SEQUENCE LISTING

<110> Koppaka, et al.

<120> MANUFACTURE OF ACTIVE HIGHLY PHOSPHORYLATED HUMAN N-ACETYLGALACTOSAMINE-6-SULFATASE ENZYMES AND USES THEREOF

<130> 30610/45573A

<150> US-61/366,714
<151> 2010-07-22

<160> 5

<170> PatentIn version 3.5

<210> 1
<211> 1125
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human Sulfatase Modifying Factor 1 (SUMF1) Polynucleotide Sequence

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gcgggcgcgg ggtcccttgc gggttcttgc ggctgcggca cgccccagcg gcctggcgcc 180

catggcagtt cggcagccgc tcaccgatac tcgcgggagg ctaacgctcc gggccccgta 240

cccggagagc ggcaactcgc gcactcaaag atggtcccca tccctgctgg agtatttaca 300

atgggcacag atgatcctca gataaagcag gatggggaag cacctgcgag gagagttact 360

attgatgcct tttacatgga tgcctatgaa gtcagtaata ctgaatttga gaagtttgtg 420

aactcaactg gctatttgac agaggctgag aagtttggcg actcctttgt ctttgaaggc 480

atgttgagtg agcaagtgaa gaccaatatt caacaggcag ttgcagctgc tccctggtgg 540

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aggccggatc atccagttct ccatgtgtcc tggaatgatg cggttgccta ctgcacttgg 660

gcagggaagc ggctgcccac ggaagctgag tgggaataca gctgtcgagg aggcctgcat 720

aatagacttt tcccctgggg caacaaactg cagcccaaag gccagcatta tgccaacatt 780

tggcagggcg agtttccggt gaccaacact ggtgaggatg gcttccaagg aactgcgcct 840

gttgatgcct tccctcccaa tggttatggc ttatacaaca tagtggggaa cgcatgggaa 900

tggacttcag actggtggac tgttcatcat tctgttgaag aaacgcttaa cccaaaaggt 960

ccccccttctg ggaaagaccg agtgaagaaa ggtggatcct acatgtgcca taggtcttat 1020

tgttacaggt atcgctgtgc tgctcggagc cagaacacac ctgatagctc tgcttcgaat 1080

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<210> 2

<211> 374
<212> PRT
<213> Homo sapiens

<220>
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<223> Human Sulfatase Modifying Factor 1 (SUMF1) Polypeptide Sequence

<400> 2

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Gly Leu Val Leu Leu Leu Leu Leu Leu Ser Leu Leu Cys Gly Ala Ala
            20                  25                  30

Gly Ser Gln Glu Ala Gly Thr Gly Ala Gly Ala Gly Ser Leu Ala Gly
        35                  40                  45

Ser Cys Gly Cys Gly Thr Pro Gln Arg Pro Gly Ala His Gly Ser Ser
    50                  55                  60

Ala Ala Ala His Arg Tyr Ser Arg Glu Ala Asn Ala Pro Gly Pro Val
65                  70                  75                  80

Pro Gly Glu Arg Gln Leu Ala His Ser Lys Met Val Pro Ile Pro Ala
                85                  90                  95

Gly Val Phe Thr Met Gly Thr Asp Asp Pro Gln Ile Lys Gln Asp Gly
            100                 105                 110

Glu Ala Pro Ala Arg Arg Val Thr Ile Asp Ala Phe Tyr Met Asp Ala
        115                 120                 125

Tyr Glu Val Ser Asn Thr Glu Phe Glu Lys Phe Val Asn Ser Thr Gly
    130                 135                 140

Tyr Leu Thr Glu Ala Glu Lys Phe Gly Asp Ser Phe Val Phe Glu Gly
145                 150                 155                 160

Met Leu Ser Glu Gln Val Lys Thr Asn Ile Gln Gln Ala Val Ala Ala
                165                 170                 175

Ala Pro Trp Trp Leu Pro Val Lys Gly Ala Asn Trp Arg His Pro Glu
            180                 185                 190

Gly Pro Asp Ser Thr Ile Leu His Arg Pro Asp His Pro Val Leu His
        195                 200                 205

Val Ser Trp Asn Asp Ala Val Ala Tyr Cys Thr Trp Ala Gly Lys Arg
    210                 215                 220

Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ser Cys Arg Gly Gly Leu His
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225 230 235 240

Asn Arg Leu Phe Pro Trp Gly Asn Lys Leu Gln Pro Lys Gly Gln His
245 250 255

Tyr Ala Asn Ile Trp Gln Gly Glu Phe Pro Val Thr Asn Thr Gly Glu
260 265 270

Asp Gly Phe Gln Gly Thr Ala Pro Val Asp Ala Phe Pro Pro Asn Gly
275 280 285

Tyr Gly Leu Tyr Asn Ile Val Gly Asn Ala Trp Glu Trp Thr Ser Asp
290 295 300

Trp Trp Thr Val His His Ser Val Glu Glu Thr Leu Asn Pro Lys Gly
305 310 315 320

Pro Pro Ser Gly Lys Asp Arg Val Lys Lys Gly Gly Ser Tyr Met Cys
325 330 335

His Arg Ser Tyr Cys Tyr Arg Tyr Arg Cys Ala Ala Arg Ser Gln Asn
340 345 350

Thr Pro Asp Ser Ser Ala Ser Asn Leu Gly Phe Arg Cys Ala Ala Asp
355 360 365

Arg Leu Pro Thr Met Asp
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<210> 3
<211> 1569
<212> DNA
<213> Homo sapiens

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<223> Human N-Acetylgalactosamine-6_Sulfatase (GALNS) Polynucleotide Sequence

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atgggatggg gtgacctcgg ggtgtatgga gagccctcca gagagacccc gaatttggac 180

cggatggctg cagaagggct gcttttccca aacttctatt ctgccaaccc tctgtgctcg 240

ccatcgaggg cggcactgct cacaggacgg ctacccatcc gcaatggctt ctacaccacc 300

aacgcccatg ccagaaacgc ctacacaccg caggagattg tgggcggcat cccagactcg 360

gagcagctcc tgccggagct tctgaagaag gccggctacg tcagcaagat tgtcggcaag 420

tggcatctgg gtcacaggcc ccagttccac cccctgaagc acggatttga tgagtggttt 480

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tacagggact gggagatggt tggcagatat tatgaagaat ttcctattaa tctgaagacg 600

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gggcagaacg tttcaggggt cacaactcac aatctggaag accacacgaa gctgcccctg 1320

atcttccacc tgggacggga cccaggggag aggttccccc tcagctttgc cagcgccgag 1380

taccaggagg ccctcagcag gatcacctcg gtcgtccagc agcaccagga ggccttggtc 1440

cccgcgcagc cccagctcaa cgtgtgcaac tgggcggtca tgaactgggc acctccgggc 1500

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<210> 4
<211> 522
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Human N-acetylgalactosamine-6-Sulfatase (GALNS) Polypeptide Sequence

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Leu Ser Ala Ala Gly Met Gly Ala Ser Gly Ala Pro Gln Pro Pro Asn
20 25 30

Ile Leu Leu Leu Leu Met Asp Asp Met Gly Trp Gly Asp Leu Gly Val
35 40 45

Tyr Gly Glu Pro Ser Arg Glu Thr Pro Asn Leu Asp Arg Met Ala Ala
50 55 60

Glu Gly Leu Leu Phe Pro Asn Phe Tyr Ser Ala Asn Pro Leu Cys Ser

65 70 75 80

Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg Leu Pro Ile Arg Asn Gly
85 90 95

Phe Tyr Thr Thr Asn Ala His Ala Arg Asn Ala Tyr Thr Pro Gln Glu
100 105 110

Ile Val Gly Gly Ile Pro Asp Ser Glu Gln Leu Leu Pro Glu Leu Leu
115 120 125

Lys Lys Ala Gly Tyr Val Ser Lys Ile Val Gly Lys Trp His Leu Gly
130 135 140

His Arg Pro Gln Phe His Pro Leu Lys His Gly Phe Asp Glu Trp Phe
145 150 155 160

Gly Ser Pro Asn Cys His Phe Gly Pro Tyr Asp Asn Lys Ala Arg Pro
165 170 175

Asn Ile Pro Val Tyr Arg Asp Trp Glu Met Val Gly Arg Tyr Tyr Glu
180 185 190

Glu Phe Pro Ile Asn Leu Lys Thr Gly Glu Ala Asn Leu Thr Gln Ile
195 200 205

Tyr Leu Gln Glu Ala Leu Asp Phe Ile Lys Arg Gln Ala Arg His His
210 215 220

Pro Phe Phe Leu Tyr Trp Ala Val Asp Ala Thr His Ala Pro Val Tyr
225 230 235 240

Ala Ser Lys Pro Phe Leu Gly Thr Ser Gln Arg Gly Arg Tyr Gly Asp
245 250 255

Ala Val Arg Glu Ile Asp Asp Ser Ile Gly Lys Ile Leu Glu Leu Leu
260 265 270

Gln Asp Leu His Val Ala Asp Asn Thr Phe Val Phe Phe Thr Ser Asp
275 280 285

Asn Gly Ala Ala Leu Ile Ser Ala Pro Glu Gln Gly Gly Ser Asn Gly
290 295 300

Pro Phe Leu Cys Gly Lys Gln Thr Thr Phe Glu Gly Gly Met Arg Glu
305 310 315 320

Pro Ala Leu Ala Trp Trp Pro Gly His Val Thr Ala Gly Gln Val Ser
325 330 335

His Gln Leu Gly Ser Ile Met Asp Leu Phe Thr Thr Ser Leu Ala Leu

340 345 350

Ala Gly Leu Thr Pro Pro Ser Asp Arg Ala Ile Asp Gly Leu Asn Leu
355 360 365

Leu Pro Thr Leu Leu Gln Gly Arg Leu Met Asp Arg Pro Ile Phe Tyr
370 375 380

Tyr Arg Gly Asp Thr Leu Met Ala Ala Thr Leu Gly Gln His Lys Ala
385 390 395 400

His Phe Trp Thr Trp Thr Asn Ser Trp Glu Asn Phe Arg Gln Gly Ile
405 410 415

Asp Phe Cys Pro Gly Gln Asn Val Ser Gly Val Thr Thr His Asn Leu
420 425 430

Glu Asp His Thr Lys Leu Pro Leu Ile Phe His Leu Gly Arg Asp Pro
435 440 445

Gly Glu Arg Phe Pro Leu Ser Phe Ala Ser Ala Glu Tyr Gln Glu Ala
450 455 460

Leu Ser Arg Ile Thr Ser Val Val Gln Gln His Gln Glu Ala Leu Val
465 470 475 480

Pro Ala Gln Pro Gln Leu Asn Val Cys Asn Trp Ala Val Met Asn Trp
485 490 495

Ala Pro Pro Gly Cys Glu Lys Leu Gly Lys Cys Leu Thr Pro Pro Glu
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Ser Ile Pro Lys Lys Cys Leu Trp Ser His
515 520

<210> 5
<211> 496
<212> PRT
<213> Homo sapiens

<400> 5

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Trp Gly Asp Leu Gly Val Tyr Gly Glu Pro Ser Arg Glu Thr Pro Asn
20 25 30

Leu Asp Arg Met Ala Ala Glu Gly Leu Leu Phe Pro Asn Phe Tyr Ser
35 40 45

Ala Asn Pro Leu Cys Ser Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg
50 55 60

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

Ala Tyr Thr Pro Gln Glu Ile Val Gly Gly Ile Pro Asp Ser Glu Gln
                85                  90                  95

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

Gly Lys Trp His Leu Gly His Arg Pro Gln Phe His Pro Leu Lys His
        115                 120                 125

Gly Phe Asp Glu Trp Phe Gly Ser Pro Asn Cys His Phe Gly Pro Tyr
    130                 135                 140

Asp Asn Lys Ala Arg Pro Asn Ile Pro Val Tyr Arg Asp Trp Glu Met
145                 150                 155                 160

Val Gly Arg Tyr Tyr Glu Glu Phe Pro Ile Asn Leu Lys Thr Gly Glu
                165                 170                 175

Ala Asn Leu Thr Gln Ile Tyr Leu Gln Glu Ala Leu Asp Phe Ile Lys
            180                 185                 190

Arg Gln Ala Arg His His Pro Phe Phe Leu Tyr Trp Ala Val Asp Ala
        195                 200                 205

Thr His Ala Arg Val Tyr Ala Ser Lys Pro Phe Leu Gly Thr Ser Gln
    210                 215                 220

Arg Gly Arg Tyr Gly Asp Ala Val Arg Glu Ile Asp Asp Ser Ile Gly
225                 230                 235                 240

Lys Ile Leu Glu Leu Leu Gln Asp Leu His Val Ala Asp Asn Thr Phe
                245                 250                 255

Val Phe Phe Thr Ser Asp Asn Gly Ala Ala Leu Ile Ser Ala Pro Glu
            260                 265                 270

Gln Gly Gly Ser Asn Gly Pro Phe Leu Cys Gly Lys Gln Thr Thr Phe
        275                 280                 285

Glu Gly Gly Met Arg Glu Pro Ala Leu Ala Trp Trp Pro Gly His Val
    290                 295                 300

Thr Ala Gly Gln Val Ser His Gln Leu Gly Ser Ile Met Asp Leu Phe
305                 310                 315                 320

Thr Thr Ser Leu Ala Leu Ala Gly Leu Thr Pro Pro Ser Asp Arg Ala
                325                 330                 335
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Ile Asp Gly Leu Asn Leu Leu Pro Thr Leu Leu Gln Gly Arg Leu Met
            340                 345                 350

Asp Arg Pro Ile Phe Tyr Tyr Arg Gly Asp Thr Leu Met Ala Ala Thr
        355                 360                 365

Leu Gly Gln His Lys Ala His Phe Trp Thr Trp Thr Asn Ser Trp Glu
    370                 375                 380

Asn Phe Arg Gln Gly Ile Asp Phe Cys Pro Gly Gln Asn Val Ser Gly
385                 390                 395                 400

Val Thr Thr His Asn Leu Glu Asp His Thr Lys Leu Pro Leu Ile Phe
                405                 410                 415

His Leu Gly Arg Asp Pro Gly Glu Arg Phe Pro Leu Ser Phe Ala Ser
            420                 425                 430

Ala Glu Tyr Gln Glu Ala Leu Ser Arg Ile Thr Ser Val Val Gln Gln
        435                 440                 445

His Gln Glu Ala Leu Val Pro Ala Gln Pro Gln Leu Asn Val Cys Asn
    450                 455                 460

Trp Ala Val Met Asn Trp Ala Pro Pro Gly Cys Glu Lys Leu Gly Lys
465                 470                 475                 480

Cys Leu Thr Pro Pro Glu Ser Ile Pro Lys Lys Cys Leu Trp Ser His
                485                 490                 495
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