Asp Gln Gln His Lys Gln Glu Leu
1730 1735 1740

His Lys Leu Met Ala Arg Cys Phe Leu Lys Leu Gly Glu Trp Gln
1745 1750 1755

Leu Asn Leu Gln Gly Ile Asn Glu Ser Thr Ile Pro Lys Val Leu
1760 1765 1770

Gln Tyr Tyr Ser Ala Ala Thr Glu His Asp Arg Ser Trp Tyr Lys
1775 1780 1785

Ala Trp His Ala Trp Ala Val Met Asn Phe Glu Ala Val Leu His
1790 1795 1800

Tyr Lys His Gln Asn Gln Ala Arg Asp Glu Lys Lys Lys Leu Arg
1805 1810 1815

His Ala Ser Gly Ala Asn Ile Thr Asn Ala Thr Thr Ala Ala Thr
1820 1825 1830

Thr Ala Ala Thr Ala Thr Thr Thr Ala Ser Thr Glu Gly Ser Asn
1835 1840 1845

Ser Glu Ser Glu Ala Glu Ser Thr Glu Asn Ser Pro Thr Pro Ser

1850						1855						1860			
Pro	Leu	Gln	Lys	Lys	Val	Thr	Glu	Asp	Leu	Ser	Lys	Thr	Leu	Leu	
1865						1870					1875				
Met	Tyr	Thr	Val	Pro	Ala	Val	Gln	Gly	Phe	Phe	Arg	Ser	Ile	Ser	
1880						1885					1890				
Leu	Ser	Arg	Gly	Asn	Asn	Leu	Gln	Asp	Thr	Leu	Arg	Val	Leu	Thr	
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Leu	Trp	Phe	Asp	Tyr	Gly	His	Trp	Pro	Asp	Val	Asn	Glu	Ala	Leu	
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Val	Glu	Gly	Val	Lys	Ala	Ile	Gln	Ile	Asp	Thr	Trp	Leu	Gln	Val	
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1955						1960					1965				
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1970						1975					1980				
Thr	Thr	Ala	Arg	His	Asn	Ala	Ala	Asn	Lys	Ile	Leu	Lys	Asn	Met	
1985						1990					1995				
Cys	Glu	His	Ser	Asn	Thr	Leu	Val	Gln	Gln	Ala	Met	Met	Val	Ser	
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2015						2020					2025				
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Val Lys Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met
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Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala
2060 2065 2070

Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr
2075 2080 2085

Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala Trp Asp Leu
2090 2095 2100

Tyr Tyr His Val Phe Arg Arg Ile Ser Lys Gln Leu Pro Gln Leu
2105 2110 2115

Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro Lys Leu Leu Met Cys
2120 2125 2130

Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Asp Pro Asn Gln
2135 2140 2145

Pro Ile Ile Arg Ile Gln Ser Ile Ala Pro Ser Leu Gln Val Ile
2150 2155 2160

Thr Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met Gly Ser Asn
2165 2170 2175

Gly His Glu Phe Val Phe Leu Leu Lys Gly His Glu Asp Leu Arg
2180 2185 2190

Gln Asp Glu Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu
2195 2200 2205

Leu Ala Asn Asp Pro Thr Ser Leu Arg Lys Asn Leu Ser Ile Gln
2210 2215 2220

Arg Tyr Ala Val Ile Pro Leu Ser Thr Asn Ser Gly Leu Ile Gly

2225

2230

2235

Trp Val Pro His Cys Asp Thr Leu His Ala Leu Ile Arg Asp Tyr
 2240 2245 2250

Arg Glu Lys Lys Lys Ile Leu Leu Asn Ile Glu His Arg Ile Met
 2255 2260 2265

Leu Arg Met Ala Pro Asp Tyr Asp His Leu Thr Leu Met Gln Lys
 2270 2275 2280

Val Glu Val Phe Glu His Ala Val Asn Asn Thr Ala Gly Asp Asp
 2285 2290 2295

Leu Ala Lys Leu Leu Trp Leu Lys Ser Pro Ser Ser Glu Val Trp
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Phe Asp Arg Arg Thr Asn Tyr Thr Arg Ser Leu Ala Val Met Ser
 2315 2320 2325

Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His Pro Ser Asn
 2330 2335 2340

Leu Met Leu Asp Arg Leu Ser Gly Lys Ile Leu His Ile Asp Phe
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Gly Asp Cys Phe Glu Val Ala Met Thr Arg Glu Lys Phe Pro Glu
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Lys Ile Pro Phe Arg Leu Thr Arg Met Leu Thr Asn Ala Met Glu
 2375 2380 2385

Val Thr Gly Leu Asp Gly Asn Tyr Arg Ile Thr Cys His Thr Val
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Met Glu Val Leu Arg Glu His Lys Asp Ser Val Met Ala Val Leu
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Glu Ala Phe Val Tyr Asp Pro Leu Leu Asn Trp Arg Leu Met Asp
2420 2425 2430

Thr Asn Thr Lys Gly Asn Lys Arg Ser Arg Thr Arg Thr Asp Ser
2435 2440 2445

Tyr Ser Ala Gly Gln Ser Val Glu Ile Leu Asp Gly Val Glu Leu
2450 2455 2460

Gly Glu Pro Ala His Lys Lys Thr Gly Thr Thr Val Pro Glu Ser
2465 2470 2475

Ile His Ser Phe Ile Gly Asp Gly Leu Val Lys Pro Glu Ala Leu
2480 2485 2490

Asn Lys Lys Ala Ile Gln Ile Ile Asn Arg Val Arg Asp Lys Leu
2495 2500 2505

Thr Gly Arg Asp Phe Ser His Asp Asp Thr Leu Asp Val Pro Thr
2510 2515 2520

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<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> human Neutral and basic amino acid transport protein rBAT
(SLC3A1) isoform 1 Uniprot Q07837

<400> 36

Met Ala Glu Asp Lys Ser Lys Arg Asp Ser Ile Glu Met Ser Met Lys
1 5 10 15

Gly Cys Gln Thr Asn Asn Gly Phe Val His Asn Glu Asp Ile Leu Glu
20 25 30

Gln Thr Pro Asp Pro Gly Ser Ser Thr Asp Asn Leu Lys His Ser Thr
35 40 45

Arg Gly Ile Leu Gly Ser Gln Glu Pro Asp Phe Lys Gly Val Gln Pro
50 55 60

Tyr Ala Gly Met Pro Lys Glu Val Leu Phe Gln Phe Ser Gly Gln Ala
65 70 75 80

Arg Tyr Arg Ile Pro Arg Glu Ile Leu Phe Trp Leu Thr Val Ala Ser
85 90 95

Val Leu Val Leu Ile Ala Ala Thr Ile Ala Ile Ile Ala Leu Ser Pro
100 105 110

Lys Cys Leu Asp Trp Trp Gln Glu Gly Pro Met Tyr Gln Ile Tyr Pro
115 120 125

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

Ile Gln Asp Lys Leu Asp Tyr Ile Thr Ala Leu Asn Ile Lys Thr Val
145 150 155 160

Trp Ile Thr Ser Phe Tyr Lys Ser Ser Leu Lys Asp Phe Arg Tyr Gly
165 170 175

Val Glu Asp Phe Arg Glu Val Asp Pro Ile Phe Gly Thr Met Glu Asp
180 185 190

Phe Glu Asn Leu Val Ala Ala Ile His Asp Lys Gly Leu Lys Leu Ile
195 200 205

Ile Asp Phe Ile Pro Asn His Thr Ser Asp Lys His Ile Trp Phe Gln
210 215 220

Leu Ser Arg Thr Arg Thr Gly Lys Tyr Thr Asp Tyr Tyr Ile Trp His
225 230 235 240

Asp Cys Thr His Glu Asn Gly Lys Thr Ile Pro Pro Asn Asn Trp Leu
245 250 255

Ser Val Tyr Gly Asn Ser Ser Trp His Phe Asp Glu Val Arg Asn Gln
260 265 270

Cys Tyr Phe His Gln Phe Met Lys Glu Gln Pro Asp Leu Asn Phe Arg
275 280 285

Asn Pro Asp Val Gln Glu Glu Ile Lys Glu Ile Leu Arg Phe Trp Leu
290 295 300

Thr Lys Gly Val Asp Gly Phe Ser Leu Asp Ala Val Lys Phe Leu Leu
305 310 315 320

Glu Ala Lys His Leu Arg Asp Glu Ile Gln Val Asn Lys Thr Gln Ile
325 330 335

Pro Asp Thr Val Thr Gln Tyr Ser Glu Leu Tyr His Asp Phe Thr Thr
340 345 350

Thr Gln Val Gly Met His Asp Ile Val Arg Ser Phe Arg Gln Thr Met
355 360 365

Asp Gln Tyr Ser Thr Glu Pro Gly Arg Tyr Arg Phe Met Gly Thr Glu
370 375 380

Ala Tyr Ala Glu Ser Ile Asp Arg Thr Val Met Tyr Tyr Gly Leu Pro
385 390 395 400

Phe Ile Gln Glu Ala Asp Phe Pro Phe Asn Asn Tyr Leu Ser Met Leu
405 410 415

Asp Thr Val Ser Gly Asn Ser Val Tyr Glu Val Ile Thr Ser Trp Met
420 425 430

Glu Asn Met Pro Glu Gly Lys Trp Pro Asn Trp Met Ile Gly Gly Pro
435 440 445

Asp Ser Ser Arg Leu Thr Ser Arg Leu Gly Asn Gln Tyr Val Asn Val
450 455 460

Met Asn Met Leu Leu Phe Thr Leu Pro Gly Thr Pro Ile Thr Tyr Tyr
465 470 475 480

Gly Glu Glu Ile Gly Met Gly Asn Ile Val Ala Ala Asn Leu Asn Glu
485 490 495

Ser Tyr Asp Ile Asn Thr Leu Arg Ser Lys Ser Pro Met Gln Trp Asp
500 505 510

Asn Ser Ser Asn Ala Gly Phe Ser Glu Ala Ser Asn Thr Trp Leu Pro
515 520 525

Thr Asn Ser Asp Tyr His Thr Val Asn Val Asp Val Gln Lys Thr Gln
530 535 540

Pro Arg Ser Ala Leu Lys Leu Tyr Gln Asp Leu Ser Leu Leu His Ala
545 550 555 560

Asn Glu Leu Leu Leu Asn Arg Gly Trp Phe Cys His Leu Arg Asn Asp
565 570 575

Ser His Tyr Val Val Tyr Thr Arg Glu Leu Asp Gly Ile Asp Arg Ile
580 585 590

Phe Ile Val Val Leu Asn Phe Gly Glu Ser Thr Leu Leu Asn Leu His
595 600 605

Asn Met Ile Ser Gly Leu Pro Ala Lys Met Arg Ile Arg Leu Ser Thr
610 615 620

Asn Ser Ala Asp Lys Gly Ser Lys Val Asp Thr Ser Gly Ile Phe Leu
625 630 635 640

Asp Lys Gly Glu Gly Leu Ile Phe Glu His Asn Thr Lys Asn Leu Leu
645 650 655

His Arg Gln Thr Ala Phe Arg Asp Arg Cys Phe Val Ser Asn Arg Ala
660 665 670

Cys Tyr Ser Ser Val Leu Asn Ile Leu Tyr Thr Ser Cys
675 680 685

<210> 37
<211> 630
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> human 4F2 cell-surface antigen heavy chain (CD98hc; SLC3A2)
isoform 1 Uniprot P08195

<400> 37

Met Glu Leu Gln Pro Pro Glu Ala Ser Ile Ala Val Val Ser Ile Pro

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

Arg Cys Arg Glu Leu Pro Ala Gln Lys Trp Trp His Thr Gly Ala Leu
210 215 220

Tyr Arg Ile Gly Asp Leu Gln Ala Phe Gln Gly His Gly Ala Gly Asn
225 230 235 240

Leu Ala Gly Leu Lys Gly Arg Leu Asp Tyr Leu Ser Ser Leu Lys Val
245 250 255

Lys Gly Leu Val Leu Gly Pro Ile His Lys Asn Gln Lys Asp Asp Val
260 265 270

Ala Gln Thr Asp Leu Leu Gln Ile Asp Pro Asn Phe Gly Ser Lys Glu
275 280 285

Asp Phe Asp Ser Leu Leu Gln Ser Ala Lys Lys Lys Ser Ile Arg Val
290 295 300

Ile Leu Asp Leu Thr Pro Asn Tyr Arg Gly Glu Asn Ser Trp Phe Ser
305 310 315 320

Thr Gln Val Asp Thr Val Ala Thr Lys Val Lys Asp Ala Leu Glu Phe
325 330 335

Trp Leu Gln Ala Gly Val Asp Gly Phe Gln Val Arg Asp Ile Glu Asn
340 345 350

Leu Lys Asp Ala Ser Ser Phe Leu Ala Glu Trp Gln Asn Ile Thr Lys
355 360 365

Gly Phe Ser Glu Asp Arg Leu Leu Ile Ala Gly Thr Asn Ser Ser Asp
370 375 380

Leu Gln Gln Ile Leu Ser Leu Leu Glu Ser Asn Lys Asp Leu Leu Leu
385 390 395 400

Thr Ser Ser Tyr Leu Ser Asp Ser Gly Ser Thr Gly Glu His Thr Lys

405

410

415

Ser Leu Val Thr Gln Tyr Leu Asn Ala Thr Gly Asn Arg Trp Cys Ser
 420 425 430

Trp Ser Leu Ser Gln Ala Arg Leu Leu Thr Ser Phe Leu Pro Ala Gln
 435 440 445

Leu Leu Arg Leu Tyr Gln Leu Met Leu Phe Thr Leu Pro Gly Thr Pro
 450 455 460

Val Phe Ser Tyr Gly Asp Glu Ile Gly Leu Asp Ala Ala Ala Leu Pro
 465 470 475 480

Gly Gln Pro Met Glu Ala Pro Val Met Leu Trp Asp Glu Ser Ser Phe
 485 490 495

Pro Asp Ile Pro Gly Ala Val Ser Ala Asn Met Thr Val Lys Gly Gln
 500 505 510

Ser Glu Asp Pro Gly Ser Leu Leu Ser Leu Phe Arg Arg Leu Ser Asp
 515 520 525

Gln Arg Ser Lys Glu Arg Ser Leu Leu His Gly Asp Phe His Ala Phe
 530 535 540

Ser Ala Gly Pro Gly Leu Phe Ser Tyr Ile Arg His Trp Asp Gln Asn
 545 550 555 560

Glu Arg Phe Leu Val Val Leu Asn Phe Gly Asp Val Gly Leu Ser Ala
 565 570 575

Gly Leu Gln Ala Ser Asp Leu Pro Ala Ser Ala Ser Leu Pro Ala Lys
 580 585 590

Ala Asp Leu Leu Leu Ser Thr Gln Pro Gly Arg Glu Glu Gly Ser Pro
 595 600 605

Leu Glu Leu Glu Arg Leu Lys Leu Glu Pro His Glu Gly Leu Leu Leu
610 615 620

Arg Phe Pro Tyr Ala Ala
625 630

<210> 38
<211> 507
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> human Large neutral amino acids transporter small subunit 1
(LAT1; SLC7A5) isoform 1 Uniprot Q01650

<400> 38

Met Ala Gly Ala Gly Pro Lys Arg Arg Ala Leu Ala Ala Pro Ala Ala
1 5 10 15

Glu Glu Lys Glu Glu Ala Arg Glu Lys Met Leu Ala Ala Lys Ser Ala
20 25 30

Asp Gly Ser Ala Pro Ala Gly Glu Gly Glu Gly Val Thr Leu Gln Arg
35 40 45

Asn Ile Thr Leu Leu Asn Gly Val Ala Ile Ile Val Gly Thr Ile Ile
50 55 60

Gly Ser Gly Ile Phe Val Thr Pro Thr Gly Val Leu Lys Glu Ala Gly
65 70 75 80

Ser Pro Gly Leu Ala Leu Val Val Trp Ala Ala Cys Gly Val Phe Ser
85 90 95

Ile Val Gly Ala Leu Cys Tyr Ala Glu Leu Gly Thr Thr Ile Ser Lys
100 105 110

Ser Gly Gly Asp Tyr Ala Tyr Met Leu Glu Val Tyr Gly Ser Leu Pro
115 120 125

Ala Phe Leu Lys Leu Trp Ile Glu Leu Leu Ile Ile Arg Pro Ser Ser
130 135 140

Gln Tyr Ile Val Ala Leu Val Phe Ala Thr Tyr Leu Leu Lys Pro Leu
145 150 155 160

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

Leu Cys Val Leu Leu Leu Thr Ala Val Asn Cys Tyr Ser Val Lys Ala
180 185 190

Ala Thr Arg Val Gln Asp Ala Phe Ala Ala Ala Lys Leu Leu Ala Leu
195 200 205

Ala Leu Ile Ile Leu Leu Gly Phe Val Gln Ile Gly Lys Gly Asp Val
210 215 220

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

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

Trp Asn Tyr Leu Asn Phe Val Thr Glu Glu Met Ile Asn Pro Tyr Arg
260 265 270

Asn Leu Pro Leu Ala Ile Ile Ile Ser Leu Pro Ile Val Thr Leu Val
275 280 285

Tyr Val Leu Thr Asn Leu Ala Tyr Phe Thr Thr Leu Ser Thr Glu Gln
290 295 300

Met Leu Ser Ser Glu Ala Val Ala Val Asp Phe Gly Asn Tyr His Leu
305 310 315 320

Gly Val Met Ser Trp Ile Ile Pro Val Phe Val Gly Leu Ser Cys Phe
325 330 335

Gly Ser Val Asn Gly Ser Leu Phe Thr Ser Ser Arg Leu Phe Phe Val
340 345 350

Gly Ser Arg Glu Gly His Leu Pro Ser Ile Leu Ser Met Ile His Pro
355 360 365

Gln Leu Leu Thr Pro Val Pro Ser Leu Val Phe Thr Cys Val Met Thr
370 375 380

Leu Leu Tyr Ala Phe Ser Lys Asp Ile Phe Ser Val Ile Asn Phe Phe
385 390 395 400

Ser Phe Phe Asn Trp Leu Cys Val Ala Leu Ala Ile Ile Gly Met Ile
405 410 415

Trp Leu Arg His Arg Lys Pro Glu Leu Glu Arg Pro Ile Lys Val Asn
420 425 430

Leu Ala Leu Pro Val Phe Phe Ile Leu Ala Cys Leu Phe Leu Ile Ala
435 440 445

Val Ser Phe Trp Lys Thr Pro Val Glu Cys Gly Ile Gly Phe Thr Ile
450 455 460

Ile Leu Ser Gly Leu Pro Val Tyr Phe Phe Gly Val Trp Trp Lys Asn
465 470 475 480

Lys Pro Lys Trp Leu Leu Gln Gly Ile Phe Ser Thr Thr Val Leu Cys
485 490 495

Gln Lys Leu Met Gln Val Val Pro Gln Glu Thr
500 505

<210> 39
<211> 535
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> human Large neutral amino acids transporter small subunit 2
(LAT2; SLC7A8) isoform 1

Uniprot Q9UHI5

<400> 39

Met Glu Glu Gly Ala Arg His Arg Asn Asn Thr Glu Lys Lys His Pro
1 5 10 15

Gly Gly Gly Glu Ser Asp Ala Ser Pro Glu Ala Gly Ser Gly Gly Gly
20 25 30

Gly Val Ala Leu Lys Lys Glu Ile Gly Leu Val Ser Ala Cys Gly Ile
35 40 45

Ile Val Gly Asn Ile Ile Gly Ser Gly Ile Phe Val Ser Pro Lys Gly
50 55 60

Val Leu Glu Asn Ala Gly Ser Val Gly Leu Ala Leu Ile Val Trp Ile
65 70 75 80

Val Thr Gly Phe Ile Thr Val Val Gly Ala Leu Cys Tyr Ala Glu Leu
85 90 95

Gly Val Thr Ile Pro Lys Ser Gly Gly Asp Tyr Ser Tyr Val Lys Asp
100 105 110

Ile Phe Gly Gly Leu Ala Gly Phe Leu Arg Leu Trp Ile Ala Val Leu
115 120 125

Val Ile Tyr Pro Thr Asn Gln Ala Val Ile Ala Leu Thr Phe Ser Asn
130 135 140

Tyr Val Leu Gln Pro Leu Phe Pro Thr Cys Phe Pro Pro Glu Ser Gly
145 150 155 160

Leu Arg Leu Leu Ala Ala Ile Cys Leu Leu Leu Thr Trp Val Asn
165 170 175

Cys Ser Ser Val Arg Trp Ala Thr Arg Val Gln Asp Ile Phe Thr Ala
180 185 190

Gly Lys Leu Leu Ala Leu Ala Leu Ile Ile Ile Met Gly Ile Val Gln
195 200 205

Ile Cys Lys Gly Glu Tyr Phe Trp Leu Glu Pro Lys Asn Ala Phe Glu
210 215 220

Asn Phe Gln Glu Pro Asp Ile Gly Leu Val Ala Leu Ala Phe Leu Gln
225 230 235 240

Gly Ser Phe Ala Tyr Gly Gly Trp Asn Phe Leu Asn Tyr Val Thr Glu
245 250 255

Glu Leu Val Asp Pro Tyr Lys Asn Leu Pro Arg Ala Ile Phe Ile Ser
260 265 270

Ile Pro Leu Val Thr Phe Val Tyr Val Phe Ala Asn Val Ala Tyr Val
275 280 285

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

Thr Phe Gly Glu Lys Leu Leu Gly Val Met Ala Trp Ile Met Pro Ile
305 310 315 320

Ser Val Ala Leu Ser Thr Phe Gly Gly Val Asn Gly Ser Leu Phe Thr
325 330 335

Ser Ser Arg Leu Phe Phe Ala Gly Ala Arg Glu Gly His Leu Pro Ser

340

345

350

Val Leu Ala Met Ile His Val Lys Arg Cys Thr Pro Ile Pro Ala Leu
 355 360 365

Leu Phe Thr Cys Ile Ser Thr Leu Leu Met Leu Val Thr Ser Asp Met
 370 375 380

Tyr Thr Leu Ile Asn Tyr Val Gly Phe Ile Asn Tyr Leu Phe Tyr Gly
 385 390 395 400

Val Thr Val Ala Gly Gln Ile Val Leu Arg Trp Lys Lys Pro Asp Ile
 405 410 415

Pro Arg Pro Ile Lys Ile Asn Leu Leu Phe Pro Ile Ile Tyr Leu Leu
 420 425 430

Phe Trp Ala Phe Leu Leu Val Phe Ser Leu Trp Ser Glu Pro Val Val
 435 440 445

Cys Gly Ile Gly Leu Ala Ile Met Leu Thr Gly Val Pro Val Tyr Phe
 450 455 460

Leu Gly Val Tyr Trp Gln His Lys Pro Lys Cys Phe Ser Asp Phe Ile
 465 470 475 480

Glu Leu Leu Thr Leu Val Ser Gln Lys Met Cys Val Val Val Tyr Pro
 485 490 495

Glu Val Glu Arg Gly Ser Gly Thr Glu Glu Ala Asn Glu Asp Met Glu
 500 505 510

Glu Gln Gln Gln Pro Met Tyr Gln Pro Thr Pro Thr Lys Asp Lys Asp
 515 520 525

Val Ala Gly Gln Pro Gln Pro
 530 535

<210> 40
<211> 523
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> human Asc-type amino acid transporter 1 (Asc-1; SLC7A10) isoform
1

Uniprot Q9NS82

<400> 40

Met Ala Gly His Thr Gln Gln Pro Ser Gly Arg Gly Asn Pro Arg Pro
1 5 10 15

Ala Pro Ser Pro Ser Pro Val Pro Gly Thr Val Pro Gly Ala Ser Glu
20 25 30

Arg Val Ala Leu Lys Lys Glu Ile Gly Leu Leu Ser Ala Cys Thr Ile
35 40 45

Ile Ile Gly Asn Ile Ile Gly Ser Gly Ile Phe Ile Ser Pro Lys Gly
50 55 60

Val Leu Glu His Ser Gly Ser Val Gly Leu Ala Leu Phe Val Trp Val
65 70 75 80

Leu Gly Gly Gly Val Thr Ala Leu Gly Ser Leu Cys Tyr Ala Glu Leu
85 90 95

Gly Val Ala Ile Pro Lys Ser Gly Gly Asp Tyr Ala Tyr Val Thr Glu
100 105 110

Ile Phe Gly Gly Leu Ala Gly Phe Leu Leu Leu Trp Ser Ala Val Leu
115 120 125

Ile Met Tyr Pro Thr Ser Leu Ala Val Ile Ser Met Thr Phe Ser Asn
130 135 140

Tyr Val Leu Gln Pro Val Phe Pro Asn Cys Ile Pro Pro Thr Thr Ala
145 150 155 160

Ser Arg Val Leu Ser Met Ala Cys Leu Met Leu Leu Thr Trp Val Asn
165 170 175

Ser Ser Ser Val Arg Trp Ala Thr Arg Ile Gln Asp Met Phe Thr Gly
180 185 190

Gly Lys Leu Leu Ala Leu Ser Leu Ile Ile Gly Val Gly Leu Leu Gln
195 200 205

Ile Phe Gln Gly His Phe Glu Glu Leu Arg Pro Ser Asn Ala Phe Ala
210 215 220

Phe Trp Met Thr Pro Ser Val Gly His Leu Ala Leu Ala Phe Leu Gln
225 230 235 240

Gly Ser Phe Ala Phe Ser Gly Trp Asn Phe Leu Asn Tyr Val Thr Glu
245 250 255

Glu Met Val Asp Ala Arg Lys Asn Leu Pro Arg Ala Ile Phe Ile Ser
260 265 270

Ile Pro Leu Val Thr Phe Val Tyr Thr Phe Thr Asn Ile Ala Tyr Phe
275 280 285

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

Thr Phe Gly Glu Lys Leu Leu Gly Tyr Phe Ser Trp Val Met Pro Val
305 310 315 320

Ser Val Ala Leu Ser Thr Phe Gly Gly Ile Asn Gly Tyr Leu Phe Thr
325 330 335

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

Leu Leu Ala Met Ile His Val Arg His Cys Thr Pro Ile Pro Ala Leu
355 360 365

Leu Val Cys Cys Gly Ala Thr Ala Val Ile Met Leu Val Gly Asp Thr
370 375 380

Tyr Thr Leu Ile Asn Tyr Val Ser Phe Ile Asn Tyr Leu Cys Tyr Gly
385 390 395 400

Val Thr Ile Leu Gly Leu Leu Leu Leu Arg Trp Arg Arg Pro Ala Leu
405 410 415

His Arg Pro Ile Lys Val Asn Leu Leu Ile Pro Val Ala Tyr Leu Val
420 425 430

Phe Trp Ala Phe Leu Leu Val Phe Ser Phe Ile Ser Glu Pro Met Val
435 440 445

Cys Gly Val Gly Val Ile Ile Ile Leu Thr Gly Val Pro Ile Phe Phe
450 455 460

Leu Gly Val Phe Trp Arg Ser Lys Pro Lys Cys Val His Arg Leu Thr
465 470 475 480

Glu Ser Met Thr His Trp Gly Gln Glu Leu Cys Phe Val Val Tyr Pro
485 490 495

Gln Asp Ala Pro Glu Glu Glu Glu Asn Gly Pro Cys Pro Pro Ser Leu
500 505 510

Leu Pro Ala Thr Asp Lys Pro Ser Lys Pro Gln
515 520

<210> 41
<211> 642

<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> human Sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)(ATB0,+; SLC6A14) isoform 1 Uniprot Q9UN76

<400> 41

Met Asp Lys Leu Lys Cys Pro Ser Phe Phe Lys Cys Arg Glu Lys Glu
1 5 10 15

Lys Val Ser Ala Ser Ser Glu Asn Phe His Val Gly Glu Asn Asp Glu
20 25 30

Asn Gln Asp Arg Gly Asn Trp Ser Lys Lys Ser Asp Tyr Leu Leu Ser
35 40 45

Met Ile Gly Tyr Ala Val Gly Leu Gly Asn Val Trp Arg Phe Pro Tyr
50 55 60

Leu Thr Tyr Ser Asn Gly Gly Gly Ala Phe Leu Ile Pro Tyr Ala Ile
65 70 75 80

Met Leu Ala Leu Ala Gly Leu Pro Leu Phe Phe Leu Glu Cys Ser Leu
85 90 95

Gly Gln Phe Ala Ser Leu Gly Pro Val Ser Val Trp Arg Ile Leu Pro
100 105 110

Leu Phe Gln Gly Val Gly Ile Thr Met Val Leu Ile Ser Ile Phe Val
115 120 125

Thr Ile Tyr Tyr Asn Val Ile Ile Ala Tyr Ser Leu Tyr Tyr Met Phe
130 135 140

Ala Ser Phe Gln Ser Glu Leu Pro Trp Lys Asn Cys Ser Ser Trp Ser
145 150 155 160

Asp Lys Asn Cys Ser Arg Ser Pro Ile Val Thr His Cys Asn Val Ser
165 170 175

Thr Val Asn Lys Gly Ile Gln Glu Ile Ile Gln Met Asn Lys Ser Trp
180 185 190

Val Asp Ile Asn Asn Phe Thr Cys Ile Asn Gly Ser Glu Ile Tyr Gln
195 200 205

Pro Gly Gln Leu Pro Ser Glu Gln Tyr Trp Asn Lys Val Ala Leu Gln
210 215 220

Arg Ser Ser Gly Met Asn Glu Thr Gly Val Ile Val Trp Tyr Leu Ala
225 230 235 240

Leu Cys Leu Leu Leu Ala Trp Leu Ile Val Gly Ala Ala Leu Phe Lys
245 250 255

Gly Ile Lys Ser Ser Gly Lys Val Val Tyr Phe Thr Ala Leu Phe Pro
260 265 270

Tyr Val Val Leu Leu Ile Leu Leu Val Arg Gly Ala Thr Leu Glu Gly
275 280 285

Ala Ser Lys Gly Ile Ser Tyr Tyr Ile Gly Ala Gln Ser Asn Phe Thr
290 295 300

Lys Leu Lys Glu Ala Glu Val Trp Lys Asp Ala Ala Thr Gln Ile Phe
305 310 315 320

Tyr Ser Leu Ser Val Ala Trp Gly Gly Leu Val Ala Leu Ser Ser Tyr
325 330 335

Asn Lys Phe Lys Asn Asn Cys Phe Ser Asp Ala Ile Val Val Cys Leu
340 345 350

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

355

360

365

Leu Gly His Met Ala His Ile Ser Gly Lys Glu Val Ser Gln Val Val
 370 375 380

Lys Ser Gly Phe Asp Leu Ala Phe Ile Ala Tyr Pro Glu Ala Leu Ala
 385 390 395 400

Gln Leu Pro Gly Gly Pro Phe Trp Ser Ile Leu Phe Phe Phe Met Leu
 405 410 415

Leu Thr Leu Gly Leu Asp Ser Gln Phe Ala Ser Ile Glu Thr Ile Thr
 420 425 430

Thr Thr Ile Gln Asp Leu Phe Pro Lys Val Met Lys Lys Met Arg Val
 435 440 445

Pro Ile Thr Leu Gly Cys Cys Leu Val Leu Phe Leu Leu Gly Leu Val
 450 455 460

Cys Val Thr Gln Ala Gly Ile Tyr Trp Val His Leu Ile Asp His Phe
 465 470 475 480

Cys Ala Gly Trp Gly Ile Leu Ile Ala Ala Ile Leu Glu Leu Val Gly
 485 490 495

Ile Ile Trp Ile Tyr Gly Gly Asn Arg Phe Ile Glu Asp Thr Glu Met
 500 505 510

Met Ile Gly Ala Lys Arg Trp Ile Phe Trp Leu Trp Trp Arg Ala Cys
 515 520 525

Trp Phe Val Ile Thr Pro Ile Leu Leu Ile Ala Ile Phe Ile Trp Ser
 530 535 540

Leu Val Gln Phe His Arg Pro Asn Tyr Gly Ala Ile Pro Tyr Pro Asp
 545 550 555 560

Trp Gly Val Ala Leu Gly Trp Cys Met Ile Val Phe Cys Ile Ile Trp
565 570 575

Ile Pro Ile Met Ala Ile Ile Lys Ile Ile Gln Ala Lys Gly Asn Ile
580 585 590

Phe Gln Arg Leu Ile Ser Cys Cys Arg Pro Ala Ser Asn Trp Gly Pro
595 600 605

Tyr Leu Glu Gln His Arg Gly Glu Arg Tyr Lys Asp Met Val Asp Pro
610 615 620

Lys Lys Glu Ala Asp His Glu Ile Pro Thr Val Ser Gly Ser Arg Lys
625 630 635 640

Pro Glu

<210> 42
<211> 634
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> human Sodium-dependent neutral amino acid transporter B(0)AT1
(B(0)AT1; SLC6A19) isoform 1 Uniprot Q695T7

<400> 42

Met Val Arg Leu Val Leu Pro Asn Pro Gly Leu Asp Ala Arg Ile Pro
1 5 10 15

Ser Leu Ala Glu Leu Glu Thr Ile Glu Gln Glu Glu Ala Ser Ser Arg
20 25 30

Pro Lys Trp Asp Asn Lys Ala Gln Tyr Met Leu Thr Cys Leu Gly Phe
35 40 45

Cys Val Gly Leu Gly Asn Val Trp Arg Phe Pro Tyr Leu Cys Gln Ser
50 55 60

His Gly Gly Gly Ala Phe Met Ile Pro Phe Leu Ile Leu Leu Val Leu
65 70 75 80

Glu Gly Ile Pro Leu Leu Tyr Leu Glu Phe Ala Ile Gly Gln Arg Leu
85 90 95

Arg Arg Gly Ser Leu Gly Val Trp Ser Ser Ile His Pro Ala Leu Lys
100 105 110

Gly Leu Gly Leu Ala Ser Met Leu Thr Ser Phe Met Val Gly Leu Tyr
115 120 125

Tyr Asn Thr Ile Ile Ser Trp Ile Met Trp Tyr Leu Phe Asn Ser Phe
130 135 140

Gln Glu Pro Leu Pro Trp Ser Asp Cys Pro Leu Asn Glu Asn Gln Thr
145 150 155 160

Gly Tyr Val Asp Glu Cys Ala Arg Ser Ser Pro Val Asp Tyr Phe Trp
165 170 175

Tyr Arg Glu Thr Leu Asn Ile Ser Thr Ser Ile Ser Asp Ser Gly Ser
180 185 190

Ile Gln Trp Trp Met Leu Leu Cys Leu Ala Cys Ala Trp Ser Val Leu
195 200 205

Tyr Met Cys Thr Ile Arg Gly Ile Glu Thr Thr Gly Lys Ala Val Tyr
210 215 220

Ile Thr Ser Thr Leu Pro Tyr Val Val Leu Thr Ile Phe Leu Ile Arg
225 230 235 240

Gly Leu Thr Leu Lys Gly Ala Thr Asn Gly Ile Val Phe Leu Phe Thr
245 250 255

Pro Asn Val Thr Glu Leu Ala Gln Pro Asp Thr Trp Leu Asp Ala Gly
260 265 270

Ala Gln Val Phe Phe Ser Phe Ser Leu Ala Phe Gly Gly Leu Ile Ser
275 280 285

Phe Ser Ser Tyr Asn Ser Val His Asn Asn Cys Glu Lys Asp Ser Val
290 295 300

Ile Val Ser Ile Ile Asn Gly Phe Thr Ser Val Tyr Val Ala Ile Val
305 310 315 320

Val Tyr Ser Val Ile Gly Phe Arg Ala Thr Gln Arg Tyr Asp Asp Cys
325 330 335

Phe Ser Thr Asn Ile Leu Thr Leu Ile Asn Gly Phe Asp Leu Pro Glu
340 345 350

Gly Asn Val Thr Gln Glu Asn Phe Val Asp Met Gln Gln Arg Cys Asn
355 360 365

Ala Ser Asp Pro Ala Ala Tyr Ala Gln Leu Val Phe Gln Thr Cys Asp
370 375 380

Ile Asn Ala Phe Leu Ser Glu Ala Val Glu Gly Thr Gly Leu Ala Phe
385 390 395 400

Ile Val Phe Thr Glu Ala Ile Thr Lys Met Pro Leu Ser Pro Leu Trp
405 410 415

Ser Val Leu Phe Phe Ile Met Leu Phe Cys Leu Gly Leu Ser Ser Met
420 425 430

Phe Gly Asn Met Glu Gly Val Val Val Pro Leu Gln Asp Leu Arg Val
435 440 445

Ile Pro Pro Lys Trp Pro Lys Glu Val Leu Thr Gly Leu Ile Cys Leu
450 455 460

Gly Thr Phe Leu Ile Gly Phe Ile Phe Thr Leu Asn Ser Gly Gln Tyr
465 470 475 480

Trp Leu Ser Leu Leu Asp Ser Tyr Ala Gly Ser Ile Pro Leu Leu Ile
485 490 495

Ile Ala Phe Cys Glu Met Phe Ser Val Val Tyr Val Tyr Gly Val Asp
500 505 510

Arg Phe Asn Lys Asp Ile Glu Phe Met Ile Gly His Lys Pro Asn Ile
515 520 525

Phe Trp Gln Val Thr Trp Arg Val Val Ser Pro Leu Leu Met Leu Ile
530 535 540

Ile Phe Leu Phe Phe Phe Val Val Glu Val Ser Gln Glu Leu Thr Tyr
545 550 555 560

Ser Ile Trp Asp Pro Gly Tyr Glu Glu Phe Pro Lys Ser Gln Lys Ile
565 570 575

Ser Tyr Pro Asn Trp Val Tyr Val Val Val Val Ile Val Ala Gly Val
580 585 590

Pro Ser Leu Thr Ile Pro Gly Tyr Ala Ile Tyr Lys Leu Ile Arg Asn
595 600 605

His Cys Gln Lys Pro Gly Asp His Gln Gly Leu Val Ser Thr Leu Ser
610 615 620

Thr Ala Ser Met Asn Gly Asp Leu Lys Tyr
625 630

<210> 43
<211> 515

<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> human Monocarboxylate transporter 10 (TAT1; SLC16A10) isoform 1

Uniprot Q8TF71

<400> 43

Met Val Leu Ser Gln Glu Glu Pro Asp Ser Ala Arg Gly Thr Ser Glu
1 5 10 15

Ala Gln Pro Leu Gly Pro Ala Pro Thr Gly Ala Ala Pro Pro Pro Gly
20 25 30

Pro Gly Pro Ser Asp Ser Pro Glu Ala Ala Val Glu Lys Val Glu Val
35 40 45

Glu Leu Ala Gly Pro Ala Thr Ala Glu Pro His Glu Pro Pro Glu Pro
50 55 60

Pro Glu Gly Gly Trp Gly Trp Leu Val Met Leu Ala Ala Met Trp Cys
65 70 75 80

Asn Gly Ser Val Phe Gly Ile Gln Asn Ala Cys Gly Val Leu Phe Val
85 90 95

Ser Met Leu Glu Thr Phe Gly Ser Lys Asp Asp Asp Lys Met Val Phe
100 105 110

Lys Thr Ala Trp Val Gly Ser Leu Ser Met Gly Met Ile Phe Phe Cys
115 120 125

Cys Pro Ile Val Ser Val Phe Thr Asp Leu Phe Gly Cys Arg Lys Thr
130 135 140

Ala Val Val Gly Ala Ala Val Gly Phe Val Gly Leu Met Ser Ser Ser
145 150 155 160

Phe Val Ser Ser Ile Glu Pro Leu Tyr Leu Thr Tyr Gly Ile Ile Phe
165 170 175

Ala Cys Gly Cys Ser Phe Ala Tyr Gln Pro Ser Leu Val Ile Leu Gly
180 185 190

His Tyr Phe Lys Lys Arg Leu Gly Leu Val Asn Gly Ile Val Thr Ala
195 200 205

Gly Ser Ser Val Phe Thr Ile Leu Leu Pro Leu Leu Leu Arg Val Leu
210 215 220

Ile Asp Ser Val Gly Leu Phe Tyr Thr Leu Arg Val Leu Cys Ile Phe
225 230 235 240

Met Phe Val Leu Phe Leu Ala Gly Phe Thr Tyr Arg Pro Leu Ala Thr
245 250 255

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

Arg Lys Lys Phe Ser Pro Pro Lys Lys Ile Phe Asn Phe Ala Ile Phe
275 280 285

Lys Val Thr Ala Tyr Ala Val Trp Ala Val Gly Ile Pro Leu Ala Leu
290 295 300

Phe Gly Tyr Phe Val Pro Tyr Val His Leu Met Lys His Val Asn Glu
305 310 315 320

Arg Phe Gln Asp Glu Lys Asn Lys Glu Val Val Leu Met Cys Ile Gly
325 330 335

Val Thr Ser Gly Val Gly Arg Leu Leu Phe Gly Arg Ile Ala Asp Tyr
340 345 350

Val Pro Gly Val Lys Lys Val Tyr Leu Gln Val Leu Ser Phe Phe Phe
355 360 365

Ile Gly Leu Met Ser Met Met Ile Pro Leu Cys Ser Ile Phe Gly Ala
370 375 380

Leu Ile Ala Val Cys Leu Ile Met Gly Leu Phe Asp Gly Cys Phe Ile
385 390 395 400

Ser Ile Met Ala Pro Ile Ala Phe Glu Leu Val Gly Ala Gln Asp Val
405 410 415

Ser Gln Ala Ile Gly Phe Leu Leu Gly Phe Met Ser Ile Pro Met Thr
420 425 430

Val Gly Pro Pro Ile Ala Gly Leu Leu Arg Asp Lys Leu Gly Ser Tyr
435 440 445

Asp Val Ala Phe Tyr Leu Ala Gly Val Pro Pro Leu Ile Gly Gly Ala
450 455 460

Val Leu Cys Phe Ile Pro Trp Ile His Ser Lys Lys Gln Arg Glu Ile
465 470 475 480

Ser Lys Thr Thr Gly Lys Glu Lys Met Glu Lys Met Leu Glu Asn Gln
485 490 495

Asn Ser Leu Leu Ser Ser Ser Ser Gly Met Phe Lys Lys Glu Ser Asp
500 505 510

Ser Ile Ile
515

<210> 44
<211> 504
<212> PRT
<213> Homo sapiens

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<221> MISC_FEATURE

<223> human Proton-coupled amino acid transporter 4 (PAT4; SLC36A4)
isoform 1 Uniprot Q6YBV0

<400> 44

Met Glu Ala Ala Ala Thr Pro Ala Ala Ala Gly Ala Ala Arg Arg Glu
1 5 10 15

Glu Leu Asp Met Asp Val Met Arg Pro Leu Ile Asn Glu Gln Asn Phe
20 25 30

Asp Gly Thr Ser Asp Glu Glu His Glu Gln Glu Leu Leu Pro Val Gln
35 40 45

Lys His Tyr Gln Leu Asp Asp Gln Glu Gly Ile Ser Phe Val Gln Thr
50 55 60

Leu Met His Leu Leu Lys Gly Asn Ile Gly Thr Gly Leu Leu Gly Leu
65 70 75 80

Pro Leu Ala Ile Lys Asn Ala Gly Ile Val Leu Gly Pro Ile Ser Leu
85 90 95

Val Phe Ile Gly Ile Ile Ser Val His Cys Met His Ile Leu Val Arg
100 105 110

Cys Ser His Phe Leu Cys Leu Arg Phe Lys Lys Ser Thr Leu Gly Tyr
115 120 125

Ser Asp Thr Val Ser Phe Ala Met Glu Val Ser Pro Trp Ser Cys Leu
130 135 140

Gln Lys Gln Ala Ala Trp Gly Arg Ser Val Val Asp Phe Phe Leu Val
145 150 155 160

Ile Thr Gln Leu Gly Phe Cys Ser Val Tyr Ile Val Phe Leu Ala Glu
165 170 175

Asn Val Lys Gln Val His Glu Gly Phe Leu Glu Ser Lys Val Phe Ile
180 185 190

Ser Asn Ser Thr Asn Ser Ser Asn Pro Cys Glu Arg Arg Ser Val Asp
195 200 205

Leu Arg Ile Tyr Met Leu Cys Phe Leu Pro Phe Ile Ile Leu Leu Val
210 215 220

Phe Ile Arg Glu Leu Lys Asn Leu Phe Val Leu Ser Phe Leu Ala Asn
225 230 235 240

Val Ser Met Ala Val Ser Leu Val Ile Ile Tyr Gln Tyr Val Val Arg
245 250 255

Asn Met Pro Asp Pro His Asn Leu Pro Ile Val Ala Gly Trp Lys Lys
260 265 270

Tyr Pro Leu Phe Phe Gly Thr Ala Val Phe Ala Phe Glu Gly Ile Gly
275 280 285

Val Val Leu Pro Leu Glu Asn Gln Met Lys Glu Ser Lys Arg Phe Pro
290 295 300

Gln Ala Leu Asn Ile Gly Met Gly Ile Val Thr Thr Leu Tyr Val Thr
305 310 315 320

Leu Ala Thr Leu Gly Tyr Met Cys Phe His Asp Glu Ile Lys Gly Ser
325 330 335

Ile Thr Leu Asn Leu Pro Gln Asp Val Trp Leu Tyr Gln Ser Val Lys
340 345 350

Ile Leu Tyr Ser Phe Gly Ile Phe Val Thr Tyr Ser Ile Gln Phe Tyr
355 360 365

Val Pro Ala Glu Ile Ile Ile Pro Gly Ile Thr Ser Lys Phe His Thr

370

375

380

Lys Trp Lys Gln Ile Cys Glu Phe Gly Ile Arg Ser Phe Leu Val Ser
 385 390 395 400

Ile Thr Cys Ala Gly Ala Ile Leu Ile Pro Arg Leu Asp Ile Val Ile
 405 410 415

Ser Phe Val Gly Ala Val Ser Ser Ser Thr Leu Ala Leu Ile Leu Pro
 420 425 430

Pro Leu Val Glu Ile Leu Thr Phe Ser Lys Glu His Tyr Asn Ile Trp
 435 440 445

Met Val Leu Lys Asn Ile Ser Ile Ala Phe Thr Gly Val Val Gly Phe
 450 455 460

Leu Leu Gly Thr Tyr Ile Thr Val Glu Glu Ile Ile Tyr Pro Thr Pro
 465 470 475 480

Lys Val Val Ala Gly Thr Pro Gln Ser Pro Phe Leu Asn Leu Asn Ser
 485 490 495

Thr Cys Leu Thr Ser Gly Leu Lys
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<210> 45
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> T2A sequence

<400> 45

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
 1 5 10 15

Gly Pro

<210> 46
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> P2A sequence

<400> 46

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
20

<210> 47
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> P2A sequence

<400> 47

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

<210> 48
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> E2A sequence

<400> 48

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser

1 5 10 15

Asn Pro Gly Pro Ser Glu
20

<210> 49
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> F2A sequence

<400> 49

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
1 5 10 15

Glu Ser Asn Pro Gly Pro
20

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> GCN2 CRISPR gRNA target sequence

<400> 50
cgctgagaaa tgactgcacg 20

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> GCN2 CRISPR gRNA target sequence

<400> 51
catatacttc ttcaccagtt 20

<210> 52

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> GCN2 CRISPR gRNA target sequence

<400> 52
atgtactcac acatctggat 20

<210> 53
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> GCN2 CRISPR gRNA target sequence

<400> 53
ttaggtgatg atctttgaac 20

<210> 54
<211> 20
<212> DNA
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<220>
<223> GCN2 CRISPR gRNA target sequence

<400> 54
tacctcccca cagtgtttct 20

<210> 55
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> GCN2 CRISPR gRNA target sequence

<400> 55
aaaatctcgc ctagaagaac 20

<210> 56
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> CHOP CRISPR gRNA target sequence

<400> 56

ccgagctctg attgaccgaa

20

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> CHOP CRISPR gRNA target sequence

<400> 57

aggaaatcga gcgcctgacc

20

<210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> CHOP CRISPR gRNA target sequence

<400> 58

ccagctggac agtgtcccga

20

<210> 59

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> CHOP CRISPR gRNA target sequence

<400> 59

ctcttgcagg tcctcatacc

20

<210> 60

<211> 20

<212> DNA

<213> Artificial Sequence

<220>
<223> CHOP CRISPR gRNA target sequence

<400> 60
gcgagtcgcc tctacttccc 20

<210> 61
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> CHOP CRISPR gRNA target sequence

<400> 61
ggctggaaaag cagcgcatga 20

<210> 62
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> ATF4 CRISPR gRNA target sequence

<400> 62
aggatcgtaa ggtttgggac 20

<210> 63
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> ATF4 CRISPR gRNA target sequence

<400> 63
taataagcag cccccccaga 20

<210> 64
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> ATF4 CRISPR gRNA target sequence

<400> 64
ccactcaccc ttgctgttgt 20

<210> 65
<211> 20
<212> DNA
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<220>
<223> ATF4 CRISPR gRNA target sequence

<400> 65
tctcttagat gattacctgg 20

<210> 66
<211> 20
<212> DNA
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<220>
<223> ATF4 CRISPR gRNA target sequence

<400> 66
gcaacgtaag cagtgtagtc 20

<210> 67
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> ATF4 CRISPR gRNA target sequence

<400> 67
tttgcagagg atgccttctc 20

<210> 68
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> eIF2alpha CRISPR gRNA target sequence

<400> 68

caggctgtca aaattcgagc 20

<210> 69

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> eIF2alpha CRISPR gRNA target sequence

<400> 69

cattcttcgt catgttgctg 20

<210> 70

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> eIF2alpha CRISPR gRNA target sequence

<400> 70

gtacttgctca tcaaagaccc 20

<210> 71

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> eIF2alpha CRISPR gRNA target sequence

<400> 71

gtaaaagaag ccctaagagc 20

<210> 72

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> eIF2alpha CRISPR gRNA target sequence

<400> 72

gaccagagac ccatctattt 20

<210> 73
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> eIF2alpha CRISPR gRNA target sequence

<400> 73
tacagaaaac atgcccatta