

SEQUENCE LISTING

<110> BASF SE

<120> 180847W001 sequence protocol

<130> PF 180847

<160> 137

<170> According Wipo Std 25

<210> 1

<211> 1764

<212> DNA

<213> K. lactis

<220>

<223> CDS Lac12 wild type

<400> 1

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| cataaagaca | ctttgggcaa | tgatcgggat | cacaaggaag | ccttgaacag | tgataatgat | 120 |
| aatacttctg | gattgaaaat | caatggtgtc | cccacgagg | acgctagaga | ggaagtgctc | 180 |
| ttaccagggt | acttgtcgaa | gcaatattac | aaattgtacg | gtttatgttt | tataacatat | 240 |
| ctgtgtgcta | ctatgcaagg | ttatgatggg | gctttaatgg | gttctatcta | taccgaagat | 300 |
| gcataatttg | aatactacca | tttggatatt | aactcatcct | ctggtactgg | tctagtgttc | 360 |
| tctattttca | acgttgggtc | aatttgcggg | gcattctttg | ttcctcttat | ggattggaaa | 420 |
| ggtagaaaac | ctgctatttt | aattgggtgt | ctgggtgttg | ttattgggtg | tattatttcg | 480 |
| tctttaacaa | caacaaagag | tgcattaatt | ggtaggtgat | ggttcgtggc | ctttttcgct | 540 |
| acaatcgcta | atgcagcagc | tccaacatac | tgtgcagaag | tggtccagc | tcacttaaga | 600 |
| ggtaagggtg | caggtcttta | taacaccctt | tgggtctgtc | gttccattgt | tgctgccttt | 660 |
| agcacttacg | gtaccaacaa | aaacttccct | aactcctcca | aggcttttaa | gattccatta | 720 |
| tacttacaaa | tgatgttccc | aggtcttgtg | tgtatatatt | gttggttaat | cccagaatct | 780 |
| ccaagatggg | tgggtgggtg | tggccgtgag | gaagaagctc | gtgaattcat | tatcaaatac | 840 |
| cacttaaatg | gcgatagaac | tcatccatta | ttggatatgg | agatggcaga | aataatagaa | 900 |
| tctttccatg | gtacagattt | atcaaaccct | ctagaaatgt | tagatgtaag | gagcttattc | 960 |
| agaacgagat | cggataggta | cagagcaatg | ttggttatac | ttatggcttg | gttcgggtcaa | 1020 |
| ttttccggta | acaatgtgtg | ttcgtactat | ttgcctacca | tgttgagaaa | tgttggtatg | 1080 |
| aagagtgtct | cattgaatgt | gttaatgaat | gggtgtttatt | ccatcgtcac | ttggatttct | 1140 |
| tcaatttgcg | gtgcattctt | tattgataag | attggttagaa | gggaagggtt | ccttggttct | 1200 |
| atctcaggtg | ctgcattagc | attgacaggt | ctatctatct | gtactgctcg | ttatgagaag | 1260 |
| actaagaaga | agagtgtctc | caatggtgca | ttgggtgttca | tttatctctt | tggtggtatc | 1320 |
| ttttcttttg | ctttcactcc | aatgcaatcc | atgtactcaa | cagaagtgtc | tacaaacttg | 1380 |
| acgagatcta | aggcccaact | cctcaacttt | gtggtttctg | gtgttgccca | atttggtta | 1440 |
| caatttgcta | ctccaaaggc | aatgaagaat | atcaaatatt | ggttctatgt | gttctacgtt | 1500 |
| ttcttcgata | ttttcgaatt | tattgttatc | tacttcttct | tcgttgaaac | taagggtaga | 1560 |
| agcttagaag | aattagaagt | tgtctttgaa | gctccaaacc | caagaaaggc | atccgttgat | 1620 |
| caagcattct | tggctcaagt | cagggcaact | ttgggtccaac | gaaatgacgt | tagagttgca | 1680 |
| aatgctcaaa | atttgaaaga | gcaagagcct | ctaaagagcg | atgctgatca | tgtcgaaaag | 1740 |
| ctttcagagg | cagaatctgt | ttaa | | | | 1764 |

<210> 2

<211> 1764

<212> DNA
<213> Artificial

<220>
<223> CDS Lac12 codon optimized

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aacacctctg gtttgaagat caacggtgtt ccaatcgaag acgctagaga agaagttttg 180
ttgccagggtt acttgtctaa gcaatactac aagttgtacg gtttgtgttt catcacctac 240
ttgtgtgcta ccatgcaagg ttacgacggt gctttgatgg gttctatcta caccgaagac 300
gcttacttga agtactacca cttggacatc aactcttctt ctggtaccgg tttggttttc 360
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tacttgcaaa tgatgttccc aggtttgggt tgtatcttcg gttggttgat cccagaatct 780
ccaagatggt tggttgggtg ttgtagagaa gaagaagcta gagaattcat catcaagtac 840
cacttgaacg gtgacagaac ccaccattg ttggacatgg aaatggctga aatcatcgaa 900
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atctctgggt ctgctttggc tttgaccggt ttgtctatct gtaccgctag atacgaaaag 1260
accaagaaga agtctgcttc taacggtgct ttggttttca tctacttggt cgggtggtatc 1320
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tctttggaag aattggaagt tgttttcgaa gctccaaacc caagaaaggc ttctgttgac 1620
caagctttct tggctcaagt tagagctacc ttggttcaaa gaaacgacgt tagagttgct 1680
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<210> 3
<211> 587
<212> PRT
<213> K. lactis

<220>
<223> Lac12

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20 25 30
Glu Ala Leu Asn Ser Asp Asn Asp Asn Thr Ser Gly Leu Lys Ile Asn
35 40 45
Gly Val Pro Ile Glu Asp Ala Arg Glu Glu Val Leu Leu Pro Gly Tyr
50 55 60
Leu Ser Lys Gln Tyr Tyr Lys Leu Tyr Gly Leu Cys Phe Ile Thr Tyr

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Leu | Cys | Ala | Thr | Met | Gln | Gly | Tyr | Asp | Gly | Ala | Leu | Met | Gly | Ser | Ile |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Tyr | Thr | Glu | Asp | Ala | Tyr | Leu | Lys | Tyr | Tyr | His | Leu | Asp | Ile | Asn | Ser |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Ser | Gly | Thr | Gly | Leu | Val | Phe | Ser | Ile | Phe | Asn | Val | Gly | Gln | Ile |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Cys | Gly | Ala | Phe | Phe | Val | Pro | Leu | Met | Asp | Trp | Lys | Gly | Arg | Lys | Pro |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ala | Ile | Leu | Ile | Gly | Cys | Leu | Gly | Val | Val | Ile | Gly | Ala | Ile | Ile | Ser |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ser | Leu | Thr | Thr | Thr | Lys | Ser | Ala | Leu | Ile | Gly | Gly | Arg | Trp | Phe | Val |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ala | Phe | Phe | Ala | Thr | Ile | Ala | Asn | Ala | Ala | Ala | Pro | Thr | Tyr | Cys | Ala |
| | | | 180 | | | | 185 | | | | | 190 | | | |
| Glu | Val | Ala | Pro | Ala | His | Leu | Arg | Gly | Lys | Val | Ala | Gly | Leu | Tyr | Asn |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Thr | Leu | Trp | Ser | Val | Gly | Ser | Ile | Val | Ala | Ala | Phe | Ser | Thr | Tyr | Gly |
| | 210 | | | | 215 | | | | | | 220 | | | | |
| Thr | Asn | Lys | Asn | Phe | Pro | Asn | Ser | Ser | Lys | Ala | Phe | Lys | Ile | Pro | Leu |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Tyr | Leu | Gln | Met | Met | Phe | Pro | Gly | Leu | Val | Cys | Ile | Phe | Gly | Trp | Leu |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ile | Pro | Glu | Ser | Pro | Arg | Trp | Leu | Val | Gly | Val | Gly | Arg | Glu | Glu | Glu |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ala | Arg | Glu | Phe | Ile | Ile | Lys | Tyr | His | Leu | Asn | Gly | Asp | Arg | Thr | His |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Pro | Leu | Leu | Asp | Met | Glu | Met | Ala | Glu | Ile | Ile | Glu | Ser | Phe | His | Gly |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Thr | Asp | Leu | Ser | Asn | Pro | Leu | Glu | Met | Leu | Asp | Val | Arg | Ser | Leu | Phe |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Arg | Thr | Arg | Ser | Asp | Arg | Tyr | Arg | Ala | Met | Leu | Val | Ile | Leu | Met | Ala |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Trp | Phe | Gly | Gln | Phe | Ser | Gly | Asn | Asn | Val | Cys | Ser | Tyr | Tyr | Leu | Pro |
| | | | 340 | | | | 345 | | | | | | 350 | | |
| Thr | Met | Leu | Arg | Asn | Val | Gly | Met | Lys | Ser | Val | Ser | Leu | Asn | Val | Leu |
| | 355 | | | | | 360 | | | | | | 365 | | | |
| Met | Asn | Gly | Val | Tyr | Ser | Ile | Val | Thr | Trp | Ile | Ser | Ser | Ile | Cys | Gly |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Ala | Phe | Phe | Ile | Asp | Lys | Ile | Gly | Arg | Arg | Glu | Gly | Phe | Leu | Gly | Ser |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Ile | Ser | Gly | Ala | Ala | Leu | Ala | Leu | Thr | Gly | Leu | Ser | Ile | Cys | Thr | Ala |
| | | | 405 | | | | | | 410 | | | | | 415 | |
| Arg | Tyr | Glu | Lys | Thr | Lys | Lys | Lys | Ser | Ala | Ser | Asn | Gly | Ala | Leu | Val |
| | | 420 | | | | | | 425 | | | | | 430 | | |
| Phe | Ile | Tyr | Leu | Phe | Gly | Gly | Ile | Phe | Ser | Phe | Ala | Phe | Thr | Pro | Met |
| | 435 | | | | | 440 | | | | | | 445 | | | |
| Gln | Ser | Met | Tyr | Ser | Thr | Glu | Val | Ser | Thr | Asn | Leu | Thr | Arg | Ser | Lys |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Ala | Gln | Leu | Leu | Asn | Phe | Val | Val | Ser | Gly | Val | Ala | Gln | Phe | Val | Asn |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Gln | Phe | Ala | Thr | Pro | Lys | Ala | Met | Lys | Asn | Ile | Lys | Tyr | Trp | Phe | Tyr |
| | | | 485 | | | | | | 490 | | | | | 495 | |
| Val | Phe | Tyr | Val | Phe | Phe | Asp | Ile | Phe | Glu | Phe | Ile | Val | Ile | Tyr | Phe |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Phe | Phe | Val | Glu | Thr | Lys | Gly | Arg | Ser | Leu | Glu | Glu | Leu | Glu | Val | Val |


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ggttcttctg aaatgttcgg ttctacccca ccaccacaat ctgaaaccac cccattccac 540
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<210> 6
 <211> 373
 <212> PRT
 <213> A. thaliana

<220>
 <223> Mur1

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20          25          30
Ile Thr Gly Ile Thr Gly Gln Asp Gly Ser Tyr Leu Thr Glu Phe Leu
35          40          45
Leu Gly Lys Gly Tyr Glu Val His Gly Leu Ile Arg Arg Ser Ser Asn
50          55          60
Phe Asn Thr Gln Arg Ile Asn His Ile Tyr Ile Asp Pro His Asn Val
65          70          75          80
Asn Lys Ala Leu Met Lys Leu His Tyr Ala Asp Leu Thr Asp Ala Ser
85          90          95
Ser Leu Arg Arg Trp Ile Asp Val Ile Lys Pro Asp Glu Val Tyr Asn
100         105         110
Leu Ala Ala Gln Ser His Val Ala Val Ser Phe Glu Ile Pro Asp Tyr
115         120         125
Thr Ala Asp Val Val Ala Thr Gly Ala Leu Arg Leu Leu Glu Ala Val
130         135         140
Arg Ser His Thr Ile Asp Ser Gly Arg Thr Val Lys Tyr Tyr Gln Ala
145         150         155         160
Gly Ser Ser Glu Met Phe Gly Ser Thr Pro Pro Pro Gln Ser Glu Thr
165         170         175
Thr Pro Phe His Pro Arg Ser Pro Tyr Ala Ala Ser Lys Cys Ala Ala
180         185         190
His Trp Tyr Thr Val Asn Tyr Arg Glu Ala Tyr Gly Leu Phe Ala Cys
195         200         205
Asn Gly Ile Leu Phe Asn His Glu Ser Pro Arg Arg Gly Glu Asn Phe
210         215         220
Val Thr Arg Lys Ile Thr Arg Ala Leu Gly Arg Ile Lys Val Gly Leu
225         230         235         240
Gln Thr Lys Leu Phe Leu Gly Asn Leu Gln Ala Ser Arg Asp Trp Gly
245         250         255
Phe Ala Gly Asp Tyr Val Glu Ala Met Trp Leu Met Leu Gln Gln Glu
260         265         270
Lys Pro Asp Asp Tyr Val Val Ala Thr Glu Glu Gly His Thr Val Glu

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| | | | | | | | |
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| gtttgctggtc | acagaggttt | ggttggttct | gctatcgtaa | gaaagttgca | agaacaaggt | | 120 |
| ttcaccaact | tggttttgaa | gacccacgct | gaattggact | tgaccagaca | agctgacgtt | | 180 |
| gaatctttct | tctctcaaga | aaagccagtt | tacgttatct | tggctgctgc | taaggttggt | | 240 |
| ggtatccacg | ctaacaacac | ctaccagct | gacttcacg | gtgttaactt | gcaaatacaa | | 300 |
| accaacgtta | tccactctgc | ttacgaacac | ggtgttaaga | agttgttggt | cttgggttct | | 360 |

| | | | | | | |
|-------------|------------|------------|-------------|-------------|------------|-----|
| tcttgtatct | acccaaagtt | cgctccacaa | ccaatcccag | aatctgcttt | gttgaccgct | 420 |
| tctttggaac | caaccaacga | atggtacgct | atcgctaaga | tcgctgggtat | caagacctgt | 480 |
| caagcttaca | gaatccaaca | cggttgggac | gctatctctg | gtatgccaac | caacttgtac | 540 |
| gggtccaaacg | acaacttcca | cccagaaaac | tctcacgttt | tgccagcttt | gatgagaaga | 600 |
| ttccacgaag | ctaaggttaa | cgggtctgaa | gaagttgttg | tttgggggtac | cggttctcca | 660 |
| ttgagagaat | tcttgcacgt | tgacgacttg | gctgacgctt | gtgttttctt | gttggacaga | 720 |
| tactctgggt | tggaacacgt | taacatcggt | tctgggtcaag | aagttaccat | cagagaattg | 780 |
| gctgaattgg | ttaaggaagt | tgttggtttc | gaaggtaagt | tgggttggga | ctgtaccaag | 840 |
| ccagacggta | ccccaaagaa | gttgatggac | tcttctaagt | tggcttcttt | gggttggacc | 900 |
| ccaaagggtt | ctttgcgcga | cggtttgtct | caaacctacg | actggtactt | gaagaacgtt | 960 |
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<210> 9

<211> 323

<212> PRT

<213> A. thaliana

<220>

<223> Ger1

<400> 9

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| Met | Ala | Glu | Thr | Ile | Gly | Ser | Glu | Val | Ser | Ser | Met | Ser | Asp | Lys | Ser |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ala | Lys | Ile | Phe | Val | Ala | Gly | His | Arg | Gly | Leu | Val | Gly | Ser | Ala | Ile |
| | | | 20 | | | | | 25 | | | | | | 30 | |
| Val | Arg | Lys | Leu | Gln | Glu | Gln | Gly | Phe | Thr | Asn | Leu | Val | Leu | Lys | Thr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| His | Ala | Glu | Leu | Asp | Leu | Thr | Arg | Gln | Ala | Asp | Val | Glu | Ser | Phe | Phe |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ser | Gln | Glu | Lys | Pro | Val | Tyr | Val | Ile | Leu | Ala | Ala | Ala | Lys | Val | Gly |
| 65 | | | | 70 | | | | | 75 | | | | | | 80 |
| Gly | Ile | His | Ala | Asn | Asn | Thr | Tyr | Pro | Ala | Asp | Phe | Ile | Gly | Val | Asn |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | Gln | Ile | Gln | Thr | Asn | Val | Ile | His | Ser | Ala | Tyr | Glu | His | Gly | Val |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| Lys | Lys | Leu | Leu | Phe | Leu | Gly | Ser | Ser | Cys | Ile | Tyr | Pro | Lys | Phe | Ala |
| | | 115 | | | | | 120 | | | | | | 125 | | |
| Pro | Gln | Pro | Ile | Pro | Glu | Ser | Ala | Leu | Leu | Thr | Ala | Ser | Leu | Glu | Pro |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Thr | Asn | Glu | Trp | Tyr | Ala | Ile | Ala | Lys | Ile | Ala | Gly | Ile | Lys | Thr | Cys |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Gln | Ala | Tyr | Arg | Ile | Gln | His | Gly | Trp | Asp | Ala | Ile | Ser | Gly | Met | Pro |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Thr | Asn | Leu | Tyr | Gly | Pro | Asn | Asp | Asn | Phe | His | Pro | Glu | Asn | Ser | His |
| | | 180 | | | | | | 185 | | | | | | 190 | |
| Val | Leu | Pro | Ala | Leu | Met | Arg | Arg | Phe | His | Glu | Ala | Lys | Val | Asn | Gly |
| | | 195 | | | | | 200 | | | | | | 205 | | |
| Ala | Glu | Glu | Val | Val | Val | Trp | Gly | Thr | Gly | Ser | Pro | Leu | Arg | Glu | Phe |
| | | | | | | 215 | | | | | 220 | | | | |
| Leu | His | Val | Asp | Asp | Leu | Ala | Asp | Ala | Cys | Val | Phe | Leu | Leu | Asp | Arg |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Tyr | Ser | Gly | Leu | Glu | His | Val | Asn | Ile | Gly | Ser | Gly | Gln | Glu | Val | Thr |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ile | Arg | Glu | Leu | Ala | Glu | Leu | Val | Lys | Glu | Val | Val | Gly | Phe | Glu | Gly |
| | | | 260 | | | | | 265 | | | | | | 270 | |
| Lys | Leu | Gly | Trp | Asp | Cys | Thr | Lys | Pro | Asp | Gly | Thr | Pro | Arg | Lys | Leu |

| | | | | | |
|-------------------------|---------------------|---------------------|---------------------|-----|-----|
| | 275 | | 280 | | 285 |
| Met | Asp Ser Ser Lys Leu | Ala Ser Leu Gly Trp | Thr Pro Lys Val Ser | | |
| 290 | | 295 | | 300 | |
| Leu Arg Asp Gly Leu Ser | Gln Thr Tyr Asp Trp | Tyr Leu Lys Asn Val | | | |
| 305 | | 310 | | 315 | 320 |
| Cys Asn Arg | | | | | |

<210> 10
 <211> 1095
 <212> DNA
 <213> H. sapiens

<220>
 <223> CDS Slc35C1 wild type

<400> 10

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| gacccctctg | cagaggcaga | ggccaacggg | gagaagccct | ttctgctgcg | ggcattgcag | 120 |
| atcgcgctgg | tggctctccct | ctactgggtc | acctccatct | ccatgggtgtt | ccttaataag | 180 |
| tacctgctgg | acagcccctc | cctgcggctg | gacaccccca | tcttcgtcac | cttctaccag | 240 |
| tgcctgggtga | ccacgctgct | gtgcaaaggc | ctcagcgctc | tggccgcctg | ctgccctggt | 300 |
| gccgtggact | tccccagctt | gcgccctggac | ctcagggtgg | cccgcagcgt | cctgcccctg | 360 |
| tcgggtggctt | tcacgggcat | gatcaccttc | aataacctct | gcctcaagta | cgtcgggtgtg | 420 |
| gccttctaca | atgtggggccg | ctcactcacc | accgtcttca | acgtgctgct | ctcctacctg | 480 |
| ctgctcaagc | agaccacctc | cttctatgcc | ctgctcacct | gcggtatcat | catcggggggc | 540 |
| ttctggcctt | gtgtggacca | ggagggggca | gaaggcacc | tgtcgtggct | gggcaccgtc | 600 |
| ttcggcgtgc | tggctagcct | ctgtgtctcg | ctcaacgcca | tctacaccac | gaaggtgctc | 660 |
| ccggcggtgg | acggcagcat | ctggcgctg | actttctaca | acaacgtcaa | cgctgcatc | 720 |
| ctcttcctgc | ccctgctcct | gctgctcggg | gagcttcagg | ccctgcgtga | ctttgccag | 780 |
| ctgggcagtg | cccacttctg | ggggatgatg | acgctgggcg | gcctgttttg | ctttgccatc | 840 |
| ggctacgtga | caggactgca | gatcaagttc | accagtccgc | tgaccacaaa | tgtgtcgggc | 900 |
| acggccaagg | cctgtgcccc | gacagtgtct | gccgtgtctt | actacgagga | gaccaagagc | 960 |
| ttcctctggt | ggacgagcaa | catgatggtg | ctgggcggct | cctccgccta | cacctgggtc | 1020 |
| aggggctggg | agatgaagaa | gactccggag | gagcccagcc | ccaaagacag | cgagaagagc | 1080 |
| gccatggggg | tgtga | | | | | 1095 |

<210> 11
 <211> 1095
 <212> DNA
 <213> Artificial

<220>
 <223> CDS Slc35C1 codon optimized

<400> 11

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| atgaacagag | ctccattgaa | gagatctaga | atcttgcaca | tggctttgac | cgggtgcttct | 60 |
| gacccatctg | ctgaagctga | agctaacggg | gaaaagccat | tcttgttgag | agctttgcaa | 120 |
| atcgctttgg | ttgtttcttt | gtactgggtt | acctctatct | ctatggtttt | cttgaacaag | 180 |
| tacttgttgg | actctccatc | tttgagattg | gacaccccaa | tcttcgttac | cttctaccaa | 240 |
| tgtttgggtta | ccaccttggt | gtgtaagggt | ttgtctgctt | tggctgcttg | ttgtccagggt | 300 |
| gctgttgact | tcccatcttt | gagattggac | ttgagagttg | ctagatctgt | tttgccattg | 360 |
| tctgttggtt | tcacggtat | gatcaccttc | aacaacttgt | gtttgaagta | cgttgggtgtt | 420 |
| gctttctaca | acgttggtag | atctttgacc | accgttttca | acgttttggt | gtcttacttg | 480 |
| ttgttgaaagc | aaaccacctc | tttctacgct | ttgttgacct | gtggtatcat | catcgggtggt | 540 |
| ttctgggttg | gtgttgacca | agaaggtgct | gaaggtacct | tgtcttggtt | gggtaccgtt | 600 |
| ttcgggtgtt | tggcttcttt | gtgtgtttct | ttgaacgcta | tctacaccac | caaggttttg | 660 |

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|------|
| ccagctgttg | acggtttctat | ctggagattg | accttctaca | acaacgttaa | cgcttgtatc | 720 |
| ttgttcttgc | cattgttggt | gttgttgggt | gaattgcaag | ctttgagaga | cttcgctcaa | 780 |
| ttgggttctg | ctcacttctg | gggtatgatg | accttgggtg | gtttgttcgg | tttcgctatc | 840 |
| ggttacgtta | ccggtttgca | aatcaagttc | acctctccat | tgaccacaaa | cgtttctggt | 900 |
| accgctaagg | cttgtgctca | aaccgttttg | gctgttttgt | actacgaaga | aaccaagtct | 960 |
| ttcttgtggt | ggacctctaa | catgatgggt | ttgggtgggt | cttctgctta | cacctgggtt | 1020 |
| agaggttggg | aaatgaagaa | gacccagaa | gaaccatctc | caaaggactc | tgaaaagtct | 1080 |
| gctatgggtg | tttga | | | | | 1095 |

<210> 12
 <211> 364
 <212> PRT
 <213> H. sapiens

<220>
 <223> Slc35C1

<400> 12

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Arg | Ala | Pro | Leu | Lys | Arg | Ser | Arg | Ile | Leu | His | Met | Ala | Leu |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Thr | Gly | Ala | Ser | Asp | Pro | Ser | Ala | Glu | Ala | Glu | Ala | Asn | Gly | Glu | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Pro | Phe | Leu | Leu | Arg | Ala | Leu | Gln | Ile | Ala | Leu | Val | Val | Ser | Leu | Tyr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Trp | Val | Thr | Ser | Ile | Ser | Met | Val | Phe | Leu | Asn | Lys | Tyr | Leu | Leu | Asp |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ser | Pro | Ser | Leu | Arg | Leu | Asp | Thr | Pro | Ile | Phe | Val | Thr | Phe | Tyr | Gln |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Cys | Leu | Val | Thr | Thr | Leu | Leu | Cys | Lys | Gly | Leu | Ser | Ala | Leu | Ala | Ala |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Cys | Cys | Pro | Gly | Ala | Val | Asp | Phe | Pro | Ser | Leu | Arg | Leu | Asp | Leu | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Ala | Arg | Ser | Val | Leu | Pro | Leu | Ser | Val | Val | Phe | Ile | Gly | Met | Ile |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Thr | Phe | Asn | Asn | Leu | Cys | Leu | Lys | Tyr | Val | Gly | Val | Ala | Phe | Tyr | Asn |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Val | Gly | Arg | Ser | Leu | Thr | Thr | Val | Phe | Asn | Val | Leu | Leu | Ser | Tyr | Leu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Leu | Leu | Lys | Gln | Thr | Ser | Phe | Tyr | Ala | Leu | Leu | Thr | Cys | Gly | Ile | |
| | | | 165 | | | | | 170 | | | | | 175 | | |
| Ile | Ile | Gly | Gly | Phe | Trp | Leu | Gly | Val | Asp | Gln | Glu | Gly | Ala | Glu | Gly |
| | | 180 | | | | | 185 | | | | | | 190 | | |
| Thr | Leu | Ser | Trp | Leu | Gly | Thr | Val | Phe | Gly | Val | Leu | Ala | Ser | Leu | Cys |
| | 195 | | | | | 200 | | | | | | 205 | | | |
| Val | Ser | Leu | Asn | Ala | Ile | Tyr | Thr | Thr | Lys | Val | Leu | Pro | Ala | Val | Asp |
| | 210 | | | | | 215 | | | | | | 220 | | | |
| Gly | Ser | Ile | Trp | Arg | Leu | Thr | Phe | Tyr | Asn | Asn | Val | Asn | Ala | Cys | Ile |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Leu | Phe | Leu | Pro | Leu | Leu | Leu | Leu | Leu | Gly | Glu | Leu | Gln | Ala | Leu | Arg |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Asp | Phe | Ala | Gln | Leu | Gly | Ser | Ala | His | Phe | Trp | Gly | Met | Met | Thr | Leu |
| | | 260 | | | | | | 265 | | | | | 270 | | |
| Gly | Gly | Leu | Phe | Gly | Phe | Ala | Ile | Gly | Tyr | Val | Thr | Gly | Leu | Gln | Ile |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Lys | Phe | Thr | Ser | Pro | Leu | Thr | His | Asn | Val | Ser | Gly | Thr | Ala | Lys | Ala |
| | 290 | | | | | 295 | | | | | 300 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ala | Gln | Thr | Val | Leu | Ala | Val | Leu | Tyr | Tyr | Glu | Glu | Thr | Lys | Ser |
| 305 | | | | | 310 | | | | 315 | | | | | | 320 |
| Phe | Leu | Trp | Trp | Thr | Ser | Asn | Met | Met | Val | Leu | Gly | Gly | Ser | Ser | Ala |
| | | | | 325 | | | | | 330 | | | | | | 335 |
| Tyr | Thr | Trp | Val | Arg | Gly | Trp | Glu | Met | Lys | Lys | Thr | Pro | Glu | Glu | Pro |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Ser | Pro | Lys | Asp | Ser | Glu | Lys | Ser | Ala | Met | Gly | Val | | | | |
| | | 355 | | | | | 360 | | | | | | | | |

<210> 13

<211> 1212

<212> DNA

<213> R. norvegicus

<220>

<223> CDS St6gal1 wild type

<400> 13

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|------|
| atgattcata | ccaacttgaa | gaaaaagttc | agcctcttca | tcctgggtctt | tctcctgttc | 60 |
| gcagtcatct | gtgttttgaa | gaaagggagc | gactatgagg | cccttacact | gcaagccaag | 120 |
| gaattccaga | tgcccaagag | ccaggagaaa | gtggccatgg | ggtctgcttc | ccaggttgtg | 180 |
| ttctcaaaca | gcaagcaaga | ccctaaggaa | gacattccaa | tcctcagtta | ccacagggtc | 240 |
| acagccaagg | tcaaaccaca | gccttccttc | caggtgtggg | acaaggactc | cacatactca | 300 |
| aaacttaacc | ccaggctgct | gaagatctgg | agaaactatc | tgaacatgaa | caaataataa | 360 |
| gtatcctaca | agggaccggg | gccaggagtc | aagttcagcg | tagaagcact | gcgttgccac | 420 |
| cttcgagacc | atgtgaacgt | gtctatgata | gaggccacag | atcttccttc | caacaccact | 480 |
| gagtgggagg | gttacctgcc | caaggagaac | tttagaacca | aggttgggcc | ttggcaaagg | 540 |
| tgtgccgtcg | tctcttctgc | aggatctctg | aaaaactccc | agcttggtcg | agagattgat | 600 |
| aatcatgatg | cagttctgag | gtttaatggg | gcccctaccg | acaacttcca | acaggatgtg | 660 |
| ggctcaaaaa | ctaccattcg | cctaataaac | tctcagttag | tcaccacaga | aaagcgcttc | 720 |
| ctcaaggaca | gtttgtacac | cgaaggaatc | ctaattgtat | gggacccatc | cgtgtatcat | 780 |
| gcagatatcc | caaagtggta | tcagaaacca | gactacaatt | tcttcgaaac | ctataagagt | 840 |
| taccgaaggc | tgaacccag | ccagccattt | tatatcctca | agccccagat | gccatgggaa | 900 |
| ctgtgggaca | tcattcagga | aatctctgca | gatctgattc | agccaaatcc | cccacctcc | 960 |
| ggcatgctgg | gtatcatcat | catgatgacg | ctgtgtgacc | aggtagatat | ttacgagttc | 1020 |
| ctcccatcca | agcgcaagac | ggacgtgtgc | tattatcacc | aaaagttctt | tgacagcgct | 1080 |
| tgcacgatgg | gtgcctacca | cccgtccttc | ttcgagaaga | atatggtgaa | gcattctaat | 1140 |
| gagggaacag | atgaagacat | ttatttgttt | gggaaagcca | ccctttctgg | cttcggaac | 1200 |
| attcgttgtt | ga | | | | | 1212 |

<210> 14

<211> 1212

<212> DNA

<213> Artificial

<220>

<223> CDS St6gal1 codon optimized

<400> 14

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|------------|------------|-------------|------------|------------|------------|-----|
| atgatccaca | ccaacttgaa | gaagaagttc | tctttgttca | tcttggtttt | cttgttgttc | 60 |
| gctgttatct | gtgttttgaa | gaagggttct | gactacgaag | ctttgacctt | gcaagctaag | 120 |
| gaattccaaa | tgccaaagtc | tcaagaaaag | gttgctatgg | gttctgcttc | tcaagttgtt | 180 |
| ttctctaact | ctaagcaaga | cccaaaggaa | gacatcccaa | tcttgtctta | ccacagagtt | 240 |
| accgctaagg | ttaagccaca | accatctttc | caagtttggg | acaaggactc | tacctactct | 300 |
| aagttgaacc | caagattgtt | gaagatctgg | agaaactact | tgaacatgaa | caagtacaag | 360 |
| gtttcttaca | agggtccagg | tccagggtgtt | aagttctctg | ttgaagcttt | gagatgtcac | 420 |

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ttgcgcgacc acgttaacgt ttctatgatc gaagctaccg acttcccatt caacaccacc 480
gaatgggaag gttacttgcc aaaggaaaac ttcagaacca aggttggtcc atggcaaaga 540
tgtgctgttg tttcttctgc tggttctttg aagaactctc aattgggtag agaaatcgac 600
aaccacgacg ctgtttttgag attcaacggg gctccaaccg acaacttcca acaagacgtt 660
ggttctaaga ccaccatcag attgatgaac tctcaattgg ttaccaccga aaagagattc 720
ttgaaggact ctttgtacac cgaaggatc ttgatcgttt gggacccatc tgttttaccac 780
gctgacatcc caaagtggta ccaaaagcca gactacaact tcttcgaaac ctacaagtct 840
tacagaagat tgaacccatc tcaaccattc tacatcttga agccacaaat gccatgggaa 900
ttgtgggaca tcatccaaga aatctctgct gacttgatcc aaccaaacc accatcttct 960
ggtatgttgg gtatcatcat catgatgacc ttgtgtgacc aagttgacat ctacgaattc 1020
ttgccatcta agagaaagac cgacgtttgt tactaccacc aaaagttctt cgactctgct 1080
tgtacatgg gtgcttacca cccattgttg ttcgaaaaga acatgggttaa gcacttgaac 1140
gaaggtagcg acgaagacat ctacttgttc ggtaaggcta ccttgtcttg tttcagaaac 1200
atcagatgtt ga 1212

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<210> 15

<211> 403

<212> PRT

<213> R. norvegicus

<220>

<223> St6gal1

<400> 15

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Met Ile His Thr Asn Leu Lys Lys Lys Phe Ser Leu Phe Ile Leu Val
1           5           10           15
Phe Leu Leu Phe Ala Val Ile Cys Val Trp Lys Lys Gly Ser Asp Tyr
          20           25           30
Glu Ala Leu Thr Leu Gln Ala Lys Glu Phe Gln Met Pro Lys Ser Gln
          35           40           45
Glu Lys Val Ala Met Gly Ser Ala Ser Gln Val Val Phe Ser Asn Ser
          50           55           60
Lys Gln Asp Pro Lys Glu Asp Ile Pro Ile Leu Ser Tyr His Arg Val
65           70           75           80
Thr Ala Lys Val Lys Pro Gln Pro Ser Phe Gln Val Trp Asp Lys Asp
          85           90           95
Ser Thr Tyr Ser Lys Leu Asn Pro Arg Leu Leu Lys Ile Trp Arg Asn
          100          105          110
Tyr Leu Asn Met Asn Lys Tyr Lys Val Ser Tyr Lys Gly Pro Gly Pro
          115          120          125
Gly Val Lys Phe Ser Val Glu Ala Leu Arg Cys His Leu Arg Asp His
          130          135          140
Val Asn Val Ser Met Ile Glu Ala Thr Asp Phe Pro Phe Asn Thr Thr
145          150          155          160
Glu Trp Glu Gly Tyr Leu Pro Lys Glu Asn Phe Arg Thr Lys Val Gly
          165          170          175
Pro Trp Gln Arg Cys Ala Val Val Ser Ser Ala Gly Ser Leu Lys Asn
          180          185          190
Ser Gln Leu Gly Arg Glu Ile Asp Asn His Asp Ala Val Leu Arg Phe
          195          200          205
Asn Gly Ala Pro Thr Asp Asn Phe Gln Gln Asp Val Gly Ser Lys Thr
          210          215          220
Thr Ile Arg Leu Met Asn Ser Gln Leu Val Thr Thr Glu Lys Arg Phe
225          230          235          240
Leu Lys Asp Ser Leu Tyr Thr Glu Gly Ile Leu Ile Val Trp Asp Pro
          245          250          255

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Ser Val Tyr His Ala Asp Ile Pro Lys Trp Tyr Gln Lys Pro Asp Tyr
 260 265 270
 Asn Phe Phe Glu Thr Tyr Lys Ser Tyr Arg Arg Leu Asn Pro Ser Gln
 275 280 285
 Pro Phe Tyr Ile Leu Lys Pro Gln Met Pro Trp Glu Leu Trp Asp Ile
 290 295 300
 Ile Gln Glu Ile Ser Ala Asp Leu Ile Gln Pro Asn Pro Pro Ser Ser
 305 310 315 320
 Gly Met Leu Gly Ile Ile Ile Met Met Thr Leu Cys Asp Gln Val Asp
 325 330 335
 Ile Tyr Glu Phe Leu Pro Ser Lys Arg Lys Thr Asp Val Cys Tyr Tyr
 340 345 350
 His Gln Lys Phe Phe Asp Ser Ala Cys Thr Met Gly Ala Tyr His Pro
 355 360 365
 Leu Leu Phe Glu Lys Asn Met Val Lys His Leu Asn Glu Gly Thr Asp
 370 375 380
 Glu Asp Ile Tyr Leu Phe Gly Lys Ala Thr Leu Ser Gly Phe Arg Asn
 385 390 395 400
 Ile Arg Cys

<210> 16
 <211> 1032
 <212> DNA
 <213> H. sapiens

<220>
 <223> CDS Fut2 wild type

<400> 16
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 ttaccggtgc agataccagt gctagcctca acatcaaagg cactgggacc cagccagctc 180
 aggggggatgt ggacgatcaa tgcaataggc cgcctgggga accagatggg cgagtacgcc 240
 aactgtacg ccctggccaa gatgaacggg cggcccgct tcatcccggc ccagatgcac 300
 agcaccttg ccccatctt cagaatcacc ctgccggtgc tgcacagcgc cacggccagc 360
 aggatccctt ggacagaacta ccacctgaac gactggatgg aggaggaata ccgccacatc 420
 ccgggggagt acgtccgctt caccggctac ccctgctcct ggaccttcta ccaccacctc 480
 cgccaggaga tcctccagga gttcaccctg caccgaccag tgcgggagga ggcccagaag 540
 ttcttgctgg gcctgcaggt gaacgggagc cggccgggca cttttgtagg ggtccatgtt 600
 cgccgagggg actatgtcca tgtcatgcca aaagtgtgga agggggtggt ggccgaccgg 660
 cgatacctac agcaggccct ggactggttc cgagctcgt acagctccct catcttcgtg 720
 gtcaccagta atggcatggc ctggtgtcgg gagaacattg acacctcca cggatgatgtg 780
 gtgtttgctg gcgatggcat tgagggctca cctgccaaag attttgctct actcacacag 840
 tgtaaccaca ccatcatgac cattgggacg ttcgggatct gggccgcata cctcacgggc 900
 ggagacacca tctacctggc caattacacc ctccccgact cccctttcct caaaatcttt 960
 aagccagagg cagccttcct gccggagtgg acagggtatt ccgcagacct gtccccctta 1020
 ctcaagcact aa 1032

<210> 17
 <211> 1032
 <212> DNA
 <213> Artificial

<220>
 <223> CDS Fut2 codon optimized

<400> 17

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ttgccagttc aaatcccagt tttggcttct acctctaagg ctttgggtcc atctcaattg 180
agaggtatgt ggaccatcaa cgctatcggt agattgggta accaaatggg tgaatacgct 240
accttgtagc ctttggctaa gatgaacggt agaccagctt tcatcccagc tcaaatgcac 300
tctaccttgg ctccaatctt cagaatcacc ttgccagttt tgcactctgc taccgcttct 360
agaatcccat ggcaaaacta ccacttgaac gactggatgg aagaagaata cagacacatc 420
ccaggtgaat acgttagatt caccgggttac ccatgttctt ggaccttcta ccaccacttg 480
agacaagaaa tcttgcaaga attcaccttg cacgaccacg ttagagaaga agctcaaaag 540
ttcttgagag gtttgcaagt taacggttct agaccaggta ccttcgttgg tgttcacggt 600
agaagaggtg actacgttca cgttatgcca aagggttggg aggggtgttg tgctgacaga 660
agatacttgc aacaagcttt ggactgggtc agagctagat actcttcttt gatcttcggt 720
gttacctcta acggtatggc ttggtgtaga gaaaacatcg acacctctca cggtgacggt 780
gttttcgctg gtgacggtat cgaaggttct ccagctaagg acttcgcttt gttgacccaa 840
tgtaaccaca ccatcatgac catcggtacc ttcggtatct gggctgctta cttgaccggt 900
ggtgacacca tctacttggc taactacacc ttgccagact ctccattctt gaagatcttc 960
aagccagaag ctgctttctt gccagaatgg accggtatcg ctgctgactt gtctccattg 1020
ttgaagcact ga 1032
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<210> 18

<211> 343

<212> PRT

<213> H. sapiens

<220>

<223> Fut2

<400> 18

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

| | | | | |
|---|-----|-----|-----|-----|
| 210 | | 215 | | 220 |
| Gln Ala Leu Asp Trp Phe Arg Ala Arg Tyr Ser Ser Leu Ile Phe Val | | | | |
| 225 | | 230 | | 235 |
| Val Thr Ser Asn Gly Met Ala Trp Cys Arg Glu Asn Ile Asp Thr Ser | | | | |
| | 245 | | 250 | |
| His Gly Asp Val Val Phe Ala Gly Asp Gly Ile Glu Gly Ser Pro Ala | | | | |
| | 260 | | 265 | |
| Lys Asp Phe Ala Leu Leu Thr Gln Cys Asn His Thr Ile Met Thr Ile | | | | |
| | 275 | | 280 | |
| Gly Thr Phe Gly Ile Trp Ala Ala Tyr Leu Thr Gly Gly Asp Thr Ile | | | | |
| | 290 | | 295 | |
| Tyr Leu Ala Asn Tyr Thr Leu Pro Asp Ser Pro Phe Leu Lys Ile Phe | | | | |
| 305 | | 310 | | 315 |
| Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Thr Gly Ile Ala Ala Asp | | | | |
| | 325 | | 330 | |
| Leu Ser Pro Leu Leu Lys His | | | | |
| | 340 | | | |

<210> 19
 <211> 1026
 <212> DNA
 <213> Artificial

<220>
 <223> CDS FUT2 chimeric

<400> 19
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 gttcaaatcc cagttttggc ttctacctct aaggctttgg gtccatctca attgagaggt 180
 atgtggacca tcaacgctat cggtagattg ggtaaccaa tgggtgaata cgctaccttg 240
 tacgctttgg ctaagatgaa cggtagacca gctttcatcc cagctcaaat gcactctacc 300
 ttggctccaa tcttcagaat caccttgcca gttttgcact ctgctaccgc ttctagaatc 360
 ccatggcaaa actaccactt gaacgactgg atggaagaag aatacagaca catcccaggt 420
 gaatacgtta gattcaccgg ttaccatgt tcttgacct tctaccacca cttgagacaa 480
 gaaatcttgc aagaattcac cttgcacgac cacgttagag aagaagctca aaagtcttg 540
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 ggtgactacg ttcacgttat gccaaagggt tggaagggtg ttgttgctga cagaagatac 660
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| Tyr | Ala | Leu | Ala | Lys | Met | Asn | Gly | Arg | Pro | Ala | Phe | Ile | Pro | Ala | Gln | |
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| Asp | Trp | Met | Glu | Glu | Glu | Tyr | Arg | His | Ile | Pro | Gly | Glu | Tyr | Val | Arg | |
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| Phe | Thr | Gly | Tyr | Pro | Cys | Ser | Trp | Thr | Phe | Tyr | His | His | Leu | Arg | Gln | |
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| Phe | Val | Gly | Val | His | Val | Arg | Arg | Gly | Asp | Tyr | Val | His | Val | Met | Pro | |
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| Lys | Val | Trp | Lys | Gly | Val | Val | Ala | Asp | Arg | Arg | Tyr | Leu | Gln | Gln | Ala | |
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| Leu | Asp | Trp | Phe | Arg | Ala | Arg | Tyr | Ser | Ser | Leu | Ile | Phe | Val | Val | Thr | |
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| Phe | Ala | Leu | Leu | Thr | Gln | Cys | Asn | His | Thr | Ile | Met | Thr | Ile | Gly | Thr | |
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| Glu | Ala | Ala | Phe | Leu | Pro | Glu | Trp | Thr | Gly | Ile | Ala | Ala | Asp | Leu | Ser | |
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| aacacctctg | gtttgaagat | caacggtgtt | ccaatcgaag | acgctagaga | agaagttttg | 180 |

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| tctatcttca | acgttgggtca | aatctgtggg | gctttcttcg | ttccattgat | ggactggaag | 420 |
| ggtagaaagc | cagctatctt | gatcggttgt | ttgggtgttg | ttatcgggtgc | tatcatctct | 480 |
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| tctacctacg | gtaccaacaa | gaacttccca | aactcttcta | aggctttcaa | gatccatttg | 720 |
| tacttgcaaa | tgatgttccc | aggtttgggt | tgtatcttcg | gttggttgat | cccagaatct | 780 |
| ccaagatggg | tggttgggtg | tggtagagaa | gaagaagcta | gagaattcat | catcaagtac | 840 |
| cacttgaacg | gtgacagaac | ccaccatttg | ttggacatgg | aaatggctga | aatcatcgaa | 900 |
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| agaaccagat | ctgacagata | cagagctatg | ttggttatct | tgatggcttg | gttcgggtcaa | 1020 |
| ttctctggta | acaacgtttg | ttcttactac | ttgccaacca | tggtgagaaa | cgttggtatg | 1080 |
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| Leu | Ser | Lys | Gln | Tyr | Tyr | Lys | Leu | Tyr | Gly | Leu | Cys | Phe | Ile | Thr | Tyr |
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| Leu | Cys | Ala | Thr | Met | Gln | Gly | Tyr | Asp | Gly | Ala | Leu | Met | Gly | Ser | Ile |
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| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Ser | Gly | Thr | Gly | Leu | Val | Phe | Ser | Ile | Phe | Asn | Val | Gly | Gln | Ile |
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| Ser | Leu | Thr | Thr | Thr | Lys | Ser | Ala | Leu | Ile | Gly | Gly | Arg | Trp | Phe | Val |
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| Ala | Phe | Phe | Ala | Thr | Ile | Ala | Asn | Ala | Ala | Ala | Pro | Thr | Tyr | Cys | Ala | |
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| Glu | Val | Ala | Pro | Ala | His | Leu | Arg | Gly | Lys | Val | Ala | Gly | Leu | Tyr | Asn | |
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| Thr | Leu | Trp | Ser | Val | Gly | Ser | Ile | Val | Ala | Ala | Phe | Ser | Thr | Tyr | Gly | |
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| Thr | Asn | Lys | Asn | Phe | Pro | Asn | Ser | Ser | Lys | Ala | Phe | Lys | Ile | Pro | Leu | |
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| Tyr | Leu | Gln | Met | Met | Phe | Pro | Gly | Leu | Val | Cys | Ile | Phe | Gly | Trp | Leu | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Ile | Pro | Glu | Ser | Pro | Arg | Trp | Leu | Val | Gly | Val | Gly | Arg | Glu | Glu | Glu | |
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| Ala | Arg | Glu | Phe | Ile | Ile | Lys | Tyr | His | Leu | Asn | Gly | Asp | Arg | Thr | His | |
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| Pro | Leu | Leu | Asp | Met | Glu | Met | Ala | Glu | Ile | Ile | Glu | Ser | Phe | His | Gly | |
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| Trp | Phe | Gly | Gln | Phe | Ser | Gly | Asn | Asn | Val | Cys | Ser | Tyr | Tyr | Leu | Pro | |
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| Ala | Phe | Phe | Ile | Asp | Lys | Ile | Gly | Arg | Arg | Glu | Gly | Phe | Leu | Gly | Ser | |
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| Ile | Ser | Gly | Ala | Ala | Leu | Ala | Leu | Thr | Gly | Leu | Ser | Ile | Cys | Thr | Ala | |
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| Arg | Tyr | Glu | Lys | Thr | Lys | Lys | Lys | Ser | Ala | Ser | Asn | Gly | Ala | Leu | Val | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| Phe | Ile | Tyr | Leu | Phe | Gly | Gly | Ile | Phe | Ser | Phe | Ala | Phe | Thr | Pro | Met | |
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| Gln | Ser | Met | Tyr | Ser | Thr | Glu | Val | Ser | Thr | Asn | Leu | Thr | Arg | Ser | Lys | |
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| Ala | Gln | Leu | Leu | Asn | Phe | Val | Val | Ser | Gly | Val | Ala | Gln | Phe | Val | Asn | |
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| Gln | Phe | Ala | Thr | Pro | Lys | Ala | Met | Lys | Asn | Ile | Lys | Tyr | Trp | Phe | Tyr | |
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| Val | Phe | Tyr | Val | Phe | Phe | Asp | Ile | Phe | Glu | Phe | Ile | Val | Ile | Tyr | Phe | |
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| Phe | Phe | Leu | Ser | Tyr | Leu | Thr | Ala | Ser | Trp | Phe | Ile | Asn | Lys | Ile | Tyr | |
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| Ser | Leu | Thr | Thr | Thr | Lys | Ser | Ala | Leu | Ile | Gly | Gly | Arg | Trp | Phe | Val | |
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| Ala | Phe | Phe | Ala | Thr | Ile | Ala | Asn | Ala | Ala | Ala | Pro | Thr | Tyr | Cys | Ala | |
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| Glu | Val | Ala | Pro | Ala | His | Leu | Arg | Gly | Lys | Val | Ala | Gly | Leu | Tyr | Asn | |
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| Thr | Leu | Trp | Ser | Val | Gly | Ser | Ile | Val | Ala | Ala | Phe | Ser | Thr | Tyr | Gly | |
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| Thr | Asn | Lys | Asn | Phe | Pro | Asn | Ser | Ser | Lys | Ala | Phe | Lys | Ile | Pro | Leu | |
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| Tyr | Leu | Gln | Met | Met | Phe | Pro | Gly | Leu | Val | Cys | Ile | Phe | Gly | Trp | Leu | |
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| Ala | Arg | Glu | Phe | Ile | Ile | Lys | Tyr | His | Leu | Asn | Gly | Asp | Arg | Thr | His | |
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| Pro | Leu | Leu | Asp | Met | Glu | Met | Ala | Glu | Ile | Ile | Glu | Ser | Phe | His | Gly | |
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| Trp | Phe | Gly | Gln | Phe | Ser | Gly | Asn | Asn | Val | Cys | Ser | Tyr | Tyr | Leu | Pro | |
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| Met | Asn | Gly | Val | Tyr | Ser | Ile | Val | Thr | Trp | Ile | Ser | Ser | Ile | Cys | Gly | |
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| Ala | Phe | Phe | Ile | Asp | Lys | Ile | Gly | Arg | Arg | Glu | Gly | Phe | Leu | Gly | Ser | |
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| Ile | Ser | Gly | Ala | Ala | Leu | Ala | Leu | Thr | Gly | Leu | Ser | Ile | Cys | Thr | Ala | |
| | | | 405 | | | | | | 410 | | | | | 415 | | |
| Arg | Tyr | Glu | Lys | Thr | Lys | Lys | Lys | Ser | Ala | Ser | Asn | Gly | Ala | Leu | Val | |
| | | | 420 | | | | 425 | | | | | | 430 | | | |
| Phe | Ile | Tyr | Leu | Phe | Gly | Gly | Ile | Phe | Ser | Phe | Ala | Phe | Thr | Pro | Met | |
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| Gln | Ser | Met | Tyr | Ser | Thr | Glu | Val | Ser | Thr | Asn | Leu | Thr | Arg | Ser | Lys | |
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| Ala | Gln | Leu | Leu | Asn | Phe | Val | Val | Ser | Gly | Val | Ala | Gln | Phe | Val | Asn | |
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| Lys | Ser | Ser | Thr | Glu | Asn | Pro | Phe | Glu | Glu | Asn | Glu | Glu | Asn | Val | Ile | | | | |
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| Thr | Asp | Tyr | Gly | Asp | Glu | His | His | Thr | Ala | Glu | Gln | Glu | Phe | Asp | Leu | | | | |
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| Ala | Phe | Phe | Ala | Thr | Ile | Ala | Asn | Ala | Ala | Ala | Pro | Thr | Tyr | Cys | Ala |
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| Glu | Val | Ala | Pro | Ala | His | Leu | Arg | Gly | Lys | Val | Ala | Gly | Leu | Tyr | Asn |
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| Thr | Leu | Trp | Ser | Val | Gly | Ser | Ile | Val | Ala | Ala | Phe | Ser | Thr | Tyr | Gly |
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| Tyr | Leu | Gln | Met | Met | Phe | Pro | Gly | Leu | Val | Cys | Ile | Phe | Gly | Trp | Leu |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Ile | Pro | Glu | Ser | Pro | Arg | Trp | Leu | Val | Gly | Val | Gly | Arg | Glu | Glu | Glu |
| | | 260 | | | | | 265 | | | | | | 270 | | |
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| Pro | Leu | Leu | Asp | Met | Glu | Met | Ala | Glu | Ile | Ile | Glu | Ser | Phe | His | Gly |
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| Thr | Asp | Leu | Ser | Asn | Pro | Leu | Glu | Met | Leu | Asp | Val | Arg | Ser | Leu | Phe |
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| Arg | Thr | Arg | Ser | Asp | Arg | Tyr | Arg | Ala | Met | Leu | Val | Ile | Leu | Met | Ala |
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| Trp | Phe | Gly | Gln | Phe | Ser | Gly | Asn | Asn | Val | Cys | Ser | Tyr | Tyr | Leu | Pro |
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| Met | Asn | Gly | Val | Tyr | Ser | Ile | Val | Thr | Trp | Ile | Ser | Ser | Ile | Cys | Gly |
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| Ala | Phe | Phe | Ile | Asp | Lys | Ile | Gly | Arg | Arg | Glu | Gly | Phe | Leu | Gly | Ser |
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| Ile | Ser | Gly | Ala | Ala | Leu | Ala | Leu | Thr | Gly | Leu | Ser | Ile | Cys | Thr | Ala |
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| Arg | Tyr | Glu | Lys | Thr | Lys | Lys | Lys | Ser | Ala | Ser | Asn | Gly | Ala | Leu | Val |
| | | 420 | | | | | | 425 | | | | | 430 | | |
| Phe | Ile | Tyr | Leu | Phe | Gly | Gly | Ile | Phe | Ser | Phe | Ala | Phe | Thr | Pro | Met |
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| Ala | Gln | Leu | Leu | Asn | Phe | Val | Val | Ser | Gly | Val | Ala | Gln | Phe | Val | Asn |
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| Gln | Phe | Ala | Thr | Pro | Lys | Ala | Met | Lys | Asn | Ile | Lys | Tyr | Trp | Phe | Tyr |
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| Val | Phe | Tyr | Val | Phe | Phe | Asp | Ile | Phe | Glu | Phe | Ile | Val | Ile | Tyr | Phe |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Phe | Phe | Met | Trp | Asp | Ser | Lys | Ser | Gly | Arg | Asn | Gln | Lys | Lys | Ile | Ser |
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| Leu | Cys | Ala | Thr | Met | Gln | Gly | Tyr | Asp | Gly | Ala | Leu | Met | Gly | Ser | Ile |
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| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Ser | Gly | Thr | Gly | Leu | Val | Phe | Ser | Ile | Phe | Asn | Val | Gly | Gln | Ile |
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| Ala | Ile | Leu | Ile | Gly | Cys | Leu | Gly | Val | Val | Ile | Gly | Ala | Ile | Ile | Ser |
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| Ser | Leu | Thr | Thr | Thr | Lys | Ser | Ala | Leu | Ile | Gly | Gly | Arg | Trp | Phe | Val |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ala | Phe | Phe | Ala | Thr | Ile | Ala | Asn | Ala | Ala | Ala | Pro | Thr | Tyr | Cys | Ala |
| | | | 180 | | | | 185 | | | | | | 190 | | |
| Glu | Val | Ala | Pro | Ala | His | Leu | Arg | Gly | Lys | Val | Ala | Gly | Leu | Tyr | Asn |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Thr | Leu | Trp | Ser | Val | Gly | Ser | Ile | Val | Ala | Ala | Phe | Ser | Thr | Tyr | Gly |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Thr | Asn | Lys | Asn | Phe | Pro | Asn | Ser | Ser | Lys | Ala | Phe | Lys | Ile | Pro | Leu |
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| Tyr | Leu | Gln | Met | Met | Phe | Pro | Gly | Leu | Val | Cys | Ile | Phe | Gly | Trp | Leu |
| | | | | 245 | | | | | 250 | | | | | 255 | |
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| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ala | Arg | Glu | Phe | Ile | Ile | Lys | Tyr | His | Leu | Asn | Gly | Asp | Arg | Thr | His |
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| Pro | Leu | Leu | Asp | Met | Glu | Met | Ala | Glu | Ile | Ile | Glu | Ser | Phe | His | Gly |
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| Thr | Asp | Leu | Ser | Asn | Pro | Leu | Glu | Met | Leu | Asp | Val | Arg | Ser | Leu | Phe |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Arg | Thr | Arg | Ser | Asp | Arg | Tyr | Arg | Ala | Met | Leu | Val | Ile | Leu | Met | Ala |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Trp | Phe | Gly | Gln | Phe | Ser | Gly | Asn | Asn | Val | Cys | Ser | Tyr | Tyr | Leu | Pro |
| | | | 340 | | | | | 345 | | | | | | 350 | |
| Thr | Met | Leu | Arg | Asn | Val | Gly | Met | Lys | Ser | Val | Ser | Leu | Asn | Val | Leu |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Met | Asn | Gly | Val | Tyr | Ser | Ile | Val | Thr | Trp | Ile | Ser | Ser | Ile | Cys | Gly |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Ala | Phe | Phe | Ile | Asp | Lys | Ile | Gly | Arg | Arg | Glu | Gly | Phe | Leu | Gly | Ser |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Ile | Ser | Gly | Ala | Ala | Leu | Ala | Leu | Thr | Gly | Leu | Ser | Ile | Cys | Thr | Ala |
| | | | | 405 | | | | | 410 | | | | | 415 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Tyr | Glu | Lys | Thr | Lys | Lys | Lys | Ser | Ala | Ser | Asn | Gly | Ala | Leu | Val |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Phe | Ile | Tyr | Leu | Phe | Gly | Gly | Ile | Phe | Ser | Phe | Ala | Phe | Thr | Pro | Met |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Gln | Ser | Met | Tyr | Ser | Thr | Glu | Val | Ser | Thr | Asn | Leu | Thr | Arg | Ser | Lys |
| | | 450 | | | | 455 | | | | | 460 | | | | |
| Ala | Gln | Leu | Leu | Asn | Phe | Val | Val | Ser | Gly | Val | Ala | Gln | Phe | Val | Asn |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Gln | Phe | Ala | Thr | Pro | Lys | Ala | Met | Lys | Asn | Ile | Lys | Tyr | Trp | Phe | Tyr |
| | | | | 485 | | | | | 490 | | | | | 495 | |
| Val | Phe | Tyr | Val | Phe | Phe | Asp | Ile | Phe | Glu | Phe | Ile | Val | Ile | Tyr | Phe |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Phe | Phe | Val | Glu | Thr | Lys | Gly | Arg | Ser | Leu | Glu | Glu | Leu | Glu | Val | Val |
| | | 515 | | | | 520 | | | | | | 525 | | | |
| Phe | Glu | Ala | Pro | Asn | Pro | Arg | Lys | Ala | Ser | Val | Asp | Gln | Ala | Phe | Leu |
| | 530 | | | | | 535 | | | | | 540 | | | | |
| Ala | Gln | Val | Arg | Ala | Thr | Leu | Val | Gln | Arg | Asn | Asp | Val | Arg | Val | Ala |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| Asn | Ala | Gln | Asn | Leu | Lys | Glu | Gln | Glu | Pro | Leu | Lys | Ser | Asp | Ala | Asp |
| | | | 565 | | | | | 570 | | | | | | 575 | |
| His | Val | Glu | Lys | Leu | Ser | Glu | Ala | Glu | Ser | Val | Lys | Lys | Leu | Leu | |
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<211> 1779

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<213> Artificial

<220>

<223> CDS LAC12-KTKKQ

<400> 31

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| cacaaggaca | ccttgggttaa | cgaccgcgac | cacaaggaag | ctttgaactc | tgacaacgac | 120 |
| aacacctctg | gtttgaagat | caacggtgtt | ccaatcgaag | acgctagaga | agaagttttg | 180 |
| ttgccagggt | acttgtctaa | gcaatactac | aagttgtacg | gtttgtgttt | catcacctac | 240 |
| ttgtgtgcta | ccatgcaagg | ttacgacggt | gctttgatgg | gttctatcta | caccgaagac | 300 |
| gcttacttga | agtactacca | cttgacatc | aactcttctt | ctggtaccgg | tttggttttc | 360 |
| tctatcttca | acgttgggtc | aatctgtggg | gctttcttcg | ttccattgat | ggactggaag | 420 |
| ggtagaaaagc | cagctatctt | gacggttgt | ttgggtgttg | ttatcggtgc | tatcatctct | 480 |
| tctttgacca | ccaccaagtc | tgctttgatc | ggtggtagat | ggttcgttgc | tttcttcgct | 540 |
| accatcgcta | acgctgctgc | tccaacctac | tgtgctgaag | ttgctccagc | tcatttgaga | 600 |
| ggtaagggtg | ctggtttgta | caacaccttg | tggctctgtt | gttctatcgt | tgctgctttc | 660 |
| tctacctacg | gtaccaacaa | gaacttccca | aactcttcta | aggctttcaa | gatccatttg | 720 |
| tacttgcaaa | tgatgttccc | aggtttggtt | tgtatcttcg | gttggttgat | cccagaatct | 780 |
| ccaagatggg | tggttggtgt | tggtagagaa | gaagaagcta | gagaattcat | catcaagtac | 840 |
| cacttgaacg | gtgacagaac | ccaccatttg | ttggacatgg | aaatggctga | aatcatcgaa | 900 |
| tctttccacg | gtaccgactt | gtctaaccba | ttggaaatgt | tggacgttag | atctttgttc | 960 |
| agaaccagat | ctgacagata | cagagctatg | ttggttatct | tgatggcttg | gttcggtcaa | 1020 |
| ttctctggta | acaacgtttg | ttcttactac | ttgccaacca | tggttgagaaa | cgttggtatg | 1080 |
| aagctgtgtt | ctttgaacgt | tttgatgaac | ggtgtttact | ctatcgttac | ctggatctct | 1140 |
| tctatctgtg | gtgctttctt | catcgacaag | atcggtagaa | gagaagggtt | cttgggttct | 1200 |
| atctctgggt | ctgctttggc | tttgaccggt | ttgtctatct | gtaccgctag | atacgaaaag | 1260 |
| accaagaaga | agtctgcttc | taacggtgct | ttggttttca | tctacttggt | cggtggtatc | 1320 |
| ttctctttcg | ctttcaccac | aatgcaatct | atgtactcta | ccgaagtttc | taccaacttg | 1380 |
| accagatcta | aggctcaatt | gttgaacttc | gttgtttctg | gtgttgctca | attcgttaac | 1440 |

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|------|
| caattcgcta | ccccaaaggc | tatgaagaac | atcaagtact | ggttctacgt | tttctacgtt | 1500 |
| ttcttcgaca | tcttcgaatt | catcgttatc | tactttcttct | tcgttgaaac | caagggtaga | 1560 |
| tctttggaag | aattggaagt | tgttttcgaa | gctccaaacc | caagaaaggc | ttctgttgac | 1620 |
| caagctttct | tggctcaagt | tagagctacc | ttggttcaaa | gaaacgacgt | tagagttgct | 1680 |
| aacgctcaaa | acttgaagga | acaagaacca | ttgaagtctg | acgctgacca | cgttgaaaag | 1740 |
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 <211> 592
 <212> PRT
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<220>
 <223> LAC12-KTKKQ

<400> 32

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| Met | Ala | Asp | His | Ser | Ser | Ser | Ser | Ser | Ser | Leu | Gln | Lys | Lys | Pro | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asn | Thr | Ile | Glu | His | Lys | Asp | Thr | Leu | Gly | Asn | Asp | Arg | Asp | His | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Ala | Leu | Asn | Ser | Asp | Asn | Asp | Asn | Thr | Ser | Gly | Leu | Lys | Ile | Asn |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Gly | Val | Pro | Ile | Glu | Asp | Ala | Arg | Glu | Glu | Val | Leu | Leu | Pro | Gly | Tyr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Ser | Lys | Gln | Tyr | Tyr | Lys | Leu | Tyr | Gly | Leu | Cys | Phe | Ile | Thr | Tyr |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Leu | Cys | Ala | Thr | Met | Gln | Gly | Tyr | Asp | Gly | Ala | Leu | Met | Gly | Ser | Ile |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Tyr | Thr | Glu | Asp | Ala | Tyr | Leu | Lys | Tyr | Tyr | His | Leu | Asp | Ile | Asn | Ser |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Ser | Gly | Thr | Gly | Leu | Val | Phe | Ser | Ile | Phe | Asn | Val | Gly | Gln | Ile |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Cys | Gly | Ala | Phe | Phe | Val | Pro | Leu | Met | Asp | Trp | Lys | Gly | Arg | Lys | Pro |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ala | Ile | Leu | Ile | Gly | Cys | Leu | Gly | Val | Val | Ile | Gly | Ala | Ile | Ile | Ser |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ser | Leu | Thr | Thr | Thr | Lys | Ser | Ala | Leu | Ile | Gly | Gly | Arg | Trp | Phe | Val |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ala | Phe | Phe | Ala | Thr | Ile | Ala | Asn | Ala | Ala | Ala | Pro | Thr | Tyr | Cys | Ala |
| | | | 180 | | | | 185 | | | | | | 190 | | |
| Glu | Val | Ala | Pro | Ala | His | Leu | Arg | Gly | Lys | Val | Ala | Gly | Leu | Tyr | Asn |
| | 195 | | | | | | 200 | | | | 205 | | | | |
| Thr | Leu | Trp | Ser | Val | Gly | Ser | Ile | Val | Ala | Ala | Phe | Ser | Thr | Tyr | Gly |
| | 210 | | | | 215 | | | | | | 220 | | | | |
| Thr | Asn | Lys | Asn | Phe | Pro | Asn | Ser | Ser | Lys | Ala | Phe | Lys | Ile | Pro | Leu |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Tyr | Leu | Gln | Met | Met | Phe | Pro | Gly | Leu | Val | Cys | Ile | Phe | Gly | Trp | Leu |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ile | Pro | Glu | Ser | Pro | Arg | Trp | Leu | Val | Gly | Val | Gly | Arg | Glu | Glu | Glu |
| | | | 260 | | | | 265 | | | | | | 270 | | |
| Ala | Arg | Glu | Phe | Ile | Ile | Lys | Tyr | His | Leu | Asn | Gly | Asp | Arg | Thr | His |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Pro | Leu | Leu | Asp | Met | Glu | Met | Ala | Glu | Ile | Ile | Glu | Ser | Phe | His | Gly |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Thr | Asp | Leu | Ser | Asn | Pro | Leu | Glu | Met | Leu | Asp | Val | Arg | Ser | Leu | Phe |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Thr | Arg | Ser | Asp | Arg | Tyr | Arg | Ala | Met | Leu | Val | Ile | Leu | Met | Ala | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Trp | Phe | Gly | Gln | Phe | Ser | Gly | Asn | Asn | Val | Cys | Ser | Tyr | Tyr | Leu | Pro | |
| | | | 340 | | | | 345 | | | | | | 350 | | | |
| Thr | Met | Leu | Arg | Asn | Val | Gly | Met | Lys | Ser | Val | Ser | Leu | Asn | Val | Leu | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Met | Asn | Gly | Val | Tyr | Ser | Ile | Val | Thr | Trp | Ile | Ser | Ser | Ile | Cys | Gly | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| Ala | Phe | Phe | Ile | Asp | Lys | Ile | Gly | Arg | Arg | Glu | Gly | Phe | Leu | Gly | Ser | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| Ile | Ser | Gly | Ala | Ala | Leu | Ala | Leu | Thr | Gly | Leu | Ser | Ile | Cys | Thr | Ala | |
| | | | 405 | | | | | | 410 | | | | | 415 | | |
| Arg | Tyr | Glu | Lys | Thr | Lys | Lys | Lys | Ser | Ala | Ser | Asn | Gly | Ala | Leu | Val | |
| | | 420 | | | | | | 425 | | | | | 430 | | | |
| Phe | Ile | Tyr | Leu | Phe | Gly | Gly | Ile | Phe | Ser | Phe | Ala | Phe | Thr | Pro | Met | |
| | 435 | | | | | 440 | | | | | 445 | | | | | |
| Gln | Ser | Met | Tyr | Ser | Thr | Glu | Val | Ser | Thr | Asn | Leu | Thr | Arg | Ser | Lys | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| Ala | Gln | Leu | Leu | Asn | Phe | Val | Val | Ser | Gly | Val | Ala | Gln | Phe | Val | Asn | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| Gln | Phe | Ala | Thr | Pro | Lys | Ala | Met | Lys | Asn | Ile | Lys | Tyr | Trp | Phe | Tyr | |
| | | | 485 | | | | | | 490 | | | | | 495 | | |
| Val | Phe | Tyr | Val | Phe | Phe | Asp | Ile | Phe | Glu | Phe | Ile | Val | Ile | Tyr | Phe | |
| | | 500 | | | | | | 505 | | | | | 510 | | | |
| Phe | Phe | Val | Glu | Thr | Lys | Gly | Arg | Ser | Leu | Glu | Glu | Leu | Glu | Val | Val | |
| | 515 | | | | | 520 | | | | | | 525 | | | | |
| Phe | Glu | Ala | Pro | Asn | Pro | Arg | Lys | Ala | Ser | Val | Asp | Gln | Ala | Phe | Leu | |
| | 530 | | | | | 535 | | | | | 540 | | | | | |
| Ala | Gln | Val | Arg | Ala | Thr | Leu | Val | Gln | Arg | Asn | Asp | Val | Arg | Val | Ala | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | |
| Asn | Ala | Gln | Asn | Leu | Lys | Glu | Gln | Glu | Pro | Leu | Lys | Ser | Asp | Ala | Asp | |
| | | | 565 | | | | | | 570 | | | | | 575 | | |
| His | Val | Glu | Lys | Leu | Ser | Glu | Ala | Glu | Ser | Val | Lys | Thr | Lys | Lys | Gln | |
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<211> 1773

<212> DNA

<213> Artificial

<220>

<223> CDS LAC12-KVD

<400> 33

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| cacaaggaca | ccttgggtaa | cgaccgcgac | cacaaggaag | ctttgaactc | tgacaacgac | 120 |
| aacacctctg | gtttgaagat | caacggtgtt | ccaatcgaag | acgctagaga | agaagttttg | 180 |
| ttgccagggt | acttgtctaa | gcaatactac | aagttgtacg | gtttgtgttt | catcacctac | 240 |
| ttgtgtgcta | ccatgcaagg | ttacgacggt | gctttgatgg | gttctatcta | caccgaagac | 300 |
| gcttacttga | agtactacca | cttggacatc | aactcttctt | ctggtaccgg | tttggttttc | 360 |
| tctatcttca | acgttggtca | aatctgtggt | gctttcttcg | ttccattgat | ggactggaag | 420 |
| ggtagaaagc | cagctatctt | gatcggttgt | ttgggtgttg | ttatcgggtgc | tatcatctct | 480 |
| tctttgacca | ccaccaagtc | tgctttgatc | ggtggtagat | ggttcgttgc | tttcttcgct | 540 |
| accatcgcta | acgctgctgc | tccaacctac | tgtgctgaag | ttgctccagc | tcacttgaga | 600 |
| ggtaagggtg | ctggtttgta | caacaccttg | tggtctgttg | gttctatcgt | tgctgctttc | 660 |
| tctacctacg | gtaccaacaa | gaacttccca | aactcttcta | aggctttcaa | gatccattg | 720 |

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tacttgcaaa | tgatgttccc | aggtttgggt | tgtatcttcg | gttggttgat | cccagaatct | 780 |
| ccaagatggg | tggttggtgt | tggtagagaa | gaagaagcta | gagaattcat | catcaagtac | 840 |
| cacttgaacg | gtgacagaac | ccaccattg | ttggacatgg | aaatggctga | aatcatcgaa | 900 |
| tctttccacg | gtaccgactt | gtctaacca | ttggaaatgt | tggaagcttag | atctttgttc | 960 |
| agaaccagat | ctgacagata | cagagctatg | ttggttatct | tgatggcttg | gttcgggtcaa | 1020 |
| ttctctggta | acaacgtttg | ttcttactac | ttgccaaacca | tggttgagaaa | cgttgggtatg | 1080 |
| aagtcgtgtt | ctttgaacgt | tttgatgaac | gggtgtttact | ctatcgttac | ctggatctct | 1140 |
| tctatctgtg | gtgctttctt | catcgacaag | atcggttagaa | gagaagggtt | cttgggttct | 1200 |
| atctctgggtg | ctgctttggc | tttgaccggg | ttgtctatct | gtaccgctag | atacgaaaag | 1260 |
| accaagaaga | agtctgcttc | taacgggtgct | ttgggttttca | tctacttggt | cggtgggtatc | 1320 |
| ttctctttcg | ctttcacc | aatgcaatct | atgtactcta | ccgaagtttc | taccaacttg | 1380 |
| accagatcta | aggctcaatt | gttgaacttc | gttggtttctg | gtgttgctca | attcggttaac | 1440 |
| caattcgcta | ccccaaaggc | tatgaagaac | atcaagtact | ggttctacgt | tttctacgtt | 1500 |
| ttcttcgaca | tcttcgaatt | catcgttatc | tacttcttct | tcgttgaaac | caagggtaga | 1560 |
| tctttggaag | aattggaagt | tggtttcgaa | gctccaaacc | caagaaaggc | ttctgttgac | 1620 |
| caagctttct | tggtctcaagt | tagagctacc | ttggttcaaa | gaaacgacgt | tagagttgct | 1680 |
| aacgctcaaa | acttgaagga | acaagaacca | ttgaagtctg | acgctgacca | cgttgaaaag | 1740 |
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<210> 34
 <211> 590
 <212> PRT
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<220>
 <223> LAC12-KVD

<400> 34

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| Met | Ala | Asp | His | Ser | Ser | Ser | Ser | Ser | Ser | Leu | Gln | Lys | Lys | Pro | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asn | Thr | Ile | Glu | His | Lys | Asp | Thr | Leu | Gly | Asn | Asp | Arg | Asp | His | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Ala | Leu | Asn | Ser | Asp | Asn | Asp | Asn | Thr | Ser | Gly | Leu | Lys | Ile | Asn |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Gly | Val | Pro | Ile | Glu | Asp | Ala | Arg | Glu | Glu | Val | Leu | Leu | Pro | Gly | Tyr |
| | | | 50 | | | 55 | | | | | 60 | | | | |
| Leu | Ser | Lys | Gln | Tyr | Tyr | Lys | Leu | Tyr | Gly | Leu | Cys | Phe | Ile | Thr | Tyr |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Leu | Cys | Ala | Thr | Met | Gln | Gly | Tyr | Asp | Gly | Ala | Leu | Met | Gly | Ser | Ile |
| | | | | 85 | | | | 90 | | | | | | 95 | |
| Tyr | Thr | Glu | Asp | Ala | Tyr | Leu | Lys | Tyr | Tyr | His | Leu | Asp | Ile | Asn | Ser |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Ser | Gly | Thr | Gly | Leu | Val | Phe | Ser | Ile | Phe | Asn | Val | Gly | Gln | Ile |
| | | | 115 | | | | 120 | | | | | | 125 | | |
| Cys | Gly | Ala | Phe | Phe | Val | Pro | Leu | Met | Asp | Trp | Lys | Gly | Arg | Lys | Pro |
| | | | | | | 135 | | | | | 140 | | | | |
| Ala | Ile | Leu | Ile | Gly | Cys | Leu | Gly | Val | Val | Ile | Gly | Ala | Ile | Ile | Ser |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ser | Leu | Thr | Thr | Thr | Lys | Ser | Ala | Leu | Ile | Gly | Gly | Arg | Trp | Phe | Val |
| | | | | | 165 | | | | 170 | | | | | | 175 |
| Ala | Phe | Phe | Ala | Thr | Ile | Ala | Asn | Ala | Ala | Ala | Pro | Thr | Tyr | Cys | Ala |
| | | | | | | | | 185 | | | | | 190 | | |
| Glu | Val | Ala | Pro | Ala | His | Leu | Arg | Gly | Lys | Val | Ala | Gly | Leu | Tyr | Asn |
| | | | | | | | 200 | | | | | 205 | | | |
| Thr | Leu | Trp | Ser | Val | Gly | Ser | Ile | Val | Ala | Ala | Phe | Ser | Thr | Tyr | Gly |
| | | | | | | | 215 | | | | | | | | 220 |

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|------|
| atggctgacc | actcttcctc | ttcgtcttct | ttgcaaaaga | agccaatcaa | caccatcgaa | 60 |
| cacaaggaca | ccttgggtaa | cgaccgcgac | cacaaggaag | ctttgaactc | tgacaacgac | 120 |
| aacacctctg | gtttgaagat | caacggtgtt | ccaatcgaag | acgctagaga | agaagttttg | 180 |
| ttgccagggt | acttgtctaa | gcaatactac | aagttgtacg | gtttgtgttt | catcacctac | 240 |
| ttgtgtgcta | ccatgcaagg | ttacgacggt | gctttgatgg | gttctatcta | caccgaagac | 300 |
| gcttacttga | agtactacca | cttggacatc | aactcttctt | ctggtagcgg | tttggttttc | 360 |
| tctatcttca | acgttgggtc | aatctgtggt | gctttcttcg | ttccattgat | ggactggaag | 420 |
| ggtagaaagc | cagctatctt | gatcggttgt | ttgggtgttg | ttatcgggtg | tatcatctct | 480 |
| tctttgacca | ccaccaagtc | tgctttgatc | ggtaggtgat | ggttcgttgc | tttcttcgct | 540 |
| accatcgcta | acgctgctgc | tccaacctac | tgtgctgaag | ttgctccagc | tcacttgaga | 600 |
| ggtaagggtg | ctggtttgta | caacaccttg | tggtctgttg | gttctatcgt | tgctgctttc | 660 |
| tctacctacg | gtaccaacaa | gaacttccca | aactcttcta | aggctttcaa | gatcccattg | 720 |
| tacttgcaaa | tgatgttccc | aggtttggtt | tgtatcttcg | gttggttgat | cccagaatct | 780 |
| ccaagatggg | tggttgggtg | tggtagagaa | gaagaagcta | gagaattcat | catcaagtac | 840 |
| cacttgaacg | gtacagaaac | ccaccatttg | ttggacatgg | aaatggctga | aatcatcgaa | 900 |
| tctttccacg | gtaccgactt | gtctaaccac | ttggaaatgt | tggacgttag | atctttgttc | 960 |
| agaaccagat | ctgacagata | cagagctatg | ttggttatct | tgatggcttg | gttcgggtcaa | 1020 |
| ttctctggta | acaacgtttg | ttcttactac | ttgccaacca | tgttgagaaa | cgttgggtatg | 1080 |
| aagtctgttt | ctttgaacgt | tttgatgaac | gggtgtttact | ctatcgttac | ctggatctct | 1140 |
| tctatctgtg | gtgctttctt | catcgacaag | atcggtagaa | gagaagggtt | cttgggttct | 1200 |
| atctctgggt | ctgctttggc | tttgaccggt | ttgtctatct | gtaccgctag | atacgaaaag | 1260 |
| accaagaaga | agtctgcttc | taacggtgct | ttggttttca | tctacttggt | cgggtggtatc | 1320 |
| ttctctttcg | ctttcacccc | aatgcaatct | atgtactcta | ccgaagtttc | taccaacttg | 1380 |
| accagatcta | aggctcaatt | gttgaacttc | gttgtttctg | gtgttgctca | attcgttaac | 1440 |
| caattcgcta | ccccaaaggc | tatgaagaac | atcaagtact | ggttctacgt | tttctacgtt | 1500 |
| ttcttcgaca | tcttcgaatt | catcgttatc | tacttcttct | tcgttgaaac | caagggtaga | 1560 |
| tctttggaag | aattggaagt | tgttttcgaa | gctccaaacc | caagaaaggc | ttctgttgac | 1620 |
| caagctttct | tggctcaagt | tagagctacc | ttggttcaaa | gaaacgacgt | tagagttgct | 1680 |
| aacgctcaaa | acttgaagga | acaagaacca | ttgaagtctg | acgctgacca | cgttgaaaag | 1740 |
| ttgtctgaag | ctgaatctgt | ttacaagggt | ttgtga | | | 1776 |

<210> 36

<211> 591

<212> PRT

<213> Artificial

<220>

<223> LAC12-YKGL

<400> 36

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | His | Ser | Ser | Ser | Ser | Ser | Leu | Gln | Lys | Lys | Pro | Ile |
| 1 | | | 5 | | | | | 10 | | | | | 15 | |
| Asn | Thr | Ile | Glu | His | Lys | Asp | Thr | Leu | Gly | Asn | Asp | Arg | Asp | His |
| | | 20 | | | | | 25 | | | | | 30 | | Lys |
| Glu | Ala | Leu | Asn | Ser | Asp | Asn | Asp | Asn | Thr | Ser | Gly | Leu | Lys | Ile |
| | | 35 | | | | | 40 | | | | 45 | | | Asn |
| Gly | Val | Pro | Ile | Glu | Asp | Ala | Arg | Glu | Glu | Val | Leu | Leu | Pro | Gly |
| | | 50 | | | | 55 | | | | 60 | | | | Tyr |
| Leu | Ser | Lys | Gln | Tyr | Tyr | Lys | Leu | Tyr | Gly | Leu | Cys | Phe | Ile | Thr |
| 65 | | | | | 70 | | | | 75 | | | | | 80 |
| Leu | Cys | Ala | Thr | Met | Gln | Gly | Tyr | Asp | Gly | Ala | Leu | Met | Gly | Ser |
| | | | | 85 | | | | | 90 | | | | | 95 |
| Tyr | Thr | Glu | Asp | Ala | Tyr | Leu | Lys | Tyr | Tyr | His | Leu | Asp | Ile | Asn |
| | | | 100 | | | | | 105 | | | | | 110 | Ser |
| Ser | Ser | Gly | Thr | Gly | Leu | Val | Phe | Ser | Ile | Phe | Asn | Val | Gly | Gln |
| | | | 115 | | | | 120 | | | | | 125 | | Ile |

| | | | | | | | | | | | | | | | |
|------------|-----|-----|-----|-----|------------|------------|-----|-----|-----|-----|------------|-----|-----|-----|------------|
| Cys 130 | Gly | Ala | Phe | Phe | Val | Pro 135 | Leu | Met | Asp | Trp | Lys 140 | Gly | Arg | Lys | Pro |
| Ala 145 | Ile | Leu | Ile | Gly | Cys 150 | Leu | Gly | Val | Val | Ile | Gly | Ala | Ile | Ile | Ser 160 |
| Ser | Leu | Thr | Thr | Thr | Lys | Ser | Ala | Leu | Ile | Gly | Gly | Arg | Trp | Phe | Val 175 |
| Ala | Phe | Phe | Ala | Thr | Ile | Ala | Asn | Ala | Ala | Ala | Pro | Thr | Tyr | Cys | Ala |
| Glu | Val | Ala | Pro | Ala | His | Leu | Arg | Gly | Lys | Val | Ala | Gly | Leu | Tyr | Asn |
| Thr | Leu | Trp | Ser | Val | Gly | Ser | Ile | Val | Ala | Ala | Phe | Ser | Thr | Tyr | Gly |
| Thr 225 | Asn | Lys | Asn | Phe | Pro 230 | Asn | Ser | Ser | Lys | Ala | Phe | Lys | Ile | Pro | Leu 240 |
| Tyr | Leu | Gln | Met | Met | Phe | Pro | Gly | Leu | Val | Cys | Ile | Phe | Gly | Trp | Leu |
| Ile | Pro | Glu | Ser | Pro | Arg | Trp | Leu | Val | Gly | Val | Gly | Arg | Glu | Glu | Glu |
| Ala | Arg | Glu | Phe | Ile | Ile | Lys | Tyr | His | Leu | Asn | Gly | Asp | Arg | Thr | His |
| Pro | Leu | Leu | Asp | Met | Glu | Met | Ala | Glu | Ile | Ile | Glu | Ser | Phe | His | Gly |
| Thr 305 | Asp | Leu | Ser | Asn | Pro 310 | Leu | Glu | Met | Leu | Asp | Val | Arg | Ser | Leu | Phe 320 |
| Arg | Thr | Arg | Ser | Asp | Arg | Tyr | Arg | Ala | Met | Leu | Val | Ile | Leu | Met | Ala |
| Trp | Phe | Gly | Gln | Phe | Ser | Gly | Asn | Asn | Val | Cys | Ser | Tyr | Tyr | Leu | Pro |
| Thr | Met | Leu | Arg | Asn | Val | Gly | Met | Lys | Ser | Val | Ser | Leu | Asn | Val | Leu |
| Met | Asn | Gly | Val | Tyr | Ser | Ile | Val | Thr | Trp | Ile | Ser | Ser | Ile | Cys | Gly |
| Ala 385 | Phe | Phe | Ile | Asp | Lys 390 | Ile | Gly | Arg | Arg | Glu | Gly | Phe | Leu | Gly | Ser 400 |
| Ile | Ser | Gly | Ala | Ala | Leu | Ala | Leu | Thr | Gly | Leu | Ser | Ile | Cys | Thr | Ala |
| Arg | Tyr | Glu | Lys | Thr | Lys | Lys | Lys | Ser | Ala | Ser | Asn | Gly | Ala | Leu | Val |
| Phe | Ile | Tyr | Leu | Phe | Gly | Gly | Ile | Phe | Ser | Phe | Ala | Phe | Thr | Pro | Met |
| Gln | Ser | Met | Tyr | Ser | Thr | Glu | Val | Ser | Thr | Asn | Leu | Thr | Arg | Ser | Lys |
| Ala 465 | Gln | Leu | Leu | Asn | Phe 470 | Val | Val | Ser | Gly | Val | Ala | Gln | Phe | Val | Asn 480 |
| Gln | Phe | Ala | Thr | Pro | Lys | Ala | Met | Lys | Asn | Ile | Lys | Tyr | Trp | Phe | Tyr |
| Val | Phe | Tyr | Val | Phe | Phe | Asp | Ile | Phe | Glu | Phe | Ile | Val | Ile | Tyr | Phe |
| Phe | Phe | Val | Glu | Thr | Lys | Gly | Arg | Ser | Leu | Glu | Glu | Leu | Glu | Val | Val |
| Phe | Glu | Ala | Pro | Asn | Pro | Arg | Lys | Ala | Ser | Val | Asp | Gln | Ala | Phe | Leu |
| Ala 545 | Gln | Val | Arg | Ala | Thr 550 | Leu | Val | Gln | Arg | Asn | Asp | Val | Arg | Val | Ala 560 |
| Asn | Ala | Gln | Asn | Leu | Lys | Glu | Gln | Glu | Pro | Leu | Lys | Ser | Asp | Ala | Asp |

His Val Glu Lys Leu Ser Glu Ala Glu Ser Val Tyr Lys Gly Leu
580 585 590

<210> 37
<211> 78
<212> DNA
<213> Artificial

<220>
<223> Coding for Tag "Rn_ST6GAL1"

<400> 37
atgatccaca ccaacttgaa gaagaagttc tctttgttca tcttggtttt cttgttgttc 60
gctgttatct gtgtttgg 78

<210> 38
<211> 26
<212> PRT
<213> Artificial

<220>
<223> Tag "Rn_ST6GAL1"

<400> 38
Met Ile His Thr Asn Leu Lys Lys Lys Phe Ser Leu Phe Ile Leu Val
1 5 10 15
Phe Leu Leu Phe Ala Val Ile Cys Val Trp
20 25

<210> 39
<211> 60
<212> DNA
<213> Artificial

<220>
<223> Coding for Tag "Sce_TMN3"

<400> 39
ttgtcttact tgaccgcttc ttggttcac aacaagatct accaccaaaa ggttaacttg 60

<210> 40
<211> 20
<212> PRT
<213> Artificial

<220>
<223> Tag "Sce_TMN3"

<400> 40
Leu Ser Tyr Leu Thr Ala Ser Trp Phe Ile Asn Lys Ile Tyr His Gln
1 5 10 15
Lys Val Asn Leu
20

<210> 41
<211> 306

<212> DNA
<213> Artificial

<220>
<223> Coding for Tag "Sce_TP05"

<400> 41
aagtggggta agtacaactt cagattgcc a ttggctgacg acatcaaggc tccaatccca 60
tctgacgctg aagaaaccgt tttcgaattg gaagactcta acgttgaaca caccttgaac 120
tctggtacca ccgttaagga atctgttgaa aacaactctg aagaagggtt catcaagggt 180
cacccaaagt cttctaccga aaaccattc gaagaaaacg aagaaaacgt tatcaccgac 240
tacggtgacg aacaccacac cgctgaacaa gaattcgact tggctgacga cagaagatac 300
gacatc 306

<210> 42
<211> 102
<212> PRT
<213> S. cerevisiae

<220>
<223> Tag "Sce_TP05"

<400> 42
Lys Trp Gly Lys Tyr Asn Phe Arg Leu Pro Leu Ala Asp Asp Ile Lys
1 5 10 15
Ala Pro Ile Pro Ser Asp Ala Glu Glu Thr Val Phe Glu Leu Glu Asp
20 25 30
Ser Asn Val Glu His Thr Leu Asn Ser Gly Thr Thr Val Lys Glu Ser
35 40 45
Val Glu Asn Asn Ser Glu Glu Gly Phe Ile Lys Val His Pro Lys Ser
50 55 60
Ser Thr Glu Asn Pro Phe Glu Glu Asn Glu Glu Asn Val Ile Thr Asp
65 70 75 80
Tyr Gly Asp Glu His His Thr Ala Glu Gln Glu Phe Asp Leu Ala Asp
85 90 95
Asp Arg Arg Tyr Asp Ile
100

<210> 43
<211> 45
<212> DNA
<213> Artificial

<220>
<223> Coding for Tag "Sce_ALG6"

<400> 43
tactacaaga tcttcacctc tggttctaag tctatgaagg acttg 45

<210> 44
<211> 15
<212> PRT
<213> S. cerevisiae

<220>
<223> Tag "Sce_ALG6"

<400> 44
Tyr Tyr Lys Ile Phe Thr Ser Gly Ser Lys Ser Met Lys Asp Leu
1 5 10 15

<210> 45
<211> 42
<212> DNA
<213> Artificial

<220>
<223> Coding for Tag "Hsa_ALG6"

<400> 45
atgtgggact ctaagtctgg tagaaaccaa aagaagatct ct

42

<210> 46
<211> 14
<212> PRT
<213> H. sapiens

<220>
<223> Tag "Hsa_ALG6"

<400> 46
Met Trp Asp Ser Lys Ser Gly Arg Asn Gln Lys Lys Ile Ser
1 5 10

<210> 47
<211> 12
<212> DNA
<213> Artificial

<220>
<223> Coding for Tag "KKLL"

<400> 47
aagaagttgt tg

12

<210> 48
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Tag "KKLL"

<400> 48
Lys Lys Leu Leu
1

<210> 49
<211> 15
<212> DNA
<213> Artificial

<220>
<223> Coding for Tag "KTKKQ"

<400> 49
aagaccaaga agcaa

15

<210> 50
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Tag "KTKKQ"

<400> 50
Lys Thr Lys Lys Gln
1 5

<210> 51
<211> 12
<212> DNA
<213> Artificial

<220>
<223> Coding for Tag "YKGL"

<400> 51
tacaagggtt tg

12

<210> 52
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Tag "YKGL"

<400> 52
Tyr Lys Gly Leu
1

<210> 53
<211> 9
<212> DNA
<213> Artificial

<220>
<223> Coding for Tag "KVD"

<400> 53
aaggttgac

9

<210> 54
<211> 3
<212> PRT
<213> Artificial

<220>
<223> Tag "KVD"

<400> 54
Lys Val Asp
1

<210> 55
<211> 500
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter PGK1

<400> 55
tgtttgcaaa aagaacaaaa ctgaaaaaac ccagacacgc tcgacttcct gtcttcctat 60
tgattgcagc ttccaatttc gtcacacaac aagggtcctag cgacggctca caggttttgt 120
aacaagcaat cgaaggttct ggaatggcgg gaaagggttt agtaccacat gctatgatgc 180
ccactgtgat ctccagagca aagttcgttc gatcgtactg ttactctctc tctttcaaac 240
agaattgtcc gaatcgtgtg acaacaacag cctgtttctca cacactcttt tcttctaacc 300
aaggggggtgg tttagtttag tagaacctcg tgaaacttac atttacatat atataaactt 360
gcataaattg gtcaatgcaa gaaatacata tttgggtcttt tctaattcgt agtttttcaa 420
gttcttagat gctttctttt tctctttttt acagatcatc aaggaagtaa ttatctactt 480
tttacaacaa atataaaaaca 500

<210> 56
<211> 416
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter ATG5

<400> 56
gtaccggata acagagtaac tggtaaaaaac ggcaaaaaaat actgtaagga agttgtctat 60
atatgtacat atggatattg cgggtataata aaaaagcttt aaaattataa agaaacccga 120
cttttatcac atataattat attataaaaa aataatggca tctgtatgaa ctgcgcatta 180
agctcacttt tttctaataga tcgaagtttt gtccggttat ccaactgtgg caagaacatc 240
gcgaggcgga gctaaacaca gaatttttgt agcgcgatga gaaacataac gcctcttttag 300
ataaattatc atcacctttt ttactactaaa taatgaagta gcatgctcag aagtgcgaat 360
gaatttttgt tcttttggtt ctagaagaac ggagatagga aacctatgat gtaagt 416

<210> 57
<211> 500
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter ALG5

<400> 57
caatatatta ttatTTTTTTT acattttattg cgatgctgct gaaaattttt tttccacctt 60
gaaacttttc tttttccatt gaaaaattag atgtgggtgtt tgggtttatt ccatttgatc 120
ttgtaacttc tatactagtc acaactaaca agtccaaagt caagtgtaca tagttatcct 180

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| attttcaccg | ttatcacttc | agtacctttt | aatttatata | tattaatgca | catggctctg | 240 |
| ttgtatcttt | cgaagcagt | tatgccattt | ttttcatgag | aaagcgaat | ttggcgtatt | 300 |
| cgaaaaaaag | tgtaaacaag | aagaaaacgt | gccaattttc | aaggctttat | cgcaattaaa | 360 |
| gtggcacaaa | ggaccatagt | cactgtggaa | aggtagtggt | atctaattgg | atgctgtaag | 420 |
| gatagattag | gtgcttttga | taacgtaaga | aagggacaaa | aacagagagg | cagccaaaaa | 480 |
| ttacacaaag | cacaacaaaa | | | | | 500 |

<210> 58
 <211> 251
 <212> DNA
 <213> *S. cerevisiae*

<220>
 <223> promoter ALG2

| | |
|-------------|------------|
| <400> 58 | |
| taaatgtata | ttcttgtaaa |
| tattataaca | tatatacgaa |
| agggtcacaa | tcacagatac |
| 60 | |
| aatttataga | tcgagagcct |
| tgcgatatagc | ttcttttttt |
| ataaacaagt | gcctggctag |
| 120 | |
| atgaacgcgc | gaacaacaaa |
| ataaatgatg | tattcatttt |
| aacatcaaaa | gattacgttc |
| 180 | |
| gccatttaag | aagtcacgaa |
| atagatacag | tagtaaagac |
| agataaaaaa | gagtcgatta |
| 240 | |
| gacaagcaaa | a |
| 251 | |

<210> 59
 <211> 313
 <212> DNA
 <213> *S. cerevisiae*

<220>
 <223> promoter OST6

| | |
|-------------|-------------|
| <400> 59 | |
| taaaaaatac | atccagcatg |
| ataccagctt | gcttccgcaa |
| acgaaacata | acttaaggta |
| 60 | |
| ccgcaattca | aaaaggcatt |
| catacgtaca | aatattaact |
| atatctgaca | ttatttagac |
| 120 | |
| tatcacaagc | agtattttatt |
| tattttattta | cttattttatt |
| cattttattca | tttccttttt |
| 180 | |
| agtcttttat | gccagtgagc |
| tactgtcgcg | aattgaaaac |
| tgcaaaaaaa | taaaatagga |
| 240 | |
| acttggattc | agaagttttg |
| ataataaaa | tgcatgtaga |
| tgagagccgc | gaactgaatc |
| 300 | |
| atacaaaaaa | aat |
| 313 | |

<210> 60
 <211> 280
 <212> DNA
 <213> *S. cerevisiae*

<220>
 <223> promoter TP05

| | |
|------------|------------|
| <400> 60 | |
| tttgctatgt | taggagctat |
| tgtgtatcgc | ttctgtaaaa |
| gcagctagca | atcgctagcc |
| 60 | |
| gttggcaagt | aatgccccaa |
| agccttggtt | tctgccactt |
| tgaaattttt | caggcctttc |
| 120 | |
| cggcatataa | atttccgcaa |
| tgaggcttta | acaatcatta |
| atcatcccat | aaggataagc |
| 180 | |
| caaaagaaca | gatcatcaat |
| ttgacgaaga | acataccagt |
| ccgtgtattt | gtttgccatt |
| 240 | |
| gtacaataaa | ataaataaaa |
| ataagtcaaa | taaatgaaaa |
| 280 | |

<210> 61
 <211> 383
 <212> DNA

<213> *S. cerevisiae*

<220>

<223> promoter ALG6

<400> 61

| | | | | | | |
|------------|------------|-------------|-------------|-------------|------------|-----|
| ttatgtaaaa | caagcgtatt | tttttatttta | taaatttatgg | taatttttcat | ttaagacctc | 60 |
| taaattcatc | taatcgaata | tctgtgtcat | ggagtttatgg | ctcccccattg | cacaccattt | 120 |
| tctctttttt | tgtttctgtg | tttcccttca | tctcctttat | tatgaaaagt | acaagtttta | 180 |
| tataatttca | acgtcggagg | ttatccggaa | atctatagtt | gaatttttgc | aggattatac | 240 |
| ttcgctcgaa | tattgtgcgt | gttaaatact | cagcgagaac | aatacttcca | agttagaaaa | 300 |
| gggatttgct | catgttaaag | caatggcact | ccgaatggac | ggtgtcagga | attcttttct | 360 |
| tcacatcagg | cttcgcatag | aaa | | | | 383 |

<210> 62

<211> 500

<212> DNA

<213> *S. cerevisiae*

<220>

<223> promoter RRN5

<400> 62

| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|-----|
| caatcggatg | gagttcaatg | cggaatctag | tgaattctgc | ttttcgaaga | caaggagttt | 60 |
| cgagccgaaa | tcgaggttgt | tatctccagt | ttccttatgg | ctacgtttct | tagacggcct | 120 |
| gtgtctaggc | tgcttctgat | catttttcac | tagcccagat | tgggtagggg | tcaagacgac | 180 |
| gaatttcaga | ttttgcggca | gtttcttctt | cccatgaagg | ggcgagcttg | ggcctgagct | 240 |
| tgaataaaga | cggtaagtaa | gacgggagag | ctttttgttg | aattttccaca | tatgcttact | 300 |
| ctatatattt | tccagtgcct | tcaagctccg | tatatattat | gtactagttt | tattacatta | 360 |
| aagatacata | actttttttt | tttttttcag | ttcactgaaa | taagaaaagg | cgggcgagggt | 420 |
| gaaaaacaaa | aaaaaaagta | tagagaaaca | gaagtggaag | aagagctagg | aaagcacagc | 480 |
| gcatacgacg | gtcacctagg | | | | | 500 |

<210> 63

<211> 305

<212> DNA

<213> *S. cerevisiae*

<220>

<223> promoter ALG8

<400> 63

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ggcttggtat | tgcaggatgt | atgaaagttt | ataaaatccc | tgctgcaa | taagagatat | 60 |
| atggtttcgt | tcactacgta | gttatagtaa | ataacctttg | cttaacccat | ttttcaaagc | 120 |
| atttttaaaa | tttactgtta | tcacttagtt | gttcttagcg | gacaacttcc | gaaaagttaa | 180 |
| atttcatttt | tcaaaacgac | aatagtggta | tagaattata | gaataacata | cgttaaaaat | 240 |
| agctgaagtt | cattacagtt | ctgtagtggt | cagcaaggca | tttgacgtct | attggatagc | 300 |
| ctacg | | | | | | 305 |

<210> 64

<211> 500

<212> DNA

<213> *S. cerevisiae*

<220>

<223> promoter CDC19

<400> 64
acagattggg agattttcat agtagaattc agcatgatag ctacgtaaat gtgttccgca 60
ccgtcacaaa gtgttttcta ctgttctttc ttctttcgtt cattcagttg agttgagtga 120
gtgctttgtt caatggatct tagctaaaat gcatattttt tctcttggtg aatgaatgct 180
tgtgatgtct tccaagtgat ttcctttcct tcccatatga tgctaggtag ctttagtgtc 240
ttcctaataaa aaaaaaaagg ctgcgccatca aaacgatatt cgttggcctt tttttctgaa 300
ttataaatac tctttggtaa cttttcattt ccaagaacct cttttttcca gttatatcat 360
gggtcccttt caaagttatt ctctactctt tttcatattc attctttttc atcctttggt 420
tttttattct taacttgttt attattctct cttgtttcta tttacaagac accaatcaaa 480
acaaataaaa catcatcaca 500

<210> 65
<211> 500
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter NUP60

<400> 65
aataaatatt ccattgaagt actgttactg aaatgagatg aactgttcag aatgtagaaa 60
tggcgccaga aatcaatcat tgttttagcaa aaacaccttt cgtctgctgc ctcggtgtgt 120
ttttcaaatt atttcagcag gtaaattaag atagttattc gagtgattgc caaatatcat 180
gttctacttc gaagacttat agctaattaa ttttttcata atgaagggtg cgttaattgt 240
tctgattagt aacatgaaac tcaaaaatca tcaaaaaaag aaaagctaaa tgtatacttt 300
tttgtctaca ttagttacct tttattacat gagaaagtta tttttcttct tttttttttt 360
ttttttttga aactttttcc tctcggaaaa taaaagatat atttacaagt gaaagcttat 420
tgtaatgtgt acttttaaac atcaaataac agacctttac atcaaataag caccgcaaga 480
tatcctaata tcgacatcca 500

<210> 66
<211> 500
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter SNF7

<400> 66
ctagtatttt cgcctctata aatggttgtt attcgagtat aatattttcaa ccgcatcaaa 60
gaaagaggta gatagcttgc gttcaacacc gttcttttct ttccccctta atttagcgct 120
tggcggttat gctatgggtga cagttaactt ttttaattat aggatgactt gtcataattgt 180
tatatgccgc atacttatgt aaagtagtta ttgaggtggg ggtgagcaga gtaacgacaa 240
cgatggagtt ccgtaactaa ccaatgctta atgttggtaa gtaatagcaa atatatatac 300
tacatagctt ttgttatatg catcatttta tacgattcat gttcgaccct tttgataaaa 360
gatgggattt ttaaataagt cgggtgggtga tttcgaatca tgaatagttg gcagagcagg 420
ggaagtacga gcttctaaag ggtaagatat tgtatttcgg acggaagcag cagaaacata 480
acagtattga taaataaggc 500

<210> 67
<211> 254
<212> DNA
<213> *S. cerevisiae*

<220>

<223> promoter GIP4

<400> 67

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ggacaatgaa | tacgttgcgc | ttgctatgtc | tttggcgcaa | attttcaatg | tttaactaat | 60 |
| acttttgacg | atctttctta | tagatgctgt | gggaaagacc | cttaaaaatg | tctgttaccc | 120 |
| tgcaatcaat | ggttgaaaca | gcaggaagac | gcataataaa | ggcatatgtt | tgaagtttgt | 180 |
| tagcgaatga | acaatgataa | aaggagtgat | tggaagctga | aggttgagga | tttagactag | 240 |
| ttttatatta | caac | | | | | 254 |

<210> 68

<211> 200

<212> DNA

<213> *S. cerevisiae*

<220>

<223> terminator RPL18B

<400> 68

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| tctagtatgg | tttgaaacct | tacaatTTTT | cttctttgtt | cctttttcct | tgtttcagtg | 60 |
| tatattaggt | tgggaaagag | ggatttttcc | ataccatatg | actgactaca | atatatacat | 120 |
| gtataataac | ttcataatct | aaacctatca | gttcagtatc | aagtcagcta | ttccgcctta | 180 |
| tgcataaacc | tacaaactat | | | | | 200 |

<210> 69

<211> 99

<212> DNA

<213> *S. cerevisiae*

<220>

<223> terminator GCV3

<400> 69

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|----|
| acaaaagctta | tacgtacgta | aagtaatttc | atatatatgt | atatatatgt | aggggaaata | 60 |
| aaacaataaa | ctcaacgtgt | acacttatgc | ttatgcatt | | | 99 |

<210> 70

<211> 200

<212> DNA

<213> *S. cerevisiae*

<220>

<223> terminator GIP2

<400> 70

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| aggcaaccag | aaggaaggag | atgaagaatg | gacataaaaa | gcaaaatgac | ttgctagatc | 60 |
| ttggcctgag | ttactctcat | gattgggacc | gaactccgat | aaataactct | aaaacatgct | 120 |
| agaatatttc | aagtaaatat | acataaatca | caaataagca | aataaacaga | taaatatctc | 180 |
| acaagaaatc | gggagccgat | | | | | 200 |

<210> 71

<211> 200

<212> DNA

<213> *S. cerevisiae*

<220>

<223> terminator FUS3

<400> 71
ccatcattat cattaataaata tcaacccgaa gaacaatgta tacatataca tatacgtaca 60
catatacata tgtacatatg acatacgtat tagccgctga ggacgcggac gtataaaaagg 120
acaatactta tatggagcta aggggagcag ttacgcaact ccgtgatcgc gcgccacggg 180
ccgtcggcgg ctgttaattg 200

<210> 72
<211> 200
<212> DNA
<213> *S. cerevisiae*

<220>
<223> terminator RPL21B

<400> 72
tctacctcgt ttggtatatt tatcgaagtt atcacattcc tatatatattgt atcctttaca 60
taagaattgc gtatagatag atactataac aattttacatg atattatttg attaaggtgc 120
atattaccat cttctcagca ggtattcaaa catatctgcc aatgtatgac cttgacatat 180
gtgaagagat tactgtggag 200

<210> 73
<211> 200
<212> DNA
<213> *S. cerevisiae*

<220>
<223> terminator RPL25

<400> 73
tctaattgggt ttaattaata aatttaatat tattttttaaa tttttcttta aatatacaat 60
aaatctttca taacatgtta aattcatgat taagcgtaaa taaagtgtag tggcagagtg 120
cacgggggttt cctgtgcctt acaaagtagg taccaatttg cgtattgcag cgagggttcc 180
ggttactatt tataattacg 200

<210> 74
<211> 200
<212> DNA
<213> *S. cerevisiae*

<220>
<223> terminator RPL27B

<400> 74
gaagcttttt tccgaaacct aacttttttc tgtgtactat tattattttc ataatgcagt 60
ttatccttca cataattaaa aattcatatt gtataaacta aaacaaacac taccactaaa 120
tatttggcca tctatctgcc atattgggtcg taacacaaaa tgcccaatgg agcctggtaa 180
gttccttatt atttaaccct 200

<210> 75
<211> 193
<212> DNA
<213> *S. cerevisiae*

<220>
<223> terminator FUM1

<400> 75
acgagctaaa tacctaataa tatacaagtt ttttatgtct tattatatga aggaaaataa 60
ggaagtggag agaatttgtg attcagcaat ggtccctccg ctaagggtccc gcctctggcc 120
agttatgtca gaagaggagc ataggcatac attccatttt tgatggctta atggggccca 180
taaatttaca tca 193

<210> 76
<211> 200
<212> DNA
<213> *S. cerevisiae*

<220>
<223> terminator HPT1

<400> 76
tagacatatc atatccttca gtaacttgaa tcatacagca gaatttgtac aatagacaac 60
gcatataact gcgaccatat gtatacgtat aactaattat tatctcaaag tttatttcct 120
tagcctcacc ggtaacctgt gaggcgcgat tacgttttcc ctctgttcac caccacgtaa 180
cgcgatattt gacacatacg 200

<210> 77
<211> 200
<212> DNA
<213> *S. cerevisiae*

<220>
<223> terminator NDE2

<400> 77
tccttgtttt atatattcat tgttccaatt caaattgttt actatcattt acgtattata 60
accagtattt ccctttattg gtcattggaag attcgcgtta cccttactcg ttaacagtga 120
tattatttgt atatgtgatg aaaatttaag aaaaaatag tcgacaacac gccgaataaa 180
caaagggttt cttcaatacc 200

<210> 78
<211> 200
<212> DNA
<213> *S. cerevisiae*

<220>
<223> terminator ARF2

<400> 78
tctaaatctg tatagaacgt ttagtcatgc ggaccttggtg tgttttgttt ctagattggt 60
ttatttttat gattgttgaa gatataaacc actgtatagt tgtataagat aggataatga 120
tggtgcactg aaaataaact tactagctct ttaatattgc aacggcttgt aacgggcgcc 180
atgatgacat tcagaattat 200

<210> 79
<211> 200
<212> DNA
<213> *S. cerevisiae*

<220>
<223> terminator RRI1

<400> 79
attcctaacg ttgctccaat gacgctgcaa tagcttatgt ttatctgcaa cgtactttta 60
atagttattc cttcttgaat ctctataagt atatctatac cgggtgacaa tttgatattt 120
tcgtacgccg ttatgtgttg gtttttggtc ttactgataa aatggcatcg agcttacaac 180
tgaagagaaa gacgatgcat 200

<210> 80
<211> 200
<212> DNA
<213> *S. cerevisiae*

<220>
<223> terminator HEM1

<400> 80
aacaaccaat atatgcatgg gctgagatag aggtacaagg aatttgtaaa tcagtaaaaa 60
aaaaaattaa cagttttttt ttttcatttt ttttttttat tcttatttat gtatgatact 120
ttattattat ttctcttaat tattttattha ttttaactaac acgatgagca cttttaactg 180
caatggttta actgtagcaa 200

<210> 81
<211> 837
<212> DNA
<213> Artificial

<220>
<223> CDS SLC35A1 codon optimized

<400> 81
atggctgctc caagagacaa cgttaccttg ttgttcaagt tgtactgttt ggctgttatg 60
accttgatgg ctgctgttta caccatcgct ttgagataca ccagaacctc tgacaaggaa 120
ttgtacttct ctaccaccgc tgtttgtatc accgaagtta tcaagttgtt gttgtctgtt 180
ggatcttgg ctaaggaaac cggttctttg ggtagattca aggcttcttt gagagaaaac 240
gttttgggtt ctccaaagga attgttgaag ttgtctgttc catctttggg ttacgctgtt 300
caaaacaaca tggctttctt ggctttgtct aacttggacg ctgctgttta ccaagttacc 360
taccaattga agatcccatg taccgctttg tgtaccgttt tgatgttgaa cagaaccttg 420
tctaagttgc aatggggtttc tgttttcatg ttgtgtgctg gtgttacctt ggttcaatgg 480
aagccagctc aagctaccaa gggtgttgtt gaacaaaacc cattgttggg tttcgggtgct 540
atcgctatcg ctgttttgtg ttctgggttc gctgttttgg cttctgttgg tggtttgtac 600
acctctgttg ttgttaagta caccgacaac atcatgaagg gtttctctgc tgctgctgct 660
atcgttttgt ctaccatcgc ttctgttatg ttgttcgggt tgcaaatac cttgaccttc 720
gctttgggta ccttgttggg ttgtgtttct atctacttgt acggtttgcc aagacaagac 780
accacctcta tccaacaagg tgaaaccgct tctaaggaaa gagttatcgg tgtttga 837

<210> 82
<211> 278
<212> PRT
<213> *H. sapiens*

<220>
<223> SLC35A1

<400> 82
Met Ala Ala Pro Arg Asp Asn Val Thr Leu Leu Phe Lys Leu Tyr Cys
1 5 10 15

Leu Ala Val Met Thr Leu Met Ala Ala Val Tyr Thr Ile Ala Leu Arg
 20 25 30
 Tyr Thr Arg Thr Ser Asp Lys Glu Leu Tyr Phe Ser Thr Thr Ala Val
 35 40 45
 Cys Ile Thr Glu Val Ile Lys Leu Leu Leu Ser Val Gly Ile Leu Ala
 50 55 60
 Lys Glu Thr Gly Ser Leu Gly Arg Phe Lys Ala Ser Leu Arg Glu Asn
 65 70 75 80
 Val Leu Gly Ser Pro Lys Glu Leu Leu Lys Leu Ser Val Pro Ser Leu
 85 90 95
 Val Tyr Ala Val Gln Asn Asn Met Ala Phe Leu Ala Leu Ser Asn Leu
 100 105 110
 Asp Ala Ala Val Tyr Gln Val Thr Tyr Gln Leu Lys Ile Pro Cys Thr
 115 120 125
 Ala Leu Cys Thr Val Leu Met Leu Asn Arg Thr Leu Ser Lys Leu Gln
 130 135 140
 Trp Val Ser Val Phe Met Leu Cys Ala Gly Val Thr Leu Val Gln Trp
 145 150 155 160
 Lys Pro Ala Gln Ala Thr Lys Val Val Val Glu Gln Asn Pro Leu Leu
 165 170 175
 Gly Phe Gly Ala Ile Ala Ile Ala Val Leu Cys Ser Gly Phe Ala Val
 180 185 190
 Leu Ala Ser Val Gly Gly Leu Tyr Thr Ser Val Val Val Lys Tyr Thr
 195 200 205
 Asp Asn Ile Met Lys Gly Phe Ser Ala Ala Ala Ile Val Leu Ser
 210 215 220
 Thr Ile Ala Ser Val Met Leu Phe Gly Leu Gln Ile Thr Leu Thr Phe
 225 230 235 240
 Ala Leu Gly Thr Leu Leu Val Cys Val Ser Ile Tyr Leu Tyr Gly Leu
 245 250 255
 Pro Arg Gln Asp Thr Thr Ser Ile Gln Gln Gly Glu Thr Ala Ser Lys
 260 265 270
 Glu Arg Val Ile Gly Val
 275

<210> 83

<211> 747

<212> DNA

<213> Artificial

<220>

<223> CDS NANP codon optimized

<400> 83

| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|-----|
| atgggtttgt | ctagagttag | agctgttttc | ttcgacttgg | acaacacctt | gatcgacacc | 60 |
| gctggtgctt | ctagaagagg | tatgttggaa | gttatcaagt | tgttgcaatc | taagtaccac | 120 |
| tacaaggaag | aagctgaaat | catctgtgac | aaggttcaag | ttaagttgtc | taaggaatgt | 180 |
| ttccacccat | acaacacctg | tatcaccgac | ttgagaacct | ctcactggga | agaagctatc | 240 |
| caagaaacca | agggtgggtgc | tgctaacaga | aagttggctg | aagaatgtta | cttcttgttg | 300 |
| aagtctacca | gattgcaaca | catgaccttg | gctgaagacg | ttaaggctat | gttgaccgaa | 360 |
| ttgagaaagg | aagttagatt | gttgttgttg | accaacggtg | acagacaaac | ccaaagagaa | 420 |
| aagatcgaag | cttgtgcttg | tcaatcttac | ttcgacgctg | ttgttgttgg | tggtgaacaa | 480 |
| agagaagaaa | agccagctcc | atctatcttc | tactactggt | gtaacttggt | gggtgttcaa | 540 |
| ccaggtgact | gtgttatggt | tggtgacacc | ttggaaaccg | acatccaagg | tggtttgaac | 600 |
| gctggtttga | aggctaccgt | ttggatcaac | aagaacggtg | tcgtttccatt | gaagtcttct | 660 |
| ccagttccac | actacatggt | ttcttctggt | ttggaattgc | cagctttggt | gcaatctatc | 720 |

gactgtaagg tttctatgtc tacctga

747

<210> 84
<211> 248
<212> PRT
<213> H. sapiens

<220>
<223> NANP

<400> 84
Met Gly Leu Ser Arg Val Arg Ala Val Phe Phe Asp Leu Asp Asn Thr
1 5 10 15
Leu Ile Asp Thr Ala Gly Ala Ser Arg Arg Gly Met Leu Glu Val Ile
20 25 30
Lys Leu Leu Gln Ser Lys Tyr His Tyr Lys Glu Glu Ala Glu Ile Ile
35 40 45
Cys Asp Lys Val Gln Val Lys Leu Ser Lys Glu Cys Phe His Pro Tyr
50 55 60
Asn Thr Cys Ile Thr Asp Leu Arg Thr Ser His Trp Glu Glu Ala Ile
65 70 75 80
Gln Glu Thr Lys Gly Gly Ala Ala Asn Arg Lys Leu Ala Glu Glu Cys
85 90 95
Tyr Phe Leu Trp Lys Ser Thr Arg Leu Gln His Met Thr Leu Ala Glu
100 105 110
Asp Val Lys Ala Met Leu Thr Glu Leu Arg Lys Glu Val Arg Leu Leu
115 120 125
Leu Leu Thr Asn Gly Asp Arg Gln Thr Gln Arg Glu Lys Ile Glu Ala
130 135 140
Cys Ala Cys Gln Ser Tyr Phe Asp Ala Val Val Val Gly Gly Glu Gln
145 150 155 160
Arg Glu Glu Lys Pro Ala Pro Ser Ile Phe Tyr Tyr Cys Cys Asn Leu
165 170 175
Leu Gly Val Gln Pro Gly Asp Cys Val Met Val Gly Asp Thr Leu Glu
180 185 190
Thr Asp Ile Gln Gly Gly Leu Asn Ala Gly Leu Lys Ala Thr Val Trp
195 200 205
Ile Asn Lys Asn Gly Ile Val Pro Leu Lys Ser Ser Pro Val Pro His
210 215 220
Tyr Met Val Ser Ser Val Leu Glu Leu Pro Ala Leu Leu Gln Ser Ile
225 230 235 240
Asp Cys Lys Val Ser Met Ser Thr
245

<210> 85
<211> 2262
<212> DNA
<213> Artificial

<220>
<223> CDS GNE codon optimized

<400> 85
atggaaacct acggttactt gcaaagagaa tcttgtttcc aaggtccaca cgaattgtac 60
ttcaagaact tgtctaagag aaacaagcaa atcatggaaa agaacggtaa caacagaaag 120
ttgagagttt gtgttgctac ctgtaacaga gctgactact ctaagttggc tccaatcatg 180

| | | | | | | |
|-------------|------------|-------------|------------|------------|-------------|------|
| ttcggatatca | agaccgaacc | agaattcttc | gaattggacg | ttgttgTTTT | gggttctcac | 240 |
| ttgatcgacg | actacggtaa | cacctacaga | atgatcgaac | aagacgactt | cgacatcaac | 300 |
| accagattgc | acaccatcgt | tagagggtgaa | gacgaagctg | ctatggttga | atctgttgggt | 360 |
| ttggcTTTTg | ttaagttgcc | agacgttttg | aacagattga | agccagacat | catgatcgtt | 420 |
| cacggtgaca | gattcgacgc | tttggcTTTT | gctacctctg | ctgctttgat | gaacatcaga | 480 |
| atcttgcaca | tcgaaggtgg | tgaagtttct | ggtaccatcg | acgactctat | cagacacgct | 540 |
| atcaccaagt | tggtctacta | ccacgtttgt | tgtaccagat | ctgctgaaca | acacttgatc | 600 |
| tctatgtgtg | aagaccacga | cagaatcttg | ttggctgggt | gtccatctta | cgacaagtgtg | 660 |
| ttgtctgcta | agaacaagga | ctacatgtct | atcatcagaa | tgtggttggg | tgacgacgtt | 720 |
| aagtctaagg | actacatcgt | tgctttgcaa | caccagttta | ccaccgacat | caagcactct | 780 |
| atcaagatgt | tcgaattgac | cttggacgct | ttgatctctt | tcaacaagag | aaccttgggt | 840 |
| ttgttcccaa | acatcgacgc | tggttctaag | gaaatggtta | gagttatgag | aaagaagggt | 900 |
| atcgaacacc | acccaaactt | cagagctgtt | aagcacgttc | cattcgacca | attcatccaa | 960 |
| ttggttgctc | acgttggttg | tatgatcggg | aactcttctt | gtggtgttag | agaagtgtgt | 1020 |
| gctttcggtg | ccccagttat | caacttgggt | accagacaaa | tcggtagaga | aaccggtgaa | 1080 |
| aacgttttgc | acgttcgcga | cgctgacacc | caagacaaga | tcttgcaagc | tttgactttg | 1140 |
| caattcggtg | agcaataccc | atgttctaag | atctacgggt | acggtaacgc | tgttccaaga | 1200 |
| atcttgaagt | tcttgaagtc | tatcgacttg | caagaaccat | tgcaaaaaga | gttctgtttc | 1260 |
| ccaccagtta | aggaaaacat | ctctcaagac | atcgaccaca | tcttggaaac | cttgtctgct | 1320 |
| ttggctgttg | acttgggttg | taccaacttg | agagttgcta | tcgtttctat | gaagggtgaa | 1380 |
| atcgtaaga | agtacaccca | attcaaccca | aagacctacg | aagaaagaat | caacttgatc | 1440 |
| ttgcaaagt | gtgttgaagc | tgctgctgaa | gctgttaagt | tgaactgtag | aatcttgggt | 1500 |
| gttggtatct | ctaccgggtg | tagagttaac | ccaagagaag | gtatcgtttt | gcactctacc | 1560 |
| aagttgatcc | aagaatggaa | ctctgttgac | ttgagaaccc | cattgtctga | caccttgcac | 1620 |
| ttgccagttt | gggttgacaa | cgacggtaac | tgtgctgctt | tggtgaaag | aaagttcggt | 1680 |
| caaggtaagg | gtttggaaaa | cttcgttacc | ttgatcaccg | gtaccggtat | cgggtggtgt | 1740 |
| atcatccacc | aacacgaatt | gatccacggt | tcttctttct | gtgctgctga | attgggtcac | 1800 |
| ttggttgttt | ctttggacgg | tccagactgt | tcttgtgggt | ctcacggttg | tatcgaagct | 1860 |
| tacgcttctg | gtatggcttt | gcaaagagaa | gctaagaagt | tgcacgacga | agacttgttg | 1920 |
| ttggttgaag | gtatgtctgt | tccaaaggac | gaagctgttg | gtgctttgca | cttgatccaa | 1980 |
| gctgctaagt | tgggtaacgc | taaggctcaa | tctatcttga | gaaccgctgg | taccgctttg | 2040 |
| ggtttgggtg | ttgttaacat | cttgcacacc | atgaacccat | ctttggttat | cttgtctggt | 2100 |
| gttttggctt | ctcactacat | ccacatcgtt | aaggacgtta | tcagacaaca | agctttgtct | 2160 |
| tctgttcaag | acgttgacgt | tgttgtttct | gacttgggtg | accagctttt | gttgggtgct | 2220 |
| gcttctatgg | ttttggacta | caccaccaga | agaatctact | ga | | 2262 |

<210> 86

<211> 753

<212> PRT

<213> H. sapiens

<220>

<223> GNE

<400> 86

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Thr | Tyr | Gly | Tyr | Leu | Gln | Arg | Glu | Ser | Cys | Phe | Gln | Gly | Pro |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| His | Glu | Leu | Tyr | Phe | Lys | Asn | Leu | Ser | Lys | Arg | Asn | Lys | Gln | Ile | Met |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Lys | Asn | Gly | Asn | Asn | Arg | Lys | Leu | Arg | Val | Cys | Val | Ala | Thr | Cys |
| | | 35 | | | | 40 | | | | | 45 | | | | |
| Asn | Arg | Ala | Asp | Tyr | Ser | Lys | Leu | Ala | Pro | Ile | Met | Phe | Gly | Ile | Lys |
| | 50 | | | | 55 | | | | 60 | | | | | | |
| Thr | Glu | Pro | Glu | Phe | Phe | Glu | Leu | Asp | Val | Val | Val | Leu | Gly | Ser | His |
| 65 | | | | 70 | | | | 75 | | | | | 80 | | |
| Leu | Ile | Asp | Asp | Tyr | Gly | Asn | Thr | Tyr | Arg | Met | Ile | Glu | Gln | Asp | Asp |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 85 | | | | | | | | 90 | | | | 95 | | | |
| Phe | Asp | Ile | Asn | Thr | Arg | Leu | His | Thr | Ile | Val | Arg | Gly | Glu | Asp | Glu |
| | | | 100 | | | | 105 | | | | | | 110 | | |
| Ala | Ala | Met | Val | Glu | Ser | Val | Gly | Leu | Ala | Leu | Val | Lys | Leu | Pro | Asp |
| | | | 115 | | | | 120 | | | | | | 125 | | |
| Val | Leu | Asn | Arg | Leu | Lys | Pro | Asp | Ile | Met | Ile | Val | His | Gly | Asp | Arg |
| | | | 130 | | | | 135 | | | | | | 140 | | |
| Phe | Asp | Ala | Leu | Ala | Leu | Ala | Thr | Ser | Ala | Ala | Leu | Met | Asn | Ile | Arg |
| 145 | | | | 150 | | | 155 | | | | | | 160 | | |
| Ile | Leu | His | Ile | Glu | Gly | Gly | Glu | Val | Ser | Gly | Thr | Ile | Asp | Asp | Ser |
| | | | 165 | | | 170 | | | | | | 175 | | | |
| Ile | Arg | His | Ala | Ile | Thr | Lys | Leu | Ala | His | Tyr | His | Val | Cys | Cys | Thr |
| | | | 180 | | | 185 | | | | | | 190 | | | |
| Arg | Ser | Ala | Glu | Gln | His | Leu | Ile | Ser | Met | Cys | Glu | Asp | His | Asp | Arg |
| | | | 195 | | | 200 | | | | | | 205 | | | |
| Ile | Leu | Leu | Ala | Gly | Cys | Pro | Ser | Tyr | Asp | Lys | Leu | Leu | Ser | Ala | Lys |
| | | | 210 | | | 215 | | | | | | 220 | | | |
| Asn | Lys | Asp | Tyr | Met | Ser | Ile | Ile | Arg | Met | Trp | Leu | Gly | Asp | Asp | Val |
| 225 | | | | 230 | | | 235 | | | | | | 240 | | |
| Lys | Ser | Lys | Asp | Tyr | Ile | Val | Ala | Leu | Gln | His | Pro | Val | Thr | Thr | Asp |
| | | | 245 | | | 250 | | | | | | 255 | | | |
| Ile | Lys | His | Ser | Ile | Lys | Met | Phe | Glu | Leu | Thr | Leu | Asp | Ala | Leu | Ile |
| | | | 260 | | | 265 | | | | | | 270 | | | |
| Ser | Phe | Asn | Lys | Arg | Thr | Leu | Val | Leu | Phe | Pro | Asn | Ile | Asp | Ala | Gly |
| | | | 275 | | | 280 | | | | | | 285 | | | |
| Ser | Lys | Glu | Met | Val | Arg | Val | Met | Arg | Lys | Lys | Gly | Ile | Glu | His | His |
| | | | 290 | | | 295 | | | | | | 300 | | | |
| Pro | Asn | Phe | Arg | Ala | Val | Lys | His | Val | Pro | Phe | Asp | Gln | Phe | Ile | Gln |
| 305 | | | | 310 | | | 315 | | | | | | 320 | | |
| Leu | Val | Ala | His | Ala | Gly | Cys | Met | Ile | Gly | Asn | Ser | Ser | Cys | Gly | Val |
| | | | 325 | | | 330 | | | | | | 335 | | | |
| Arg | Glu | Val | Gly | Ala | Phe | Gly | Thr | Pro | Val | Ile | Asn | Leu | Gly | Thr | Arg |
| | | | 340 | | | 345 | | | | | | 350 | | | |
| Gln | Ile | Gly | Arg | Glu | Thr | Gly | Glu | Asn | Val | Leu | His | Val | Arg | Asp | Ala |
| | | | 355 | | | 360 | | | | | | 365 | | | |
| Asp | Thr | Gln | Asp | Lys | Ile | Leu | Gln | Ala | Leu | His | Leu | Gln | Phe | Gly | Lys |
| | | | 370 | | | 375 | | | | | | 380 | | | |
| Gln | Tyr | Pro | Cys | Ser | Lys | Ile | Tyr | Gly | Asp | Gly | Asn | Ala | Val | Pro | Arg |
| 385 | | | | 390 | | | 395 | | | | | | 400 | | |
| Ile | Leu | Lys | Phe | Leu | Lys | Ser | Ile | Asp | Leu | Gln | Glu | Pro | Leu | Gln | Lys |
| | | | 405 | | | 410 | | | | | | 415 | | | |
| Lys | Phe | Cys | Phe | Pro | Pro | Val | Lys | Glu | Asn | Ile | Ser | Gln | Asp | Ile | Asp |
| | | | 420 | | | 425 | | | | | | 430 | | | |
| His | Ile | Leu | Glu | Thr | Leu | Ser | Ala | Leu | Ala | Val | Asp | Leu | Gly | Gly | Thr |
| | | | 435 | | | 440 | | | | | | 445 | | | |
| Asn | Leu | Arg | Val | Ala | Ile | Val | Ser | Met | Lys | Gly | Glu | Ile | Val | Lys | Lys |
| | | | 450 | | | 455 | | | | | | 460 | | | |
| Tyr | Thr | Gln | Phe | Asn | Pro | Lys | Thr | Tyr | Glu | Glu | Arg | Ile | Asn | Leu | Ile |
| 465 | | | | 470 | | | 475 | | | | | | 480 | | |
| Leu | Gln | Met | Cys | Val | Glu | Ala | Ala | Ala | Glu | Ala | Val | Lys | Leu | Asn | Cys |
| | | | 485 | | | 490 | | | | | | 495 | | | |
| Arg | Ile | Leu | Gly | Val | Gly | Ile | Ser | Thr | Gly | Gly | Arg | Val | Asn | Pro | Arg |
| | | | | | | | | | | | | | | | |

| | | |
|---------------------|---------------------|-------------------------|
| 530 | 535 | 540 |
| Val Asp Asn Asp Gly | Asn Cys Ala Ala Leu | Ala Glu Arg Lys Phe Gly |
| 545 | 550 | 555 |
| Gln Gly Lys Gly Leu | Glu Asn Phe Val Thr | Leu Ile Thr Gly Thr Gly |
| 565 | 570 | 575 |
| Ile Gly Gly Gly Ile | Ile His Gln His Glu | Leu Ile His Gly Ser Ser |
| 580 | 585 | 590 |
| Phe Cys Ala Ala Glu | Leu Gly His Leu Val | Val Ser Leu Asp Gly Pro |
| 595 | 600 | 605 |
| Asp Cys Ser Cys Gly | Ser His Gly Cys Ile | Glu Ala Tyr Ala Ser Gly |
| 610 | 615 | 620 |
| Met Ala Leu Gln Arg | Glu Ala Lys Lys Leu | His Asp Glu Asp Leu Leu |
| 625 | 630 | 635 |
| Leu Val Glu Gly Met | Ser Val Pro Lys Asp | Glu Ala Val Gly Ala Leu |
| 645 | 650 | 655 |
| His Leu Ile Gln Ala | Ala Lys Leu Gly Asn | Ala Lys Ala Gln Ser Ile |
| 660 | 665 | 670 |
| Leu Arg Thr Ala Gly | Thr Ala Leu Gly Leu | Gly Val Val Asn Ile Leu |
| 675 | 680 | 685 |
| His Thr Met Asn Pro | Ser Leu Val Ile Leu | Ser Gly Val Leu Ala Ser |
| 690 | 695 | 700 |
| His Tyr Ile His Ile | Val Lys Asp Val Ile | Arg Gln Gln Ala Leu Ser |
| 705 | 710 | 715 |
| Ser Val Gln Asp Val | Asp Val Val Val Ser | Asp Leu Val Asp Pro Ala |
| 725 | 730 | 735 |
| Leu Leu Gly Ala Ala | Ser Met Val Leu Asp | Tyr Thr Thr Arg Arg Ile |
| 740 | 745 | 750 |

Tyr

<210> 87

<211> 2178

<212> DNA

<213> Artificial

<220>

<223> CDS GNE codon optimized

<400> 87

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| agagctgact | actctaagtt | ggctccaatc | atgttcggta | tcaagtctca | ccctgacatc | 120 |
| ttcgacttgg | aagttgttgt | tttgggttct | cacttgatcg | acgactacgg | taacaccttc | 180 |
| agaatgatcg | aacaagacga | cttcgacatc | ggttctaagt | tgcacaccat | cgtttagaggt | 240 |
| gaagacgaag | ctgctatggg | tgaatctgtt | ggtttggcct | tggttaagtt | gccagacggt | 300 |
| ttgcaaagat | tggtccaga | catcttggtt | gttcacgggt | acagattcga | cgctttggct | 360 |
| ttggctaccg | ctgctgcttt | gatgaacatc | agaatccttg | acttggaagg | tggtgaagtt | 420 |
| tctggtacca | tcgacgactc | tatcagacac | gctatctcta | agttggctca | ctaccacgct | 480 |
| gtttgtacct | tgtctgctga | aagacacttg | atctctatgt | gtgaagacca | ctctagaatc | 540 |
| ttgttggctg | gttgctccatc | ttacgacaag | ttgttgtctg | cttacaagag | ggacgactac | 600 |
| gctgacatca | tcaagtcttg | gatcgggtgac | gacgttaagg | aacaagacta | catcgttgct | 660 |
| ttgcaacacc | ctgttaccac | cgacatcaag | aactctatca | agatctacga | attgatgttg | 720 |
| gacgctttga | tctctttcaa | caagaagacc | ttgatcttgt | tcccaaacat | cgacgctggg | 780 |
| tctaaggaaa | tggttagagt | tatgagaaga | aagggtatcg | aacaacacca | aaacttcaga | 840 |
| gctgttaagc | acgttccatt | cgaccaattc | atccaattgg | ttgctcacgc | tgtttgtatg | 900 |
| atcggttaact | cttcttgtgg | tggttagagaa | gctggtgctt | tcggtacccc | agttatcaac | 960 |
| ttgggtacca | gacaaaccgg | tagagaaacc | ggtgaaaacg | ttttgcacgt | tagggacgct | 1020 |
| gacactcaca | acaagatcta | ccacgctttg | gaattgcaat | tcggttaagag | atacccttgt | 1080 |

| | | | | | | |
|-------------|-------------|-------------|--------------|-------------|-------------|------|
| tctaagatct | acggtgacgg | taacgctgtt | caaagaatct | tgaagttctt | gcaaaccatc | 1140 |
| gacttgctctg | aaccattgca | aaagaagttc | tgtttccac | cagttaagga | atgtatctct | 1200 |
| caagacatcg | accacatctt | ggaaactcaa | tctgctttgt | ctgttgactt | gggtgggtacc | 1260 |
| aacttgagag | ttgggtatcgt | ttctatgaag | ggtaagggtg | ttaagaagta | cgttcaattg | 1320 |
| aaccctaaga | ccttcgaaga | aagaatcgaa | ttgatcttga | ccatgtgtaa | gcaagctatg | 1380 |
| gctgacgctg | ttcacttgaa | ctgtagaatc | ttgggtgttg | gtgtttctac | cggtggtaga | 1440 |
| gttaaccctc | aagacggtgt | tgttttgcac | tctaccaagt | tgatcaagga | atggctcttct | 1500 |
| gttgacatca | gaacccatt | gtcttctgct | ttgcacttgc | cagtttgggt | tgacaacgac | 1560 |
| ggtaactgtg | ctgctttggc | tgaaagaaag | ttcggtcacg | gtaagggtgt | tgaaaacttc | 1620 |
| gttaccatca | tcaccgggtac | cggtatcggg | gggtgggtatca | tccaacacaa | cgaattgatc | 1680 |
| cacggtaaca | ccttctgtgc | tgctgaattg | ggtcacatcg | ttgtttcttt | ggaagggtcca | 1740 |
| gaatgtatgt | gtgggtggta | cggttgatc | gaagcttact | cttctgggtt | ggctttgcaa | 1800 |
| agagaagcta | agagattgca | cgacgaagac | ttgttggttg | ttgaagggtat | gaccttgaac | 1860 |
| aacaaggaac | aagttaacgc | tatccacttg | atcaacgctg | ctagattggg | taactctaag | 1920 |
| gctgaaaccg | ttttgcacac | cgctgggtacc | gctttgggtt | tgggtatcgt | taacatcttg | 1980 |
| cacatgatca | acccttcttt | ggttatcttg | tctgggtgtt | tggctgttca | ctacgaaacc | 2040 |
| ccagttagac | aagttatcgg | tcaaagagct | ttgttgaccg | ctcaagggtac | caagggttatg | 2100 |
| gttctgact | tggaagacc | tgctttgttg | gggtgctgctt | ctatggtttt | ggactacacc | 2160 |
| accagaagaa | cctactga | | | | | 2178 |

<210> 88

<211> 725

<212> PRT

<213> ?D. rerio

<220>

<223> GNE

<400> 88

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

| | | |
|---|-----|-----|
| 210 | 215 | 220 |
| Val Thr Thr Asp Ile Lys Asn Ser Ile Lys Ile Tyr Glu Leu Met Leu | | |
| 225 | 230 | 235 |
| Asp Ala Leu Ile Ser Phe Asn Lys Lys Thr Leu Ile Leu Phe Pro Asn | | 240 |
| | 245 | 250 |
| Ile Asp Ala Gly Ser Lys Glu Met Val Arg Val Met Arg Arg Lys Gly | | 255 |
| | 260 | 265 |
| Ile Glu Gln His Gln Asn Phe Arg Ala Val Lys His Val Pro Phe Asp | | 270 |
| | 275 | 280 |
| Gln Phe Ile Gln Leu Val Ala His Ala Val Cys Met Ile Gly Asn Ser | | 285 |
| | 290 | 295 |
| Ser Cys Gly Val Arg Glu Ala Gly Ala Phe Gly Thr Pro Val Ile Asn | | 300 |
| 305 | 310 | 315 |
| Leu Gly Thr Arg Gln Thr Gly Arg Glu Thr Gly Glu Asn Val Leu His | | 320 |
| | 325 | 330 |
| Val Arg Asp Ala Asp Thr His Asn Lys Ile Tyr His Ala Leu Glu Leu | | 335 |
| | 340 | 345 |
| Gln Phe Gly Lys Arg Tyr Pro Cys Ser Lys Ile Tyr Gly Asp Gly Asn | | 350 |
| | 355 | 360 |
| Ala Val Gln Arg Ile Leu Lys Phe Leu Gln Thr Ile Asp Leu Ser Glu | | 365 |
| | 370 | 375 |
| Pro Leu Gln Lys Lys Phe Cys Phe Pro Pro Val Lys Glu Cys Ile Ser | | 380 |
| 385 | 390 | 395 |
| Gln Asp Ile Asp His Ile Leu Glu Thr Gln Ser Ala Leu Ser Val Asp | | 400 |
| | 405 | 410 |
| Leu Gly Gly Thr Asn Leu Arg Val Gly Ile Val Ser Met Lys Gly Lys | | 415 |
| | 420 | 425 |
| Val Val Lys Lys Tyr Val Gln Leu Asn Pro Lys Thr Phe Glu Glu Arg | | 430 |
| | 435 | 440 |
| Ile Glu Leu Ile Leu Thr Met Cys Lys Gln Ala Met Ala Asp Ala Val | | 445 |
| | 450 | 455 |
| His Leu Asn Cys Arg Ile Leu Gly Val Gly Val Ser Thr Gly Gly Arg | | 460 |
| 465 | 470 | 475 |
| Val Asn Pro Gln Asp Gly Val Val Leu His Ser Thr Lys Leu Ile Lys | | 480 |
| | 485 | 490 |
| Glu Trp Ser Ser Val Asp Ile Arg Thr Pro Leu Ser Ser Ala Leu His | | 495 |
| | 500 | 505 |
| Leu Pro Val Trp Val Asp Asn Asp Gly Asn Cys Ala Ala Leu Ala Glu | | 510 |
| | 515 | 520 |
| Arg Lys Phe Gly His Gly Lys Gly Val Glu Asn Phe Val Thr Ile Ile | | 525 |
| | 530 | 535 |
| Thr Gly Thr Gly Ile Gly Gly Gly Ile Ile Gln His Asn Glu Leu Ile | | 540 |
| 545 | 550 | 555 |
| His Gly Asn Thr Phe Cys Ala Ala Glu Leu Gly His Ile Val Val Ser | | 560 |
| | 565 | 570 |
| Leu Glu Gly Pro Glu Cys Met Cys Gly Gly His Gly Cys Ile Glu Ala | | 575 |
| | 580 | 585 |
| Tyr Ser Ser Gly Leu Ala Leu Gln Arg Glu Ala Lys Arg Leu His Asp | | 590 |
| | 595 | 600 |
| Glu Asp Leu Leu Leu Val Glu Gly Met Thr Leu Asn Asn Lys Glu Gln | | 605 |
| | 610 | 615 |
| Val Asn Ala Ile His Leu Ile Asn Ala Ala Arg Leu Gly Asn Ser Lys | | 620 |
| 625 | 630 | 635 |
| Ala Glu Thr Val Leu His Thr Ala Gly Thr Ala Leu Gly Leu Gly Ile | | 640 |
| | 645 | 650 |
| Val Asn Ile Leu His Met Ile Asn Pro Ser Leu Val Ile Leu Ser Gly | | 655 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Tyr | Gly | Glu | His | Lys | Arg | His | Leu | Glu | Phe | Ser | His | Asp | Gln | Tyr | Arg |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Glu | Leu | Gln | Arg | Tyr | Ala | Glu | Glu | Val | Gly | Ile | Phe | Phe | Thr | Ala | Ser |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gly | Met | Asp | Glu | Met | Ala | Val | Glu | Phe | Leu | His | Glu | Leu | Asn | Val | Pro |
| | | 115 | | | | | 120 | | | | 125 | | | | |
| Phe | Phe | Lys | Val | Gly | Ser | Gly | Asp | Thr | Asn | Asn | Phe | Pro | Tyr | Leu | Glu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Lys | Thr | Ala | Lys | Lys | Gly | Arg | Pro | Met | Val | Ile | Ser | Ser | Gly | Met | Gln |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ser | Met | Asp | Thr | Met | Lys | Gln | Val | Tyr | Gln | Ile | Val | Lys | Pro | Leu | Asn |
| | | | | 165 | | | | 170 | | | | | | 175 | |
| Pro | Asn | Phe | Cys | Phe | Leu | Gln | Cys | Thr | Ser | Ala | Tyr | Pro | Leu | Gln | Pro |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Glu | Asp | Val | Asn | Leu | Arg | Val | Ile | Ser | Glu | Tyr | Gln | Lys | Leu | Phe | Pro |
| | 195 | | | | | | 200 | | | | 205 | | | | |
| Asp | Ile | Pro | Ile | Gly | Tyr | Ser | Gly | His | Glu | Thr | Gly | Ile | Ala | Ile | Ser |
| 210 | | | | | 215 | | | | | | 220 | | | | |
| Val | Ala | Ala | Val | Ala | Leu | Gly | Ala | Lys | Val | Leu | Glu | Arg | His | Ile | Thr |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Leu | Asp | Lys | Thr | Trp | Lys | Gly | Ser | Asp | His | Ser | Ala | Ser | Leu | Glu | Pro |
| | | | | 245 | | | | 250 | | | | | | 255 | |
| Gly | Glu | Leu | Ala | Glu | Leu | Val | Arg | Ser | Val | Arg | Leu | Val | Glu | Arg | Ala |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Leu | Gly | Ser | Pro | Thr | Lys | Gln | Leu | Leu | Pro | Cys | Glu | Met | Ala | Cys | Asn |
| | 275 | | | | | 280 | | | | | | 285 | | | |
| Glu | Lys | Leu | Gly | Lys | Ser | Val | Val | Ala | Lys | Val | Lys | Ile | Pro | Glu | Gly |
| 290 | | | | | | 295 | | | | | 300 | | | | |
| Thr | Ile | Leu | Thr | Met | Asp | Met | Leu | Thr | Val | Lys | Val | Gly | Glu | Pro | Lys |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Gly | Tyr | Pro | Pro | Glu | Asp | Ile | Phe | Asn | Leu | Val | Gly | Lys | Lys | Val | Leu |
| | | | | 325 | | | | 330 | | | | | | 335 | |
| Val | Thr | Val | Glu | Glu | Asp | Asp | Thr | Ile | Met | Glu | Glu | Leu | Val | Asp | Asn |
| | | | 340 | | | | | 345 | | | | | | 350 | |
| His | Gly | Lys | Lys | Ile | Lys | Ser | | | | | | | | | |
| | | 355 | | | | | | | | | | | | | |

<210> 91
 <211> 1080
 <212> DNA
 <213> Artificial

<220>
 <223> CDS NANS codon optimized

| | |
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| <400> 91 | |
| atgccattga agttcgaatt gtgtccaggt agaatgatcg gtggtaacaa cccttgtttc | 60 |
| atcatcgctg aaatcggtca aaaccaccaa ggtgacatcg aaatcgctaa gaagatgatc | 120 |
| aagatggcta aggactgtgg tgctgactgt gctaagttcc aaaagtctga attggaatac | 180 |
| aagttcaaca agaaggcttt ggaaagacca tacacctcta agcactcttg gggtgaagacc | 240 |
| tacggtgaac acaagagaca cttggaattc tctcacgaac aatacagaga attgcaacaa | 300 |
| tacgctaagc aagttggtat cttcttcacc gcttctggta tggacgaaat ggctgttgaa | 360 |
| ttcttgacag aattggacgt tccattcttc aaggttggtt ctggtgacac caacaacttc | 420 |
| ccatacttga agaagaccgc tcaaaagggt agaccaatgg ttgtttcttc tggtatgcaa | 480 |
| tctatggaaa ccatgcaaca cgtttacaag atcgttaagg aacacaacca aaacttctgt | 540 |

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|------|
| atcttgcaat | gtacctctgc | ttaccctttg | gaaccagaag | acgttaactt | gagagttatc | 600 |
| accgaatacc | aaaaggaatt | cccagacatc | ccaatcggtt | actctgggtc | cgaatctggt | 660 |
| atcaacatca | ccgttggtgc | tgttgctttg | ggtgctaagg | ttgttgaaag | acacgttacc | 720 |
| ttggacaagt | cttggagggg | ttctgaccac | gctgcttctt | tggaaccaga | agaattggct | 780 |
| gaattggtta | gatctatcag | aatcgttgaa | agagctttgg | gtaccgggtt | gaagagaatg | 840 |
| ttgccatgtg | aagttccatg | tcacgacaag | ttgggtaagt | ctgttggtgc | taagacctct | 900 |
| atcccaaagg | gtaccgaatt | gaccttggac | atgttggctg | ttaagggtgc | tgaaccaaag | 960 |
| ggtgttgctc | cagaagaaat | cttccaattg | gttggttaaga | aggttaccac | cgacgttgaa | 1020 |
| gaagacgaat | ctatcaccga | agacgttggt | gactcttacg | gtaagaaggc | taaggcttga | 1080 |

<210> 92

<211> 359

<212> PRT

<213> ?D. rerio

<220>

<223> NANS

<400> 92

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Pro | Leu | Lys | Phe | Glu | Leu | Cys | Pro | Gly | Arg | Met | Ile | Gly | Gly | Asn | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Asn | Pro | Cys | Phe | Ile | Ile | Ala | Glu | Ile | Gly | Gln | Asn | His | Gln | Gly | Asp | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ile | Glu | Ile | Ala | Lys | Lys | Met | Ile | Lys | Met | Ala | Lys | Asp | Cys | Gly | Ala | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| Asp | Cys | Ala | Lys | Phe | Gln | Lys | Ser | Glu | Leu | Glu | Tyr | Lys | Phe | Asn | Lys | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Lys | Ala | Leu | Glu | Arg | Pro | Tyr | Thr | Ser | Lys | His | Ser | Trp | Gly | Lys | Thr | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Tyr | Gly | Glu | His | Lys | Arg | His | Leu | Glu | Phe | Ser | His | Glu | Gln | Tyr | Arg | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Glu | Leu | Gln | Gln | Tyr | Ala | Lys | Gln | Val | Gly | Ile | Phe | Phe | Thr | Ala | Ser | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Gly | Met | Asp | Glu | Met | Ala | Val | Glu | Phe | Leu | His | Glu | Leu | Asp | Val | Pro | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Phe | Phe | Lys | Val | Gly | Ser | Gly | Asp | Thr | Asn | Asn | Phe | Pro | Tyr | Leu | Lys | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Lys | Thr | Ala | Gln | Lys | Gly | Arg | Pro | Met | Val | Val | Ser | Ser | Gly | Met | Gln | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Ser | Met | Glu | Thr | Met | Gln | His | Val | Tyr | Lys | Ile | Val | Lys | Glu | His | Asn | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Gln | Asn | Phe | Cys | Ile | Leu | Gln | Cys | Thr | Ser | Ala | Tyr | Pro | Leu | Glu | Pro | |
| | | 180 | | | | | 185 | | | | | | 190 | | | |
| Glu | Asp | Val | Asn | Leu | Arg | Val | Ile | Thr | Glu | Tyr | Gln | Lys | Glu | Phe | Pro | |
| | 195 | | | | | 200 | | | | | | 205 | | | | |
| Asp | Ile | Pro | Ile | Gly | Tyr | Ser | Gly | His | Glu | Ser | Gly | Ile | Asn | Ile | Thr | |
| | 210 | | | | 215 | | | | | | 220 | | | | | |
| Val | Gly | Ala | Val | Ala | Leu | Gly | Ala | Lys | Val | Val | Glu | Arg | His | Val | Thr | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Leu | Asp | Lys | Ser | Trp | Lys | Gly | Ser | Asp | His | Ala | Ala | Ser | Leu | Glu | Pro | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Glu | Glu | Leu | Ala | Glu | Leu | Val | Arg | Ser | Ile | Arg | Ile | Val | Glu | Arg | Ala | |
| | | 260 | | | | | 265 | | | | | | 270 | | | |
| Leu | Gly | Thr | Gly | Leu | Lys | Arg | Met | Leu | Pro | Cys | Glu | Val | Pro | Cys | His | |
| | 275 | | | | | 280 | | | | | | 285 | | | | |
| Asp | Lys | Leu | Gly | Lys | Ser | Val | Val | Ala | Lys | Thr | Ser | Ile | Pro | Lys | Gly | |

| | | |
|---|-----|-----|
| 290 | 295 | 300 |
| Thr Glu Leu Thr Leu Asp Met Leu Ala Val Lys Val Ala Glu Pro Lys | | |
| 305 | 310 | 315 |
| Gly Val Ala Pro Glu Glu Ile Phe Gln Leu Val Gly Lys Lys Val Thr | | |
| | 325 | 330 |
| Thr Asp Val Glu Glu Asp Glu Ser Ile Thr Glu Asp Val Val Asp Ser | | |
| | 340 | 345 |
| Tyr Gly Lys Lys Ala Lys Ala | | 350 |
| 355 | | |

<210> 93
 <211> 1305
 <212> DNA
 <213> Artificial

<220>
 <223> CDS CMAS codon optimized

<400> 93

| | | | | | | |
|-------------|------------|-------------|-------------|------------|------------|------|
| atggactctg | ttgaaaaggg | tgctgctacc | tctgtttcta | acccaagagg | tagaccatct | 60 |
| agaggtagac | caccaaagtt | gcaaagaaac | tctagagggtg | gtcaaggtag | aggtgttgaa | 120 |
| aagccaccac | acttggctgc | tttgatcttg | gctagagggtg | gttctaaggg | tatccattg | 180 |
| aagaacatca | agcacttggc | tggtgtttcca | ttgatcgggtt | gggttttgag | agctgctttg | 240 |
| gactctgggtg | ctttccaatc | tggttgggtt | tctaccgacc | acgacgaaat | cgaaaacgtt | 300 |
| gctaagcaat | tcggtgctca | agttcacaga | agatcttctg | aagtttctaa | ggactcttct | 360 |
| acctcttttg | acgctatcat | cgaattcttg | aactaccaca | acgaagttga | catcgttggt | 420 |
| aacatccaag | ctacctctcc | atgtttgcac | ccaaccgact | tgcaaaaagg | tgctgaaatg | 480 |
| atcagagaag | aaggttacga | ctctgttttc | tctgttggtta | gaagacacca | attcagatgg | 540 |
| tctgaaatcc | aaaaggggtg | tagagaagtt | accgaaccat | tgaacttgaa | cccagctaaa | 600 |
| agaccaagaa | gacaagactg | ggacggtgaa | ttgtacgaaa | acggttcttt | ctacttcgct | 660 |
| aagagacact | tgatcgaaat | gggttacttg | caagggtggt | agatggctta | ctacgaaatg | 720 |
| agagctgaac | actctgttga | catcgacgtt | gacatcgact | ggccaatcgc | tgaacaaaga | 780 |
| gttttgagat | acggttactt | cggtaaggaa | aagttgaagg | aaatcaagtt | gttggtttgt | 840 |
| aacatcgacg | gttggttgac | caacggtcac | atctacgttt | ctggtgacca | aaaggaaatc | 900 |
| atctcttacg | acgttaagga | cgctatcggt | atctctttgt | tgaagaagtc | tggtatcgaa | 960 |
| gtagattga | tctctgaaag | agcttggtct | aagcaaacct | tgtcttcttt | gaagttggac | 1020 |
| tgtaagatgg | aagtttctgt | ttctgacaag | ttggctgttg | ttgacgaatg | gagaaaggaa | 1080 |
| atgggtttgt | gttggaagga | agttgcttac | ttgggtaacg | aagtttctga | cgaagaatgt | 1140 |
| ttgaagagag | ttggtttgtc | tggtgctcca | gctgacgctt | gttctaccgc | tcaaaaggct | 1200 |
| gttggttaca | tctgtaagtg | taacggtggt | agaggtgcta | tcagagaatt | cgctgaacac | 1260 |
| atctgtttgt | tgatggaaaa | ggttaacaac | tcttgtcaaa | agtga | | 1305 |

<210> 94
 <211> 434
 <212> PRT
 <213> H. sapiens

<220>
 <223> CMAS

<400> 94

| | |
|---|----|
| Met Asp Ser Val Glu Lys Gly Ala Ala Thr Ser Val Ser Asn Pro Arg | |
| 1 | 5 |
| Gly Arg Pro Ser Arg Gly Arg Pro Pro Lys Leu Gln Arg Asn Ser Arg | |
| | 20 |
| Gly Gly Gln Gly Arg Gly Val Glu Lys Pro Pro His Leu Ala Ala Leu | |
| | 25 |
| | 30 |

<220>

<223> CDS CMAS codon optimized

<400> 95

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atggacgctg ttaacgaaaa cggtaagaga gctatgaagg acgactctca cggtaactct 60
acctctccaa agagaagaaa gtctagacac atctctgctt tgatcttggc tagagggtgg 120
tctaagggtg tccattgaa gaacatcaag atgttggctg gtgttccatt gatcggttgg 180
gttatcagag ctgctgttga ctctaacggt ttcaactctg tttgggtttc taccgaccac 240
gaagaaatcg ctaagggttg tttggcttgg ggtgctaagg ttcacaagag atctccagaa 300
gtttctcaag actcttcttc ttctttggac accatcagag aattctctag acaacacaga 360
gaagttgacg ttatctgtaa catccaagct acctctccat gtttgcaccc taagcacttg 420
accgaagctg ttgaattgat caccaagcaa ggttacgact ctgttttctc tgttgttaga 480
agacacaact tcagatggaa ggaagttgaa aagggtgggtg actgttctac cgaaccaatg 540
aacttgaacc ctgctttag tagccaagaaga caagactgggt ctggtgaatt gtgtgaaaac 600
ggttctttct acttcgctaa gaaggaattg atcgaacaag gtttgttgca aggtggtaag 660
aagacctact acgaaatgaa gccagaatac tctgttgaca tcgacgttga catcgactgg 720
ccagttgctg aacaaagagt tttgagattc ggttacttcg gtaaggacaa gccagaagtt 780
gtagattgtg tgttgtgtaa cgtttctgggt tgtttgaccg acggtcaa atctacacct 840
gcttctgggtg aagaaatgggt ttctatcaac atcagggacc aaatcggtat ctctatgttg 900
aagaaggaag gtgttaaggt tatcttgttg gaaacctacc ctatcgctaa ggctttggct 960
gtagattgtg ctgaaagaat ggggtgtcca ttgttgcacc acatggacga caagttgaag 1020
gaagttgaaa gaatcatggt tgaagaaaag ttggaatgga aggaagttgc ttacttgggt 1080
aacgacgaag ctgacgttaa gtgtttggaa ttggctgggt tgtctgggtg tccagttgac 1140
gctccaaccg ttgctttgaa ccacaccaag tacacctgtc acaacgctgc tggtcacggt 1200
gctgttagag aattcgctga acacatcttg ttgttgaaga agaaggctaa gtctcaa atg 1260
gaacaagaca gaatcttag ggacgtttc tga 1293
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<210> 96

<211> 430

<212> PRT

<213> ?D. rerio

<220>

<223> CMAS

<400> 96

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

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | His | Asn | Phe | Arg | Trp | Lys | Glu | Val | Glu | Lys | Gly | Gly | Asp | Cys | Ser | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Thr | Glu | Pro | Met | Asn | Leu | Asn | Pro | Ala | Cys | Arg | Pro | Arg | Arg | Gln | Asp | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Trp | Ser | Gly | Glu | Leu | Cys | Glu | Asn | Gly | Ser | Phe | Tyr | Phe | Ala | Lys | Lys | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Glu | Leu | Ile | Glu | Gln | Gly | Leu | Leu | Gln | Gly | Gly | Lys | Lys | Thr | Tyr | Tyr | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Glu | Met | Lys | Pro | Glu | Tyr | Ser | Val | Asp | Ile | Asp | Val | Asp | Ile | Asp | Trp | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Pro | Val | Ala | Glu | Gln | Arg | Val | Leu | Arg | Phe | Gly | Tyr | Phe | Gly | Lys | Asp | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Lys | Pro | Glu | Val | Val | Arg | Leu | Leu | Leu | Cys | Asn | Val | Ser | Gly | Cys | Leu | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Thr | Asp | Gly | Gln | Ile | Tyr | Thr | Ser | Ala | Ser | Gly | Glu | Glu | Met | Val | Ser | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Ile | Asn | Ile | Arg | Asp | Gln | Ile | Gly | Ile | Ser | Met | Leu | Lys | Lys | Glu | Gly | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Val | Lys | Val | Ile | Leu | Leu | Glu | Thr | Tyr | Pro | Ile | Ala | Lys | Ala | Leu | Ala | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Val | Arg | Leu | Ser | Glu | Arg | Met | Gly | Cys | Pro | Leu | Leu | His | His | Met | Asp | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Asp | Lys | Leu | Lys | Glu | Val | Glu | Arg | Ile | Met | Val | Glu | Glu | Lys | Leu | Glu | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Trp | Lys | Glu | Val | Ala | Tyr | Leu | Gly | Asn | Asp | Glu | Ala | Asp | Val | Lys | Cys | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Leu | Glu | Leu | Ala | Gly | Leu | Ser | Gly | Val | Pro | Val | Asp | Ala | Pro | Thr | Val | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| Ala | Leu | Asn | His | Thr | Lys | Tyr | Thr | Cys | His | Asn | Ala | Ala | Gly | His | Gly | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| Ala | Val | Arg | Glu | Phe | Ala | Glu | His | Ile | Leu | Leu | Leu | Lys | Lys | Lys | Ala | |
| | | | | 405 | | | | 410 | | | | | | 415 | | |
| Lys | Ser | Gln | Met | Glu | Gln | Asp | Arg | Ile | Cys | Arg | Asp | Ala | Phe | | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |

<210> 97

<211> 1221

<212> DNA

<213> Artificial

<220>

<223> CDS St6GAL1 (human / rat#2 construct) codon optimized

<400> 97

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| atgatccaca | ccaacttgaa | gaagaagttc | tctttgttca | tcttggtttt | cttgttgttc | 60 |
| gctgttatct | gtgtttggaa | ggaaaagaag | aagggttctt | actacgactc | tttcaagttg | 120 |
| caaaccaagg | aattccaagt | tttgaagtct | ttgggtaagt | tggctatggg | ttctgactct | 180 |
| caatctgttt | cttcttcttc | tacccaagac | ccacacagag | gtagacaaac | cttgggttct | 240 |
| ttgagagggt | tggctaaggc | taagccagaa | gcttctttcc | aagtttggaa | caaggactct | 300 |
| tcttctaaga | acttgatccc | aagattgcaa | aagatctgga | agaactactt | gtctatgaac | 360 |
| aagtacaagg | tttcttacaa | gggtccaggt | ccaggtatca | agttctctgc | tgaagctttg | 420 |
| agatgtcact | tgcgcgacca | cgttaacgtt | tctatggttg | aagttaccga | cttccatttc | 480 |
| aacacctctg | aatgggaagg | ttacttgcca | aaggaatcta | tcagaaccaa | ggctgggtcca | 540 |
| tggggtagat | gtgctgttgt | ttcttctgct | ggttctttga | agtcttctca | attgggtaga | 600 |
| gaaatcgacg | accacgacgc | tgttttgaga | ttcaacgggtg | ctccaaccgc | taacttccaa | 660 |
| caagacgttg | gtaccaagac | caccatcaga | ttgatgaact | ctcaattggt | taccaccgaa | 720 |

```

aagagattct tgaaggactc tttgtacaac gaaggtatct tgatcgtttg ggacccatct 780
gtttaccact ctgacatccc aaagtgggtac caaaaccag actacaactt cttcaacaac 840
tacaagacct acagaaagtt gcacccaaac caaccattct acatcttgaa gccacaaatg 900
ccatgggaat tgtgggacat cttgcaagaa atctctccag aagaaatcca accaaaccca 960
ccatcttctg gtatgttggg tatcatcatc atgatgacct tgtgtgacca agttgacatc 1020
tacgaattct tgccatctaa gagaaagacc gacgtttgtt actactacca aaagttcttc 1080
gactctgctt gtacatggg tgcttaccac ccattgttgt acgaaaagaa cttgggtaag 1140
cacttgaacc aaggtaccga cgaagacatc tacttgttgg gtaaggctac cttgccaggt 1200
ttcagaacca tccactgttg a 1221

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<210> 98
 <211> 406
 <212> PRT
 <213> Artificial

<220>
 <223> St6GAL1 (human / rat#2 construct)

<400> 98

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | His | Thr | Asn | Leu | Lys | Lys | Lys | Phe | Ser | Leu | Phe | Ile | Leu | Val | 1 | 5 | 10 | 15 |
| Phe | Leu | Leu | Phe | Ala | Val | Ile | Cys | Val | Trp | Lys | Glu | Lys | Lys | Lys | Gly | 20 | 25 | 30 | |
| Ser | Tyr | Tyr | Asp | Ser | Phe | Lys | Leu | Gln | Thr | Lys | Glu | Phe | Gln | Val | Leu | 35 | 40 | 45 | |
| Lys | Ser | Leu | Gly | Lys | Leu | Ala | Met | Gly | Ser | Asp | Ser | Gln | Ser | Val | Ser | 50 | 55 | 60 | |
| Ser | Ser | Ser | Thr | Gln | Asp | Pro | His | Arg | Gly | Arg | Gln | Thr | Leu | Gly | Ser | 65 | 70 | 75 | 80 |
| Leu | Arg | Gly | Leu | Ala | Lys | Ala | Lys | Pro | Glu | Ala | Ser | Phe | Gln | Val | Trp | 85 | 90 | 95 | |
| Asn | Lys | Asp | Ser | Ser | Ser | Lys | Asn | Leu | Ile | Pro | Arg | Leu | Gln | Lys | Ile | 100 | 105 | 110 | |
| Trp | Lys | Asn | Tyr | Leu | Ser | Met | Asn | Lys | Tyr | Lys | Val | Ser | Tyr | Lys | Gly | 115 | 120 | 125 | |
| Pro | Gly | Pro | Gly | Ile | Lys | Phe | Ser | Ala | Glu | Ala | Leu | Arg | Cys | His | Leu | 130 | 135 | 140 | |
| Arg | Asp | His | Val | Asn | Val | Ser | Met | Val | Glu | Val | Thr | Asp | Phe | Pro | Phe | 145 | 150 | 155 | 160 |
| Asn | Thr | Ser | Glu | Trp | Glu | Gly | Tyr | Leu | Pro | Lys | Glu | Ser | Ile | Arg | Thr | 165 | 170 | 175 | |
| Lys | Ala | Gly | Pro | Trp | Gly | Arg | Cys | Ala | Val | Val | Ser | Ser | Ala | Gly | Ser | 180 | 185 | 190 | |
| Leu | Lys | Ser | Ser | Gln | Leu | Gly | Arg | Glu | Ile | Asp | Asp | His | Asp | Ala | Val | 195 | 200 | 205 | |
| Leu | Arg | Phe | Asn | Gly | Ala | Pro | Thr | Ala | Asn | Phe | Gln | Gln | Asp | Val | Gly | 210 | 215 | 220 | |
| Thr | Lys | Thr | Thr | Ile | Arg | Leu | Met | Asn | Ser | Gln | Leu | Val | Thr | Thr | Glu | 225 | 230 | 235 | 240 |
| Lys | Arg | Phe | Leu | Lys | Asp | Ser | Leu | Tyr | Asn | Glu | Gly | Ile | Leu | Ile | Val | 245 | 250 | 255 | |
| Trp | Asp | Pro | Ser | Val | Tyr | His | Ser | Asp | Ile | Pro | Lys | Trp | Tyr | Gln | Asn | 260 | 265 | 270 | |
| Pro | Asp | Tyr | Asn | Phe | Phe | Asn | Asn | Tyr | Lys | Thr | Tyr | Arg | Lys | Leu | His | 275 | 280 | 285 | |
| Pro | Asn | Gln | Pro | Phe | Tyr | Ile | Leu | Lys | Pro | Gln | Met | Pro | Trp | Glu | Leu | | | | |

| | | | | |
|---|-----|-----|-----|-----|
| 290 | | 295 | | 300 |
| Trp Asp Ile Leu Gln Glu Ile Ser Pro Glu Glu Ile Gln Pro Asn Pro | | | | |
| 305 | | 310 | | 315 |
| Pro Ser Ser Gly Met Leu Gly Ile Ile Ile Met Met Thr Leu Cys Asp | | | | |
| | 325 | | 330 | 335 |
| Gln Val Asp Ile Tyr Glu Phe Leu Pro Ser Lys Arg Lys Thr Asp Val | | | | |
| | 340 | | 345 | 350 |
| Cys Tyr Tyr Tyr Gln Lys Phe Phe Asp Ser Ala Cys Thr Met Gly Ala | | | | |
| | 355 | | 360 | 365 |
| Tyr His Pro Leu Leu Tyr Glu Lys Asn Leu Val Lys His Leu Asn Gln | | | | |
| | 370 | | 375 | 380 |
| Gly Thr Asp Glu Asp Ile Tyr Leu Leu Gly Lys Ala Thr Leu Pro Gly | | | | |
| 385 | | 390 | | 395 |
| Phe Arg Thr Ile His Cys | | | | 400 |
| | 405 | | | |

<210> 99

<211> 1002

<212> DNA

<213> Artificial

<220>

<223> CDS St3GAL4 (human / rat#2 construct) codon optimized

<400> 99

| | |
|---|------|
| atgatccaca ccaacttgaa gaagaagttc tctttgttca tcttggtttt cttgttgttc | 60 |
| gctgttatct gtgtttggag agaagacaga tacatcgaat tgttctactt cccaatccca | 120 |
| gaaaagaagg aaccatgttt gcaaggtgaa gctgaatcta aggcttctaa gttgttcggt | 180 |
| aactactctc gcgaccaacc aatcttcttg agattggaag actacttctg ggттаagacc | 240 |
| ccatctgctt acgaattgcc atacggtacc aagggttctg aagacttggt gttgagagtt | 300 |
| ttggctatca cctcttcttc tatcccaaag aacatccaat ctttgagatg tagaagatgt | 360 |
| gttggtgttg gtaacggtca cagattgaga aactcttctt tgggtgacgc tatcaacaag | 420 |
| tacgacgttg ttatcagatt gaacaacgct ccagttgctg gttacgaagg tgacgttggt | 480 |
| tctaagacca ccatgagatt gttctaccca gaatctgctc acttcgaccc aaaggttgaa | 540 |
| aacaaccag acacctgtgt gggtttgtgt gctttcaagg ctatggactt ccactggatc | 600 |
| gaaaccatct tgtctgacaa gaagagagtt agaaagggtt tctggaagca accaccattg | 660 |
| atctgggacg ttaaccctaa gcaaatcaga atcttgaacc cattcttcat ggaaatcgct | 720 |
| gctgacaagt tggtgtcttt gccaatgcaa caaccaagaa agatcaagca aaagccaacc | 780 |
| accggtttgt tggctatcac cttggctttg cacttggtgt acttggttca catcgctggt | 840 |
| ttcggttacc cagacgctta caacaagaag caaaccatcc actactacga acaaatcacc | 900 |
| ttgaagtcta tggctgggtc tggtcacaac gtttctcaag aagctttggc tatcaagaga | 960 |
| atgttggaata tgggtgctat caagaacttg acctcttct ga | 1002 |

<210> 100

<211> 333

<212> PRT

<213> Artificial

<220>

<223> St3GAL4 (human / rat#2 construct)

<400> 100

| | |
|---|----|
| Met Ile His Thr Asn Leu Lys Lys Lys Phe Ser Leu Phe Ile Leu Val | |
| 1 | 5 |
| Phe Leu Leu Phe Ala Val Ile Cys Val Trp Arg Glu Asp Arg Tyr Ile | |
| 20 | 25 |
| | 30 |

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

<210> 101

<211> 1221

<212> DNA

<213> Artificial

<220>

<223> CDS St6GAL1 codon optimized

<400> 101

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| atgatccaca | ccaacttgaa | gaagaagttc | tcttggtgtg | ttttggtttt | cttggtgttc | 60 |
| gctgttatct | gtgtttggaa | ggaaaagaag | aagggttctt | actacgactc | tttcaagttg | 120 |
| caaaccaagg | aattccaagt | tttgaagtct | ttgggtaagt | tggtctatggg | ttctgactct | 180 |
| caatctgttt | cttcttcttc | tacccaagac | ccacacagag | gtagacaaac | cttgggttct | 240 |
| ttgagagggt | tggttaaggc | taagccagaa | gcttctttcc | aagtttggaa | caaggactct | 300 |
| tcttctaaga | acttgatccc | aagattgcaa | aagatctgga | agaactactt | gtctatgaac | 360 |
| aagtacaagg | tttcttacaa | gggtccaggt | ccaggtatca | agttctctgc | tgaagctttg | 420 |
| agatgtcact | tgcgcgacca | cgttaacgtt | tctatggttg | aagttaccga | cttcccatcc | 480 |

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aacacctctg aatgggaagg ttacttgcca aaggaatcta tcagaaccaa ggctgggtcca 540
tggggtagat gtgctgttgt ttcttctgct ggttctttga agtcttctca attgggtaga 600
gaaatcgacg accacgacgc tgttttgaga ttcaacgggtg ctccaaccgc taacttccaa 660
caagacgttg gtaccaagac caccatcaga ttgatgaact ctcaattggg taccaccgaa 720
aagagattct tgaaggactc tttgtacaac gaaggatatc tgatcgtttg ggacccatct 780
gtttaccact ctgacatccc aaagtgggtac caaaaccag actacaactt cttcaacaac 840
tacaagacct acagaaagtt gcacccaaac caaccattct acatcttgaa gccacaaatg 900
ccatgggaat tgtgggacat cttgcaagaa atctctccag aagaaatcca accaaaccca 960
ccatcttctg gtatgttggg tatcatcatc atgatgacct tgtgtgacca agttgacatc 1020
tacgaattct tgccatctaa gagaaagacc gacgtttgtt actactacca aaagttcttc 1080
gactctgctt gtaccatggg tgcttaccac ccattgttgt acgaaaagaa cttgggttaag 1140
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<210> 102

<211> 406

<212> PRT

<213> H. sapiens

<220>

<223> St6GAL1

<400> 102

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20          25          30
Ser Tyr Tyr Asp Ser Phe Lys Leu Gln Thr Lys Glu Phe Gln Val Leu
35          40          45
Lys Ser Leu Gly Lys Leu Ala Met Gly Ser Asp Ser Gln Ser Val Ser
50          55          60
Ser Ser Ser Thr Gln Asp Pro His Arg Gly Arg Gln Thr Leu Gly Ser
65          70          75          80
Leu Arg Gly Leu Ala Lys Ala Lys Pro Glu Ala Ser Phe Gln Val Trp
85          90          95
Asn Lys Asp Ser Ser Ser Lys Asn Leu Ile Pro Arg Leu Gln Lys Ile
100         105         110
Trp Lys Asn Tyr Leu Ser Met Asn Lys Tyr Lys Val Ser Tyr Lys Gly
115         120         125
Pro Gly Pro Gly Ile Lys Phe Ser Ala Glu Ala Leu Arg Cys His Leu
130         135         140
Arg Asp His Val Asn Val Ser Met Val Glu Val Thr Asp Phe Pro Phe
145         150         155         160
Asn Thr Ser Glu Trp Glu Gly Tyr Leu Pro Lys Glu Ser Ile Arg Thr
165         170         175
Lys Ala Gly Pro Trp Gly Arg Cys Ala Val Val Ser Ser Ala Gly Ser
180         185         190
Leu Lys Ser Ser Gln Leu Gly Arg Glu Ile Asp Asp His Asp Ala Val
195         200         205
Leu Arg Phe Asn Gly Ala Pro Thr Ala Asn Phe Gln Gln Asp Val Gly
210         215         220
Thr Lys Thr Thr Ile Arg Leu Met Asn Ser Gln Leu Val Thr Thr Glu
225         230         235         240
Lys Arg Phe Leu Lys Asp Ser Leu Tyr Asn Glu Gly Ile Leu Ile Val
245         250         255
Trp Asp Pro Ser Val Tyr His Ser Asp Ile Pro Lys Trp Tyr Gln Asn

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Met Val Ser Lys Ser Arg Trp Lys Leu Leu Ala Met Leu Ala Leu Val
 1 5 10 15
 Leu Val Val Met Val Trp Tyr Ser Ile Ser Arg Glu Asp Arg Tyr Ile
 20 25 30
 Glu Leu Phe Tyr Phe Pro Ile Pro Glu Lys Lys Glu Pro Cys Leu Gln
 35 40 45
 Gly Glu Ala Glu Ser Lys Ala Ser Lys Leu Phe Gly Asn Tyr Ser Arg
 50 55 60
 Asp Gln Pro Ile Phe Leu Arg Leu Glu Asp Tyr Phe Trp Val Lys Thr
 65 70 75 80
 Pro Ser Ala Tyr Glu Leu Pro Tyr Gly Thr Lys Gly Ser Glu Asp Leu
 85 90 95
 Leu Leu Arg Val Leu Ala Ile Thr Ser Ser Ile Pro Lys Asn Ile
 100 105 110
 Gln Ser Leu Arg Cys Arg Arg Cys Val Val Val Gly Asn Gly His Arg
 115 120 125
 Leu Arg Asn Ser Ser Leu Gly Asp Ala Ile Asn Lys Tyr Asp Val Val
 130 135 140
 Ile Arg Leu Asn Asn Ala Pro Val Ala Gly Tyr Glu Gly Asp Val Gly
 145 150 155 160
 Ser Lys Thr Thr Met Arg Leu Phe Tyr Pro Glu Ser Ala His Phe Asp
 165 170 175
 Pro Lys Val Glu Asn Asn Pro Asp Thr Leu Leu Val Leu Val Ala Phe
 180 185 190
 Lys Ala Met Asp Phe His Trp Ile Glu Thr Ile Leu Ser Asp Lys Lys
 195 200 205
 Arg Val Arg Lys Gly Phe Trp Lys Gln Pro Pro Leu Ile Trp Asp Val
 210 215 220
 Asn Pro Lys Gln Ile Arg Ile Leu Asn Pro Phe Phe Met Glu Ile Ala
 225 230 235 240
 Ala Asp Lys Leu Leu Ser Leu Pro Met Gln Gln Pro Arg Lys Ile Lys
 245 250 255
 Gln Lys Pro Thr Thr Gly Leu Leu Ala Ile Thr Leu Ala Leu His Leu
 260 265 270
 Cys Asp Leu Val His Ile Ala Gly Phe Gly Tyr Pro Asp Ala Tyr Asn
 275 280 285
 Lys Lys Gln Thr Ile His Tyr Tyr Glu Gln Ile Thr Leu Lys Ser Met
 290 295 300
 Ala Gly Ser Gly His Asn Val Ser Gln Glu Ala Leu Ala Ile Lys Arg
 305 310 315 320
 Met Leu Glu Met Gly Ala Ile Lys Asn Leu Thr Ser Phe
 325 330

<210> 105

<211> 1764

<212> DNA

<213> Artificial

<220>

<223> LAC12 re-coded codon optimized

<400> 105

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| atggctgatac actcttcctc ctcttcttcc tctcaaaaga agccaattaa cactattgaa | 60 |
| cacaaggata ctttgggtaa cgatcgagat cacaaggaag ctttgaactc cgataacgat | 120 |
| aacacttccg gtttgaagat taacggtgtc ccaattgaag atgctagaga agaagtcttg | 180 |
| ttgccagggtt acttgtccaa gcaatactac aagttatacg gtttgtgttt cattacttac | 240 |

| | | | | | | |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| ttgtgtgcta | ctatgcaagg | ttacgatggg | gctttgatgg | gttccattta | cactgaagat | 300 |
| gcttacttaa | agtactacca | cttggatatt | aactcctcct | ccggtactgg | tttggctttc | 360 |
| tccattttca | acgtcgggtc | aatttgtggg | gctttcttcg | tcccattgat | ggattggaag | 420 |
| ggtagaaagc | cagctatttt | gattggttgt | ttgggtgtcg | tcattgggtgc | tattatttcc | 480 |
| tccttgacta | ctactaagtc | cgctttgatt | ggtaggtgat | ggttcgtcgc | tttcttcgct | 540 |
| actattgcta | acgctgctgc | tccaacttac | tgtgctgaag | tcgctccagc | tcacttaaga | 600 |
| ggtaaggctg | ctggtttgta | caacactttg | tgggtccgtcg | gttccattgt | cgctgctttc | 660 |
| tccacttacg | gtactaacia | gaacttccca | aactcctcca | aggctttcaa | gattccattg | 720 |
| tacttacaaa | tgatgttccc | aggtttgggtc | tgtattttcg | gttggttgat | tccagaatcc | 780 |
| ccaagatggg | tggtcgggtg | cggtagagaa | gaagaggcta | gagaattcat | tattaagtac | 840 |
| cacttgaacg | gtgatagaac | tcacccattg | ttggatatgg | aaatggctga | aattattgaa | 900 |
| tccttccacg | gtactgattt | gtccaaccca | ttggaaatgt | tggatgtcag | atccttgttc | 960 |
| agaactagat | ccgatagata | cagagctatg | ttggtcattt | tgatggcttg | gttcgggtcaa | 1020 |
| ttctccggta | acaacgtctg | ttcctactac | ttgccaaacta | tgttgagaaa | cgtcgggtatg | 1080 |
| aagagtgtct | ccttgaacgt | cttgatgaac | gggtgtctact | ccattgtcac | ttggattttc | 1140 |
| tccatttgtg | gtgcttttct | cattgataag | attggtagaa | gagaagggtt | cttgggtttc | 1200 |
| atttccgggtg | ctgctttggc | tttgactggg | ttgtccattt | gtactgctag | atacgaagag | 1260 |
| actaagaaga | agtcgccttc | caacgggtgct | ttggctcttca | tttacttggt | cggtgggtatt | 1320 |
| ttctccttcg | ctttcactcc | aatgcaatcc | atgtactcca | ctgaagtctc | cactaacttg | 1380 |
| actagatcca | aggctcaatt | gttaaacttc | gttgtctccg | gtgtcgtcga | attcgtcaac | 1440 |
| caattcgcta | ctccaaaggc | tatgaagaac | attaagtact | ggttctacgt | cttctacgtc | 1500 |
| ttcttcgata | ttttcgaatt | cattgtcatt | tacttcttct | tcgtcgaagc | taagggtaga | 1560 |
| tccttggaag | aattggaagt | cgtcttcgaa | gctccaaacc | caagaaaggc | ttccgtcgat | 1620 |
| caagctttct | tggctcaagt | cagagctact | ttgggtccaaa | gaaacgatgt | cagagtcgct | 1680 |
| aacgtcctaa | acttaaagga | acaagaacca | ttaaagtccg | atgctgatca | cgtcgaaaag | 1740 |
| ttgtccgaag | ctgaatccgt | ctga | | | | 1764 |

<210> 106

<211> 587

<212> PRT

<213> K. lactis

<220>

<223> LAC12 re-coded

<400> 106

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

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Leu | Thr | Thr | Thr | Lys | Ser | Ala | Leu | Ile | Gly | Gly | Arg | Trp | Phe | Val | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Ala | Phe | Phe | Ala | Thr | Ile | Ala | Asn | Ala | Ala | Ala | Pro | Thr | Tyr | Cys | Ala | |
| | | | 180 | | | | | 185 | | | | | | 190 | | |
| Glu | Val | Ala | Pro | Ala | His | Leu | Arg | Gly | Lys | Val | Ala | Gly | Leu | Tyr | Asn | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Thr | Leu | Trp | Ser | Val | Gly | Ser | Ile | Val | Ala | Ala | Phe | Ser | Thr | Tyr | Gly | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Thr | Asn | Lys | Asn | Phe | Pro | Asn | Ser | Ser | Lys | Ala | Phe | Lys | Ile | Pro | Leu | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Tyr | Leu | Gln | Met | Met | Phe | Pro | Gly | Leu | Val | Cys | Ile | Phe | Gly | Trp | Leu | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Ile | Pro | Glu | Ser | Pro | Arg | Trp | Leu | Val | Gly | Val | Gly | Arg | Glu | Glu | Glu | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Ala | Arg | Glu | Phe | Ile | Ile | Lys | Tyr | His | Leu | Asn | Gly | Asp | Arg | Thr | His | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Pro | Leu | Leu | Asp | Met | Glu | Met | Ala | Glu | Ile | Ile | Glu | Ser | Phe | His | Gly | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Thr | Asp | Leu | Ser | Asn | Pro | Leu | Glu | Met | Leu | Asp | Val | Arg | Ser | Leu | Phe | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Arg | Thr | Arg | Ser | Asp | Arg | Tyr | Arg | Ala | Met | Leu | Val | Ile | Leu | Met | Ala | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Trp | Phe | Gly | Gln | Phe | Ser | Gly | Asn | Asn | Val | Cys | Ser | Tyr | Tyr | Leu | Pro | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Thr | Met | Leu | Arg | Asn | Val | Gly | Met | Lys | Ser | Val | Ser | Leu | Asn | Val | Leu | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Met | Asn | Gly | Val | Tyr | Ser | Ile | Val | Thr | Trp | Ile | Ser | Ser | Ile | Cys | Gly | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| Ala | Phe | Phe | Ile | Asp | Lys | Ile | Gly | Arg | Arg | Glu | Gly | Phe | Leu | Gly | Ser | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| Ile | Ser | Gly | Ala | Ala | Leu | Ala | Leu | Thr | Gly | Leu | Ser | Ile | Cys | Thr | Ala | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| Arg | Tyr | Glu | Lys | Thr | Lys | Lys | Lys | Ser | Ala | Ser | Asn | Gly | Ala | Leu | Val | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| Phe | Ile | Tyr | Leu | Phe | Gly | Gly | Ile | Phe | Ser | Phe | Ala | Phe | Thr | Pro | Met | |
| | | 435 | | | | | 440 | | | | | 445 | | | | |
| Gln | Ser | Met | Tyr | Ser | Thr | Glu | Val | Ser | Thr | Asn | Leu | Thr | Arg | Ser | Lys | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| Ala | Gln | Leu | Leu | Asn | Phe | Val | Val | Ser | Gly | Val | Ala | Gln | Phe | Val | Asn | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| Gln | Phe | Ala | Thr | Pro | Lys | Ala | Met | Lys | Asn | Ile | Lys | Tyr | Trp | Phe | Tyr | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| Val | Phe | Tyr | Val | Phe | Phe | Asp | Ile | Phe | Glu | Phe | Ile | Val | Ile | Tyr | Phe | |
| | | | 500 | | | | | 505 | | | | | 510 | | | |
| Phe | Phe | Val | Glu | Thr | Lys | Gly | Arg | Ser | Leu | Glu | Glu | Leu | Glu | Val | Val | |
| | | 515 | | | | | 520 | | | | | 525 | | | | |
| Phe | Glu | Ala | Pro | Asn | Pro | Arg | Lys | Ala | Ser | Val | Asp | Gln | Ala | Phe | Leu | |
| | | | | | | 535 | | | | | 540 | | | | | |
| Ala | Gln | Val | Arg | Ala | Thr | Leu | Val | Gln | Arg | Asn | Asp | Val | Arg | Val | Ala | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | |
| Asn | Ala | Gln | Asn | Leu | Lys | Glu | Gln | Glu | Pro | Leu | Lys | Ser | Asp | Ala | Asp | |
| | | | | 565 | | | | | 570 | | | | | 575 | | |
| His | Val | Glu | Lys | Leu | Ser | Glu | Ala | Glu | Ser | Val | | | | | | |
| | | | 580 | | | | | 585 | | | | | | | | |

<211> 78
<212> DNA
<213> *S. cerevisiae*

<220>
<223> ST6GAL1 (Golgi targeting #2)

<400> 107
atgatccaca ccaacttgaa gaagaagttc tctttgttca tcttggtttt cttgttgttc 60
gctgttatct gtgttttg 78

<210> 108
<211> 500
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter PAB1

<400> 108
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atgaccatat aagagggtcat actgtatgaa gccacaaagc agatagatca atcatgttta 120
acgaaaactg ttaatcgaag attatctctt tttttttttc tctttccttt ttacaaagaa 180
aatTTTTTTT gcgctttttg ccatcaccat cgcaagttct gggacaattg ttctctttcg 240
ctccagttcc aaggaaagag gtttctgttt tacttaatag aaagtgtcat cttgtatTTT 300
atatctcttc tttcttgtgt aaaattcttt agttttgatt ttgtatTTTT aggacagtga 360
gctacgaagt aacattttta cttaataacc gtttgaagca tagagcaggc cctggtacca 420
ccaccttaata tctggctttt tattcaataa aaactcaaaa aaaaaaatcc aaaaaaact 480
aaaaaaccaa taaaaataaa 500

<210> 109
<211> 500
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter RPL17B

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aagtaggcgt gggaagtga gctctttcgc tctttctgtg atgatctcct tccagctagg 120
ctcggttcga ccttgaggtc tgcccctagc tccttcctat tccaaacgga ataccaaag 180
tccagcccgt gacaatgcag cagggtggct aatttttcat ccagagtttg cagaatgttg 240
gttctcacia actcagagag aattggcgga tgatgggtaa ctgtgagagg aagtgtctgg 300
atttgatcgt atttgttaaa ttcatcaaca ctttttatgc agagggtgtag tagttaggt 360
agcccctagt aattgggtgtt tattattgtc tatatagaaa tttcttttta gtgtagcttg 420
tactctttcc ctgcattatt tttgttttat tgacttttgt cttggtgaat caaaaaatta 480
acgaaacgaa caaatttaaa 500

<210> 110
<211> 365
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter RPL1A

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ctgcattatt ttttagtcctt tttatagaga catgaacatt caattacttt caaggataaa 120
tattctaata ttcatattat tcacttatgt atttttaacg aaactctact ccattctact 180
gggatcgggc atacttttacg ggggtgcacgg attttagcag tctttttctt tcttggcttt 240
tgcgagatgc cttgagagga agatTTTTTTT ttcactcaaa acctctgtct tgtacatatc 300
tagaacatgt ttcattgata ttggacgtta ctatttcaat ttaacagtca accagtcgtc 360
caaaa 365

<210> 111
<211> 450
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter RPL31B

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caggtgatgg tgccatttcc gcccttctcg ttagagccgg aacgcagatg agctgccctc 120
tggcgcccgc gtcctcgcg tggttaagttc actactaggc tgggaagtgt atggtgtcct 180
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caactggaag ggcgcgaaac cgagggtaat gcgacagagg gcactgacgt tgtttcgtaa 300
ccttgtaagc tctttctgat ggtagtgctt catgtacatg tttactctat tatttgacca 360
gtctcattgt tgataggttc cttagtttta catagtcttg ggtcttagta tatttcaatt 420
gcacgagcag ataatccaaa gtacttgaaa 450

<210> 112
<211> 500
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter RPL32

<400> 112
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agaatcgttt tattaaaata cttttaaaga attttagattt tgataattag ttcattctct 120
tttacaaaga taatcaccaa acagggacaa tacactgaac gataaaaagta tgtgacatat 180
agaatgctag aatgaatagc ctagactgca ttgttatgag agcaacgttt gatatttgtg 240
gcgattggaa caaacatagt acatgccaaa atgagatgaa atgtccaatt tgaactgatt 300
aacatacacg cgcaagctcg tatttgttta ctggtacacc tagagttagc cgatcaaaga 360
gacagtggca gatatatggg aaaattttct ccggaagatt gcatgcgaga gtctcataac 420
cagtcatttc ccaagataca attctcggag ctgttatact aacaaacttt taattttcat 480
tttttttttt ttttgattag 500

<210> 113
<211> 500
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter RPL33A

<400> 113

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| taactttact | cattcacctc | atcgagaatg | gaaaaactaa | tgaaaaattc | agccctaaga | 60 |
| aaaatgctcg | aaatacatat | cgtagtagtt | accacacctt | cgttgcaatt | ttttccacgg | 120 |
| caatattaac | atccttacct | ctttacaccc | ttacacttcc | tttgattact | tttttttttc | 180 |
| ttctctcagt | ttgtttcgcg | tacacacctt | gggtgcccgt | cgaagaattc | tccgctcaat | 240 |
| ggaacgtacg | gaggtcatac | tcagcttccc | tctagcagta | cagtcgttag | acagagctga | 300 |
| ttcatctttt | ccggcctaaa | ctcgtatcct | gtccctccct | tctactcttc | accggcatga | 360 |
| tacctttgcc | tcccgtttgg | caaaatattc | gctatcaagc | tttaattttac | gtgtattaat | 420 |
| cactagttca | aaacttgagt | tattttgcct | tgagcaattg | taagaatccg | taagaaacca | 480 |
| acaatcaaat | aaattgaaaa | | | | | 500 |

<210> 114

<211> 500

<212> DNA

<213> *S. cerevisiae*

<220>

<223> promoter RPL6B

<400> 114

| | | | | | | |
|------------|------------|-------------|------------|-------------|------------|-----|
| cttgtcttaa | tctgaaagtt | actaataata | ataaagacaa | aatatcaccc | atgcacaaaa | 60 |
| atgtatgggt | cataattttt | tttcttgcct | tcaaaaatcg | ttgttagctg | caaaatggcg | 120 |
| gtgaaacaca | tagttgtggt | tatgcgtccc | ctccgggagg | ccgcagatgg | aggatgcccc | 180 |
| catgtgctga | ttctccccgt | aggcggcgag | taatatcctc | gcctaacctg | gacttgccgt | 240 |
| gctaagtcgg | ccttctaggc | tgcgcttccg | ttcagcatcg | tttacggtag | agggagcaca | 300 |
| tgggcggaaa | caaacctcat | tctggctcctg | tgcttgccca | tttgcaactgt | atagagtgtg | 360 |
| tgagtttcaa | ttaatgttgt | aggcgcgagg | ccctgtaata | tggcagttga | tcaaaagtca | 420 |
| atagataatt | ttcaagcaaa | atctcattta | ggtttgacta | ctttcttgaa | cttgaagag | 480 |
| aagcaaatat | attcaacgaa | | | | | 500 |

<210> 115

<211> 500

<212> DNA

<213> *S. cerevisiae*

<220>

<223> promoter RPS19B

<400> 115

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|-----|
| taacttcata | atctaaacct | atcagttcag | tatcaagtca | gctattccgc | cctatgcata | 60 |
| aacctacaaa | ctatcattca | cacacttttc | ccattttttt | tcaatactac | tttacatccg | 120 |
| aacatttttag | caaccacac | catatacctt | tggtgcacta | ttgattttct | tcctgatgtc | 180 |
| agctttttgt | gctttgacaa | aaaaatcgcg | tctacgtccg | tccgttctcc | ctgaataaat | 240 |
| taggcgcgtt | tgagcccagc | aggacggagc | tctagtgaca | agccctgggtg | tttggtgagg | 300 |
| ttttgcacat | tgctgttctt | tctactgtat | tgagatctcc | agttttacggc | tccctgggag | 360 |
| ccaccgtaa | cgcggttggt | gtgcccattt | caataagcga | acattagtga | agatacaatc | 420 |
| gttaaaatgg | actaatgaaa | ttttaaaagt | ggattttttg | gaatattgac | aacaaaggta | 480 |
| tagaaccaaa | gataataaag | | | | | 500 |

<210> 116

<211> 500

<212> DNA

<213> *S. cerevisiae*

<220>

<223> promoter RPS26B

<400> 116
aataacgcta ggcgtctatc gtaacataac agagtgtttt attatctata tagtgatatt 60
taccttaaatt tcttgctctt aagcgtgtct caatttactt tcaaaaagaa agataaatac 120
acataatcaa acaggaaaag tatgttataa gagcgaataa tgtgataaag gagcaaagtg 180
gaaggaaaga attataaaga atgacgttgc cgtaaagcca atttttcaac caacaaaatt 240
gcaatagttt caagcaaatt atgggtgtgtc cgggattggc ggtagtaaat tgtaaaacaa 300
tagctgggtca atagttgata ttcataccga cactataatc cacaaaagat ggggtgacatt 360
gatggctgaa atggtagagg caagaaaatt ttttaaagca ataaggcata gacgtttcta 420
ttaatccttt gttttattca gtattttcga tatttcctct ttactaactt caatttactg 480
aatttgtatg taatttttag 500

<210> 117
<211> 500
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter RPS27B

<400> 117
ttacttacgt ctattataac cttccgcgta aaaaagaaat attgacatcc tttcttgtat 60
ttagcccata cattttcacc catgcacccat tggattataa agaaaaaaat ttaataaaaa 120
tctgccgggg aaatttcaga agaaaaaagg aaggtgtgtt cgcatttaac acgggccacc 180
ataaactttt gtttgccacc catctagacg ggatccgccc cgccaaggc tctcttcctc 240
tagctaggca atgtggctct cggaaaggaa actcccacca ggacgtggtg ggaaatgcag 300
caattcccct ctgcttcccg ctgacctttc ttggggccag tttagtaagt atgctctcat 360
ctttcatgtg tgctgtaact tgcaagtcac taacactatc tataattgat attagacgtt 420
aaaagtctta tatagcattt gcttttattt agagaatacg aaaacacacc agataattag 480
tgcatatata ttagatcaat 500

<210> 118
<211> 332
<212> DNA
<213> *S. cerevisiae*

<220>
<223> promoter RPS8A

<400> 118
acacaccagg acaaaaagta tgtgctatgg tcatatgagt aatggaacta catattattt 60
tgaatgctac aggacctctc tttgaatgga atagatagtg gaaaaagtaa acttaactaa 120
aagggatgat ataaattgtg acaggagcag tgcactaaac tgaatccttt gtgtacccaa 180
aaaatcaagc ctcttatgaa acgccgagtt tttcacaaga agagatgaaa agaaacccaa 240
gcatatttca agataagaaa aaaattccgc aacttttcta cgttctttat ttactaaca 300
agcgtcatta aattttctat tacagttaca aa 332

<210> 119
<211> 200
<212> DNA
<213> *S. cerevisiae*

<220>
<223> terminator HEM1

<400> 119
aacaaccaat atatgcatgg gctgagatag aggtacaagg aatttgtaaa tcagtaaaaa 60

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| aaaaaattaa | cagttttttt | ttttcatttt | ttttttttat | tcttatttat | gtatgatact | 120 |
| ttattattat | ttctcttaat | tatttattta | tttaactaac | acgatgagca | cttttaactg | 180 |
| caatggttaa | actgtagcaa | | | | | 200 |

<210> 120
 <211> 200
 <212> DNA
 <213> *S. cerevisiae*

<220>
 <223> terminator RPL18B

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| <400> 120 | | | | | | |
| tctagtatgg | tttgaaacct | tacaattttt | cttctttggt | cctttttcct | tgtttcagtg | 60 |
| tatattaggt | tgggaaagag | ggatttttcc | ataccatatg | actgactaca | atatatacat | 120 |
| gtataataac | ttcataatct | aaacctatca | gttcagtatc | aagtcagcta | ttccgcccta | 180 |
| tgcataaacc | tacaaactat | | | | | 200 |

<210> 121
 <211> 200
 <212> DNA
 <213> *S. cerevisiae*

<220>
 <223> terminator RPL1B

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| <400> 121 | | | | | | |
| tcacttccga | gcgattaata | catatctcca | tctttttaaa | tacctttttt | aatacgtatg | 60 |
| actctaagta | gtaaaagtat | tatgcatagt | tttagccaga | tatttttggg | cccggaatat | 120 |
| atcttttcgg | gaagctcgga | gtatattgca | ccgatccgat | tcttactcca | tatcatgccca | 180 |
| tttttctttc | ctttctcagc | | | | | 200 |

<210> 122
 <211> 200
 <212> DNA
 <213> *S. cerevisiae*

<220>
 <223> terminator RPL22B

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| <400> 122 | | | | | | |
| atagacactc | acatgtatat | taattttataa | aatgctattc | atatcataat | tcaccaccct | 60 |
| taatatatcc | ttttgtccct | cttttgattt | acatatttta | tttttgcaat | atgtcacttc | 120 |
| acgaaaatta | gtgaaaaata | gaaaagaaaa | agaaatgctt | tagcttttga | aacacgaaga | 180 |
| tcatcaaaaa | actttaagaa | | | | | 200 |

<210> 123
 <211> 200
 <212> DNA
 <213> *S. cerevisiae*

<220>
 <223> terminator RPL6A

| | | | | | | |
|------------|------------|------------|------------|------------|------------|----|
| <400> 123 | | | | | | |
| atataattat | tttaacgaac | ttctataata | atatatatgc | aggtaaaatt | ataatttaac | 60 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| tacagtttca | taagtgcatt | tgtattgagc | attgggtttt | tattcgcata | tttatatctt | 120 |
| cattgcggca | atcacccaga | gaaagggcgt | gaaaagaaaa | aggaatacat | tatttcaagt | 180 |
| tcctttgatc | tttctataa | | | | | 200 |

<210> 124
 <211> 200
 <212> DNA
 <213> *S. cerevisiae*

<220>
 <223> terminator RPL8B

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| <400> 124 | | | | | | |
| attcatatat | agaatttcga | acatcgtaat | ataattatat | tttgatact | tacttaattc | 60 |
| ccgttttctt | ttgtatgaat | ttttgaaaaa | taatagagca | acattatact | tttaagcgcg | 120 |
| gcactagttc | atcaatgtcg | ggttttgcca | agcaaaacta | attggggcag | ctatttatat | 180 |
| ttgaaagaat | cagcgtcact | | | | | 200 |

<210> 125
 <211> 200
 <212> DNA
 <213> *S. cerevisiae*

<220>
 <223> terminator RPS16B

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| <400> 125 | | | | | | |
| gaaaatttca | agattttttc | cagaaatctc | ttcacttttc | tttgacatc | tattgtatta | 60 |
| aaaaactttt | tacttacata | tactgtatat | cttcctataa | cgggtaaaac | gttaatttag | 120 |
| aatcattccc | aaaacttcat | ttccttatca | tgctttgcca | tgtgatgcc | aatagaattg | 180 |
| tcttgtgcgt | tcacgaaatg | | | | | 200 |

<210> 126
 <211> 200
 <212> DNA
 <213> *S. cerevisiae*

<220>
 <223> terminator RPS2

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| <400> 126 | | | | | | |
| gcttgtgtgc | tacaaattat | aaaatagttt | tttataatca | accattaaat | aattttgtac | 60 |
| acttataata | acactttatt | tctcgttcca | attatgcgat | gcatgtgcct | tccgtttaga | 120 |
| gtgagcatta | tcaaataata | agtcaaatcc | ttttggcatt | tattttgatt | gaaaccagct | 180 |
| ctgtccttaa | ctcttttgcc | | | | | 200 |

<210> 127
 <211> 200
 <212> DNA
 <213> *S. cerevisiae*

<220>
 <223> terminator RPS4A

| | | | | | | |
|------------|------------|------------|------------|------------|------------|----|
| <400> 127 | | | | | | |
| atttcataac | aacttaatta | ttttcttctt | ttgtatatct | ccattaatgt | ttattagaaa | 60 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ttgaatttta | aaataataca | tcgtatcttc | ctttttcgac | tggcagtaat | ataacgtata | 120 |
| atatatatat | taggtgtgtg | tatatatatc | cgtattgtaa | tattgatagt | aaaaatacgc | 180 |
| taaccctgaa | atagaaggcg | | | | | 200 |

<210> 128
 <211> 837
 <212> DNA
 <213> Homo sapiens

<220>
 <223> CDS SLC35A1 wild type

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| <400> 128 | | | | | | |
| atggctgccc | cgagagacaa | tgtcacttta | ttattcaagt | tatactgctt | ggcagtgatg | 60 |
| accctgatgg | ctgcagtcta | taccatagct | ttaagataca | caaggacatc | agacaaagaa | 120 |
| ctctactttt | caaccacagc | cgtgtgtatc | acagaagtta | taaagttatt | gctaagtgtg | 180 |
| ggaatttttag | ctaaagaaac | tggtagtctg | ggtagattca | aagcatcttt | aagagaaaat | 240 |
| gtcttgggga | gccccaaagg | actgttgaag | ttaagtgtgc | catcgttagt | gtatgctgtt | 300 |
| cagaacaaca | tggcttttct | agctcttagc | aatctggatg | cagcagtgta | ccaggtgacc | 360 |
| taccagttga | agattccgtg | tactgcttta | tgcactgttt | taatgttaaa | ccggacactc | 420 |
| agcaaattac | agtgggtttc | agtttttatg | ctgtgtgctg | gagttacgct | tgtacagtgg | 480 |
| aaaccagccc | aagctacaaa | agtgggtggg | gaacaaaatc | cattattagg | gtttggcgct | 540 |
| atagctattg | ctgtattgtg | ctcaggattt | gcagttcttg | caagtgttgg | tggcctctac | 600 |
| acttctgttg | tggttaagta | cacagacaac | atcatgaaag | gcttttctgc | agcagcggcc | 660 |
| attgtccttt | ccaccattgc | ttcagtaatg | ctgtttggat | tacagataac | actcaccttt | 720 |
| gccctgggta | ctcttcttgt | atgtgtttcc | atatatctct | atggattacc | cagacaagac | 780 |
| actacatcca | tccaacaagg | agaaacagct | tcaaaggaga | gagttattgg | tgtgtga | 837 |

<210> 129
 <211> 747
 <212> DNA
 <213> Homo sapiens

<220>
 <223> CDS NANP wild type

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| <400> 129 | | | | | | |
| atggggctga | gccgcgtgcg | ggcgggttttc | tttgacttgg | acaacactct | catcgacacg | 60 |
| gccggggcga | gcaggagagg | catgttggag | gtgataaaac | tcttacaatc | aaaataccat | 120 |
| tataaagaag | aggctgaaat | catctgtgat | aaagttcaag | ttaaactcag | caaggaatgt | 180 |
| tttcatcctt | acaatacatg | cattactgat | ttaaggactt | cacattggga | agaagcaatc | 240 |
| caggaaacaa | aaggtggtgc | agccaataga | aaattggctg | aagaatgtta | tttcctttgg | 300 |
| aaatctacac | gtttacagca | tatgacacta | gcagaagacg | tcaaagccat | gcttactgaa | 360 |
| cttcgaaagg | aggtccgcct | acttctatta | acgaatgggg | acagacagac | ccagagggag | 420 |
| aagattgagg | cttgtgcctg | tcagtcctat | tttgacgctg | ttgtttagg | tggagagcag | 480 |
| agagaggaga | aaccagcacc | gtccatattt | tattactgct | gcaatcttct | cggagtacaa | 540 |
| cctggggact | gtgtgatggg | cgggtgacaca | ttagaaaccg | acatccaagg | aggcctcaat | 600 |
| gcaggattga | aagcaacagt | ctggatcaat | aaaaatggaa | tagtgccact | gaagtcctcc | 660 |
| ccagttccgc | attacatggg | ttcttctgtg | ctagagttac | ctgctctctt | acaaagtata | 720 |
| gactgcaaag | tcagtatgtc | cacttaa | | | | 747 |

<210> 130
 <211> 2262
 <212> DNA
 <213> Homo sapiens

<220>

<223> CDS GNE wild type

<400> 130

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|--------------|------|
| atggaaacct | atggttatct | gcagagggag | tcattgctttc | aaggacctca | tgaactctat | 60 |
| tttaagaacc | tctcaaaacg | aaacaagcaa | atcatggaga | agaatggaaa | taaccgaaag | 120 |
| ctgcgggttt | gtgttgctac | ttgtaaccgt | gcagattatt | ctaaacttgc | cccgatcatg | 180 |
| tttggcatta | aaaccgaacc | tgagttcttt | gaacttgatg | ttgtggtagt | tggtctctac | 240 |
| ctgatatag | actatggaaa | tacatatcga | atgattgaac | aagatgactt | tgacattaac | 300 |
| accaggctac | acacaattgt | gagggggagaa | gatgaggcag | ccatgggtgga | gtcagtaggc | 360 |
| ctggccctag | tgaagctgcc | agatgtcctt | aatcgccctga | agcctgatat | catgattgtt | 420 |
| catggagaca | ggtttgatgc | cctggctctg | gccacatctg | ctgccttgat | gaacatccga | 480 |
| atccttcaca | ttgaaggtgg | ggaagtcagt | gggaccattg | atgactctat | cagacatgcc | 540 |
| ataacaaaac | tggctcatta | tcattgtgtg | tgaccccgca | gtgcagagca | gcacctgata | 600 |
| tccatgtgtg | aggaccatga | tcgcatcctt | ttggcaggct | gcccttccta | tgacaaactt | 660 |
| ctctcagcca | agaacaaaaga | ctacatgagc | atcattcgca | tgtggctagg | tgatgatgta | 720 |
| aaatctaaag | attacattgt | tgactacag | caccctgtga | ccactgacat | taagcattcc | 780 |
| ataaaaatgt | ttgaattaac | attggatgca | cttatctcat | ttaacaagcg | gaccctagtc | 840 |
| ctgtttccaa | atattgacgc | agggagcaaa | gagatggttc | gagtgatgcg | gaagaagggc | 900 |
| attgagcatc | atcccaactt | tcgtgcagtt | aaacacgtcc | catttgacca | gtttatacac | 960 |
| ttggttgccc | atgctggctg | tatgattggg | aacagcagct | gtgggggttcg | agaagtggga | 1020 |
| gcttttgga | cacctgtgat | caacctggga | acacgtcaga | ttggaagaga | aacaggggag | 1080 |
| aatgttcttc | atgtccggga | tgctgacacc | caagacaaaa | tattgcaagc | actgcacctt | 1140 |
| cagtttggtg | aacagtaccc | ttgttcaaag | atatatgggg | atggaaatgc | tgttccaagg | 1200 |
| attttgaagt | ttctcaaatt | tatcgatctt | caagagccac | tgcaaaaaga | attctgcttt | 1260 |
| cctcctgtga | aggagaatat | ctctcaagat | attgaccata | ttcttgaaac | tctaagtgcc | 1320 |
| ttggccgttg | atcttggcgg | gacgaacctc | cgagttgcaa | tagtcagcat | gaagggtgaa | 1380 |
| atagttaaga | agtatactca | gttcaatcct | aaaacctatg | aagagaggat | taatttaatc | 1440 |
| ctacagatgt | gtgtggaagc | tgacgcagaa | gctgtaaaac | tgaactgcag | aattttggga | 1500 |
| gtaggcattt | ccacaggtgg | ccgtgtaaat | cctcggaag | gaattgtgct | gcattcaacc | 1560 |
| aaactgatcc | aagagtggaa | ctctgtggac | cttaggacct | ccctttctga | cactttgcat | 1620 |
| ctccctgtgt | gggtagacaa | tgatggcaac | tgtgctgccc | tggcggaaaag | gaaatttggc | 1680 |
| caaggaaagg | gactggaaaa | ctttgttaca | cttatcacag | gcacaggaat | cgggtgggtgga | 1740 |
| attatccatc | agcatgaatt | gatccacgga | agctccttct | gtgctgcaga | actgggccac | 1800 |
| cttgttgtgt | ctctggatgg | gcctgattgt | tcctgtggaa | gccatgggtg | cattgaagca | 1860 |
| tacgcctctg | gaatggcctt | gcagagggag | gcaaaaaagc | tccatgatga | ggacctgctc | 1920 |
| ttgggtggaag | ggatgtcagt | gccaaaagat | gaggctgtgg | gtgcgctcca | tctcatccaa | 1980 |
| gctgcgaaac | ttggcaatgc | gaaggcccag | agcatcctaa | gaacagctgg | aacagctttg | 2040 |
| ggctctgggg | ttgtgaacat | cctccatacc | atgaatccct | cccttgatg | cctctccgga | 2100 |
| gtcctggcca | gtcactatat | ccacattgtc | aaagacgtca | ttcgccagca | ggccttgtcc | 2160 |
| tccgtgcagg | acgtggatgt | ggtggtttcg | gatttggttg | acccgcccct | gctgggtgct | 2220 |
| gccagcatgg | ttctggacta | cacaacacgc | aggatctact | ag | | 2262 |

<210> 131

<211> 2178

<212> DNA

<213> Danio rerio

<220>

<223> CDS GNE wild type

<400> 131

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| atggagcggt | tggagaagcc | aaagaaagaa | agactccgcg | tgtgcgtggc | cacttgcaac | 60 |
| cgagcggact | actccaaact | ggcacccatc | atgtttggca | tcaaattctca | cccggacatc | 120 |
| tttgacctgg | aggtgggtgt | gctgggttca | catctcattg | acgattacgg | aaacacgttc | 180 |
| cgtatgattg | agcaggatga | ctttgacatc | ggctccaaat | tacacaccat | agtttcgcgt | 240 |

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| gaggatgagg | ctgccatggt | ggagtctgtc | ggcctggcgc | tcgtcaagct | tcccgatgtc | 300 |
| ctccaacgtc | tcgcgccccga | cattctgtctg | gttcatgggtg | accgttttga | tgctttggct | 360 |
| ctggcgacgg | cggcggtctt | gatgaacatt | cggatattgc | atctggaggg | tggagaagtg | 420 |
| agcggaaacca | tcgacgactc | cattcgccat | gccatctcca | aactggcaca | ctaccacgcc | 480 |
| gtgtgcacgc | tctctgccga | gagacacctc | atctccatgt | gcgaagatca | ctctcgcatac | 540 |
| ttactggccg | gctgcccgtc | gtacgacaag | ctgctctccg | cctacaaacg | agacgattat | 600 |
| gcggacatca | tcaagtcgtg | gatcggggac | gacgtgaagg | aacaggacta | tattgtagcc | 660 |
| ctccagcatc | ctgttaccac | agatatcaag | aactccatca | agatctacga | gttaatgctg | 720 |
| gacgtctca | tttctttcaa | caagaaaact | ctcatttctt | tcccgaatat | tgacgcaggc | 780 |
| agtaaggaga | tggttcgtgt | gatgcggcgg | aagggaatcg | agcagcatca | gaactttcgt | 840 |
| gcagtaaagc | atgtgccgtt | cgatcagttc | atccagctgg | tggctcacgc | agtctgcatg | 900 |
| atcggaaaca | gcagctgtgg | agttcgggaa | gccggagcgt | tcgggacgcc | tgtcataaat | 960 |
| ctggggactc | ggcagacagg | cagagaaaca | ggggaaaatg | ttctacatgt | gcgagacgca | 1020 |
| gacactcata | ataaaaatcta | tcatgccctc | gagctgcagt | ttggaaaacg | ctacccttgc | 1080 |
| tccaagatct | atggagatgg | aaacgcagtc | cagcgcattt | taaagttcct | gcagaccatc | 1140 |
| gacctctcag | agcctctgca | gaagaagttc | tgttttcttc | cagtaaagga | gtgcatctcg | 1200 |
| caagacatcg | accacatttt | ggagaccag | agcgcacttt | ctgtcgacct | gggggggaaca | 1260 |
| aacctgcgtg | tcggcatcgt | cagcatgaag | ggtaaagtgg | tcaagaagta | cgtacagtta | 1320 |
| aatcccaaga | cgtttgagga | gaggatagag | ctgattctga | ccatgtgtaa | acaggccatg | 1380 |
| gcagatgccg | ttcaccttaa | ctgcaggatc | ctgggtgtgg | gtgtgagcac | agggggccgt | 1440 |
| gtgaaccctc | aggatgggtg | cgttcttcac | tccaccaagc | taataaagga | gtggagttcg | 1500 |
| gtggacatcc | gcacgcccc | ctccagtgcc | ctgcatctgc | ccgtgtgggt | cgataatgat | 1560 |
| gggaactgcg | ctgctctggc | tgagaggaag | tttggccatg | gcaaaggcgt | ggagaacttt | 1620 |
| gttaccatta | tcactggaac | cggatattgga | ggtggtataa | tccagcataa | tgagctgatac | 1680 |
| catggcaaca | cattttgcgc | agctgaactg | ggacacatcg | tggtgtcgct | ggaaggacca | 1740 |
| gaatgcatgt | gtggaggcca | cggctgcata | gaggcctatt | catcaggtct | cgctctgcag | 1800 |
| agagaagcca | agagactcca | tgacaggagc | ttgctgctgg | tggagggaat | gactctgaat | 1860 |
| aacaaagaac | aggtgaacgc | cattcatctg | atcaacgctg | ctcgactcgg | caactccaaa | 1920 |
| gcagagactg | tccttcacac | cgcgggtaca | gctttgggtt | tgggcatcgt | gaacatcctg | 1980 |
| cacatgatca | acccgtctct | ggtcattctg | tctggggttc | tggcggtgca | ttatgagact | 2040 |
| ccgggtccgcc | aggtgatcgg | ccagcgggcg | ctgctcaccg | cacaggggac | caaagtcatg | 2100 |
| gtgtccgacc | tggaggacc | agcgtctgta | ggagccgcta | gtatgggtgct | ggattacacc | 2160 |
| acccgcagaa | cttactga | | | | | 2178 |

<210> 132

<211> 1080

<212> DNA

<213> Homo sapiens

<220>

<223> CDS NANS wild type

<400> 132

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| atgccgctgg | agctggagct | gtgtcccggg | cgctgggtgg | gcgggcaaca | cccgtgcttc | 60 |
| atcattgccg | agatcggcca | gaaccaccag | ggcgacctgg | acgtagccaa | gcgcatgatac | 120 |
| cgcattggcca | aggagtgtgg | ggctgattgt | gctaagtctc | agaagagtga | gctagaatttc | 180 |
| aagtttaatc | ggaaagcctt | ggagaggcca | tacacctcga | agcattcctg | gggggaagacg | 240 |
| tacgggggagc | acaaacgaca | tctggagttc | agccatgacc | agtacaggga | gctgcagagg | 300 |
| tacgccgagg | aggttgggat | cttcttcact | gcctctggca | tggatgagat | ggcagttgaa | 360 |
| ttcctgcatg | aactgaatgt | tccatttttc | aaagttggat | ctggagacac | taataatttt | 420 |
| ccttatctgg | aaaagacagc | caaaaaaggt | cgcccaatgg | tgatctccag | tgggatgcag | 480 |
| tcaatggaca | ccatgaagca | agtttatcag | atcgtgaagc | ccctcaacct | caacttctgc | 540 |
| ttcttgcatg | gtaccagcgc | ataccgcctc | cagcctgagg | acgtcaacct | gcgggtcatc | 600 |
| tcggaatatc | agaagctctt | tcctgacatt | cccatagggt | attctgggca | tgaacaggc | 660 |
| atagcgatat | ctgtggccgc | agtggctctg | ggggccaagg | tgttggaacg | tcacataact | 720 |
| ttggacaaga | cctggaaggg | gagtgaccac | tcggcctcgc | tggagcctgg | agaactggcc | 780 |

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|------|
| gagctgggtgc | ggtcagtgcg | tcttgtggag | cgtgccctgg | gctccccaac | caagcagctg | 840 |
| ctgccctgtg | agatggcctg | caatgagaag | ctgggcaagt | ctgtgggtggc | caaagtga | 900 |
| attccggaag | gcaccattct | aacaatggac | atgctcaccg | tgaaggtggg | tgagcccaaa | 960 |
| ggctatcctc | ctgaagacat | ctttaatcta | gtgggcaaga | aggtcctggg | cactgttgaa | 1020 |
| gaggatgaca | ccatcatgga | agaattggta | gataatcatg | gcaaaaaaat | caagtcttaa | 1080 |

<210> 133

<211> 1080

<212> DNA

<213> Danio rerio

<220>

<223> CDS NANS (A) wild type

<400> 133

| | | | | | | |
|-------------|------------|------------|------------|-------------|-------------|------|
| atgccactta | aatttgaatt | atgtcccggc | cgcatgatcg | gaggaaacaa | tccgtgcttc | 60 |
| attattgcag | aaatcggaca | gaatcatcag | ggagacattg | agattgccaa | gaaaatgata | 120 |
| aaaatggcaa | aggactgtgg | tgcaactgtg | gcaaagtttc | agaagagtga | gctggagtat | 180 |
| aaattcaata | agaaagctct | tgaacggcca | tacacctcca | aacactcctg | ggggaaaaaca | 240 |
| tacggagagc | ataagcgaca | cctggagttc | agtcatgagc | agtacaggga | gctgcagcag | 300 |
| tacgctaaac | aagtgggcat | cttcttcact | gcgtctggaa | tggacgagat | ggctgtagaa | 360 |
| ttcctccatg | aactcgatgt | gccttttttc | aaagttggat | ctggcgacac | caacaacttt | 420 |
| ccttacctca | agaaaactgc | ccaaaaagga | cgccccatgg | tagtgtccag | cgggatgcag | 480 |
| tccatggaaa | ccatgcagca | cgtttataag | attgtcaagg | agcacaatca | gaacttttgc | 540 |
| atcctgcagt | gcacaagtgc | atatccactt | gaacctgagg | acgtcaacct | gcgggttatc | 600 |
| acggaatatc | agaaagaatt | cccagacatt | cccatcggtt | actcgggtca | tgaaagtgga | 660 |
| atcaacatca | cagtcggggc | agttgctctg | ggagccaaag | ttgtggagcg | gcatgtgacc | 720 |
| ctggataaga | gctggaaagg | tagtgatcat | gcagcgtctc | tggaaaccaga | agagctggct | 780 |
| gagctgggtga | ggatccatcc | cattgtggag | agagcttttg | gactggactg | gaaacgcata | 840 |
| ctgccatgtg | aggtgccatg | ccatgataag | ctcgggaagt | cgggtgggtg | aaagacctcc | 900 |
| attccaaaag | gtacagaact | cacccttgac | atgctggcag | tgaaagtagc | tgaacccaag | 960 |
| ggtgtagctc | cagaagaaat | cttcagctg | gtggggaaga | aagtgaccac | agatgtggag | 1020 |
| gaggacgaga | gcattactga | agatgtagtc | gacagctatg | gcaaaaaagc | taaagcttga | 1080 |

<210> 134

<211> 1305

<212> DNA

<213> Homo sapiens

<220>

<223> CDS CMAS wild type

<400> 134

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| atggactcgg | tggagaaggg | ggccgccacc | tccgtctcca | acccgcgggg | gcgaccgtcc | 60 |
| cggggccggc | cgccgaagct | gcagcgcaac | tctcgcggcg | gccagggccg | aggtgtggag | 120 |
| aagccccgcg | acctggcagc | cctaattctg | gcccggggag | gcagcaaagg | catccccctg | 180 |
| aagaacatta | agcacctggc | gggggtcccc | ctcattggct | gggtcctgcg | tgcggccctg | 240 |
| gattcagggg | ccttccagag | tgtatgggtt | tcgacagacc | atgatgaaat | tgagaatgtg | 300 |
| gccaaacaat | ttgggtgcaca | agttcatcga | agaagttctg | aagtttcaaa | agacagctct | 360 |
| acctcactag | atgccatcat | agaatttctt | aattatcata | atgaggttga | cattgttagga | 420 |
| aatattcaag | ctacttctcc | atgtttacat | cctactgatc | ttcaaaaagt | tgcagaaatg | 480 |
| attcgagaag | aaggatatga | ttctgttttc | tctgttgtga | gacgccatca | gtttcgatgg | 540 |
| agtgaatttc | agaaaggagt | tcgtgaagtg | accgaacctc | tgaattttaa | tccagctaaa | 600 |
| cggcctcgtc | gacaagactg | ggatggagaa | ttatatgaaa | atggctcatt | ttattttgct | 660 |
| aaaagacatt | tgatagagat | gggttacttg | cagggtggaa | aaatggcata | ctacgaaatg | 720 |
| cgagctgaac | atagtgtgga | tatagatgtg | gatattgatt | ggcctattgc | agagcaaaga | 780 |

| | | | | | | | |
|------------|------------|-------------|------------|-------------|-------------|------------|------|
| gtattaagat | atggctat | ttt | tgcaaaagag | aagcttaagg | aaataaaaact | tttggtttgc | 840 |
| aatattgatg | gatgtctcac | caatggccac | at | tttatgtat | caggagacca | aaaagaaata | 900 |
| atatcttatg | atgtaaaaga | tgctattggg | ataagtttat | ttaaagaaaag | tggtattgag | | 960 |
| gtgaggctaa | tctcagaaag | ggcctgttca | aagcagacgc | tgtcttcttt | aaaactggat | | 1020 |
| tgcaaaatgg | aagtcagtgt | atcagacaag | ctagcagttg | tagatgaatg | gagaaaagaa | | 1080 |
| atgggcctgt | gctggaaaga | agtggcatat | cttggaaatg | aagtgtctga | tgaagagtgc | | 1140 |
| ttgaagagag | tgggcctaag | tggcgctcct | gctgatgcct | gttctactgc | ccagaaggct | | 1200 |
| gttggataca | tttgcaaatg | taatgggtggc | cgtggtgcca | tccgagaatt | tgcagagcac | | 1260 |
| atttgcctac | taatggaaaa | ggttaataat | tcatgccaaa | aatag | | | 1305 |

<210> 135

<211> 1293

<212> DNA

<213> Danio rerio

<220>

<223> CDS CMAS (A) wild type

<400> 135

| | | | | | | |
|------------|------------|------------|-------------|-------------|-------------|------|
| atggacgcag | taaatgaaaa | cggtaaacgc | gctatgaagg | acgacagtca | tgggaacagt | 60 |
| accagcccaa | aacgaagaaa | atccagacac | atctctgctc | ttattctggc | ccgtggaggg | 120 |
| agtaaaggaa | tccccctgaa | gaacattaag | atgcttgcat | gggttccccct | gatcggatgg | 180 |
| gtgatcagag | cggctgtgga | ctccaatgtc | tttaacagtg | tttgggtgtc | tactgatcac | 240 |
| gaagagatcg | ccaaagtggc | cttggccttg | ggtgcaaagg | tgcacaagag | gagcccagaa | 300 |
| gtgtcccagg | actcctccag | ctcactggac | accattcggg | agttcagcag | acagcaccga | 360 |
| gaggtggatg | ttatctgtaa | catccaggcc | acgtctccgt | gtttgcaccc | aaaacatctc | 420 |
| acagaggctg | tggaactcat | aacgaaacaa | gggtacgatt | cagtcttctc | tgttggtccgc | 480 |
| aggcacaatt | ttcgaaggaa | agaggttgag | aaaggaggag | attgcagcac | tgaaccgatg | 540 |
| aacctgaacc | cagcttgcat | gccgcggcgt | caggactgga | gtggagaact | gtgtgaaaat | 600 |
| ggctcttttt | acttcgcaaa | gaaagagctc | atagaacaag | ggcttcttca | gggtggaaaag | 660 |
| aaaacatact | atgaaatgaa | gcctgagtac | agcgtggata | ttgatgtgga | catagactgg | 720 |
| cctgttgctg | agcaaagagt | tctgagggtt | ggatactttg | ggaaggacaa | acctgaagtt | 780 |
| gtgaggctct | tgctgtgtaa | cgtgtctgga | tgtctgacag | acggtcagat | ctacacctca | 840 |
| gcgagtggag | aggagatggt | gtccatcaac | atcagagacc | agatcggcat | cagcatgctt | 900 |
| aagaaagaag | gagtgaagg | gattttactt | gaaacatacc | ccatagcaaa | agcattagct | 960 |
| gtcagactgt | ctgagaggat | gggctgtcct | ctcctgcacc | acatggacga | caaactgaag | 1020 |
| gaggtggaga | gaatcatggt | ggaggaaaag | ctggagtggga | aagaggtggc | gtatttaggg | 1080 |
| aatgatgaag | cagatgtgaa | gtgtctggaa | ttggcagggt | tgagtggagt | acctgtggac | 1140 |
| gccccgacgg | tggcgctcaa | ccacactaaa | tatacctgcc | acaacgcagc | gggtcacggg | 1200 |
| gcagtgcgcg | agtttgccga | acacatcctt | ctcctgaaga | agaaggccaa | gtctcagatg | 1260 |
| gagcaggaca | gaatctgcag | agatgcattt | taa | | | 1293 |

<210> 136

<211> 1221

<212> DNA

<213> Homo sapiens

<220>

<223> CDS St6GAL1 wild type

<400> 136

| | | | | | | |
|------------|------------|------------|-------------|-------------|------------|-----|
| atgattcaca | ccaacctgaa | gaaaaagttc | agctgctgctg | tcctggctctt | tcttctgttt | 60 |
| gcagtcatct | gtgtgtggaa | ggaaaagaag | aaaggagatt | actatgattc | ctttaaattg | 120 |
| caaaccaagg | aattccaggt | gttaaagagt | ctggggaaat | tggccatggg | gtctgattcc | 180 |
| cagtctgtat | cctcaagcag | cacccaggac | ccccacaggg | gccgccagac | cctcggcagt | 240 |
| ctcagaggcc | tagccaaggc | caaaccagag | gcctccttcc | aggtgtggaa | caaggacagc | 300 |

| | | | | | | |
|------------|------------|-------------|-------------|------------|-------------|------|
| tcttccaaaa | accttatccc | taggctgcaa | aagatctgga | agaattacct | aagcatgaac | 360 |
| aagtacaaa | tgctctacaa | ggggccagga | ccaggcatca | agttcagtgc | agaggccctg | 420 |
| cgctgccacc | tccgggacca | tgtgaatgta | tccatggtag | aggtcacaga | ttttcccttc | 480 |
| aatacctctg | aatgggaggg | ttatctgccc | aaggagagca | ttaggaccaa | ggctgggcct | 540 |
| tggggcaggt | gtgctgttgt | gtcgtcagcg | ggatctctga | agtcctcca | actaggcaga | 600 |
| gaaatcgatg | atcatgacgc | agtcctgagg | tttaatgggg | caccacagc | caacttccaa | 660 |
| caagatgtgg | gcacaaaaac | taccattcgc | ctgatgaact | ctcagttggg | taccacagag | 720 |
| aagcgcttcc | tcaaagacag | tttgtacaat | gaagggaatcc | taattgtatg | ggacccatct | 780 |
| gtataccact | cagatatccc | aaagtgggtac | cagaatccgg | attataattt | ctttaacaac | 840 |
| tacaagactt | atcgtaagct | gcacccaat | cagccctttt | acatcctcaa | gccccagatg | 900 |
| ccttgggagc | tatgggacat | tcttcaagaa | atctccccag | aagagattca | gccaaacccc | 960 |
| ccatcctctg | ggatgcttgg | tatcatcatc | atgatgacgc | tgtgtgacca | ggtggatatt | 1020 |
| tatgagttcc | tcccatccaa | gcgcaagact | gacgtgtgct | actactacca | gaagttcttc | 1080 |
| gatagtgcc | gcacgatggg | tgccctaccac | ccgctgctct | atgagaagaa | tttgggtgaag | 1140 |
| catctcaacc | agggcacaga | tgaggacatc | tacctgcttg | gaaaagccac | actgcctggc | 1200 |
| ttccggacca | ttcactgcta | a | | | | 1221 |

<210> 137

<211> 1002

<212> DNA

<213> Homo sapiens

<220>

<223> CDS St3GAL4 wild type

<400> 137

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|------|
| atggtcagca | agtcccgctg | gaagctcctg | gccatgttgg | ctctggtcct | ggctcgtcatg | 60 |
| gtgtgggtatt | ccatctcccc | ggaagacagg | tacatcgagc | ttttttat | tcccatccca | 120 |
| gagaagaagg | agccgtgcct | ccagggtgag | gcagagagca | aggcctctaa | gctctttggc | 180 |
| aactactccc | gggatcagcc | catcttcctg | cggcttgagg | attatttctg | ggtcaagacg | 240 |
| ccatctgctt | acgagctgcc | ctatgggacc | aaggggagtg | aggatctgct | cctccgggtg | 300 |
| ctagccatca | ccagctcctc | catccccaag | aacatccaga | gcctcaggtg | ccgccgctgt | 360 |
| gtggtcgtgg | ggaacgggca | ccggctgcgg | aacagctcac | tgggagatgc | catcaacaag | 420 |
| tacgatgtgg | tcatcagatt | gaacaatgcc | ccagtggctg | gctatgaggg | tgacgtgggc | 480 |
| tccaagacca | ccatgcgtct | cttctaccct | gaatctgccc | acttcgaccc | caaagtagaa | 540 |
| aacaaccag | acacactcct | cgtcctggta | gctttcaagg | caatggactt | ccactggatt | 600 |
| gagaccatcc | tgagtataaa | gaagcgggtg | cgaagggtt | tctggaaaca | gcctcccctc | 660 |
| atctgggatg | tcaatcctaa | acagattcgg | attctcaacc | ccttcttcat | ggagattgca | 720 |
| gctgacaaac | tgctgagcct | gccaatgcaa | cagccacgga | agattaagca | gaagcccacc | 780 |
| acgggcctgt | tggccatcac | gctggccctc | cacctctgtg | acttggtgca | cattgccggc | 840 |
| tttggctacc | cagacgccta | caacaagaag | cagaccattc | actactatga | gcagatcacg | 900 |
| ctcaagtcca | tggcggggtc | aggccataat | gtctcccaag | aggccctggc | cattaagcgg | 960 |
| atgctggaga | tgggagctat | caagaacctc | acgtccttct | ga | | 1002 |