SEQUENCE LISTING

<110> Boehringer Ingelheim International GmbH

<120> MAMMALIAN CELLS FOR PRODUCING A SECRETED PROTEIN

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<151> 2016-03-18

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Leu Arg Arg Met Ala Ile Ser Glu Gly Gly Leu Leu Thr Asp Glu Ile
    50                  55                  60
Arg Cys Gln Val Trp Pro Lys Leu Leu Asn Val Asn Thr Cys Glu Pro
65                  70                  75                  80
Pro Pro Val Ser Arg Lys Asp Leu Arg Gln Leu Ser Lys Asp Tyr Gln
                85                  90                  95
Gln Val Leu Leu Asp Val Arg Arg Ser Leu Arg Arg Phe Pro Pro Gly
            100                 105                 110
Met Pro Asp Glu Gln Arg Glu Gly Leu Gln Glu Glu Leu Ile Asp Ile
        115                 120                 125
Ile Leu Leu Ile Leu Asp Arg Asn Pro Gln Leu His Tyr Tyr Gln Gly
    130                 135                 140
Tyr His Asp Ile Val Val Thr Phe Leu Leu Val Val Gly Glu Arg Leu
145                 150                 155                 160
Ala Thr Ser Leu Val Glu Lys Leu Ser Thr His His Leu Arg Asp Phe
                165                 170                 175
Met Asp Pro Thr Met Asp Asn Thr Lys His Ile Leu Asn Tyr Leu Met
            180                 185                 190
Pro Ile Ile Asp Gln Val Asn Pro Glu Leu His Asp Phe Met Gln Ser
        195                 200                 205
Ala Glu Val Gly Thr Ile Phe Ala Leu Ser Trp Leu Ile Thr Trp Phe
    210                 215                 220
Gly His Val Leu Ser Asp Phe Arg His Val Val Arg Leu Tyr Asp Phe
225                 230                 235                 240
Phe Leu Ala Cys His Pro Leu Met Pro Ile Tyr Phe Ala Ala Val Ile
                245                 250                 255
Val Leu Tyr Arg Glu Gln Glu Val Leu Asp Cys Asp Cys Asp Met Ala
            260                 265                 270
Ser Val His His Leu Leu Ser Gln Ile Pro Gln Asp Leu Pro Tyr Glu
        275                 280                 285
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Thr Leu Ile Ser Arg Ala Gly Asp Leu Phe Val Gln Phe Pro Pro Ser
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Glu Leu Ala Arg Glu Ala Ala Ala Gln Gln Glu Ala Glu Arg Thr Ala
305                 310                 315                 320
Ala Ser Thr Phe Lys Asp Phe Glu Leu Ala Ser Ala Gln Gln Arg Pro
                325                 330                 335
Asp Met Val Leu Arg Gln Arg Phe Arg Gly Leu Leu Arg Pro Glu Thr
            340                 345                 350
Arg Thr Lys Asp Val Leu Thr Lys Pro Arg Thr Asn Arg Phe Val Lys
        355                 360                 365
Leu Ala Val Met Gly Leu Thr Val Ala Leu Gly Ala Ala Ala Leu Ala
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<223> CERS2

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Tyr Ala Lys Ala Ser Asp Leu Tyr Ile Thr Leu Pro Leu Ala Leu Val
        35                  40                  45
Phe Leu Val Ile Arg Tyr Phe Phe Glu Leu Tyr Val Ala Thr Pro Leu
    50                  55                  60
Ala Ala Leu Leu Asn Val Lys Glu Lys Thr Arg Leu Arg Ala Pro Pro
65                  70                  75                  80
Asn Val Thr Leu Glu His Phe Tyr Leu Thr Asn Gly Lys Gln Pro Lys
                85                  90                  95
Gln Val Glu Val Glu Leu Leu Ser Arg Gln Ser Gly Leu Ser Gly Arg
            100                 105                 110
Gln Ile Glu Arg Trp Phe Arg Arg Arg Arg Asn Gln Asp Arg Pro Ser
        115                 120                 125
Leu Leu Lys Lys Phe Arg Glu Ala Ser Trp Arg Phe Thr Phe Tyr Leu
    130                 135                 140
Ile Ala Phe Val Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe
145                 150                 155                 160
Tyr Asp Leu Arg Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Ile Val
                165                 170                 175
Pro Ser Gln Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser
            180                 185                 190
Leu Leu Phe Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu
        195                 200                 205
Gln Ile Ile His His Val Ala Thr Ile Ile Leu Leu Ser Phe Ser Trp
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    210                 215                 220
Phe Ala Asn Tyr Val Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp
225                 230                 235                 240
Ser Ser Asp Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly
                245                 250                 255
Trp Lys Asn Thr Cys Asn Asn Ile Phe Ile Val Phe Ala Ile Val Phe
            260                 265                 270
Ile Ile Thr Arg Leu Val Ile Met Pro Phe Trp Ile Leu His Cys Thr
        275                 280                 285
Leu Val Tyr Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe
    290                 295                 300
Phe Asn Ile Met Met Ala Val Leu Gln Met Leu His Ile Phe Trp Ala
305                 310                 315                 320
Tyr Phe Ile Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val
                325                 330                 335
Glu Asp Glu Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu
            340                 345                 350
Glu Ala Ala Ala Gly Ala Gly Ala Lys Ser Arg Leu Leu Ser Asn Gly
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His Pro Ile Leu Asn Asn Asn His Pro Lys Asn Asp
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<223> ATF6b

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Pro Ser Asp Ile Gln Thr Lys Val Glu Pro Ala Ser Pro Ser Ser Ser
        35                  40                  45
Val Asn Ser Glu Ala Ser Leu Leu Ser Ala Asp Ser Pro Ser Gln Ala
    50                  55                  60
Phe Ile Gly Glu Glu Val Leu Glu Val Lys Thr Glu Ser Pro Ser Pro
65                  70                  75                  80
Pro Gly Cys Leu Leu Trp Asp Val Pro Ala Pro Ser Leu Gly Ala Val
                85                  90                  95
Gln Ile Ser Met Gly Pro Ser Pro Val Ser Ser Ser Gly Lys Ala Pro
            100                 105                 110
Ala Thr Arg Lys Pro Pro Leu Gln Pro Lys Pro Val Val Leu Thr Thr
        115                 120                 125
Val Gln Val Pro Pro Arg Ala Gly Pro Pro Ser Thr Thr Val Leu Leu
    130                 135                 140
Gln Pro Leu Val Gln Gln Pro Ala Val Ser Pro Val Val Leu Ile Gln
145                 150                 155                 160
Gly Ala Ile Arg Val Gln Pro Glu Gly Pro Ala Pro Ala Val Pro Arg
                165                 170                 175
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Pro Glu Arg Lys Ser Ile Val Pro Ala Pro Leu Pro Gly Asn Ser Cys
            180                 185                 190
Pro Pro Glu Val Asp Ala Lys Leu Leu Lys Arg Gln Gln Arg Met Ile
        195                 200                 205
Lys Asn Arg Glu Ser Ala Cys Gln Ser Arg Arg Lys Lys Lys Glu Tyr
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Leu Gln Gly Leu Glu Ala Arg Leu Gln Ala Val Leu Ala Asp Asn Gln
225                 230                 235                 240
Gln Leu Arg Arg Glu Asn Ala Ala Leu Arg Arg Arg Leu Glu Thr Leu
                245                 250                 255
Leu Thr Glu Asn Ser Glu Leu Lys Leu Gly Ser Gly Asn Arg Lys Val
            260                 265                 270
Val Cys Ile Met Val Phe Leu Leu Phe Ile Ala Phe Asn Phe Gly Pro
        275                 280                 285
Val Ser Ile Ser Glu Pro Pro Pro Ala Pro Ile Ser Pro Arg Met Ser
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Arg Glu Glu Ala Arg Pro Arg Arg His Leu Leu Glu Phe Ser Glu Gln
305                 310                 315                 320
Gly Pro Ala His Gly Val Glu Pro Leu Gln Lys Ala Ala Arg Gly Pro
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Glu Glu Arg Gln Pro Ser Pro Ala Gly Arg Pro Ser Phe Arg Asn Leu
            340                 345                 350
Thr Ala Phe Pro Gly Gly Ala Lys Glu Leu Leu Leu Arg Asp Leu Asp
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Gln Leu Phe Leu Ala Ser Asp Cys Arg His Phe Asn Arg Thr Glu Ser
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385                 390                 395                 400
Gly Arg Arg Arg Met Pro His Arg Ala Gln Glu Arg Gln Lys Ser Gln
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Leu Arg Lys Lys Ser Pro Pro Val Lys Pro Val Pro Thr Gln Pro Pro
            420                 425                 430
Gly Pro Pro Glu Arg Asp Pro Val Gly Gln Leu Gln Leu Tyr Arg His
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Pro Gly Arg Ser Gln Pro Glu Phe Leu Asp Ala Ile Asp Arg Arg Glu
    450                 455                 460
Asp Thr Phe Tyr Val Val Ser Phe Arg Arg Asp His Leu Leu Leu Pro
465                 470                 475                 480
Ala Ile Ser His Asn Lys Thr Ser Arg Pro Lys Met Ser Leu Val Met
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Pro Ala Met Ala Pro Asn Glu Thr Val Ser Gly Arg Gly Pro Pro Gly
            500                 505                 510
Asp Tyr Glu Glu Met Met Gln Ile Glu Cys Glu Val Met Asp Thr Arg
        515                 520                 525
Val Ile His Ile Lys Thr Ser Thr Val Pro Pro Ser Leu Arg Lys Gln
    530                 535                 540
Pro Ser Pro Thr Pro Gly Asn Thr Thr Gly Gly Pro Leu Pro Ala Ser
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<213> Artificial Sequence

<220>
<223> shCerS2#2_oligonucleotide_reverse

<400> 21
cctgtgatgt agaggtgagg cttgtcagtc agtggccaaa acaagcctca gacctctaca 60

tcac 64

<210> 22
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> shAtf6b#1_oligonucleotide_forward

<400> 22

tgctgtccat cttcacactg aggaccgttt tggccactga ctgacggtcc tcagtgaaga 60

tgga 64

<210> 23
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> shAtf6b#1_oligonucleotide_reverse

<400> 23
cctgtccatc ttcactgagg accgtcagtc agtggccaaa acggtcctca gtgtgaagat 60

ggac 64

<210> 24
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> mAb1 heavy chain

<400> 24

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

```
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
        195                 200                 205
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
    210                 215                 220
Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
225                 230                 235                 240
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
                245                 250                 255
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            260                 265                 270
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
        275                 280                 285
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    290                 295                 300
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
305                 310                 315                 320
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                325                 330                 335
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
            340                 345                 350
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        355                 360                 365
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    370                 375                 380
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385                 390                 395                 400
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                405                 410                 415
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            420                 425                 430
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        435                 440                 445
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455                 460

<210> 25
<211> 233
<212> PRT
<213> Artificial Sequence


<220>
<223> mAb1 light chain

<400> 25
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1               5                   10                  15
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ser Ser
        35                  40                  45
Ile Asn Tyr Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
    50                  55                  60
Leu Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
```

65 70 75 80
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
85 90 95
Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Trp Ser Ser
100 105 110
Asn Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr
115 120 125
Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140
Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
145 150 155 160
Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205
Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
210 215 220
Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 26
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> mAb2 heavy chain

<400> 26
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15
Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Tyr Ser Ile
35 40 45
Thr Ser Gly Tyr Ser Trp Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly
50 55 60
Leu Glu Trp Val Ala Ser Ile Thr Tyr Asp Gly Ser Thr Asn Tyr Asn
65 70 75 80
Pro Ser Val Lys Gly Arg Ile Thr Ile Ser Arg Asp Asp Ser Lys Asn
85 90 95
Thr Phe Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Gly Ser His Tyr Phe Gly His Trp His Phe Ala
115 120 125
Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

```
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460
Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 27
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> mAb2 light chain

<400> 27

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1               5                   10                  15
Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
            20                  25                  30
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val
```

```
        35                  40                  45
Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60
Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Tyr Leu Glu Ser Gly
65                  70                  75                  80
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
                85                  90                  95
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
            100                 105                 110
Gln Ser His Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu
        115                 120                 125
Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
    130                 135                 140
Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145                 150                 155                 160
Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
                165                 170                 175
Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
            180                 185                 190
Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
        195                 200                 205
Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
    210                 215                 220
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
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<210> 28
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> hsa-miRNA-1287_oligonucleotide_forward

<400> 28
tgctgtgctg gatcagtggt tcgagtcgtt ttggccactg actgacgact cgaaccacat 60

ccagca 66

<210> 29
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> hsa-miR-1287_oligonucleotide_reverse

<400> 29
cctgtgctgg atgtggttcg agtcgtcagt cagtggccaa aacgactcga accactgatc 60

cagcac 66

<210> 30
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> hsa-miRNA-1978_oligonucleotide_forward

<400> 30
tgctgggttt ggtcctagcc tttctagttt tggccactga ctgactagaa aggctaacca 60

aacc 64

<210> 31
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> hsa-miR-1978_oligonucleotide_reverse

<400> 31
cctgggtttg gttagccttt ctagtcagtc agtggccaaa actagaaagg ctaggaccaa 60

accc 64

<210> 32
<211> 22
<212> RNA
<213> Homo sapiens

<220>
<223> hsa-miRNA-1287

<400> 32
ugcuggauca gugguucgag uc 22

<210> 33
<211> 21
<212> RNA
<213> Homo sapiens

<220>
<223> hsa-miRNA-1978

<400> 33
gguuuggucc uagccuuucu a 21

<210> 34
<211> 22
<212> RNA
<213> Artificial Sequence

<220>
<223> negative control miRNA

<400> 34
gaaauguacu gcgcguggag ac 22

<210> 35
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> shAtf6B#2_oligonucleotide_forward

<400> 35
tgctgttcac ttccagaacc tcctctgttt tggccactga ctgacagagg aggctggaag 60

tgaa 64

<210> 36
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> shAtf6b#2_oligonucleotide_reverse

<400> 36
cctgttcact tccagcctcc tctgtcagtc agtggccaaa acagaggagg ttctggaagt 60

gaac 64

<210> 37
<211> 21
<212> RNA
<213> Artificial Sequence

<220>

<223> shAtf6b#2

<400> 37
uucacuucca gaaccuccuc u 21

<210> 38
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> siRNA NT-control#1

<400> 38
ugguuuacau gucgacuaa 19

<210> 39
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> siRNA NT-control#2

<400> 39
ugguuuacau guuguguga 19

<210> 40
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> siRNA NT-control#3

<400> 40
ugguuuacau guuuucuga 19

<210> 41
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> siRNA NT-control#4

<400> 41
ugguuuacau guuuuccua 19

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> qPCR primer (Atf6b) forward

<400> 42
gagcaggatg tcccgtttga 20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> qPCR primer (Atf6b) reverse

<400> 43
agctcaggga ggaggaagag 20

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> qPCR primer (Tbc1D20) forward

<400> 44
ccctgaacag tgatcccacc 20

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> qPCR primer (Tbc1D20) reverse

<400> 45
atccttcctt gacacaggcg 20

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> qPCR primer (CerS2) forward

<400> 46
cccatacaga gcatcgtccc 20

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> qPCR primer (CerS2) reverse

<400> 47
ggcaaaccag gagaagctga 20

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

<220>
<223> qPCR primer (CHOP) forward

<400> 48
gaccctgttt ctttcccttc ag 22

<210> 49
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> qPCR primer (CHOP) reverse

<400> 49
ggactgggtt ctgctttcag g 21

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

<220>
<223> qPCR primer (GRP78) forward

<400> 50
accacctatt cctgcgttgg 20

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

<220>
<223> qPCR primer (GRP78) reverse

<400> 51
agaccgtgtt ctcgggattg 20

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> qPCR primer (Herpud1) forward

<400> 52
gaagagtccc aaccagcgtc 20

<210> 53
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> qPCR primer (Herpud1) reverse

<400> 53
atgtcgcttt tcctgctttg g 21