

SEQUENCE LISTING

<110> UBI Pharma Inc.
United BioPharma Inc.
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Chen, Hui-Jung

<120> AFUCOSYLATED ANTIBODIES AND MANUFACTURE THEREOF

<130> UBIP1004B-US

<140> TBD

<141> 2018-05-08

<160> 17

<170> PatentIn version 3.5

<210> 1

<211> 1728

<212> DNA

<213> mouse

<400> 1

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<211> 575
<212> PRT
<213> human

<400> 2

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20 25 30

Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
35 40 45

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

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
65 70 75 80

Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
85 90 95

Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
100 105 110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
115 120 125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
130 135 140

Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
145 150 155 160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
165 170 175

Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
180 185 190

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
195 200 205

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
210 215 220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
225 230 235 240

Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
245 250 255

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
260 265 270

Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
275 280 285

Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
290 295 300

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
305 310 315 320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
325 330 335

Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
340 345 350

Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
355 360 365

Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
370 375 380

His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
385 390 395 400

Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Thr Leu Leu Lys Glu
405 410 415

Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
420 425 430

Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
435 440 445

Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
450 455 460

Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
465 470 475 480

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
485 490 495

Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
500 505 510

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

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Ile Asn
530 535 540

Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
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Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
565 570 575

<210> 3

<211> 1728

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of F83M modified enzyme, where positions
1093-1095, 1225-1227, and 1357-1359 in wild-type FUT8 gene have
been changed

<400> 3

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agggagctgt ccaagatcct ggccaagctg gagaggctga agcagcagaa cgaggacctg	180
aggaggatgg ccgagtccct gaggatcccc gagggcccca tcgaccaggg caccgccacc	240
ggcagggctga gggctgctgga ggagcagctg gtgaaggcca aggagcagat cgagaactac	300
aagaagcagg ccaggaacgg cctgggcaag gaccacgaga tcctgaggag gaggatcgag	360
aacggcgcca aggagctgtg gttcttcctg cagtccgagc tgaagaagct gaagcacctg	420
gagggcaacg agctgcagag gcacgccgac gagatcctgc tggacctggg ccaccacgag	480
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ccccctacc tgcccctggc cgtgcccagag gacctggccg acaggctgct gagggtgcac      960
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tactccaact acgagttcat ctccgacaac tccatctcct ggtccgccgg cctgcacaac      1320
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gacttcctgg tgtgcacctt ctctcccag gtgtgcaggg tggcctacga gatcatgcag      1440
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aagggcacga acaggaagct gggcaagacc ggcctgtacc cctcctacaa ggtgaggagg      1680
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<210> 4
<211> 575
<212> PRT
<213> Artificial Sequence

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<220>
<223> Amino acid sequence of F83M modified enzyme, where the residues
      at positions 365, 409, and 453 in wild-type FUT8 protein have
      been changed

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<400> 4

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Met Arg Ala Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
1           5           10          15

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Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
          20           25           30

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Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
35 40 45

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

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
65 70 75 80

Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
85 90 95

Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
100 105 110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
115 120 125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
130 135 140

Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
145 150 155 160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
165 170 175

Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
180 185 190

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
195 200 205

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
210 215 220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
225 230 235 240

Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
245 250 255

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
260 265 270

Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
275 280 285

Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
290 295 300

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
305 310 315 320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
325 330 335

Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
340 345 350

Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Ala Arg Thr Asp
355 360 365

Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
370 375 380

His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
385 390 395 400

Lys Lys Arg Val Tyr Leu Ala Thr Ala Asp Pro Thr Leu Leu Lys Glu
405 410 415

Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
420 425 430

Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
435 440 445

Gly Val Ile Leu Ala Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
450 455 460

Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
465 470 475 480

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
485 490 495

Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
500 505 510

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

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Ile Asn
530 535 540

Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
545 550 555 560

Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
565 570 575

<210> 5

<211> 1728

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acids sequence of F8M1 modified enzyme, where positions
1105-1107 in wild-type FUT8 gene have been changed

<400> 5

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aacggcgcca aggagctgtg gttcttcctg cagtccgagc tgaagaagct gaagcacctg 420
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<210> 6

<211> 575

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of F8M1 modified, where the residue at position 369 in wild-type FUT8 protein has been changed

<400> 6

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Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
20 25 30

Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
35 40 45

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

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
65 70 75 80

Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
85 90 95

Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
100 105 110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
115 120 125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
130 135 140

Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
145 150 155 160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
165 170 175

Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
180 185 190

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
195 200 205

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
210 215 220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
225 230 235 240

Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
245 250 255

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
260 265 270

Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
275 280 285

Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
290 295 300

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
305 310 315 320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
325 330 335

Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
340 345 350

Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
355 360 365

Glu Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
370 375 380

His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
385 390 395 400

Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Thr Leu Leu Lys Glu
405 410 415

Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
420 425 430

Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
435 440 445

Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
450 455 460

Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
465 470 475 480

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
485 490 495

Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
500 505 510

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

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Ile Asn
530 535 540

Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
545 550 555 560

Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
565 570 575

<210> 7
<211> 1728
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of F8M2 modified enzyme, where at positions
1225-1227 in wild-type FUT8 gene has been changed

<400> 7
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gagaaggagg ccaaggacct gaccgagctg gtgcagagga ggatcaccta cctgcagaac	600
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aagaagaggg tgtacctggc caccaaggac cccaccctgc tgaaggaggc caagaccaag	1260
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<210> 8
 <211> 575
 <212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of F8M2 modified enzyme, where the residue at position 409 in wild-type FUT8 protein has been chagned

<400> 8

Met Arg Ala Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
1 5 10 15

Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
20 25 30

Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
35 40 45

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

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
65 70 75 80

Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
85 90 95

Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
100 105 110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
115 120 125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
130 135 140

Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
145 150 155 160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
165 170 175

Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
180 185 190

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
195 200 205

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
210 215 220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
225 230 235 240

Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
245 250 255

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
260 265 270

Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
275 280 285

Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
290 295 300

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
305 310 315 320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
325 330 335

Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
340 345 350

Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
355 360 365

Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
370 375 380

His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
385 390 395 400

Lys Lys Arg Val Tyr Leu Ala Thr Lys Asp Pro Thr Leu Leu Lys Glu
405 410 415

Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
420 425 430

Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
435 440 445

Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
450 455 460

Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
465 470 475 480

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
485 490 495

Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
500 505 510

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

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Ile Asn
530 535 540

Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
545 550 555 560

Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
565 570 575

<210> 9

<211> 1728

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of F8M3 modified enzyme, where positions
1405-1407 in wild-type FUT8 gene have been changed

<400> 9

atgagggcct ggaccggctc ctggaggttg atcatgctga tcctgttcgc ctggggcacc	60
ctgctgttct acatcggcgg ccacctggtg agggacaacg accaccccga ccactcctcc	120
agggagctgt ccaagatcct ggccaagctg gagaggctga agcagcagaa cgaggacctg	180
aggaggatgg ccgagtccct gaggatcccc gagggcccca tcgaccaggg caccgccacc	240
ggcagggatga gggtgctgga ggagcagctg gtgaaggcca aggagcagat cgagaactac	300
aagaagcagg ccaggaacgg cctgggcaag gaccacgaga tcctgaggag gaggatcgag	360
aacggcgcca aggagctgtg gttcttcctg cagtccgagc tgaagaagct gaagcacctg	420
gagggcaacg agctgcagag gcacgccgac gagatcctgc tggacctggg ccaccacgag	480
aggtccatca tgaccgacct gtactacctg tcccagaccg acggcgccgg cgactggagg	540
gagaaggagg ccaaggacct gaccgagctg gtgcagagga ggatcaccta cctgcagaac	600
ccaaggact gctccaaggc caggaagctg gtgtgcaaca tcaacaaggg ctgcggctac	660
ggctgccagc tgcaccacgt ggtgtactgc ttcatgatcg cctacggcac ccagaggacc	720
ctgatcctgg agtcccagaa ctggaggtac gccaccggcg gctgggagac cgtgttcagg	780
cccgtgtccg agacctgcac cgacaggtcc ggcctgtcca ccggccactg gtccggcgag	840
gtgaacgaca agaacatcca ggtggtggag ctgcccacg tggactccct gcaccccagg	900
ccccctacc tgcccctggc cgtgcccag gacctggccg acaggctgct gaggggtgcac	960
ggcgaccccg ccgtgtggtg ggtgtcccag ttcgtgaagt acctgatcag gccccagccc	1020
tgggtggaga aggagatcga ggaggccacc aagaagctgg gcttcaagca ccccgatgc	1080
ggcgtgcacg tgaggaggac cgacaaggtg ggcaccgagg ccgccttcca ccccatcgag	1140
gagtacatgg tgcacgtgga ggagcacttc cagctgctgg ccaggaggat gcaggtggac	1200
aagaagaggg tgtacctggc caccgacgac cccaccctgc tgaaggaggc caagaccaag	1260
tactccaact acgagttcat ctccgacaac tccatctcct ggtccgccgg cctgcacaac	1320
aggtacaccg agaactccct gaggggcgtg atcctggaca tccacttcct gtcccaggcc	1380
gacttcctgg tgtgcacctt cgtgtcccag gtgtgcaggg tggcctacga gatcatgcag	1440
accctgcacc ccgacgcctc cgccaacttc cactccctgg acgacatcta ctacttcggc	1500
ggccagaacg cccacaacca gatcgccgtg tacccccaca agcccaggac cgaggaggag	1560
atccccatgg agcccggcga catcatcggc gtggccggca accactggga cggctactcc	1620

aagggcatca acaggaagct gggcaagacc ggcctgtacc cctcctacaa ggtgagggag 1680

aagatcgaga ccgtgaagta cccacactac cccgaggccg agaagtga 1728

<210> 10

<211> 575

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of F83M modified enzyme, where the residue at position 469 in wild-type FUT8 protein has been changed

<400> 10

Met Arg Ala Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
1 5 10 15

Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
20 25 30

Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
35 40 45

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

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
65 70 75 80

Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
85 90 95

Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
100 105 110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
115 120 125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
130 135 140

Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
145 150 155 160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
165 170 175

Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
180 185 190

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
195 200 205

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
210 215 220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
225 230 235 240

Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
245 250 255

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
260 265 270

Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
275 280 285

Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
290 295 300

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
305 310 315 320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
325 330 335

Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
340 345 350

Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
355 360 365

Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
370 375 380

His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
385 390 395 400

Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Thr Leu Leu Lys Glu
405 410 415

Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
420 425 430

Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
435 440 445

Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
450 455 460

Cys Thr Phe Ser Val Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
465 470 475 480

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
485 490 495

Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
500 505 510

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

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Ile Asn
530 535 540

Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
545 550 555 560

Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
565 570 575

<210> 11

<211> 1665

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of F8D1 modified enzyme, where positions 1087-1149 in wild-type FUT8 gene have been deleted

<400> 11

atgagggcct ggaccggctc ctggaggtgg atcatgctga tcctgttcgc ctggggcacc	60
ctgctgttct acatcggcgg ccacctggtg agggacaacg accaccccga ccactcctcc	120
agggagctgt ccaagatcct ggccaagctg gagaggctga agcagcagaa cgaggacctg	180
aggaggatgg ccgagtccct gaggatcccc gagggcccca tcgaccaggg caccgccacc	240
ggcaggggtga ggggtgctgga ggagcagctg gtgaaggcca aggagcagat cgagaactac	300
aagaagcagg ccaggaacgg cctgggcaag gaccacgaga tcctgaggag gaggatcgag	360
aacggcgcca aggagctgtg gttcttcctg cagtccgagc tgaagaagct gaagcacctg	420
gagggcaacg agctgcagag gcacgccgac gagatcctgc tggacctggg ccaccacgag	480
aggtccatca tgaccgacct gtactacctg tcccagaccg acggcgccgg cgactggagg	540
gagaaggagg ccaaggacct gaccgagctg gtgcagagga ggatcaccta cctgcagaac	600
cccaaggact gtcceaaggc caggaagctg gtgtgcaaca tcaacaaggg ctgcggctac	660
ggctgccagc tgcaccacgt ggtgtactgc ttcatgatcg cctacggcac ccagaggacc	720
ctgatcctgg agtcccagaa ctggaggtac gccaccggcg gctgggagac cgtgttcagg	780
cccgtgtccg agacctgcac cgacaggctc ggctgtcca ccggccactg gtccggcgag	840
gtgaacgaca agaacatcca ggtggtggag ctgcccacgc tggactccct gcaccccagg	900
ccccctacc tgcccctggc cgtgcccag gacctggccg acaggctgct gaggggtgcac	960
ggcgaccccg ccgtgtggtg ggtgtcccag ttcgtgaagt acctgatcag gccccagccc	1020
tggctggaga aggagatcga ggaggccacc aagaagctgg gcttcaagca cccgtgatc	1080
ggcgtggtgc acgtggagga gcacttccag ctgctggcca ggaggatgca ggtggacaag	1140
aagaggggtg acctggccac cgacgacccc accctgctga aggaggccaa gaccaagtac	1200
tccaactacg agttcatctc cgacaactcc atctcctggt ccgccggcct gcacaacagg	1260
tacaccgaga actccctgag gggcgtgatc ctggacatcc acttcctgtc ccaggccgac	1320
ttcctggtgt gcaccttctc ctcccaggtg tgcagggtgg cctacgagat catgcagacc	1380

ctgcaccccg acgcctccgc caacttccac tccctggacg acatctacta cttcggcggc 1440
cagaacgccc acaaccagat cgccgtgtac cccacaagc ccaggaccga ggaggagatc 1500
cccatggagc ccggcgacat catcggcgtg gccggcaacc actgggacgg ctactccaag 1560
ggcatcaaca ggaagctggg caagaccggc ctgtaccctt cctacaaggt gagggagaag 1620
atcgagaccg tgaagtaccc cacctacccc gagggcgaga agtga 1665

<210> 12
<211> 548
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of F8D1 modified enzyme, where the residues
at positions 365-386 in wild-type FUT8 protein have been deleted

<400> 12

Met Arg Ala Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
1 5 10 15

Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
20 25 30

Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
35 40 45

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

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
65 70 75 80

Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
85 90 95

Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
100 105 110

Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
115 120 125

Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
130 135 140

Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
145 150 155 160

Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
165 170 175

Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
180 185 190

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
195 200 205

Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
210 215 220

His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
225 230 235 240

Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
245 250 255

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
260 265 270

Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
275 280 285

Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
290 295 300

Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
305 310 315 320

Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
325 330 335

Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
340 345 350

Leu Gly Phe Lys His Pro Val Ile Gly His Phe Gln Leu Leu Ala Arg
355 360 365

Arg Met Gln Val Asp Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro
370 375 380

Thr Leu Leu Lys Glu Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile
385 390 395 400

Ser Asp Asn Ser Ile Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr
405 410 415

Glu Asn Ser Leu Arg Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln
420 425 430

Ala Asp Phe Leu Val Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala
435 440 445

Tyr Glu Ile Met Gln Thr Leu His Pro Asp Ala Ser Ala Asn Phe His
450 455 460

Ser Leu Asp Asp Ile Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln
465 470 475 480

Ile Ala Val Tyr Pro His Lys Pro Arg Thr Glu Glu Glu Ile Pro Met
485 490 495

Glu Pro Gly Asp Ile Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr
500 505 510

Ser Lys Gly Ile Asn Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser
515 520 525

Tyr Lys Val Arg Glu Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro
530 535 540

Glu Ala Glu Lys
545

<210> 13
 <211> 1119
 <212> DNA
 <213> Mouse

<400> 13
 atgcccacg ccccgccctc ctgcccctcc tccaggaact ccggcgacgg cgacaagggc 60
 aagcccagga aggtggccct gatcaccggc atcaccggcc aggacggctc ctacctggcc 120
 gagttcctgc tggagaaggg ctacgaggtg cacggcatcg tgaggaggtc ctcctccttc 180
 aacaccggca ggatcgagca cctgtacaag aacccccagg ccacatcga gggcaacatg 240
 aagctgcact acggcgacct gaccgactcc acctgcctgg tgaagatcat caacgaggtg 300
 aagcccaccg agatctacaa cctggggcgcc cagtcccacg tgaagatctc cttcgacctg 360
 gccgagtaca ccgccgacgt ggacggcgctg ggcaccctga ggctgctgga cgccatcaag 420
 acctgcggcc tgatcaactc cgtgaagtgc taccaggcct ccacctccga gctgtacggc 480
 aaggtgcagg agatccccca gaaggagacc acccccttct accccaggtc cccctacggc 540
 gccgccaagc tgtacgccta ctggatcgtg gtgaacttca gggaggccta caacctgttc 600
 gccgtgaacg gcatcctgtt caaccacgag tccccagga ggggcgccaa cttcgtgacc 660
 aggaagatct ccaggctcgt ggccaagatc tacctgggcc agctggagtg cttctccctg 720
 ggcaacctgg acgccaagag ggactggggc cacgccaagg actacgtgga ggccatgtgg 780
 ctgatgctgc agaacgacga gcccaggagc ttcgtgatcg ccaccggcga ggtgcactcc 840
 gtgagggagt tcgtggagaa gtccttcctg cacatcgga agaccatcgt gtgggagggc 900
 aagaacgaga acgaggtggg caggtgcaag gagaccggca agatccacgt gaccgtggac 960
 ctgaagtact acaggccac cgaggtggac ttcctgcagg gcgactgctc caaggcccag 1020
 cagaagctga actggaagcc cagggtggcc ttcgacgagc tggtagggga gatggtgcag 1080
 gccgacgtgg agctgatgag gaccaacccc aacgcctga 1119

<210> 14
 <211> 372
 <212> PRT
 <213> Mouse

<400> 14

Met Ala His Ala Pro Ala Ser Cys Pro Ser Ser Arg Asn Ser Gly Asp
 1 5 10 15

Gly Asp Lys Gly Lys Pro Arg Lys Val Ala Leu Ile Thr Gly Ile Thr
20 25 30

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

Glu Val His Gly Ile Val Arg Arg Ser Ser Ser Phe Asn Thr Gly Arg
50 55 60

Ile Glu His Leu Tyr Lys Asn Pro Gln Ala His Ile Glu Gly Asn Met
65 70 75 80

Lys Leu His Tyr Gly Asp Leu Thr Asp Ser Thr Cys Leu Val Lys Ile
85 90 95

Ile Asn Glu Val Lys Pro Thr Glu Ile Tyr Asn Leu Gly Ala Gln Ser
100 105 110

His Val Lys Ile Ser Phe Asp Leu Ala Glu Tyr Thr Ala Asp Val Asp
115 120 125

Gly Val Gly Thr Leu Arg Leu Leu Asp Ala Ile Lys Thr Cys Gly Leu
130 135 140

Ile Asn Ser Val Lys Phe Tyr Gln Ala Ser Thr Ser Glu Leu Tyr Gly
145 150 155 160

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

Ser Pro Tyr Gly Ala Ala Lys Leu Tyr Ala Tyr Trp Ile Val Val Asn
180 185 190

Phe Arg Glu Ala Tyr Asn Leu Phe Ala Val Asn Gly Ile Leu Phe Asn
195 200 205

His Glu Ser Pro Arg Arg Gly Ala Asn Phe Val Thr Arg Lys Ile Ser
210 215 220

Arg Ser Val Ala Lys Ile Tyr Leu Gly Gln Leu Glu Cys Phe Ser Leu
225 230 235 240

Gly Asn Leu Asp Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val
245 250 255

Glu Ala Met Trp Leu Met Leu Gln Asn Asp Glu Pro Glu Asp Phe Val
260 265 270

Ile Ala Thr Gly Glu Val His Ser Val Arg Glu Phe Val Glu Lys Ser
275 280 285

Phe Met His Ile Gly Lys Thr Ile Val Trp Glu Gly Lys Asn Glu Asn
290 295 300

Glu Val Gly Arg Cys Lys Glu Thr Gly Lys Ile His Val Thr Val Asp
305 310 315 320

Leu Lys Tyr Tyr Arg Pro Thr Glu Val Asp Phe Leu Gln Gly Asp Cys
325 330 335

Ser Lys Ala Gln Gln Lys Leu Asn Trp Lys Pro Arg Val Ala Phe Asp
340 345 350

Glu Leu Val Arg Glu Met Val Gln Ala Asp Val Glu Leu Met Arg Thr
355 360 365

Asn Pro Asn Ala
370

<210> 15

<211> 1119

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of GMD4M modified enzyme, where positions
463-465, 469-471, 535-537, and 547-549 in wild-type GMD gene have
been changed

<400> 15

atggcccacg ccccccgcctc ctgcccctcc tccaggaact ccggcgacgg cgacaagggc 60

aagcccagga aggtggccct gatcaccggc atcaccggcc aggacggctc ctacctggcc 120

gagttcctgc tggagaaggg ctacgaggtg cacggcatcg tgaggaggtc ctcctccttc	180
aacaccggca ggatcgagca cctgtacaag aacccccagg cccacatcga gggcaacatg	240
aagctgcact acggcgacct gaccgactcc acctgcctgg tgaagatcat caacgaggtg	300
aagcccaccg agatctacaa cctgggcgcc cagtcccacg tgaagatctc cttcgacctg	360
gccgagtaca ccgccgacgt ggacggcgtg ggcaccctga ggctgctgga cgccatcaag	420
acctgcggcc tgatcaactc cgtgaagttc taccaggcct ccgcctccgc cctgtacggc	480
aaggtgcagg agatcccca gaaggagacc acccccttct accccaggtc ccccgccggc	540
gccgccgccc tgtacgccta ctggatcgtg gtgaacttca gggaggccta caacctgttc	600
gccgtgaacg gcatcctgtt caaccacgag tccccagga ggggcgcaa cttcgtgacc	660
aggaagatct ccagggtccgt ggccaagatc tacctgggcc agctggagtg cttctccctg	720
ggcaacctgg acgccaagag ggactggggc cacgccaagg actacgtgga ggccatgtgg	780
ctgatgctgc agaacgacga gcccaggac ttcgtgatcg ccaccggcga ggtgcactcc	840
gtgagggagt tcgtggagaa gtccttcatg cacatcggca agaccatcgt gtgggagggc	900
aagaacgaga acgaggtggg caggtgcaag gagaccggca agatccacgt gaccgtggac	960
ctgaagtact acaggccac cgaggtggac ttcctgcagg gcgactgctc caaggcccag	1020
cagaagctga actggaagcc caggggtggc ttcgacgagc tgggtgaggga gatggtgcag	1080
gccgacgtgg agctgatgag gaccaacccc aacgcctga	1119

<210> 16
 <211> 372
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of GMD4M modified enzyme, where at positions
 155, 157, 179, and 183 in wild-type GMD protein have been changed

<400> 16

Met	Ala	His	Ala	Pro	Ala	Ser	Cys	Pro	Ser	Ser	Arg	Asn	Ser	Gly	Asp
1				5				10						15	

Gly	Asp	Lys	Gly	Lys	Pro	Arg	Lys	Val	Ala	Leu	Ile	Thr	Gly	Ile	Thr
			20					25					30		

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

Glu Val His Gly Ile Val Arg Arg Ser Ser Ser Phe Asn Thr Gly Arg
50 55 60

Ile Glu His Leu Tyr Lys Asn Pro Gln Ala His Ile Glu Gly Asn Met
65 70 75 80

Lys Leu His Tyr Gly Asp Leu Thr Asp Ser Thr Cys Leu Val Lys Ile
85 90 95

Ile Asn Glu Val Lys Pro Thr Glu Ile Tyr Asn Leu Gly Ala Gln Ser
100 105 110

His Val Lys Ile Ser Phe Asp Leu Ala Glu Tyr Thr Ala Asp Val Asp
115 120 125

Gly Val Gly Thr Leu Arg Leu Leu Asp Ala Ile Lys Thr Cys Gly Leu
130 135 140

Ile Asn Ser Val Lys Phe Tyr Gln Ala Ser Ala Ser Ala Leu Tyr Gly
145 150 155 160

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

Ser Pro Ala Gly Ala Ala Ala Leu Tyr Ala Tyr Trp Ile Val Val Asn
180 185 190

Phe Arg Glu Ala Tyr Asn Leu Phe Ala Val Asn Gly Ile Leu Phe Asn
195 200 205

His Glu Ser Pro Arg Arg Gly Ala Asn Phe Val Thr Arg Lys Ile Ser
210 215 220

Arg Ser Val Ala Lys Ile Tyr Leu Gly Gln Leu Glu Cys Phe Ser Leu
225 230 235 240

Gly Asn Leu Asp Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val

245

250

255

Glu Ala Met Trp Leu Met Leu Gln Asn Asp Glu Pro Glu Asp Phe Val
 260 265 270

Ile Ala Thr Gly Glu Val His Ser Val Arg Glu Phe Val Glu Lys Ser
 275 280 285

Phe Met His Ile Gly Lys Thr Ile Val Trp Glu Gly Lys Asn Glu Asn
 290 295 300

Glu Val Gly Arg Cys Lys Glu Thr Gly Lys Ile His Val Thr Val Asp
 305 310 315 320

Leu Lys Tyr Tyr Arg Pro Thr Glu Val Asp Phe Leu Gln Gly Asp Cys
 325 330 335

Ser Lys Ala Gln Gln Lys Leu Asn Trp Lys Pro Arg Val Ala Phe Asp
 340 345 350

Glu Leu Val Arg Glu Met Val Gln Ala Asp Val Glu Leu Met Arg Thr
 355 360 365

Asn Pro Asn Ala
 370

<210> 17

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence deleted in F8D1 mutant gene

<400> 17

cacgtgagga ggaccgacaa ggtgggcacc gaggccgcct tccaccccat cgaggagtac 60

atg 63