

2015-04-06_13150-70136PCT_Seq_Listing_ST25
SEQUENCE LISTING

<110> MINERVA BIOTECHNOLOGIES

<120> ANTI-NME ANTIBODY

<130> 13150-70136PCT

<160> 162

<170> PatentIn version 3.5

<210> 1

<211> 1255

<212> PRT

<213> Artificial Sequence

<220>

<223> full-length MUC1 Receptor

<400> 1

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
1 5 10 15

Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
20 25 30

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

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
50 55 60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65 70 75 80

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
85 90 95

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
100 105 110

Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
115 120 125

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
130 135 140

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
145 150 155 160

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
165 170 175

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
180 185 190

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Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
195 200 205

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
210 215 220

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
225 230 235 240

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
245 250 255

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
260 265 270

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
275 280 285

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
290 295 300

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
305 310 315 320

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
325 330 335

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
340 345 350

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
355 360 365

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
370 375 380

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
385 390 395 400

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
405 410 415

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
420 425 430

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
435 440 445

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
450 455 460

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Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
465 470 475 480

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
485 490 495

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
500 505 510

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
515 520 525

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
530 535 540

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
545 550 555 560

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
565 570 575

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
580 585 590

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
595 600 605

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
610 615 620

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
625 630 635 640

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
645 650 655

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
660 665 670

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
675 680 685

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
690 695 700

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
705 710 715 720

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
725 730 735

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Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
740 745 750

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
755 760 765

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
770 775 780

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
785 790 795 800

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
805 810 815

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
820 825 830

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
835 840 845

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
850 855 860

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
865 870 875 880

Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
885 890 895

Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
900 905 910

Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
915 920 925

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn
930 935 940

Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val His Asn Val Thr Ser
945 950 955 960

Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly
965 970 975

Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe
980 985 990

Ser Ile Pro Ser His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His
995 1000 1005

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Ser	Thr	Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His	Ser	Ser	Val	Pro
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Pro	Leu	Thr	Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	Ser	Thr
	1025					1030					1035			
Gly	Val	Ser	Phe	Phe	Phe	Leu	Ser	Phe	His	Ile	Ser	Asn	Leu	Gln
	1040					1045					1050			
Phe	Asn	Ser	Ser	Leu	Glu	Asp	Pro	Ser	Thr	Asp	Tyr	Tyr	Gln	Glu
	1055					1060					1065			
Leu	Gln	Arg	Asp	Ile	Ser	Glu	Met	Phe	Leu	Gln	Ile	Tyr	Lys	Gln
	1070					1075					1080			
Gly	Gly	Phe	Leu	Gly	Leu	Ser	Asn	Ile	Lys	Phe	Arg	Pro	Gly	Ser
	1085					1090					1095			
Val	Val	Val	Gln	Leu	Thr	Leu	Ala	Phe	Arg	Glu	Gly	Thr	Ile	Asn
	1100					1105					1110			
Val	His	Asp	Val	Glu	Thr	Gln	Phe	Asn	Gln	Tyr	Lys	Thr	Glu	Ala
	1115					1120					1125			
Ala	Ser	Arg	Tyr	Asn	Leu	Thr	Ile	Ser	Asp	Val	Ser	Val	Ser	Asp
	1130					1135					1140			
Val	Pro	Phe	Pro	Phe	Ser	Ala	Gln	Ser	Gly	Ala	Gly	Val	Pro	Gly
	1145					1150					1155			
Trp	Gly	Ile	Ala	Leu	Leu	Val	Leu	Val	Cys	Val	Leu	Val	Ala	Leu
	1160					1165					1170			
Ala	Ile	Val	Tyr	Leu	Ile	Ala	Leu	Ala	Val	Cys	Gln	Cys	Arg	Arg
	1175					1180					1185			
Lys	Asn	Tyr	Gly	Gln	Leu	Asp	Ile	Phe	Pro	Ala	Arg	Asp	Thr	Tyr
	1190					1195					1200			
His	Pro	Met	Ser	Glu	Tyr	Pro	Thr	Tyr	His	Thr	His	Gly	Arg	Tyr
	1205					1210					1215			
Val	Pro	Pro	Ser	Ser	Thr	Asp	Arg	Ser	Pro	Tyr	Glu	Lys	Val	Ser
	1220					1225					1230			
Ala	Gly	Asn	Gly	Gly	Ser	Ser	Leu	Ser	Tyr	Thr	Asn	Pro	Ala	Val
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Ala	Ala	Ala	Ser	Ala	Asn	Leu								
	1250					1255								

<210> 2
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-terminal MUC-1 signaling sequence

<400> 2

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
 1 5 10 15

Val Leu Thr

<210> 3
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-terminal MUC-1 signaling sequence

<400> 3

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
 1 5 10 15

Val Leu Thr Val Val Thr Ala
 20

<210> 4
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-terminal MUC-1 signaling sequence

<400> 4

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
 1 5 10 15

Val Leu Thr Val Val Thr Gly
 20

<210> 5
 <211> 146
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> truncated MUC1 receptor isoform having nat-PSMGFR at its
 N-terminus

<400> 5

Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys
1 5 10 15

Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val
20 25 30

Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val Pro
35 40 45

Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala Leu
50 55 60

Ala Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg Lys
65 70 75 80

Asn Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His Pro
85 90 95

Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro Pro
100 105 110

Ser Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn Gly
115 120 125

Gly Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Ala Ser Ala
130 135 140

Asn Leu
145

<210> 6
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Native Primary Sequence of the MUC1 Growth Factor Receptor
<400> 6

Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys
1 5 10 15

Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val
20 25 30

Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
35 40 45

<210> 7
<211> 44
<212> PRT
<213> Artificial Sequence

<220>

<223> Native Primary Sequence of the MUC1 Growth Factor Receptor

<400> 7

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
1 5 10 15

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
20 25 30

Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
35 40

<210> 8

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> "SPY" functional variant of the native Primary Sequence of the
MUC1 Growth Factor Receptor

<400> 8

Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys
1 5 10 15

Thr Glu Ala Ala Ser Pro Tyr Asn Leu Thr Ile Ser Asp Val Ser Val
20 25 30

Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
35 40 45

<210> 9

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> SPY" functional variant of the native Primary Sequence of the
MUC1 Growth Factor Receptor

<400> 9

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
1 5 10 15

Glu Ala Ala Ser Pro Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
20 25 30

Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
35 40

<210> 10

<211> 216

<212> DNA

<213> Artificial Sequence

Val Ala Ala Ala Ser Ala Asn Leu
65 70

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gtcctattat tgccatggag attttaagag atgatgctat atgtgaatgg aaaagactgc 540
 tgggacctgc aaactctgga gtggcacgca cagatgcttc tgaaagcatt agagccctct 600
 ttggaacaga tggcataaga aatgcagcgc atggccctga ttcttttgct tctgcggcca 660
 gagaaatgga gttgtttttt ccttcaagtg gaggttggtg gccggcaaac actgctaaat 720
 ttactaattg tacctgttgc attgttaaac cccatgctgt cagtgaaggt atgttgaata 780
 cactatattc agtacatttt gttaatagga gagcaatggt tattttcttg atgtacttta 840
 tgtatagaaa ataa 854

<210> 13
 <211> 283
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NME7 amino acid sequence

<400> 13

Asp Pro Glu Thr Met Asn His Ser Glu Arg Phe Val Phe Ile Ala Glu
 1 5 10 15

Trp Tyr Asp Pro Asn Ala Ser Leu Leu Arg Arg Tyr Glu Leu Leu Phe
 20 25 30

Tyr Pro Gly Asp Gly Ser Val Glu Met His Asp Val Lys Asn His Arg
 35 40 45

Thr Phe Leu Lys Arg Thr Lys Tyr Asp Asn Leu His Leu Glu Asp Leu
 50 55 60

Phe Ile Gly Asn Lys Val Asn Val Phe Ser Arg Gln Leu Val Leu Ile
 65 70 75 80

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

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

Ile Ile Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys Leu Lys
 115 120 125

Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val Asp His
 130 135 140

Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr Thr Gly
 145 150 155 160

Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp
 165 170 175

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Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr Asp Ala
180 185 190

Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg Asn Ala
195 200 205

Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met Glu Leu
210 215 220

Phe Phe Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe
225 230 235 240

Thr Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser Glu Gly
245 250 255

Met Leu Asn Thr Leu Tyr Ser Val His Phe Val Asn Arg Arg Ala Met
260 265 270

Phe Ile Phe Leu Met Tyr Phe Met Tyr Arg Lys
275 280

<210> 14
<211> 534
<212> DNA
<213> Artificial Sequence

<220>
<223> NM23-H1 nucleotide sequence

<400> 14
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tgtgatacag gaaccatggc caactgtgag cgtaccttca ttgcgatcaa accagatggg 120
gtccagcggg gtcttggtgg agagattatc aagcgttttg agcagaaagg attccgcctt 180
gttggtctga aattcatgca agcttccgaa gatcttctca aggaacacta cgttgacctg 240
aaggaccgtc cattctttgc cggcctggtg aaatacatgc actcagggcc ggtagttgcc 300
atggtctggg aggggctgaa tgtggtgaag acgggccgag tcatgctcgg ggagaccaac 360
cctgcagact ccaagcctgg gaccatccgt ggagacttct gcatacaagt tggcaggaac 420
attatacatg gcagtgattc tgtggagagt gcagagaagg agatcggctt gtggtttcac 480
cctgaggaac tggtagatta cacgagctgt gctcagaact ggatctatga atga 534

<210> 15
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> NM23-H1 describes amino acid sequence

<400> 15

Met Val Leu Leu Ser Thr Leu Gly Ile Val Phe Gln Gly Glu Gly Pro
1 5 10 15

Pro Ile Ser Ser Cys Asp Thr Gly Thr Met Ala Asn Cys Glu Arg Thr
20 25 30

Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly Leu Val Gly Glu
35 40 45

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

Phe Met Gln Ala Ser Glu Asp Leu Leu Lys Glu His Tyr Val Asp Leu
65 70 75 80

Lys Asp Arg Pro Phe Phe Ala Gly Leu Val Lys Tyr Met His Ser Gly
85 90 95

Pro Val Val Ala Met Val Trp Glu Gly Leu Asn Val Val Lys Thr Gly
100 105 110

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

Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg Asn Ile Ile His Gly
130 135 140

Ser Asp Ser Val Glu Ser Ala Glu Lys Glu Ile Gly Leu Trp Phe His
145 150 155 160

Pro Glu Glu Leu Val Asp Tyr Thr Ser Cys Ala Gln Asn Trp Ile Tyr
165 170 175

Glu

<210> 16
<211> 534
<212> DNA
<213> Artificial Sequence

<220>
<223> NM23-H1 S120G mutant nucleotide sequence

<400> 16
atggtgctac tgtctacttt agggatcgctc tttcaaggcg aggggcctcc tatctcaagc 60
tgtgatacag gaaccatggc caactgtgag cgtaccttca ttgcatcaa accagatggg 120
gtccagcggg gtcttggtggg agagattatc aagcggtttg agcagaaagg attccgcctt 180
gttggtctga aattcatgca agcttccgaa gatcttctca aggaacacta cgttgacctg 240
aaggaccgtc cattctttgc cggcctggtg aaatacatgc actcagggcc ggtagttgcc 300
atggtctggg aggggctgaa tgtggtgaag acgggccgag tcatgctcgg ggagaccaac 360

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cctgcagact ccaagcctgg gaccatccgt ggagacttct gcatacaagt tggcaggaac 420
attatacatg gcggtgattc tgtggagagt gcagagaagg agatcggctt gtggtttcac 480
cctgaggaac tggtagatta cacgagctgt gctcagaact ggatctatga atga 534

<210> 17
<211> 177
<212> PRT
<213> Artificial sequence

<220>
<223> NM23-H1 S120G mutant amino acid sequence

<400> 17

Met Val Leu Leu Ser Thr Leu Gly Ile Val Phe Gln Gly Glu Gly Pro
1 5 10 15

Pro Ile Ser Ser Cys Asp Thr Gly Thr Met Ala Asn Cys Glu Arg Thr
20 25 30

Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly Leu Val Gly Glu
35 40 45

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

Phe Met Gln Ala Ser Glu Asp Leu Leu Lys Glu His Tyr Val Asp Leu
65 70 75 80

Lys Asp Arg Pro Phe Phe Ala Gly Leu Val Lys Tyr Met His Ser Gly
85 90 95

Pro Val Val Ala Met Val Trp Glu Gly Leu Asn Val Val Lys Thr Gly
100 105 110

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

Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg Asn Ile Ile His Gly
130 135 140

Gly Asp Ser Val Glu Ser Ala Glu Lys Glu Ile Gly Leu Trp Phe His
145 150 155 160

Pro Glu Glu Leu Val Asp Tyr Thr Ser Cys Ala Gln Asn Trp Ile Tyr
165 170 175

Glu

<210> 18
<211> 459

<212> DNA

<213> Artificial Sequence

<220>

<223> NM23-H2 nucleotide sequence

<400> 18

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gtgggcgaga tcatcaagcg cttcgagcag aagggattcc gcctcgtggc catgaagttc      120
ctccgggcct ctgaagaaca cctgaagcag cactacattg acctgaaaga ccgaccattc      180
ttccctgggc tgggtgaagta catgaactca gggccggttg tggccatggt ctgggagggg      240
ctgaacgtgg tgaagacagg ccgagtgatg cttggggaga ccaatccagc agattcaaag      300
ccaggcacca ttcgtgggga cttctgcatt caggttggca ggaacatcat tcatggcagt      360
gattcagtaa aaagtgctga aaaagaaatc agcctatggt ttaagcctga agaactggtt      420
gactacaagt cttgtgctca tgactgggtc tatgaataa      459

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<210> 19

<211> 152

<212> PRT

<213> Artificial Sequence

<220>

<223> NM23-H2 amino acid sequence

<400> 19

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Met Ala Asn Leu Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val
1      5      10      15

```

```

Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly
20      25      30

```

```

Phe Arg Leu Val Ala Met Lys Phe Leu Arg Ala Ser Glu Glu His Leu
35      40      45

```

```

Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe Pro Gly Leu
50      55      60

```

```

Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val Trp Glu Gly
65      70      75      80

```

```

Leu Asn Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro
85      90      95

```

```

Ala Asp Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val
100      105      110

```

```

Gly Arg Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys
115      120      125

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```

Glu Ile Ser Leu Trp Phe Lys Pro Glu Glu Leu Val Asp Tyr Lys Ser
130      135      140

```

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Cys Ala His Asp Trp Val Tyr Glu
145 150

<210> 20
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NM23-H7-2 sequence optimized for E. coli expression

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ctggaagacc tgtttattgg caacaaagtc aatgtgttct ctcgtcagct ggtgctgac 120
gattatggcg accagtacac cgcgcgtcaa ctgggtagtc gcaaagaaaa aacgctggcc 180
ctgattaaac cggatgcaat ctccaaagct ggcgaaatta tcgaaattat caacaaagcg 240
ggtttcacca tcacgaaact gaaaatgatg atgctgagcc gtaaagaagc cctggatttt 300
catgtcgacc accagtctcg cccgtttttc aatgaactga ttcaattcat caccacgggt 360
ccgattatcg caatggaaat tctgctgat gacgctatct gcgaatggaa acgcctgctg 420
ggcccggcaa actcaggtgt tgcgcgtacc gatgccagtg aatccattcg cgctctgttt 480
ggcaccgatg gtatccgtaa tgcagcacat ggtccggact cattcgcatc ggagctcgt 540
gaaatggaac tgttttttccc gagctctggc gggtgcggtc cggcaaacac cgccaaattt 600
accaattgta cgtgctgtat tgtcaaaccg cacgcagtgt cagaaggcct gctgggtaaa 660
attctgatgg caatccgtga tgctggcttt gaaatctcgg ccatgcagat gttcaacatg 720
gaccgcgtta acgtcgaaga attctacgaa gtttacaaag gcgtgggttac cgaatatcac 780
gatatgggta cggaaatgta ctccgggtccg tgcgtcgcga tggaaattca gcaaaacaat 840
gccacaaaaa cgtttcgtga attctgtggc cgggcagatc cggaaatcgc acgtcatctg 900
cgtccgggta ccctgcgcgc aatttttggc aaaacgaaaa tccagaacgc tgtgcactgt 960
accgatctgc cggaagacgg tctgctggaa gttcaatact ttttcaaaat tctggataat 1020
tga 1023

<210> 21
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NM23-H7-2 sequence optimized for E. coli expression

<400> 21

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

Asp Asn Leu His Leu Glu Asp Leu Phe Ile Gly Asn Lys Val Asn Val
20 25 30

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

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Leu Arg Ala Ile Phe Gly Lys Thr Lys Ile Gln Asn Ala Val His Cys
305 310 315 320

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

Ile Leu Asp Asn
340

<210> 22
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-A

<400> 22
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aaagaagcat tggattttca tgtagatcac cagtcaagac cctttttcaa tgagctgac 180
cagtttatta caactgggtcc tattattgcc atggagattt taagagatga tgctatatgt 240
gaatggaaaa gactgctggg acctgcaaac tctggagtgg cacgcacaga tgcttctgaa 300
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<210> 23
<211> 132
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<220>
<223> Human NME7-A

<400> 23

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Gly Glu Ile Ile Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys
20 25 30

Leu Lys Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val
35 40 45

Asp His Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr
50 55 60

Thr Gly Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys
65 70 75 80

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Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr
85 90 95

Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg
100 105 110

Asn Ala Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met
115 120 125

Glu Leu Phe Phe
130

<210> 24
<211> 444
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-A1

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aaagaagcat tggattttca tgtagatcac cagtcaagac cctttttcaa tgagctgac 180
cagtttatta caactgggtcc tattattgcc atggagattt taagagatga tgctatatgt 240
gaatggaaaa gactgctggg acctgcaaac tctggagtgg cacgcacaga tgcttctgaa 300
agcattagag ccctctttgg aacagatggc ataagaaatg cagcgcatgg ccctgattct 360
tttgcttctg cggccagaga aatggagttg ttttttcctt caagtggagg ttgtgggccg 420
gcaaacactg ctaaatttac ttga 444

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<211> 147
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7-A1

<400> 25

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1 5 10 15

Gly Glu Ile Ile Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys
20 25 30

Leu Lys Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val
35 40 45

Asp His Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr
50 55 60

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Thr Gly Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys
65 70 75 80

Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr
85 90 95

Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg
100 105 110

Asn Ala Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met
115 120 125

Glu Leu Phe Phe Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala
130 135 140

Lys Phe Thr
145

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<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-A2

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aagaatcatc gcaccttttt aaagcggacc aaatatgata acctgcactt ggaagattta 180
tttataggca acaaagtga tgtcttttct cgacaactgg tattaattga ctatggggat 240
caatatacag ctcgccagct gggcagtagg aaagaaaaaa cgctagccct aattaaacca 300
gatgcaatat caaaggctgg agaaataatt gaaataataa acaaagctgg atttactata 360
accaaactca aaatgatgat gctttcaagg aaagaagcat tggattttca ttagatcac 420
cagtcaagac cttttttcaa tgagctgac cagtttatta caactgggtcc tattattgcc 480
atggagattt taagagatga tgctatatgt gaatggaaaa gactgctggg acctgcaaac 540
tctggagtgg cacgcacaga tgcttctgaa agcattagag ccctctttgg aacagatggc 600
ataagaaatg cagcgcagtg ccctgattct tttgcttctg cggccagaga aatggagttg 660
tttttttga 669

<210> 27
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7-A2

<400> 27

Met Asn His Ser Glu Arg Phe Val Phe Ile Ala Glu Trp Tyr Asp Pro
 1 5 10 15

Asn Ala Ser Leu Leu Arg Arg Tyr Glu Leu Leu Phe Tyr Pro Gly Asp
 20 25 30

Gly Ser Val Glu Met His Asp Val Lys Asn His Arg Thr Phe Leu Lys
 35 40 45

Arg Thr Lys Tyr Asp Asn Leu His Leu Glu Asp Leu Phe Ile Gly Asn
 50 55 60

Lys Val Asn Val Phe Ser Arg Gln Leu Val Leu Ile Asp Tyr Gly Asp
 65 70 75 80

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

Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala Gly Glu Ile Ile Glu Ile
 100 105 110

Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys Leu Lys Met Met Met Leu
 115 120 125

Ser Arg Lys Glu Ala Leu Asp Phe His Val Asp His Gln Ser Arg Pro
 130 135 140

Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr Thr Gly Pro Ile Ile Ala
 145 150 155 160

Met Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp Lys Arg Leu Leu
 165 170 175

Gly Pro Ala Asn Ser Gly Val Ala Arg Thr Asp Ala Ser Glu Ser Ile
 180 185 190

Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg Asn Ala Ala His Gly Pro
 195 200 205

Asp Ser Phe Ala Ser Ala Ala Arg Glu Met Glu Leu Phe Phe
 210 215 220

<210> 28
 <211> 714
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human NME7-A3

<400> 28
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aagaatcatc gcaccttttt aaagcggacc aaatatgata acctgcactt ggaagattta	180
tttataggca acaaagtga tgtcttttct cgacaactgg tattaattga ctatggggat	240
caatatacag ctgccagct gggcagtagg aaagaaaaaa cgctagccct aattaaacca	300
gatgcaatat caaaggctgg agaaataatt gaaataataa acaaagctgg atttactata	360
accaaactca aaatgatgat gctttcaagg aaagaagcat tggattttca tgtagatcac	420
cagtcaagac cttttttcaa tgagctgac cagtttatta caactggtcc tattattgcc	480
atggagattt taagagatga tgctatatgt gaatggaaaa gactgctggg acctgcaaac	540
tctggagtgg cacgcacaga tgcttctgaa agcattagag ccctctttgg aacagatggc	600
ataagaaatg cagcgcattg ccctgattct ttgtcttctg cggccagaga aatggagtgt	660
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 <211> 237
 <212> PRT
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<220>
 <223> Human NME7-A3

<400> 29

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			20					25					30		

Gly	Ser	Val	Glu	Met	His	Asp	Val	Lys	Asn	His	Arg	Thr	Phe	Leu	Lys
		35					40					45			

Arg	Thr	Lys	Tyr	Asp	Asn	Leu	His	Leu	Glu	Asp	Leu	Phe	Ile	Gly	Asn
	50					55					60				

Lys	Val	Asn	Val	Phe	Ser	Arg	Gln	Leu	Val	Leu	Ile	Asp	Tyr	Gly	Asp
65					70					75				80	

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

Leu	Ile	Lys	Pro	Asp	Ala	Ile	Ser	Lys	Ala	Gly	Glu	Ile	Ile	Glu	Ile
			100					105					110		

Ile	Asn	Lys	Ala	Gly	Phe	Thr	Ile	Thr	Lys	Leu	Lys	Met	Met	Met	Leu
		115					120					125			

Ser	Arg	Lys	Glu	Ala	Leu	Asp	Phe	His	Val	Asp	His	Gln	Ser	Arg	Pro
	130					135					140				

Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr Thr Gly Pro Ile Ile Ala
145 150 155 160

Met Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp Lys Arg Leu Leu
165 170 175

Gly Pro Ala Asn Ser Gly Val Ala Arg Thr Asp Ala Ser Glu Ser Ile
180 185 190

Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg Asn Ala Ala His Gly Pro
195 200 205

Asp Ser Phe Ala Ser Ala Ala Arg Glu Met Glu Leu Phe Phe Pro Ser
210 215 220

Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe Thr
225 230 235

<210> 30
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
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gatcgggtta atgttgagga attctatgaa gtttataaag gagtagtgac cgaatatcat 180
gacatggtga cagaaatgta ttctggccct tgtgtagcaa tggagattca acagaataat 240
gctacaaaga catttcgaga attttgtgga cctgctgata ctgaaattgc ccggcattta 300
cgccctggaa ctctcagagc aatctttggt aaaactaaga tccagaatgc tgttcactgt 360
actgatctgc cagaggatgg cctattagag gttcaatact tcttctga 408

<210> 31
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7-B

<400> 31

Met Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser Glu Gly
1 5 10 15

Leu Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile
20 25 30

Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe
35 40 45

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Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr
50 55 60

Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn
65 70 75 80

Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile
85 90 95

Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr
100 105 110

Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu
115 120 125

Leu Glu Val Gln Tyr Phe Phe
130 135

<210> 32
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-B1

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gatcggttta atgttgagga attctatgaa gtttataaag gagtagtgac cgaatatcat 180
gacatggtga cagaaatgta ttctggccct tgtgtagcaa tggagattca acagaataat 240
gctacaaaga catttcgaga attttgtgga cctgctgac ctgaaattgc ccggcattta 300
cgccctggaa ctctcagagc aatcttttgt aaaactaaga tccagaatgc tggtcactgt 360
actgatctgc cagaggatgg cctattagag gttcaatact tcttcaagat cttggataat 420
tagtga 426

<210> 33
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7-B1

<400> 33

Met Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser Glu Gly
1 5 10 15

Leu Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile
20 25 30

2015-04-06_13150-70136PCT_Seq_Listing_ST25

Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe
35 40 45

Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr
50 55 60

Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn
65 70 75 80

Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile
85 90 95

Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr
100 105 110

Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu
115 120 125

Leu Glu Val Gln Tyr Phe Phe Lys Ile Leu Asp Asn
130 135 140

<210> 34
<211> 453
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-B2

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cgagatgcag gttttgaaat ctcagctatg cagatgttca atatggatcg ggttaatgtt 180
gaggaattct atgaagttaa taaaggagta gtgaccgaat atcatgacat ggtgacagaa 240
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cgagaatttt gtggacctgc tgatcctgaa attgcccggc atttacgccc tggaactctc 360
agagcaatct ttggtaaaac taagatccag aatgctgttc actgtactga tctgccagag 420
gatggcctat tagaggttca atacttcttc tga 453

<210> 35
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7-B2

<400> 35

Met Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe Thr
1 5 10 15

2015-04-06_13150-70136PCT_Seq_Listing_ST25

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

Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile Ser
35 40 45

Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe Tyr
50 55 60

Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr Glu
65 70 75 80

Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn Ala
85 90 95

Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile Ala
100 105 110

Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr Lys
115 120 125

Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu Leu
130 135 140

Glu Val Gln Tyr Phe Phe
145 150

<210> 36
<211> 471
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-B3

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cgagatgcag gttttgaaat ctcagctatg cagatgttca atatggatcg ggtaaatgtt 180
gaggaattct atgaagtta taaaggagta gtgaccgaat atcatgacat ggtgacagaa 240
atgtattctg gcccttgtgt agcaatggag attcaacaga ataatgctac aaagacattt 300
cgagaatttt gtggacctgc tgatcctgaa attgcccggc atttacgcc tggaactctc 360
agagcaatct ttggtaaaac taagatccag aatgctgttc actgtactga tctgccagag 420
gatggcctat tagaggttca atacttcttc aagatcttgg ataattagtg a 471

<210> 37
<211> 155
<212> PRT
<213> Artificial Sequence

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<220>

<223> Human NME7-B3

<400> 37

Met Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe Thr
1 5 10 15

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

Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile Ser
35 40 45

Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe Tyr
50 55 60

Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr Glu
65 70 75 80

Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn Ala
85 90 95

Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile Ala
100 105 110

Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr Lys
115 120 125

Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu Leu
130 135 140

Glu Val Gln Tyr Phe Phe Lys Ile Leu Asp Asn
145 150 155

<210> 38

<211> 864

<212> DNA

<213> Artificial Sequence

<220>

<223> Human NME7-AB

<400> 38

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aaagaagcat tggattttca tgtagatcac cagtcaagac cctttttcaa tgagctgac	180
cagtttatta caactggtcc tattattgcc atggagattt taagagatga tgctatatgt	240
gaatggaaaa gactgctggg acctgcaaac tctggagtgg cacgcacaga tgcttctgaa	300
agcattagag ccctctttgg aacagatggc ataagaaatg cagcgcatgg ccctgattct	360
tttgcttctg cggccagaga aatggagttg ttttttcctt caagtggagg ttgtgggccg	420

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gcaaacactg ctaaatttac taattgtacc tgttgcatg ttaaacccca tgctgtcagt 480
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gtagtgaccg aatatcatga catggtgaca gaaatgtatt ctggcccttg ttagcaatg 660
gagattcaac agaataatgc tacaaagaca tttcgagaat tttgtggacc tgctgacct 720
gaaattgccc ggcatttacg ccctggaact ctcagagcaa tctttggtaa aactaagatc 780
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<211> 286
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7-AB

<400> 39

Met Glu Lys Thr Leu Ala Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala
1 5 10 15

Gly Glu Ile Ile Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys
20 25 30

Leu Lys Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val
35 40 45

Asp His Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr
50 55 60

Thr Gly Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys
65 70 75 80

Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr
85 90 95

Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg
100 105 110

Asn Ala Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met
115 120 125

Glu Leu Phe Phe Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala
130 135 140

Lys Phe Thr Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser
145 150 155 160

Glu Gly Leu Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe
 165 170 175

Glu Ile Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu
 180 185 190

Glu Phe Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met
 195 200 205

Val Thr Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln
 210 215 220

Asn Asn Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro
 225 230 235 240

Glu Ile Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly
 245 250 255

Lys Thr Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp
 260 265 270

Gly Leu Leu Glu Val Gln Tyr Phe Phe Lys Ile Leu Asp Asn
 275 280 285

<210> 40
 <211> 846
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human NME7-AB1

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 aaagaagcat tggattttca tgtagatcac cagtcaagac cctttttcaa tgagctgatc 180
 cagtttatta caactgggtcc tattattgcc atggagattt taagagatga tgctatatgt 240
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 agcattagag ccctcttttg aacagatggc ataagaaatg cagcgcatgg ccctgattct 360
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 gcaaacactg ctaaatttac taattgtacc tgttgcattg ttaaacccca tgctgtcagt 480
 gaaggactgt tgggaaagat cctgatggct atccgagatg caggttttga aatctcagct 540
 atgcagatgt tcaatatgga tcgggttaat gttgaggaat tctatgaagt ttataaagga 600
 gtagtgaccg aatatcatga catggtgaca gaaatgtatt ctggcccttg tgtagcaatg 660
 gagattcaac agaataatgc tacaaagaca tttcgagaat tttgtggacc tgctgatcct 720
 gaaattgccc ggcatttacg ccctggaact ctcagagcaa tctttggtaa aactaagatc 780
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<210> 41
 <211> 281
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human NME7-AB1

<400> 41

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 1 5 10 15

Gly Glu Ile Ile Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys
 20 25 30

Leu Lys Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val
 35 40 45

Asp His Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr
 50 55 60

Thr Gly Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys
 65 70 75 80

Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr
 85 90 95

Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg
 100 105 110

Asn Ala Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met
 115 120 125

Glu Leu Phe Phe Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala
 130 135 140

Lys Phe Thr Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser
 145 150 155 160

Glu Gly Leu Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe
 165 170 175

Glu Ile Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu
 180 185 190

Glu Phe Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met
 195 200 205

Val Thr Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln
 210 215 220

Asn Asn Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro
225 230 235 240

Glu Ile Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly
245 250 255

Lys Thr Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp
260 265 270

Gly Leu Leu Glu Val Gln Tyr Phe Phe
275 280

<210> 42
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-A sequence optimized for E. coli expression

<400> 42
atggaaaaaa cgctggccct gattaaaccg gatgcaatct ccaaagctgg cgaaattatc 60
gaaattatca acaaagcggg ttccaccatc acgaaactga aaatgatgat gctgagccgt 120
aaagaagccc tggattttca tgtcgaccac cagtctcgcc cgtttttcaa tgaactgatt 180
caattcatca ccacgggtcc gattatcgca atggaaattc tgcgtgatga cgctatctgc 240
gaatggaaac gcctgctggg cccggcaaac tcaggtgttg cgcgtaccga tgccagtga 300
tccattcgcg ctctgtttgg caccgatggg atccgtaatg cagcacatgg tccggactca 360
ttcgcacgag cagctcgtga aatggaactg tttttctga 399

<210> 43
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7-A sequence optimized for E. coli expression

<400> 43

Met Glu Lys Thr Leu Ala Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala
1 5 10 15

Gly Glu Ile Ile Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys
20 25 30

Leu Lys Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val
35 40 45

Asp His Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr
50 55 60

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Thr Gly Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys
65 70 75 80

Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr
85 90 95

Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg
100 105 110

Asn Ala Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met
115 120 125

Glu Leu Phe Phe
130

<210> 44
<211> 444
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-A1 sequence optimized for E. coli expression

<400> 44
atggaaaaaa cgctggccct gattaaaccg gatgcaatct ccaaagctgg cgaaattatc 60
gaaattatca acaaagcggg tttcaccatc acgaaactga aaatgatgat gctgagccgt 120
aaagaagccc tggattttca tgtcgaccac cagtctcgcc cgtttttcaa tgaactgatt 180
caattcatca ccacgggtcc gattatcgca atggaaaattc tgcgtgatga cgctatctgc 240
gaatggaaac gcctgctggg cccggcaaac tcagggtgttg cgcgtaccga tgccagtga 300
tccattcgcg ctctgttttg caccgatggg atccgtaatg cagcacatgg tccggactca 360
ttcgcatcgg cagctcgtga aatggaactg tttttcccga gctctggcgg ttgcggtccg 420
gcaaacaccg ccaaatttac ctga 444

<210> 45
<211> 147
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7-A1 sequence optimized for E. coli expression

<400> 45

Met Glu Lys Thr Leu Ala Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala
1 5 10 15

Gly Glu Ile Ile Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys
20 25 30

Leu Lys Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val
35 40 45

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Asp His Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr
50 55 60

Thr Gly Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys
65 70 75 80

Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr
85 90 95

Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg
100 105 110

Asn Ala Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met
115 120 125

Glu Leu Phe Phe Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala
130 135 140

Lys Phe Thr
145

<210> 46
<211> 669
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-A2 sequence optimized for E. coli expression

<400> 46
atgaatcact ccgaacgctt tgtttttatc gccgaatggt atgacccgaa tgcttcctg 60
ctgcgccgct acgaactgct gttttatccg ggcgatggta gcgtggaaat gcatgacgtt 120
aaaaatcacc gtacctttct gaaacgcacg aaatatgata atctgcatct ggaagacctg 180
tttattggca acaaagtcaa tgtgttctct cgtcagctgg tgctgatcga ttatggcgac 240
cagtacaccg cgcgtcaact gggtagtcgc aaagaaaaaa cgctggccct gattaaaccg 300
gatgcaatct ccaaagctgg cgaaattatc gaaattatca acaaagcggg tttcaccatc 360
acgaaactga aaatgatgat gctgagccgt aaagaagccc tggattttca tgtcgaccac 420
cagtctcgcc cgtttttcaa tgaactgatt caattcatca ccacgggtcc gattatcgca 480
atggaaattc tgcgtgatga cgctatctgc gaatggaaac gcctgctggg cccggcaaac 540
tcagggtgttg cgcgtaccga tgccagtga tccattcgcg ctctgtttgg caccgatggt 600
atccgtaatg cagcacatgg tccggactca ttcgcatcgg cagctcgtga aatggaactg 660
tttttctga 669

<210> 47
<211> 222
<212> PRT
<213> Artificial Sequence

<220>

<223> Human NME7-A2 sequence optimized for E. coli expression

<400> 47

Met Asn His Ser Glu Arg Phe Val Phe Ile Ala Glu Trp Tyr Asp Pro
1 5 10 15

Asn Ala Ser Leu Leu Arg Arg Tyr Glu Leu Leu Phe Tyr Pro Gly Asp
20 25 30

Gly Ser Val Glu Met His Asp Val Lys Asn His Arg Thr Phe Leu Lys
35 40 45

Arg Thr Lys Tyr Asp Asn Leu His Leu Glu Asp Leu Phe Ile Gly Asn
50 55 60

Lys Val Asn Val Phe Ser Arg Gln Leu Val Leu Ile Asp Tyr Gly Asp
65 70 75 80

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

Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala Gly Glu Ile Ile Glu Ile
100 105 110

Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys Leu Lys Met Met Met Leu
115 120 125

Ser Arg Lys Glu Ala Leu Asp Phe His Val Asp His Gln Ser Arg Pro
130 135 140

Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr Thr Gly Pro Ile Ile Ala
145 150 155 160

Met Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp Lys Arg Leu Leu
165 170 175

Gly Pro Ala Asn Ser Gly Val Ala Arg Thr Asp Ala Ser Glu Ser Ile
180 185 190

Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg Asn Ala Ala His Gly Pro
195 200 205

Asp Ser Phe Ala Ser Ala Ala Arg Glu Met Glu Leu Phe Phe
210 215 220

<210> 48

<211> 714

<212> DNA

<213> Artificial sequence

<220>

<223> Human NME7-A3 sequence optimized for E. coli expression

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```

<400> 48
atgaatcact ccgaacgctt tgtttttatc gccgaatggt atgacccgaa tgcttccctg      60
ctgcgccgct acgaactgct gttttatccg ggcgatggta gcgtggaaat gcatgacgtt    120
aaaaatcacc gtacctttct gaaacgcacg aaatatgata atctgcatct ggaagacctg    180
tttattggca acaaagtcaa tgtgttctct cgtcagctgg tgctgatcga ttatggcgac    240
cagtacaccg cgcgtcaact gggtagtcgc aaagaaaaaa cgctggccct gattaaaccg    300
gatgcaatct ccaaagctgg cgaaattatc gaaattatca acaaagcggg tttcaccatc    360
acgaaactga aaatgatgat gctgagccgt aaagaagccc tggattttca tgtcgaccac    420
cagtctcgcc cgtttttcaa tgaactgatt caattcatca ccacgggtcc gattatcgca    480
atggaaattc tgcgtgatga cgctatctgc gaatggaaac gcctgctggg cccggcaaac    540
tcagggtgtg cgcgtaccga tgccagtga tccattcgcg ctctgtttgg caccgatggt    600
atccgtaatg cagcacatgg tccggactca ttcgcatcgg cagctcgtga aatggaactg    660
tttttccgga gctctggcgg ttgcgggtccg gcaaacaccg ccaaatttac ctga      714

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```

<210> 49
<211> 237
<212> PRT
<213> Artificial Sequence

```

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<220>
<223> Human NME7-A3 sequence optimized for E. coli expression

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<400> 49

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```

Met Asn His Ser Glu Arg Phe Val Phe Ile Ala Glu Trp Tyr Asp Pro
1          5          10          15

```

```

Asn Ala Ser Leu Leu Arg Arg Tyr Glu Leu Leu Phe Tyr Pro Gly Asp
20          25          30

```

```

Gly Ser Val Glu Met His Asp Val Lys Asn His Arg Thr Phe Leu Lys
35          40          45

```

```

Arg Thr Lys Tyr Asp Asn Leu His Leu Glu Asp Leu Phe Ile Gly Asn
50          55          60

```

```

Lys Val Asn Val Phe Ser Arg Gln Leu Val Leu Ile Asp Tyr Gly Asp
65          70          75          80

```

```

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

```

```

Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala Gly Glu Ile Ile Glu Ile
100         105         110

```

```

Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys Leu Lys Met Met Met Leu
115         120         125

```

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Ser Arg Lys Glu Ala Leu Asp Phe His Val Asp His Gln Ser Arg Pro
130 135 140

Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr Thr Gly Pro Ile Ile Ala
145 150 155 160

Met Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp Lys Arg Leu Leu
165 170 175

Gly Pro Ala Asn Ser Gly Val Ala Arg Thr Asp Ala Ser Glu Ser Ile
180 185 190

Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg Asn Ala Ala His Gly Pro
195 200 205

Asp Ser Phe Ala Ser Ala Ala Arg Glu Met Glu Leu Phe Phe Pro Ser
210 215 220

Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe Thr
225 230 235

<210> 50
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-B sequence optimized for E. coli expression

<400> 50
atgaattgta cgtgctgtat tgtcaaaccg cacgcagtgt cagaaggcct gctgggtaaa 60
attctgatgg caatccgtga tgctggcttt gaaatctcgg ccatgcagat gttcaacatg 120
gaccgcgtta acgtcgaaga attctacgaa gtttacaaag gcgtgggttac cgaatatcac 180
gatatgggta cggaatgta ctccgggtccg tgcgtcgcga tggaaattca gcaaaacaat 240
gccacaaaaa cgtttcgtga attctgtggg cgggcagatc cggaaatcgc acgtcatctg 300
cgtccgggta ccctgcgcgc aatttttggg aaaacgaaaa tccagaacgc tgtgcactgt 360
accgatctgc cggaagacgg tctgctggaa gttcaatact ttttctga 408

<210> 51
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7-B sequence optimized for E. coli expression

<400> 51

Met Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser Glu Gly
1 5 10 15

Leu Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile
20 25 30

Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe
 35 40 45

Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr
 50 55 60

Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn
 65 70 75 80

Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile
 85 90 95

Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr
 100 105 110

Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu
 115 120 125

Leu Glu Val Gln Tyr Phe Phe
 130 135

<210> 52
 <211> 423
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human NME7-B1 sequence optimized for E. coli expression

<400> 52
 atgaattgta cgtgctgtat tgtcaaaccg cacgcagtgt cagaaggcct gctgggtaaa 60
 attctgatgg caatccgtga tgctggcttt gaaatctcgg ccatgcagat gttcaacatg 120
 gaccgcgtta acgtcgaaga attctacgaa gtttacaaag gcgtgggttac cgaatatcac 180
 gatatgggta cggaaatgta ctccgggtccg tgcgtcgcga tggaaattca gcaaaacaat 240
 gccacaaaaa cgtttcgtga attctgtggg ccggcagatc cggaaatcgc acgtcatctg 300
 cgtccgggta ccctgcgcgc aatttttggg aaaacgaaaa tccagaacgc tgtgcactgt 360
 accgatctgc cggaagacgg tctgctggaa gttcaatact ttttcaaaat tctggataat 420
 tga 423

<210> 53
 <211> 140
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human NME7-B1 sequence optimized for E. coli expression

<400> 53

Met Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser Glu Gly
 1 5 10 15

Leu Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile
20 25 30

Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe
35 40 45

Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr
50 55 60

Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn
65 70 75 80

Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile
85 90 95

Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr
100 105 110

Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu
115 120 125

Leu Glu Val Gln Tyr Phe Phe Lys Ile Leu Asp Asn
130 135 140

<210> 54
<211> 453
<212> DNA
<213> Artificial sequence

<220>
<223> Human NME7-B2 sequence optimized for E. coli expression

<400> 54
atgccgagct ctggcgggttg cgggtccggca aacaccgccca aatttaccaa ttgtacgtgc 60
tgtattgtca aaccgcacgc agtgtcagaa ggctgtctgg gtaaaattct gatggcaatc 120
cgtgatgctg gctttgaaat ctcggccatg cagatgttca acatggaccg cgtaacgtc 180
gaagaattct acgaagttta caaaggcgtg gttaccgaat atcacgatat ggttacggaa 240
atgtactccg gtccgtgcgt cgcgatggaa attcagcaaa acaatgccac caaaacgttt 300
cgtgaattct gtggtccggc agatccggaa atcgcacgtc atctgcgtcc gggtagcctg 360
cgcgcaattt ttggtaaaac gaaaatccag aacgctgtgc actgtaccga tctgccggaa 420
gacggtctgc tggaagttca atactttttc tga 453

<210> 55
<211> 150
<212> PRT
<213> Artificial sequence

<220>
<223> Human NME7-B2 sequence optimized for E. coli expression

<400> 55

Met Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe Thr
1 5 10 15

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

Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile Ser
35 40 45

Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe Tyr
50 55 60

Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr Glu
65 70 75 80

Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn Ala
85 90 95

Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile Ala
100 105 110

Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr Lys
115 120 125

Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu Leu
130 135 140

Glu Val Gln Tyr Phe Phe
145 150

<210> 56

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> Human NME7-B3 sequence optimized for E. coli expression

<400> 56

atgccgagct ctggcggttg cgggccgga aacaccgcca aatttaccaa ttgtacgtgc	60
tgtattgtca aaccgcacgc agtgtcagaa ggcctgctgg gtaaaattct gatggcaatc	120
cgtgatgctg gctttgaaat ctcggccatg cagatgttca acatggaccg cgttaacgtc	180
gaagaattct acgaagttaa caaaggcgtg gttaccgaat atcacgatat gggtacggaa	240
atgtactccg gtccgtgcgt cgcgatggaa attcagcaaa acaatgccac caaaacgttt	300
cgtgaattct gtggtccggc agatccggaa atcgcacgtc atctgcgtcc gggtaccctg	360
cgcgcaattt ttggtaaaac gaaaatccag aacgctgtgc actgtaccga tctgccggaa	420
gacggtctgc tggaagtcca atactttttc aaaattctgg ataattga	468

<210> 57
 <211> 155
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human NME7-B3 sequence optimized for E. coli expression

<400> 57

Met Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe Thr
 1 5 10 15

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

Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile Ser
 35 40 45

Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe Tyr
 50 55 60

Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr Glu
 65 70 75 80

Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn Ala
 85 90 95

Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile Ala
 100 105 110

Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr Lys
 115 120 125

Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu Leu
 130 135 140

Glu Val Gln Tyr Phe Phe Lys Ile Leu Asp Asn
 145 150 155

<210> 58
 <211> 861
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human NME7-AB sequence optimized for E. coli expression

<400> 58

atggaaaaaa cgctggccct gattaaaccg gatgcaatct ccaaagctgg cgaaattatc	60
gaaattatca acaaagcggg ttccaccatc acgaaactga aaatgatgat gctgagccgt	120
aaagaagccc tggattttca tgtcgaccac cagtctcgcc cgtttttcaa tgaactgatt	180
caattcatca ccacgggtcc gattatcgca atggaaattc tgcgtgatga cgctatctgc	240
gaatggaaac gcctgctggg cccggcaaac tcaggtgttg cgcgtaaccga tgccagtga	300

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tccattcgcg ctctgtttgg caccgatggg atccgtaatg cagcacatgg tccggactca 360
ttcgcacatcgg cagctcgtga aatggaactg tttttcccga gctctggcgg ttgcggtccg 420
gcaaacaccg ccaaatttac caattgtacg tgctgtattg tcaaaccgca cgcagtgtca 480
gaaggcctgc tgggtaaaat tctgatggca atccgtgatg ctggctttga aatctcggcc 540
atgcagatgt tcaacatgga ccgcgttaac gtcgaagaat tctacgaagt ttacaaaggc 600
gtggttaccg aatatcacga tatggttacg gaaatgtact ccggtccgtg cgtcgcgatg 660
gaaattcagc aaaacaatgc caccaaaacg tttcgtgaat tctgtgggcc ggcagatccg 720
gaaatcgcac gtcactcgcg tccgggtacc ctgcgcgcaa tttttggtaa aacgaaaatc 780
cagaacgctg tgcactgtac cgatctgccg gaagacgggc tgctggaagt tcaatacttt 840
ttcaaaattc tggataattg a 861
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<210> 59
 <211> 286
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human NME7-AB sequence optimized for E. coli expression
 <400> 59

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Met Glu Lys Thr Leu Ala Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala
1      5      10     15

Gly Glu Ile Ile Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys
20     25     30

Leu Lys Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val
35     40     45

Asp His Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr
50     55     60

Thr Gly Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys
65     70     75     80

Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr
85     90     95

Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg
100    105    110

Asn Ala Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met
115    120    125

Glu Leu Phe Phe Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala
130    135    140
```

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Lys Phe Thr Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser
145 150 155 160

Glu Gly Leu Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe
165 170 175

Glu Ile Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu
180 185 190

Glu Phe Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met
195 200 205

Val Thr Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln
210 215 220

Asn Asn Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro
225 230 235 240

Glu Ile Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly
245 250 255

Lys Thr Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp
260 265 270

Gly Leu Leu Glu Val Gln Tyr Phe Phe Lys Ile Leu Asp Asn
275 280 285

<210> 60
<211> 846
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-AB1 sequence optimized for E. coli expression

<400> 60
atggaaaaaa cgctggccct gattaaaccg gatgcaatct ccaaagctgg cgaaattatc 60
gaaattatca acaaagcggg tttcaccatc acgaaactga aaatgatgat gctgagccgt 120
aaagaagccc tggattttca tgctgaccac cagtctcgcc cgtttttcaa tgaactgatt 180
caattcatca ccacgggtcc gattatcgca atggaaattc tgcgtgatga cgctatctgc 240
gaatggaaac gcctgctggg cccggcaaac tcaggtgttg cgcgtaccga tgccagtga 300
tccattcgcg ctctgtttgg caccgatggg atccgtaatg cagcacatgg tccggactca 360
ttcgcacgag cagctcgtga aatggaactg tttttcccga gctctggcgg ttgcgggtccg 420
gcaaacaccg ccaaatttac caattgtacg tgctgtattg tcaaaccgca cgcagtgtca 480
gaaggcctgc tgggtaaaat tctgatggca atccgtgatg ctggccttga aatctcggcc 540
atgcagatgt tcaacatgga ccgcgttaac gtcgaagaat tctacgaagt ttacaaaggc 600
gtggttaccg aatatcacga tatggttacg gaaatgtact ccggtccgtg cgtcgcgatg 660
gaaattcagc aaaacaatgc caccaaaacg tttcgtgaat tctgtgggtcc ggcagatccg 720

gaaatcgcac gtcactgtcg tccgggtacc ctgcgcgcaa tttttggtaa aacgaaaatc 780
 cagaacgctg tgcactgtac cgatctgccg gaagacggtc tgctggaagt tcaatacttt 840
 ttctga 846

<210> 61
 <211> 281
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Human NME7-AB1 sequence optimized for E. coli expression

<400> 61

Met Glu Lys Thr Leu Ala Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala
 1 5 10 15

Gly Glu Ile Ile Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys
 20 25 30

Leu Lys Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val
 35 40 45

Asp His Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr
 50 55 60

Thr Gly Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys
 65 70 75 80

Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr
 85 90 95

Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg
 100 105 110

Asn Ala Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met
 115 120 125

Glu Leu Phe Phe Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala
 130 135 140

Lys Phe Thr Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser
 145 150 155 160

Glu Gly Leu Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe
 165 170 175

Glu Ile Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu
 180 185 190

Glu Phe Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met
 195 200 205

Val Thr Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln
210 215 220

Asn Asn Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro
225 230 235 240

Glu Ile Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly
245 250 255

Lys Thr Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp
260 265 270

Gly Leu Leu Glu Val Gln Tyr Phe Phe
275 280

<210> 62
<211> 570
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding Mouse NME6

<400> 62
atgacctcca tcttgccaag tccccaagct cttcagctca cactagccct gatcaagcct 60
gatgcagttg cccacccact gatcctggag gctgttcac agcagattct gagcaacaag 120
ttcctcattg tacgaacgag ggaactgcag tggaagctgg aggactgccg gaggttttac 180
cgagagcatg aagggcgttt tttctatcag cggctggtgg agttcatgac aagtgggcca 240
atccgagcct atatccttgc ccacaaagat gccatccaac tttggaggac actgatggga 300
cccaccagag tatttcgagc acgctatata gcccagatt caattcgtgg aagtttgggc 360
ctcactgaca cccgaaatac tacccatggc tcagactccg tggtttccgc cagcagagag 420
attgcagcct tcttcctga cttcagtga cagcgtggt atgaggagga ggaacccag 480
ctgcggtgtg gtcctgtgca ctacagtcca gaggaaggta tccactgtgc agctgaaaca 540
ggaggccaca aacaacctaa caaacctag 570

<210> 63
<211> 189
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse NME6

<400> 63

Met Thr Ser Ile Leu Arg Ser Pro Gln Ala Leu Gln Leu Thr Leu Ala
1 5 10 15

Leu Ile Lys Pro Asp Ala Val Ala His Pro Leu Ile Leu Glu Ala Val
20 25 30

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His Gln Gln Ile Leu Ser Asn Lys Phe Leu Ile Val Arg Thr Arg Glu
35 40 45

Leu Gln Trp Lys Leu Glu Asp Cys Arg Arg Phe Tyr Arg Glu His Glu
50 55 60

Gly Arg Phe Phe Tyr Gln Arg Leu Val Glu Phe Met Thr Ser Gly Pro
65 70 75 80

Ile Arg Ala Tyr Ile Leu Ala His Lys Asp Ala Ile Gln Leu Trp Arg
85 90 95

Thr Leu Met Gly Pro Thr Arg Val Phe Arg Ala Arg Tyr Ile Ala Pro
100 105 110

Asp Ser Ile Arg Gly Ser Leu Gly Leu Thr Asp Thr Arg Asn Thr Thr
115 120 125

His Gly Ser Asp Ser Val Val Ser Ala Ser Arg Glu Ile Ala Ala Phe
130 135 140

Phe Pro Asp Phe Ser Glu Gln Arg Trp Tyr Glu Glu Glu Glu Pro Gln
145 150 155 160

Leu Arg Cys Gly Pro Val His Tyr Ser Pro Glu Glu Gly Ile His Cys
165 170 175

Ala Ala Glu Thr Gly Gly His Lys Gln Pro Asn Lys Thr
180 185

<210> 64
<211> 585
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding Human NME6

<400> 64
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ctcactctag ccctgatcaa gcctgacgca gtcgcccata cactgattct ggaggctgtt 120
catcagcaga ttctaagcaa caagttcctg attgtacgaa tgagagaact actgtggaga 180
aaggaagatt gccagagggt ttaccgagag catgaagggc gttttttcta tcagaggctg 240
gtggagttca tggccagcgg gccaatccga gcctacatcc ttgccacaa ggatgccatc 300
cagctctgga ggacgctcat gggacccacc agagtgttcc gagcacgcca tgtggcccca 360
gattctatcc gtgggagttt cggcctcact gacacccgca acaccacca tggttcggac 420
tctgtggttt cagccagcag agagattgca gccttcttcc ctgacttcag tgaacagcgc 480
tggtatgagg aggaagagcc ccagttgcgc tgtggccctg tgtgctatag cccagaggga 540

ggtgtccact atgtagctgg aacaggaggc ctaggaccag cctga

585

<210> 65
 <211> 194
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human NME6

<400> 65

Met Thr Gln Asn Leu Gly Ser Glu Met Ala Ser Ile Leu Arg Ser Pro
 1 5 10 15

Gln Ala Leu Gln Leu Thr Leu Ala Leu Ile Lys Pro Asp Ala Val Ala
 20 25 30

His Pro Leu Ile Leu Glu Ala Val His Gln Gln Ile Leu Ser Asn Lys
 35 40 45

Phe Leu Ile Val Arg Met Arg Glu Leu Leu Trp Arg Lys Glu Asp Cys
 50 55 60

Gln Arg Phe Tyr Arg Glu His Glu Gly Arg Phe Phe Tyr Gln Arg Leu
 65 70 75 80

Val Glu Phe Met Ala Ser Gly Pro Ile Arg Ala Tyr Ile Leu Ala His
 85 90 95

Lys Asp Ala Ile Gln Leu Trp Arg Thr Leu Met Gly Pro Thr Arg Val
 100 105 110

Phe Arg Ala Arg His Val Ala Pro Asp Ser Ile Arg Gly Ser Phe Gly
 115 120 125

Leu Thr Asp Thr Arg Asn Thr Thr His Gly Ser Asp Ser Val Val Ser
 130 135 140

Ala Ser Arg Glu Ile Ala Ala Phe Phe Pro Asp Phe Ser Glu Gln Arg
 145 150 155 160

Trp Tyr Glu Glu Glu Glu Pro Gln Leu Arg Cys Gly Pro Val Cys Tyr
 165 170 175

Ser Pro Glu Gly Gly Val His Tyr Val Ala Gly Thr Gly Gly Leu Gly
 180 185 190

Pro Ala

<210> 66
 <211> 525

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding Human NME6 1

<400> 66

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atgacccaga atctggggag tgagatggcc tcaatcttgc gaagccctca ggctctccag      60
ctcactctag ccctgatcaa gcctgacgca gtcgcccac cactgattct ggaggctgtt      120
catcagcaga ttctaagcaa caagttcctg attgtacgaa tgagagaact actgtggaga      180
aaggaagatt gccagagggt ttaccgagag catgaagggc gttttttcta tcagaggctg      240
gtggagttca tggccagcgg gccaatccga gcctacatcc ttgcccacaa ggatgccatc      300
cagctctgga ggacgctcat gggacccacc agagtgttcc gagcacgcca tgtggcccca      360
gattctatcc gtgggagttt cggcctcact gacacccgca acaccacca tggttcggac      420
tctgtggttt cagccagcag agagattgca gccttcttcc ctgacttcag tgaacagcgc      480
tggtatgagg aggaagagcc ccagttgcgc tgtggccctg tgtga                      525

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<210> 67

<211> 174

<212> PRT

<213> Artificial Sequence

<220>

<223> Human NME6 1

<400> 67

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Met Thr Gln Asn Leu Gly Ser Glu Met Ala Ser Ile Leu Arg Ser Pro
1          5          10          15

```

```

Gln Ala Leu Gln Leu Thr Leu Ala Leu Ile Lys Pro Asp Ala Val Ala
20          25          30

```

```

His Pro Leu Ile Leu Glu Ala Val His Gln Gln Ile Leu Ser Asn Lys
35          40          45

```

```

Phe Leu Ile Val Arg Met Arg Glu Leu Leu Trp Arg Lys Glu Asp Cys
50          55          60

```

```

Gln Arg Phe Tyr Arg Glu His Glu Gly Arg Phe Phe Tyr Gln Arg Leu
65          70          75          80

```

```

Val Glu Phe Met Ala Ser Gly Pro Ile Arg Ala Tyr Ile Leu Ala His
85          90          95

```

```

Lys Asp Ala Ile Gln Leu Trp Arg Thr Leu Met Gly Pro Thr Arg Val
100         105         110

```

```

Phe Arg Ala Arg His Val Ala Pro Asp Ser Ile Arg Gly Ser Phe Gly
115        120        125

```

Leu Thr Asp Thr Arg Asn Thr Thr His Gly Ser Asp Ser Val Val Ser
 130 135 140

Ala Ser Arg Glu Ile Ala Ala Phe Phe Pro Asp Phe Ser Glu Gln Arg
 145 150 155 160

Trp Tyr Glu Glu Glu Glu Pro Gln Leu Arg Cys Gly Pro Val
 165 170

<210> 68
 <211> 468
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding Human NME6 2

<400> 68
 atgctcactc tagccctgat caagcctgac gcagtcgccc atccactgat tctggaggct 60
 gttcatcagc agattctaag caacaagttc ctgattgtac gaatgagaga actactgtgg 120
 agaaaggaag attgccagag gttttaccga gagcatgaag ggcgtttttt ctatcagagg 180
 ctggtggagt tcatggccag cgggccaatc cgagcctaca tccttgccca caaggatgcc 240
 atccagctct ggaggacgct catgggaccc accagagtgt tccgagcacg ccatgtggcc 300
 ccagattcta tccgtgggag tttcggcctc actgacaccc gcaacaccac ccatggttcg 360
 gactctgtgg tttcagccag cagagagatt gcagccttct tccctgactt cagtgaacag 420
 cgctggtatg aggaggaaga gccccagttg cgctgtggcc ctgtgtga 468

<210> 69
 <211> 155
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human NME6 2

<400> 69

Met Leu Thr Leu Ala Leu Ile Lys Pro Asp Ala Val Ala His Pro Leu
 1 5 10 15

Ile Leu Glu Ala Val His Gln Gln Ile Leu Ser Asn Lys Phe Leu Ile
 20 25 30

Val Arg Met Arg Glu Leu Leu Trp Arg Lys Glu Asp Cys Gln Arg Phe
 35 40 45

Tyr Arg Glu His Glu Gly Arg Phe Phe Tyr Gln Arg Leu Val Glu Phe
 50 55 60

Met Ala Ser Gly Pro Ile Arg Ala Tyr Ile Leu Ala His Lys Asp Ala
 65 70 75 80

Ile Gln Leu Trp Arg Thr Leu Met Gly Pro Thr Arg Val Phe Arg Ala
85 90 95

Arg His Val Ala Pro Asp Ser Ile Arg Gly Ser Phe Gly Leu Thr Asp
100 105 110

Thr Arg Asn Thr Thr His Gly Ser Asp Ser Val Val Ser Ala Ser Arg
115 120 125

Glu Ile Ala Ala Phe Phe Pro Asp Phe Ser Glu Gln Arg Trp Tyr Glu
130 135 140

Glu Glu Glu Pro Gln Leu Arg Cys Gly Pro Val
145 150 155

<210> 70
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding Human NME6 3

<400> 70
atgctcactc tagccctgat caagcctgac gcagtcgccc atccactgat tctggaggct 60
gttcatcagc agattctaag caacaagttc ctgattgtac gaatgagaga actactgtgg 120
agaaaggaag attgccagag gttttaccga gagcatgaag ggcgtttttt ctatcagagg 180
ctggttgagat tcatggccag cgggccaatc cgagcctaca tccttgccca caaggatgcc 240
atccagctct ggaggacgct catgggaccc accagagtgt tccgagcacg ccatgtggcc 300
ccagattcta tccgtgggag tttcggcctc actgacaccc gcaacaccac ccatggttcg 360
gactctgtgg tttcagccag cagagagatt gcagccttct tccctgactt cagtgaacag 420
cgctggtatg aggaggaaga gccccagttg cgctgtggcc ctgtgtgcta tagcccagag 480
ggaggtgtcc actatgtagc tggaacagga ggcctaggac cagcctga 528

<210> 71
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME6 3

<400> 71

Met Leu Thr Leu Ala Leu Ile Lys Pro Asp Ala Val Ala His Pro Leu
1 5 10 15

Ile Leu Glu Ala Val His Gln Gln Ile Leu Ser Asn Lys Phe Leu Ile
20 25 30

Val Arg Met Arg Glu Leu Leu Trp Arg Lys Glu Asp Cys Gln Arg Phe
35 40 45

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Tyr Arg Glu His Glu Gly Arg Phe Phe Tyr Gln Arg Leu Val Glu Phe
50 55 60

Met Ala Ser Gly Pro Ile Arg Ala Tyr Ile Leu Ala His Lys Asp Ala
65 70 75 80

Ile Gln Leu Trp Arg Thr Leu Met Gly Pro Thr Arg Val Phe Arg Ala
85 90 95

Arg His Val Ala Pro Asp Ser Ile Arg Gly Ser Phe Gly Leu Thr Asp
100 105 110

Thr Arg Asn Thr Thr His Gly Ser Asp Ser Val Val Ser Ala Ser Arg
115 120 125

Glu Ile Ala Ala Phe Phe Pro Asp Phe Ser Glu Gln Arg Trp Tyr Glu
130 135 140

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

Gly Gly Val His Tyr Val Ala Gly Thr Gly Gly Leu Gly Pro Ala
165 170 175

<210> 72
<211> 585
<212> DNA
<213> Artificial sequence

<220>
<223> Human NME6 sequence optimized for E. coli expression

<400> 72
atgacgcaaa atctgggctc ggaaatggca agtatcctgc gctccccgca agcactgcaa 60
ctgaccctgg ctctgatcaa accggacgct gttgctcatc cgctgattct ggaagcggtc 120
caccagcaaa ttctgagcaa caaatttctg atcgtgcgta tgcgcgaact gctgtggcgt 180
aaagaagatt gccagcgttt ttatcgcgaa catgaaggcc gtttctttta tcaacgcctg 240
gttgaattca tggcctctgg tccgattcgc gcatatatcc tggctcacia agatgcgatt 300
cagctgtggc gtaccctgat ggggccgacg cgcgtctttc gtgcacgtca tgtggcaccg 360
gactcaatcc gtggctcggt cggtctgacc gatacgcgca ataccacgca cggtagcgac 420
tctgttgta gtgcgtcccg tgaaatcgcg gcctttttcc cggacttctc cgaacagcgt 480
tggtacgaag aagaagaacc gcaactgcgc tgtggccccg tctgttattc tccggaaggt 540
ggtgtccatt atgtggcggg cacgggtggt ctgggtccgg catga 585

<210> 73
<211> 194
<212> PRT
<213> Artificial sequence

<220>

<223> Human NME6 sequence optimized for E. coli expression

<400> 73

Met Thr Gln Asn Leu Gly Ser Glu Met Ala Ser Ile Leu Arg Ser Pro
 1 5 10 15

Gln Ala Leu Gln Leu Thr Leu Ala Leu Ile Lys Pro Asp Ala Val Ala
 20 25 30

His Pro Leu Ile Leu Glu Ala Val His Gln Gln Ile Leu Ser Asn Lys
 35 40 45

Phe Leu Ile Val Arg Met Arg Glu Leu Leu Trp Arg Lys Glu Asp Cys
 50 55 60

Gln Arg Phe Tyr Arg Glu His Glu Gly Arg Phe Phe Tyr Gln Arg Leu
 65 70 75 80

Val Glu Phe Met Ala Ser Gly Pro Ile Arg Ala Tyr Ile Leu Ala His
 85 90 95

Lys Asp Ala Ile Gln Leu Trp Arg Thr Leu Met Gly Pro Thr Arg Val
 100 105 110

Phe Arg Ala Arg His Val Ala Pro Asp Ser Ile Arg Gly Ser Phe Gly
 115 120 125

Leu Thr Asp Thr Arg Asn Thr Thr His Gly Ser Asp Ser Val Val Ser
 130 135 140

Ala Ser Arg Glu Ile Ala Ala Phe Phe Pro Asp Phe Ser Glu Gln Arg
 145 150 155 160

Trp Tyr Glu Glu Glu Glu Pro Gln Leu Arg Cys Gly Pro Val Cys Tyr
 165 170 175

Ser Pro Glu Gly Gly Val His Tyr Val Ala Gly Thr Gly Gly Leu Gly
 180 185 190

Pro Ala

<210> 74

<211> 525

<212> DNA

<213> Artificial Sequence

<220>

<223> Human NME6 1 sequence optimized for E. coli expression

<400> 74

atgacgcaaa atctgggctc ggaaatggca agtatcctgc gctccccgca agcactgcaa

60

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ctgaccctgg ctctgatcaa accggacgct gttgctcatc cgctgattct ggaagcggtc      120
caccagcaaa ttctgagcaa caaatctctg atcgtgcgta tgcgcgaact gctgtggcgt      180
aaagaagatt gccagcgttt ttatcgcgaa catgaaggcc gtttctttta tcaacgcctg      240
gttgaattca tggcctctgg tccgattcgc gcatatatcc tggctcacia agatgacgatt      300
cagctgtggc gtaccctgat ggggtccgacg cgcgtctttc gtgcacgtca tgtggcaccg      360
gactcaatcc gtggctcggt cggctctgacc gatacgcgca ataccacgca cggtagcgac      420
tctgttggtta gtgcgtcccg tgaaatcgcg gcctttttcc cggacttctc cgaacagcgt      480
tggtacgaag aagaagaacc gcaactgcgc tgtggcccgg tctga                        525

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<210> 75
 <211> 174
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human NME6 1 sequence optimized for E. coli expression
 <400> 75

Met Thr Gln Asn Leu Gly Ser Glu Met Ala Ser Ile Leu Arg Ser Pro
1 5 10 15

Gln Ala Leu Gln Leu Thr Leu Ala Leu Ile Lys Pro Asp Ala Val Ala
20 25 30

His Pro Leu Ile Leu Glu Ala Val His Gln Gln Ile Leu Ser Asn Lys
35 40 45

Phe Leu Ile Val Arg Met Arg Glu Leu Leu Trp Arg Lys Glu Asp Cys
50 55 60

Gln Arg Phe Tyr Arg Glu His Glu Gly Arg Phe Phe Tyr Gln Arg Leu
65 70 75 80

Val Glu Phe Met Ala Ser Gly Pro Ile Arg Ala Tyr Ile Leu Ala His
85 90 95

Lys Asp Ala Ile Gln Leu Trp Arg Thr Leu Met Gly Pro Thr Arg Val
100 105 110

Phe Arg Ala Arg His Val Ala Pro Asp Ser Ile Arg Gly Ser Phe Gly
115 120 125

Leu Thr Asp Thr Arg Asn Thr Thr His Gly Ser Asp Ser Val Val Ser
130 135 140

Ala Ser Arg Glu Ile Ala Ala Phe Phe Pro Asp Phe Ser Glu Gln Arg
145 150 155 160

Trp Tyr Glu Glu Glu Glu Pro Gln Leu Arg Cys Gly Pro Val
 165 170

<210> 76
 <211> 468
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human NME6 2 sequence optimized for E. coli expression

<400> 76
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 gtccaccagc aaattctgag caacaaattt ctgatactgc gtatgcgcga actgctgtgg 120
 cgtaaagaag attgccagcg tttttatcgc gaacatgaag gccgtttctt ttatcaacgc 180
 ctggttgaat tcatggcctc tgggccgatt cgcgcatata tcctggctca caaagatgcg 240
 attcagctgt ggcgtaccct gatgggtccg acgcgcgtct ttcgtgcacg tcatgtggca 300
 ccggactcaa tccgtggctc gttcgggtctg accgatacgc gcaataccac gcacggtagc 360
 gactctgttg ttagtgcgtc ccgtgaaatc gcggcctttt tcccggactt ctccgaacag 420
 cgttggtacg aagaagaaga accgcaactg cgctgtggcc cggtctga 468

<210> 77
 <211> 155
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human NME6 2 sequence optimized for E. coli expression

<400> 77

Met Leu Thr Leu Ala Leu Ile Lys Pro Asp Ala Val Ala His Pro Leu
 1 5 10 15

Ile Leu Glu Ala Val His Gln Gln Ile Leu Ser Asn Lys Phe Leu Ile
 20 25 30

Val Arg Met Arg Glu Leu Leu Trp Arg Lys Glu Asp Cys Gln Arg Phe
 35 40 45

Tyr Arg Glu His Glu Gly Arg Phe Phe Tyr Gln Arg Leu Val Glu Phe
 50 55 60

Met Ala Ser Gly Pro Ile Arg Ala Tyr Ile Leu Ala His Lys Asp Ala
 65 70 75 80

Ile Gln Leu Trp Arg Thr Leu Met Gly Pro Thr Arg Val Phe Arg Ala
 85 90 95

Arg His Val Ala Pro Asp Ser Ile Arg Gly Ser Phe Gly Leu Thr Asp
 100 105 110

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Thr Arg Asn Thr Thr His Gly Ser Asp Ser Val Val Ser Ala Ser Arg
115 120 125

Glu Ile Ala Ala Phe Phe Pro Asp Phe Ser Glu Gln Arg Trp Tyr Glu
130 135 140

Glu Glu Glu Pro Gln Leu Arg Cys Gly Pro Val Met Leu Thr Leu Ala
145 150 155 1

Leu Ile Lys Pro Asp Ala Val Ala His Pro Leu Ile Leu Glu Ala Val
10 15 20

His Gln Gln Ile Leu Ser Asn Lys Phe Leu Ile Val Arg Met Arg Glu
25 30 35

Leu Leu Trp Arg Lys Glu Asp Cys Gln Arg Phe Tyr Arg Glu His Glu
40 45 50

Gly Arg Phe Phe Tyr Gln Arg Leu Val Glu Phe Met Ala Ser Gly Pro
55 60 65

Ile Arg Ala Tyr Ile Leu Ala His Lys Asp Ala Ile Gln Leu Trp Arg
70 75 80 85

Thr Leu Met Gly Pro Thr Arg Val Phe Arg Ala Arg His Val Ala Pro
90 95 100

Asp Ser Ile Arg Gly Ser Phe Gly Leu Thr Asp Thr Arg Asn Thr Thr
105 110 115

His Gly Ser Asp Ser Val Val Ser Ala Ser Arg Glu Ile Ala Ala Phe
120 125 130

Phe Pro Asp Phe Ser Glu Gln Arg Trp Tyr Glu Glu Glu Glu Pro Gln
135 140 145

Leu Arg Cys Gly Pro Val
150 155

<210> 78
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME6 3 sequence optimized for E. coli expression

<400> 78
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gtccaccagc aaattctgag caacaaattt ctgatcgtgc gtatgcgcga actgctgtgg 120
cgtaaagaag attgccagcg tttttatcgc gaacatgaag gccgtttctt ttatcaacgc 180
ctggttgaat tcatggcctc tgggccgatt cgcgcatata tcctggctca caaagatgcg 240

2015-04-06_13150-70136PCT_Seq_Listing_ST25

attcagctgt ggcgtaccct gatgggtccg acgcgcgtct ttcgtgcacg tcatgtggca 300
ccggactcaa tccgtggctc gttcgggtctg accgatacgc gcaataccac gcacggtagc 360
gactctgttg ttagtgcgtc ccgtgaaatc gcggcctttt tcccggactt ctccgaacag 420
cgttggtacg aagaagaaga accgcaactg cgctgtggcc cggctctgta ttctccggaa 480
ggtggtgtcc attatgtggc gggcacgggt ggtctgggtc cggcatga 528

<210> 79
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME6 3 sequence optimized for E. coli expression
<400> 79

Met Leu Thr Leu Ala Leu Ile Lys Pro Asp Ala Val Ala His Pro Leu
1 5 10 15

Ile Leu Glu Ala Val His Gln Gln Ile Leu Ser Asn Lys Phe Leu Ile
20 25 30

Val Arg Met Arg Glu Leu Leu Trp Arg Lys Glu Asp Cys Gln Arg Phe
35 40 45

Tyr Arg Glu His Glu Gly Arg Phe Phe Tyr Gln Arg Leu Val Glu Phe
50 55 60

Met Ala Ser Gly Pro Ile Arg Ala Tyr Ile Leu Ala His Lys Asp Ala
65 70 75 80

Ile Gln Leu Trp Arg Thr Leu Met Gly Pro Thr Arg Val Phe Arg Ala
85 90 95

Arg His Val Ala Pro Asp Ser Ile Arg Gly Ser Phe Gly Leu Thr Asp
100 105 110

Thr Arg Asn Thr Thr His Gly Ser Asp Ser Val Val Ser Ala Ser Arg
115 120 125

Glu Ile Ala Ala Phe Phe Pro Asp Phe Ser Glu Gln Arg Trp Tyr Glu
130 135 140

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

Gly Gly Val His Tyr Val Ala Gly Thr Gly Gly Leu Gly Pro Ala
165 170 175

<210> 80
<211> 1306

<212> DNA

<213> Artificial Sequence

<220>

<223> OriGene-NME7-1 full length

<400> 80

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gacgttgat acgactccta tagggcggcc gggaattcgt cgactggatc cggtagcgag      60
gagatctgcc gccgcgatcg ccatgaatca tagtgaaaga ttcgttttca ttgcagagtg      120
gtatgatcca aatgcttcac ttcttcgacg ttatgagctt ttattttacc caggggatgg      180
atctgttgaa atgcatgatg taaagaatca tcgcaccttt ttaaagcgga ccaaatatga      240
taacctgcac ttggaagatt tatttatagg caacaaagtg aatgtcttct ctcgacaact      300
gggtattaatt gactatgggg atcaatatac agctcgccag ctgggcagta ggaaagaaaa      360
aacgctagcc ctaattaaac cagatgcaat atcaaaggct ggagaaataa ttgaaataat      420
aaacaaagct ggatttacta taaccaaact caaaatgatg atgctttcaa ggaaagaagc      480
attggatttt catgtagatc accagtcaag accctttttc aatgagctga tccagtttat      540
tacaactggc cctattattg ccatggagat ttaagagat gatgctatat gtgaatggaa      600
aagactgctg ggacctgcaa actctggagt ggacgcgaca gatgcttctg aaagcattag      660
agccctcttt ggaacagatg gcataagaaa tgcagcgcat ggccctgatt cttttgcttc      720
tgcggccaga gaaatggagt tgttttttcc ttcaagtgga ggttggtggc cggcaaacac      780
tgctaaattt actaattgta cctgttgcat tgttaaacct catgctgtca gtgaaggact      840
gttgggaaag atcctgatgg ctatccgaga tgcagggttt gaaatctcag ctatgcagat      900
gttcaatatg gatcgggtta atgttgagga attctatgaa gttataaaag gagtagtgac      960
cgaatatcat gacatggtga cagaaatgta ttctggccct tgtgtagcaa tggagattca     1020
acagaataat gctacaaaga catttcgaga attttgtgga cctgctgata ctgaaattgc     1080
ccggcattta cgccctggaa ctctcagagc aatctttggt aaaactaaga tccagaatgc     1140
tgttcactgt actgatctgc cagaggatgg cctattagag gttcaatact tcttcaagat     1200
cttggataat acgcgtacgc ggccgctcga gcagaaactc atctcagaag aggatctggc     1260
agcaaataat atcctggatt acaaggatga cgacgataag gtttaa                        1306

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<210> 81

<211> 407

<212> PRT

<213> Artificial Sequence

<220>

<223> OriGene-NME7-1 full length

<400> 81

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Met Asn His Ser Glu Arg Phe Val Phe Ile Ala Glu Trp Tyr Asp Pro
1           5           10           15

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Asn Ala Ser Leu Leu Arg Arg Tyr Glu Leu Leu Phe Tyr Pro Gly Asp
20           25           30

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

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Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn Ala Thr Lys Thr
305 310 315 320

Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile Ala Arg His Leu
325 330 335

Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr Lys Ile Gln Asn
340 345 350

Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu Leu Glu Val Gln
355 360 365

Tyr Phe Phe Lys Ile Leu Asp Asn Thr Arg Thr Arg Arg Leu Glu Gln
370 375 380

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

Lys Asp Asp Asp Asp Lys Val
405

<210> 82
<211> 376
<212> PRT
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<220>
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<400> 82

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Asn Ala Ser Leu Leu Arg Arg Tyr Glu Leu Leu Phe Tyr Pro Gly Asp
20 25 30

Gly Ser Val Glu Met His Asp Val Lys Asn His Arg Thr Phe Leu Lys
35 40 45

Arg Thr Lys Tyr Asp Asn Leu His Leu Glu Asp Leu Phe Ile Gly Asn
50 55 60

Lys Val Asn Val Phe Ser Arg Gln Leu Val Leu Ile Asp Tyr Gly Asp
65 70 75 80

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

Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala Gly Glu Ile Ile Glu Ile
100 105 110

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Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys Leu Lys Met Met Met Leu
115 120 125

Ser Arg Lys Glu Ala Leu Asp Phe His Val Asp His Gln Ser Arg Pro
130 135 140

Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr Thr Gly Pro Ile Ile Ala
145 150 155 160

Met Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp Lys Arg Leu Leu
165 170 175

Gly Pro Ala Asn Ser Gly Val Ala Arg Thr Asp Ala Ser Glu Ser Ile
180 185 190

Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg Asn Ala Ala His Gly Pro
195 200 205

Asp Ser Phe Ala Ser Ala Ala Arg Glu Met Glu Leu Phe Phe Pro Ser
210 215 220

Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe Thr Asn Cys Thr
225 230 235 240

Cys Cys Ile Val Lys Pro His Ala Val Ser Glu Gly Leu Leu Gly Lys
245 250 255

Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile Ser Ala Met Gln
260 265 270

Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe Tyr Glu Val Tyr
275 280 285

Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr Glu Met Tyr Ser
290 295 300

Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn Ala Thr Lys Thr
305 310 315 320

Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile Ala Arg His Leu
325 330 335

Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr Lys Ile Gln Asn
340 345 350

Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu Leu Glu Val Gln
355 360 365

Tyr Phe Phe Lys Ile Leu Asp Asn
370 375

<210> 83
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Abnova Partial NME7-B

<400> 83

Asp Arg Val Asn Val Glu Glu Phe Tyr Glu Val Tyr Lys Gly Val Val
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Thr Glu Tyr His Asp Met Val Thr Glu Met Tyr Ser Gly Pro Cys Val
 20 25 30

Ala Met Glu Ile Gln Gln Asn Asn Ala Thr Lys Thr Phe Arg Glu Phe
 35 40 45

Cys Gly Pro Ala Asp Pro Glu Ile Ala Arg His Leu Arg Pro Gly Thr
 50 55 60

Leu Arg Ala Ile Phe Gly Lys Thr Lys Ile Gln Asn Ala Val His Cys
 65 70 75 80

Thr Asp Leu Pro Glu Asp Gly Leu Leu Glu Val Gln Tyr Phe Phe Lys
 85 90 95

Ile Leu

<210> 84
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding Histidine Tag

<400> 84
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27

<210> 85
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding Strept II Tag

<400> 85
 accggttgga gccatcctca gttcgaaaag taatga

36

<210> 86
 <211> 35
 <212> PRT
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<220>

<223> N-10 peptide

<400> 86

Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr
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Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln
20 25 30

Ser Gly Ala
35

<210> 87

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> C-10 peptide

<400> 87

Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys
1 5 10 15

Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val
20 25 30

Ser Asp Val
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<210> 88

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Immunizing peptides derived from human NME7

<400> 88

Leu Ala Leu Ile Lys Pro Asp Ala
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<210> 89

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Immunizing peptides derived from human NME7

<400> 89

Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val Asp His
1 5 10 15

Gln Ser

<210> 90
 <211> 10
 <212> PRT
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<220>
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 <400> 90

Ala Leu Asp Phe His Val Asp His Gln Ser
 1 5 10

<210> 91
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Immunizing peptides derived from human NME7
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Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp Lys Arg Leu
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<210> 92
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 <400> 92

Phe Asn Glu Leu Ile Gln Phe Ile Thr Thr Gly Pro
 1 5 10

<210> 93
 <211> 8
 <212> PRT
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<220>
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Arg Asp Asp Ala Ile Cys Glu Trp
 1 5

<210> 94
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<220>
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 <400> 94

Ser Gly Val Ala Arg Thr Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe
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Gly Thr Asp Gly Ile Arg Asn Ala Ala
20 25

<210> 95
<211> 9
<212> PRT
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<220>
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<400> 95

Glu Leu Phe Phe Pro Ser Ser Gly Gly
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<210> 96
<211> 26
<212> PRT
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<220>
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<400> 96

Lys Phe Thr Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser
1 5 10 15

Glu Gly Leu Leu Gly Lys Ile Leu Met Ala
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<210> 97
<211> 36
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<400> 97

Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile Ser Ala Met Gln Met
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Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe Tyr Glu Val Tyr Lys
20 25 30

Gly Val Val Thr
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<400> 98

Glu Phe Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp
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<210> 99

<211> 43

<212> PRT

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<220>

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<400> 99

Glu Ile Gln Gln Asn Asn Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly
1 5 10 15

Pro Ala Asp Pro Glu Ile Ala Arg His Leu Arg Pro Gly Thr Leu Arg
20 25 30

Ala Ile Phe Gly Lys Thr Lys Ile Gln Asn Ala
35 40

<210> 100

<211> 8

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<210> 101

<211> 7

<212> PRT

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<400> 101

Phe Arg Glu Phe Cys Gly Pro
1 5

<210> 102

<211> 23

<212> PRT

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<223> Immunizing peptides derived from human NME7

<400> 102

Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu Leu Glu Val Gln Tyr
 1 5 10 15

Phe Phe Lys Ile Leu Asp Asn
 20

<210> 103
 <211> 9
 <212> PRT
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<400> 103

Ile Gln Asn Ala Val His Cys Thr Asp
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<210> 104
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 104

Thr Asp Leu Pro Glu Asp Gly Leu Leu Glu Val Gln Tyr Phe Phe Lys
 1 5 10 15

Ile Leu Asp Asn
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<210> 105
 <211> 13
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<220>
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<400> 105

Pro Glu Asp Gly Leu Leu Glu Val Gln Tyr Phe Phe Lys
 1 5 10

<210> 106
 <211> 12
 <212> PRT
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<220>
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<400> 106

Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys
 1 5 10

<210> 107
 <211> 16
 <212> PRT
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<220>
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<400> 107

Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val Asp His Gln Ser
 1 5 10 15

<210> 108
 <211> 9
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<220>
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<400> 108

Asn Glu Leu Ile Gln Phe Ile Thr Thr
 1 5

<210> 109
 <211> 14
 <212> PRT
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<220>
 <223> Immunizing peptides derived from human NME7

<400> 109

Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp Lys Arg Leu
 1 5 10

<210> 110
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<220>
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<400> 110

Ser Gly Val Ala Arg Thr Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe
 1 5 10 15

Gly Thr Asp Gly Ile
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<210> 111
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<400> 111

Ser	Gly	Val	Ala	Arg	Thr	Asp	Ala	Ser	Glu	Ser
1				5					10	

<210> 112

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<220>

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<400> 112

Ala	Leu	Phe	Gly	Thr	Asp	Gly	Ile
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<210> 113

<211> 14

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<400> 113

Asn	Cys	Thr	Cys	Cys	Ile	Val	Lys	Pro	His	Ala	Val	Ser	Glu
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<210> 114

<211> 11

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<400> 114

Leu	Gly	Lys	Ile	Leu	Met	Ala	Ile	Arg	Asp	Ala
1				5					10	

<210> 115

<211> 16

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<220>

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<400> 115

Glu	Ile	Ser	Ala	Met	Gln	Met	Phe	Asn	Met	Asp	Arg	Val	Asn	Val	Glu
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<211> 8

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<220>

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<400> 116

Glu Val Tyr Lys Gly Val Val Thr
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<211> 8

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<400> 117

Glu Tyr His Asp Met Val Thr Glu
1 5

<210> 118

<211> 15

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<220>

<223> Immunizing peptides derived from human NME7

<400> 118

Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile Ala Arg His Leu Arg
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<210> 119

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<400> 119

Ala Ile Phe Gly Lys Thr Lys Ile Gln Asn Ala Val
1 5 10

<210> 120

<211> 18

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<400> 120

Leu Pro Glu Asp Gly Leu Leu Glu Val Gln Tyr Phe Phe Lys Ile Leu
1 5 10 15

Asp Asn

<210> 121
 <211> 17
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<400> 121

Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met Glu Leu Phe Phe
 1 5 10 15

Pro

<210> 122
 <211> 7
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<400> 122

Ile Cys Glu Trp Lys Arg Leu
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<400> 123

Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala
 1 5 10

<210> 124
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<400> 124

His Ala Val Ser Glu Gly Leu Leu Gly Lys
 1 5 10

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<400> 125

Val Thr Glu Met Tyr Ser Gly Pro
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<211> 9

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<400> 126

Asn Ala Thr Lys Thr Phe Arg Glu Phe
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<210> 127

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<400> 127

Ala Ile Arg Asp Ala Gly Phe Glu Ile
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<400> 129

Asp His Gln Ser Arg Pro Phe Phe
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<400> 130

Ala Ile Cys Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn
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<223> Immunizing peptides derived from human NME7

<400> 131

Val Asp His Gln Ser Arg Pro Phe
1 5

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<223> Immunizing peptides derived from human NME7

<400> 132

Pro Asp Ser Phe Ala Ser
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<210> 133

<211> 18

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<400> 133

Lys Ala Gly Glu Ile Ile Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile
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Thr Lys

<210> 134

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<223> Immunizing peptides derived from human NME1

<400> 134

Met Ala Asn Cys Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val
1 5 10 15

Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu
20 25

<210> 135
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<400> 135

Val Asp Leu Lys Asp Arg Pro Phe
1 5

<210> 136
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<220>
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<400> 136

His Gly Ser Asp Ser Val Glu Ser Ala Glu Lys Glu Ile Gly Leu Trp
1 5 10 15

Phe

<210> 137
<211> 25
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<220>
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<400> 137

Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly Leu
1 5 10 15

Val Gly Glu Ile Ile Lys Arg Phe Glu
20 25

<210> 138
<211> 30
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<220>
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<400> 138

Val Asp Leu Lys Asp Arg Pro Phe Phe Ala Gly Leu Val Lys Tyr Met
1 5 10 15

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20 25 30

<210> 139
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<400> 139

Asn Ile Ile His Gly Ser Asp Ser Val Glu Ser Ala Glu Lys Glu Ile
1 5 10 15

Gly Leu Trp Phe His Pro Glu Glu Leu Val
20 25

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Lys Pro Asp Gly Val Gln Arg Gly Leu Val Gly Glu Ile Ile
1 5 10

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1 5 10 15

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<400> 142

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<400> 143

Asp Ala Gly Phe Glu Ile Ser Ala Met Gln Met Phe Asn Met Asp Arg
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Val Asn Val Glu
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<210> 144

<211> 16

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<400> 144

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 1 5 10 15

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<211> 29

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<223> peptide B3

<400> 145

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 1 5 10 15

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<211> 376
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<400> 147

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20 25 30

Gly Ser Val Glu Met His Asp Val Lys Asn His Arg Thr Phe Leu Lys
35 40 45

Arg Thr Lys Tyr Asp Asn Leu His Leu Glu Asp Leu Phe Ile Gly Asn
50 55 60

Lys Val Asn Val Phe Ser Arg Gln Leu Val Leu Ile Asp Tyr Gly Asp
65 70 75 80

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

Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala Gly Glu Ile Ile Glu Ile
100 105 110

Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys Leu Lys Met Met Met Leu
115 120 125

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Ser Arg Lys Glu Ala Leu Asp Phe His Val Asp His Gln Ser Arg Pro
130 135 140

Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr Thr Gly Pro Ile Ile Ala
145 150 155 160

Met Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp Lys Arg Leu Leu
165 170 175

Gly Pro Ala Asn Ser Gly Val Ala Arg Thr Asp Ala Ser Glu Ser Ile
180 185 190

Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg Asn Ala Ala His Gly Pro
195 200 205

Asp Ser Phe Ala Ser Ala Ala Arg Glu Met Glu Leu Phe Phe Pro Ser
210 215 220

Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe Thr Asn Cys Thr
225 230 235 240

Cys Cys Ile Val Lys Pro His Ala Val Ser Glu Gly Leu Leu Gly Lys
245 250 255

Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile Ser Ala Met Gln
260 265 270

Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe Tyr Glu Val Tyr
275 280 285

Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr Glu Met Tyr Ser
290 295 300

Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn Ala Thr Lys Thr
305 310 315 320

Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile Ala Arg His Leu
325 330 335

Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr Lys Ile Gln Asn
340 345 350

Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu Leu Glu Val Gln
355 360 365

Tyr Phe Phe Lys Ile Leu Asp Asn
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<210> 148
<211> 1023
<212> DNA
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<220>

<223> Human NME7 b

<400> 148

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ggaacagatg gcataagaaa tgcagcgcat ggccctgatt cttttgcttc tgcggccaga      540
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atcctgatgg ctatccgaga tgcaggtttt gaaatctcag ctatgcagat gttcaatatg      720
gatcgggtta atgttgagga attctatgaa gtttataaag gagtagtgac cgaatatcat      780
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gctacaaaga catttcgaga attttggtgga cctgctgata ctgaaattgc ccggcattta      900
cgccctggaa ctctcagagc aatctttggt aaaactaaga tccagaatgc tgttcactgt      960
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<210> 149

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> Human NME7 b

<400> 149

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Asp Asn Leu His Leu Glu Asp Leu Phe Ile Gly Asn Lys Val Asn Val
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Phe Ser Arg Gln Leu Val Leu Ile Asp Tyr Gly Asp Gln Tyr Thr Ala
          35          40          45

Arg Gln Leu Gly Ser Arg Lys Glu Lys Thr Leu Ala Leu Ile Lys Pro
          50          55          60

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

Ile Leu Asp Asn
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<210> 150
<211> 861
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-AB

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cagtttatta caactggtcc tattattgcc atggagattt taagagatga tgctatatgt 240
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tttgcttctg cggccagaga aatggagtgt ttttttcctt caagtggagg ttgtgggccg 420
gcaaacactg ctaaattttac taattgtacc tgttgcattg ttaaacccca tgctgtcagt 480
gaaggactgt tgggaaagat cctgatggct atccgagatg caggttttga aatctcagct 540
atgcagatgt tcaatatgga tcgggttaat gttgaggaat tctatgaagt ttataaagga 600
gtagtgaccg aatatcatga catggtgaca gaaatgtatt ctggcccttg tgtagcaatg 660
gagattcaac agaataatgc taaaagaca tttcgagaat tttgtggacc tgctgatcct 720
gaaattgccc ggcattttacg ccctggaact ctgagagcaa tctttggtaa aactaagatc 780
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<210> 151
<211> 286
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7-AB

<400> 151

Met Glu Lys Thr Leu Ala Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala
1 5 10 15

Gly Glu Ile Ile Glu Ile Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys
20 25 30

Leu Lys Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val
35 40 45

Asp His Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr
50 55 60

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Thr Gly Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys
65 70 75 80

Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr
85 90 95

Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg
100 105 110

Asn Ala Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met
115 120 125

Glu Leu Phe Phe Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala
130 135 140

Lys Phe Thr Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser
145 150 155 160

Glu Gly Leu Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe
165 170 175

Glu Ile Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu
180 185 190

Glu Phe Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met
195 200 205

Val Thr Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln
210 215 220

Asn Asn Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro
225 230 235 240

Glu Ile Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly
245 250 255

Lys Thr Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp
260 265 270

Gly Leu Leu Glu Val Gln Tyr Phe Phe Lys Ile Leu Asp Asn
275 280 285

<210> 152
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7 x1

<400> 152
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ggcccttggt tagcaatgga gattcaacag aataatgcta caaagacatt tcgagaattt 600
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<210> 153
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human NME7 x1

<400> 153

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Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr Thr Gly
20 25 30

Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp
35 40 45

Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr Asp Ala
50 55 60

Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg Asn Ala
65 70 75 80

Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met Glu Leu
85 90 95

Phe Phe Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe
100 105 110

Thr Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser Glu Gly
115 120 125

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

Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe
145 150 155 160

Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr
165 170 175

Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn
180 185 190

Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile
195 200 205

Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr
210 215 220

Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu
225 230 235 240

Leu Glu Val Gln Tyr Phe Phe Lys Ile Leu Asp Asn
245 250

<210> 154
<211> 1128
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7 a (optimized for E coli expression)

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gatgcaatct ccaaagctgg cgaaattatc gaaattatca acaaagcggg tttcaccatc 360
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cagtctcgcc cgtttttcaa tgaactgatt caattcatca ccacgggtcc gattatcgca 480
atggaaattc tgcgtgatga cgctatctgc gaatggaaac gcctgctggg cccggcaaac 540
tcaggtgttg cgcgtaccga tgccagtga tccattcgcg ctctgtttgg caccgatggt 600
atccgtaatg cagcacatgg tccggactca ttcgcatcgg cagctcgtga aatggaactg 660
tttttcccg gctctggcgg ttgcgggtccg gcaaaccacg ccaaatttac caattgtacg 720
tgctgtattg tcaaaccgca cgcagtgtca gaaggcctgc tgggtaaaat tctgatggca 780
atccgtgatg ctggctttga aatctcggcc atgcagatgt tcaacatgga ccgcgttaac 840

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tttcgtgaat tctgtggtcc ggcagatccg gaaatcgcac gtcactctgcg tccgggtacc 1020
ctgcgcgcaa tttttggtaa aacgaaaatc cagaacgctg tgcactgtac cgatctgccg 1080
gaagacgggtc tgctggaagt tcaatacttt ttcaaaattc tggataat 1128

<210> 155
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> Human NME7 a (optimized for E coli expression)
<400> 155

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1 5 10 15

Asn Ala Ser Leu Leu Arg Arg Tyr Glu Leu Leu Phe Tyr Pro Gly Asp
20 25 30

Gly Ser Val Glu Met His Asp Val Lys Asn His Arg Thr Phe Leu Lys
35 40 45

Arg Thr Lys Tyr Asp Asn Leu His Leu Glu Asp Leu Phe Ile Gly Asn
50 55 60

Lys Val Asn Val Phe Ser Arg Gln Leu Val Leu Ile Asp Tyr Gly Asp
65 70 75 80

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

Leu Ile Lys Pro Asp Ala Ile Ser Lys Ala Gly Glu Ile Ile Glu Ile
100 105 110

Ile Asn Lys Ala Gly Phe Thr Ile Thr Lys Leu Lys Met Met Met Leu
115 120 125

Ser Arg Lys Glu Ala Leu Asp Phe His Val Asp His Gln Ser Arg Pro
130 135 140

Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr Thr Gly Pro Ile Ile Ala
145 150 155 160

Met Glu Ile Leu Arg Asp Asp Ala Ile Cys Glu Trp Lys Arg Leu Leu
165 170 175

Gly Pro Ala Asn Ser Gly Val Ala Arg Thr Asp Ala Ser Glu Ser Ile
180 185 190

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Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg Asn Ala Ala His Gly Pro
195 200 205

Asp Ser Phe Ala Ser Ala Ala Arg Glu Met Glu Leu Phe Phe Pro Ser
210 215 220

Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala Lys Phe Thr Asn Cys Thr
225 230 235 240

Cys Cys Ile Val Lys Pro His Ala Val Ser Glu Gly Leu Leu Gly Lys
245 250 255

Ile Leu Met Ala Ile Arg Asp Ala Gly Phe Glu Ile Ser Ala Met Gln
260 265 270

Met Phe Asn Met Asp Arg Val Asn Val Glu Glu Phe Tyr Glu Val Tyr
275 280 285

Lys Gly Val Val Thr Glu Tyr His Asp Met Val Thr Glu Met Tyr Ser
290 295 300

Gly Pro Cys Val Ala Met Glu Ile Gln Gln Asn Asn Ala Thr Lys Thr
305 310 315 320

Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile Ala Arg His Leu
325 330 335

Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr Lys Ile Gln Asn
340 345 350

Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu Leu Glu Val Gln
355 360 365

Tyr Phe Phe Lys Ile Leu Asp Asn Thr Gly
370 375

<210> 156

<211> 1020

<212> DNA

<213> Artificial Sequence

<220>

<223> Human NME7 b (optimized for E coli expression)

<400> 156

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gattatggcg accagtacac cgcgcgtcaa ctgggtagtc gcaaagaaaa aacgctggcc 180

ctgattaaac cggatgcaat ctccaaagct ggcgaaatta tcgaaattat caacaaagcg 240

ggtttcacca tcacgaaact gaaaatgatg atgctgagcc gtaaagaagc cctggatttt 300

2015-04-06_13150-70136PCT_Seq_Listing_ST25

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catgtcgacc accagtctcg cccgtttttc aatgaactga ttcaattcat caccacgggt      360
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ggccccggcaa actcaggtgt tgcgcgtacc gatgccagtg aatccattcg cgctctgttt      480
ggcaccgatg gtatccgtaa tgcagcacat ggtccggact cattcgcatac ggagctcgt      540
gaaatggaac tgttttttccc gagctctggc ggttgcggtc cggcaaacac cgccaaattt      600
accaattgta cgtgctgtat tgtcaaaccg cacgcagtgt cagaaggcct gctgggtaaa      660
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gaccgcgtta acgtcgaaga attctacgaa gtttacaag gcgtgggttac cgaatatcac      780
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gccacaaaaa cgtttcgtga attctgtggt ccggcagatc cggaaatcgc acgtcatctg      900
cgtccgggta ccctgcgcgc aatttttggg aaaacgaaaa tccagaacgc tgtgcactgt      960
accgatctgc cggaagacgg tctgctggaa gttcaatact ttttcaaaat tctggataat     1020

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<210> 157
 <211> 342
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human NME7 b (optimized for E coli expression)
 <400> 157

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Asp Asn Leu His Leu Glu Asp Leu Phe Ile Gly Asn Lys Val Asn Val
 20 25 30

Phe Ser Arg Gln Leu Val Leu Ile Asp Tyr Gly Asp Gln Tyr Thr Ala
 35 40 45

Arg Gln Leu Gly Ser Arg Lys Glu Lys Thr Leu Ala Leu Ile Lys Pro
 50 55 60

Asp Ala Ile Ser Lys Ala Gly Glu Ile Ile Glu Ile Ile Asn Lys Ala
 65 70 75 80

Gly Phe Thr Ile Thr Lys Leu Lys Met Met Met Leu Ser Arg Lys Glu
 85 90 95

Ala Leu Asp Phe His Val Asp His Gln Ser Arg Pro Phe Phe Asn Glu
 100 105 110

Leu Ile Gln Phe Ile Thr Thr Gly Pro Ile Ile Ala Met Glu Ile Leu
 115 120 125

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Arg Asp Asp Ala Ile Cys Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn
130 135 140

Ser Gly Val Ala Arg Thr Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe
145 150 155 160

Gly Thr Asp Gly Ile Arg Asn Ala Ala His Gly Pro Asp Ser Phe Ala
165 170 175

Ser Ala Ala Arg Glu Met Glu Leu Phe Phe Pro Ser Ser Gly Gly Cys
180 185 190

Gly Pro Ala Asn Thr Ala Lys Phe Thr Asn Cys Thr Cys Cys Ile Val
195 200 205

Lys Pro His Ala Val Ser Glu Gly Leu Leu Gly Lys Ile Leu Met Ala
210 215 220

Ile Arg Asp Ala Gly Phe Glu Ile Ser Ala Met Gln Met Phe Asn Met
225 230 235 240

Asp Arg Val Asn Val Glu Glu Phe Tyr Glu Val Tyr Lys Gly Val Val
245 250 255

Thr Glu Tyr His Asp Met Val Thr Glu Met Tyr Ser Gly Pro Cys Val
260 265 270

Ala Met Glu Ile Gln Gln Asn Asn Ala Thr Lys Thr Phe Arg Glu Phe
275 280 285

Cys Gly Pro Ala Asp Pro Glu Ile Ala Arg His Leu Arg Pro Gly Thr
290 295 300

Leu Arg Ala Ile Phe Gly Lys Thr Lys Ile Gln Asn Ala Val His Cys
305 310 315 320

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

Ile Leu Asp Asn Thr Gly
340

<210> 158
<211> 858
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7-AB (optimized for E coli expression)

<400> 158
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gaaattatca acaaagcggg tttcaccatc acgaaaactga aaatgatgat gctgagccgt 120
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caattcatca ccacgggtcc gattatcgca atggaaattc tgcgtgatga cgctatctgc      240
gaatggaaac gcctgctggg cccggcaaac tcagggtgttg cgcgtaccga tgccagtga      300
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ttcgcatcgg cagctcgtga aatggaactg tttttcccga gctctggcgg ttgcggtccg      420
gcaaacaccg ccaaatttac caattgtacg tgctgtattg tcaaaccgca cgcagtgtca      480
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gaaatcgcac gtcactcgcg tccgggtacc ctgcgcgcaa tttttggtaa aacgaaaatc      780
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<210> 159
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human NME7-AB (optimized for E coli expression)
 <400> 159

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 20 25 30

Leu Lys Met Met Met Leu Ser Arg Lys Glu Ala Leu Asp Phe His Val
 35 40 45

Asp His Gln Ser Arg Pro Phe Phe Asn Glu Leu Ile Gln Phe Ile Thr
 50 55 60

Thr Gly Pro Ile Ile Ala Met Glu Ile Leu Arg Asp Asp Ala Ile Cys
 65 70 75 80

Glu Trp Lys Arg Leu Leu Gly Pro Ala Asn Ser Gly Val Ala Arg Thr
 85 90 95

Asp Ala Ser Glu Ser Ile Arg Ala Leu Phe Gly Thr Asp Gly Ile Arg
 100 105 110

Asn Ala Ala His Gly Pro Asp Ser Phe Ala Ser Ala Ala Arg Glu Met
 115 120 125

2015-04-06_13150-70136PCT_Seq_Listing_ST25

Glu Leu Phe Phe Pro Ser Ser Gly Gly Cys Gly Pro Ala Asn Thr Ala
130 135 140

Lys Phe Thr Asn Cys Thr Cys Cys Ile Val Lys Pro His Ala Val Ser
145 150 155 160

Glu Gly Leu Leu Gly Lys Ile Leu Met Ala Ile Arg Asp Ala Gly Phe
165 170 175

Glu Ile Ser Ala Met Gln Met Phe Asn Met Asp Arg Val Asn Val Glu
180 185 190

Glu Phe Tyr Glu Val Tyr Lys Gly Val Val Thr Glu Tyr His Asp Met
195 200 205

Val Thr Glu Met Tyr Ser Gly Pro Cys Val Ala Met Glu Ile Gln Gln
210 215 220

Asn Asn Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro
225 230 235 240

Glu Ile Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly
245 250 255

Lys Thr Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp
260 265 270

Gly Leu Leu Glu Val Gln Tyr Phe Phe Lys Ile Leu Asp Asn Thr Gly
275 280 285

<210> 160
<211> 756
<212> DNA
<213> Artificial Sequence

<220>
<223> Human NME7 X1 (optimized for E coli expression)

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cgtgatgacg ctatctgcga atggaaacgc ctgctgggcc cggcaaactc aggtgttgcg 180
cgtaccgatg ccagtgaatc cattcgcgct ctgtttggca ccgatggtat ccgtaatgca 240
gcacatggtc cggactcatt cgcacgcgca gctcgtgaaa tggaactgtt tttcccagagc 300
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aaaccgcacg cagtgtcaga aggcctgctg ggtaaaattc tgatggcaat ccgtgatgct 420
ggctttgaaa tctcggccat gcagatgttc aacatggacc gcgttaacgt cgaagaattc 480
tacgaagttt acaaaggcgt ggttaccgaa tatcacgata tggttacgga aatgtactcc 540

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ctggaagttc		aatacttttt	caaaattctg	gataat			756	

<210> 161
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human NME7 X1 (optimized for E coli expression)

<400> 161

Met	Met	Met	Leu	Ser	Arg	Lys	Glu	Ala	Leu	Asp	Phe	His	Val	Asp	His
1				5					10					15	

Gln	Ser	Arg	Pro	Phe	Phe	Asn	Glu	Leu	Ile	Gln	Phe	Ile	Thr	Thr	Gly
			20					25					30		

Pro	Ile	Ile	Ala	Met	Glu	Ile	Leu	Arg	Asp	Asp	Ala	Ile	Cys	Glu	Trp
		35					40				45				

Lys	Arg	Leu	Leu	Gly	Pro	Ala	Asn	Ser	Gly	Val	Ala	Arg	Thr	Asp	Ala
	50					55					60				

Ser	Glu	Ser	Ile	Arg	Ala	Leu	Phe	Gly	Thr	Asp	Gly	Ile	Arg	Asn	Ala
65					70					75					80

Ala	His	Gly	Pro	Asp	Ser	Phe	Ala	Ser	Ala	Ala	Arg	Glu	Met	Glu	Leu
				85					90					95	

Phe	Phe	Pro	Ser	Ser	Gly	Gly	Cys	Gly	Pro	Ala	Asn	Thr	Ala	Lys	Phe
			100					105					110		

Thr	Asn	Cys	Thr	Cys	Cys	Ile	Val	Lys	Pro	His	Ala	Val	Ser	Glu	Gly
		115					120					125			

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

Ser	Ala	Met	Gln	Met	Phe	Asn	Met	Asp	Arg	Val	Asn	Val	Glu	Glu	Phe
145					150					155					160

Tyr	Glu	Val	Tyr	Lys	Gly	Val	Val	Thr	Glu	Tyr	His	Asp	Met	Val	Thr
				165					170					175	

Glu	Met	Tyr	Ser	Gly	Pro	Cys	Val	Ala	Met	Glu	Ile	Gln	Gln	Asn	Asn
			180					185					190		

Ala Thr Lys Thr Phe Arg Glu Phe Cys Gly Pro Ala Asp Pro Glu Ile
 195 200 205

Ala Arg His Leu Arg Pro Gly Thr Leu Arg Ala Ile Phe Gly Lys Thr
 210 215 220

Lys Ile Gln Asn Ala Val His Cys Thr Asp Leu Pro Glu Asp Gly Leu
 225 230 235 240

Leu Glu Val Gln Tyr Phe Phe Lys Ile Leu Asp Asn Thr Gly
 245 250

<210> 162

<211> 91

<212> PRT

<213> Artificial Sequence

<220>

<223> DM10 domain of NME7

<400> 162

Met Asn His Ser Glu Arg Phe Val Phe Ile Ala Glu Trp Tyr Asp Pro
 1 5 10 15

Asn Ala Ser Leu Leu Arg Arg Tyr Glu Leu Leu Phe Tyr Pro Gly Asp
 20 25 30

Gly Ser Val Glu Met His Asp Val Lys Asn His Arg Thr Phe Leu Lys
 35 40 45

Arg Thr Lys Tyr Asp Asn Leu His Leu Glu Asp Leu Phe Ile Gly Asn
 50 55 60

Lys Val Asn Val Phe Ser Arg Gln Leu Val Leu Ile Asp Tyr Gly Asp
 65 70 75 80

Gln Tyr Thr Ala Arg Gln Leu Gly Ser Arg Lys
 85 90