

SEQUENCE LISTING

<110> The Regents of the University of Colorado, a body corporate

<120> COMPOSITIONS AND METHODS FOR TREATMENT OF HOMOCYSTINURIA

<130> 2089.1003PCT2

<140> PCT/US2016/XXXXX

<141> 2016-11-XX

<150> US 14/935,690

<151> 2015-11-09

<160> 16

<170> PatentIn version 3.5

<210> 1

<211> 1656

<212> DNA

<213> Homo sapiens

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<210> 2
 <211> 551
 <212> PRT
 <213> Homo sapiens

<400> 2

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Pro	Glu	Asp	Lys	Glu	Ala	Lys	Glu	Pro	Leu	Trp	Ile	Arg	Pro	Asp	Ala
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Pro	Ser	Arg	Cys	Thr	Trp	Gln	Leu	Gly	Arg	Pro	Ala	Ser	Glu	Ser	Pro
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His	His	His	Thr	Ala	Pro	Ala	Lys	Ser	Pro	Lys	Ile	Leu	Pro	Asp	Ile
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Leu Lys Lys Ile Gly Asp Thr Pro Met Val Arg Ile Asn Lys Ile Gly
85 90 95

Lys Lys Phe Gly Leu Lys Cys Glu Leu Leu Ala Lys Cys Glu Phe Phe
100 105 110

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

Asp Ala Glu Arg Asp Gly Thr Leu Lys Pro Gly Asp Thr Ile Ile Glu
130 135 140

Pro Thr Ser Gly Asn Thr Gly Ile Gly Leu Ala Leu Ala Ala Val
145 150 155 160

Arg Gly Tyr Arg Cys Ile Ile Val Met Pro Glu Lys Met Ser Ser Glu
165 170 175

Lys Val Asp Val Leu Arg Ala Leu Gly Ala Glu Ile Val Arg Thr Pro
180 185 190

Thr Asn Ala Arg Phe Asp Ser Pro Glu Ser His Val Gly Val Ala Trp
195 200 205

Arg Leu Lys Asn Glu Ile Pro Asn Ser His Ile Leu Asp Gln Tyr Arg
210 215 220

Asn Ala Ser Asn Pro Leu Ala His Tyr Asp Thr Thr Ala Asp Glu Ile
225 230 235 240

Leu Gln Gln Cys Asp Gly Lys Leu Asp Met Leu Val Ala Ser Val Gly
245 250 255

Thr Gly Gly Thr Ile Thr Gly Ile Ala Arg Lys Leu Lys Glu Lys Cys
260 265 270

Pro Gly Cys Arg Ile Ile Gly Val Asp Pro Glu Gly Ser Ile Leu Ala
275 280 285

Glu Pro Glu Glu Leu Asn Gln Thr Glu Gln Thr Thr Tyr Glu Val Glu
290 295 300

Gly Ile Gly Tyr Asp Phe Ile Pro Thr Val Leu Asp Arg Thr Val Val
305 310 315 320

Asp Lys Trp Phe Lys Ser Asn Asp Glu Glu Ala Phe Thr Phe Ala Arg
325 330 335

Met Leu Ile Ala Gln Glu Gly Leu Leu Cys Gly Gly Ser Ala Gly Ser
340 345 350

Thr Val Ala Val Ala Val Lys Ala Ala Gln Glu Leu Gln Glu Gly Gln
355 360 365

Arg Cys Val Val Ile Leu Pro Asp Ser Val Arg Asn Tyr Met Thr Lys
370 375 380

Phe Leu Ser Asp Arg Trp Met Leu Gln Lys Gly Phe Leu Lys Glu Glu
385 390 395 400

Asp Leu Thr Glu Lys Lys Pro Trp Trp Trp His Leu Arg Val Gln Glu
405 410 415

Leu Gly Leu Ser Ala Pro Leu Thr Val Leu Pro Thr Ile Thr Cys Gly
420 425 430

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

Val Asp Glu Ala Gly Val Ile Leu Gly Met Val Thr Leu Gly Asn Met
450 455 460

Leu Ser Ser Leu Leu Ala Gly Lys Val Gln Pro Ser Asp Gln Val Gly
465 470 475 480

Lys Val Ile Tyr Lys Gln Phe Lys Gln Ile Arg Leu Thr Asp Thr Leu
485 490 495

Gly Arg Leu Ser His Ile Leu Glu Met Asp His Phe Ala Leu Val Val
500 505 510

His Glu Gln Ile Gln Tyr His Ser Thr Gly Lys Ser Ser Gln Arg Gln
515 520 525

Met Val Phe Gly Val Val Thr Ala Ile Asp Leu Leu Asn Phe Val Ala
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Ala Gln Glu Arg Asp Gln Lys
545 550

<210> 3
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 3

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

Pro Ser Arg Cys Thr Trp Gln Leu Gly Arg Pro Ala Ser Glu Ser Pro
50 55 60

His His His Thr Ala Pro Ala Lys Ser Pro Lys Ile Leu Pro Asp Ile
65 70 75 80

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

Lys Lys Phe Gly Leu Lys Cys Glu Leu Leu Ala Lys Cys Glu Phe Phe
100 105 110

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

Asp Ala Glu Arg Asp Gly Thr Leu Lys Pro Gly Asp Thr Ile Ile Glu
130 135 140

Pro Thr Ser Gly Asn Thr Gly Ile Gly Leu Ala Leu Ala Ala Ala Val
145 150 155 160

Arg Gly Tyr Arg Cys Ile Ile Val Met Pro Glu Lys Met Ser Ser Glu
165 170 175

Lys Val Asp Val Leu Arg Ala Leu Gly Ala Glu Ile Val Arg Thr Pro
180 185 190

Thr Asn Ala Arg Phe Asp Ser Pro Glu Ser His Val Gly Val Ala Trp
195 200 205

Arg Leu Lys Asn Glu Ile Pro Asn Ser His Ile Leu Asp Gln Tyr Arg
210 215 220

Asn Ala Ser Asn Pro Leu Ala His Tyr Asp Thr Thr Ala Asp Glu Ile
225 230 235 240

Leu Gln Gln Cys Asp Gly Lys Leu Asp Met Leu Val Ala Ser Val Gly
245 250 255

Thr Gly Gly Thr Ile Thr Gly Ile Ala Arg Lys Leu Lys Glu Lys Cys
260 265 270

Pro Gly Cys Arg Ile Ile Gly Val Asp Pro Glu Gly Ser Ile Leu Ala
275 280 285

Glu Pro Glu Glu Leu Asn Gln Thr Glu Gln Thr Thr Tyr Glu Val Glu
290 295 300

Gly Ile Gly Tyr Asp Phe Ile Pro Thr Val Leu Asp Arg Thr Val Val
305 310 315 320

Asp Lys Trp Phe Lys Ser Asn Asp Glu Glu Ala Phe Thr Phe Ala Arg
325 330 335

Met Leu Ile Ala Gln Glu Gly Leu Leu Cys Gly Gly Ser Ala Gly Ser
340 345 350

Thr Val Ala Val Ala Val Lys Ala Ala Gln Glu Leu Gln Glu Gly Gln
355 360 365

Arg Cys Val Val Ile Leu Pro Asp Ser Val Arg Asn Tyr Met Thr Lys
370 375 380

Phe Leu Ser Asp Arg Trp Met Leu Gln Lys Gly Phe Leu Lys Glu Glu
385 390 395 400

Asp Leu Thr Glu Lys Lys Pro Trp Trp Trp His Leu Arg
405 410

<210> 4
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

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<210> 6
 <211> 35
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 <213> Artificial Sequence

<220>
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<400> 6	
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<210> 7
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 7
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<210> 8
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 8
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<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 9
ggagatatac catgccgtca gaaaccccgc 30

<210> 10
<211> 30
<212> DNA
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<220>
<223> Synthetic oligonucleotide

<400> 10
gcggggtttc tgacggcatg gtatatctcc 30

<210> 11
<211> 23
<212> DNA
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<220>
<223> Synthetic oligonucleotide

<400> 11
tgggtccgac gggtagcccg cac 23

<210> 12
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 12
gtgcgggcta cccgtcggac cca

23

<210> 13
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated human C15S mutant CBS polypeptide

<400> 13

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Pro Glu Asp Lys Glu Ala Lys Glu Pro Leu Trp Ile Arg Pro Asp Ala
35 40 45

Pro Ser Arg Cys Thr Trp Gln Leu Gly Arg Pro Ala Ser Glu Ser Pro
50 55 60

His His His Thr Ala Pro Ala Lys Ser Pro Lys Ile Leu Pro Asp Ile
65 70 75 80

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

Lys Lys Phe Gly Leu Lys Cys Glu Leu Leu Ala Lys Cys Glu Phe Phe
100 105 110

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

Asp Ala Glu Arg Asp Gly Thr Leu Lys Pro Gly Asp Thr Ile Ile Glu
130 135 140

Pro Thr Ser Gly Asn Thr Gly Ile Gly Leu Ala Leu Ala Ala Ala Val
145 150 155 160

Arg Gly Tyr Arg Cys Ile Ile Val Met Pro Glu Lys Met Ser Ser Glu
165 170 175

Lys Val Asp Val Leu Arg Ala Leu Gly Ala Glu Ile Val Arg Thr Pro
180 185 190

Thr Asn Ala Arg Phe Asp Ser Pro Glu Ser His Val Gly Val Ala Trp
195 200 205

Arg Leu Lys Asn Glu Ile Pro Asn Ser His Ile Leu Asp Gln Tyr Arg
210 215 220

Asn Ala Ser Asn Pro Leu Ala His Tyr Asp Thr Thr Ala Asp Glu Ile
225 230 235 240

Leu Gln Gln Cys Asp Gly Lys Leu Asp Met Leu Val Ala Ser Val Gly
245 250 255

Thr Gly Gly Thr Ile Thr Gly Ile Ala Arg Lys Leu Lys Glu Lys Cys
260 265 270

Pro Gly Cys Arg Ile Ile Gly Val Asp Pro Glu Gly Ser Ile Leu Ala
275 280 285

Glu Pro Glu Glu Leu Asn Gln Thr Glu Gln Thr Thr Tyr Glu Val Glu
290 295 300

Gly Ile Gly Tyr Asp Phe Ile Pro Thr Val Leu Asp Arg Thr Val Val
305 310 315 320

Asp Lys Trp Phe Lys Ser Asn Asp Glu Glu Ala Phe Thr Phe Ala Arg
325 330 335

Met Leu Ile Ala Gln Glu Gly Leu Leu Cys Gly Gly Ser Ala Gly Ser
340 345 350

Thr Val Ala Val Ala Val Lys Ala Ala Gln Glu Leu Gln Glu Gly Gln
355 360 365

Arg Cys Val Val Ile Leu Pro Asp Ser Val Arg Asn Tyr Met Thr Lys
370 375 380

Phe Leu Ser Asp Arg Trp Met Leu Gln Lys Gly Phe Leu Lys Glu Glu
385 390 395 400

Asp Leu Thr Glu Lys Lys Pro Trp Trp Trp His Leu Arg
405 410

<210> 14
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Truncated human C15S mutant CBS Nucleotide

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caggaagggtc tgctgtgcgg tggttcagca ggttcgacgg tcgcagtggc agttaagct	1080
gcgcaggaac tgcaagaagg tcaacgttgt gtcgtgattc tgccggattc tgttcgcaac	1140
tacatgacca aatttctgag tgaccgttgg atgctgcaaa aaggcttcct gaaagaagaa	1200
gatctgaccg agaaaaaacc gtggtggtgg cacctgcgct aa	1242

<210> 15
 <211> 1656
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Full length human C15S mutant CBS nucleotide

<400> 15	
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ccgctgtgga ttctgccgga cgcaccgtca cgctgtacct ggcagctggg tcgtccggca	180
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ctgaagaaaa ttggtgacac cccgatgggt cgtatcaaca aaatcggcaa aaaattcggg	300
ctgaaatgcg aactgctggc taaatgtgaa tttttcaatg cgggcgggtt cgtgaaagat	360
cgtatctcac tgcgcatgat tgaagatgct gaacgcgacg gcaccctgaa accgggtgat	420
acgattatcg aaccgacctc tggcaacacg ggtatcggtc tggcactggc ggcggcagtc	480
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gaatcccatg tgggtgttgc atggcgcctg aaaaacgaaa tcccgaattc gcacattctg	660
gatcagtatc gtaacgctag caatccgctg gcgcattacg ataccacggc cgacgaaatc	720

ctgcagcaat gtgatggcaa actggacatg ctggctcgctt ctgtgggtac cggcgggtacc 780
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 cacatcctgg aaatggacca tttcgcgctg gttgtgcacg aacagattca ataccatagc 1560
 accggcaaat catcgcagcg ccaaatggtc tttggtgtcg tgacggccat tgatctgctg 1620
 aatttcgtgg ccgcacaaga acgtgaccag aaataa 1656

<210> 16
 <211> 551
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Full length human C15S mutant CBS polypeptide

<400> 16

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 20 25 30

Pro Glu Asp Lys Glu Ala Lys Glu Pro Leu Trp Ile Arg Pro Asp Ala
 35 40 45

Pro Ser Arg Cys Thr Trp Gln Leu Gly Arg Pro Ala Ser Glu Ser Pro
50 55 60

His His His Thr Ala Pro Ala Lys Ser Pro Lys Ile Leu Pro Asp Ile
65 70 75 80

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

Lys Lys Phe Gly Leu Lys Cys Glu Leu Leu Ala Lys Cys Glu Phe Phe
100 105 110

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

Asp Ala Glu Arg Asp Gly Thr Leu Lys Pro Gly Asp Thr Ile Ile Glu
130 135 140

Pro Thr Ser Gly Asn Thr Gly Ile Gly Leu Ala Leu Ala Ala Ala Val
145 150 155 160

Arg Gly Tyr Arg Cys Ile Ile Val Met Pro Glu Lys Met Ser Ser Glu
165 170 175

Lys Val Asp Val Leu Arg Ala Leu Gly Ala Glu Ile Val Arg Thr Pro
180 185 190

Thr Asn Ala Arg Phe Asp Ser Pro Glu Ser His Val Gly Val Ala Trp
195 200 205

Arg Leu Lys Asn Glu Ile Pro Asn Ser His Ile Leu Asp Gln Tyr Arg
210 215 220

Asn Ala Ser Asn Pro Leu Ala His Tyr Asp Thr Thr Ala Asp Glu Ile
225 230 235 240

Leu Gln Gln Cys Asp Gly Lys Leu Asp Met Leu Val Ala Ser Val Gly
245 250 255

Thr Gly Gly Thr Ile Thr Gly Ile Ala Arg Lys Leu Lys Glu Lys Cys
260 265 270

Pro Gly Cys Arg Ile Ile Gly Val Asp Pro Glu Gly Ser Ile Leu Ala
275 280 285

Glu Pro Glu Glu Leu Asn Gln Thr Glu Gln Thr Thr Tyr Glu Val Glu
290 295 300

Gly Ile Gly Tyr Asp Phe Ile Pro Thr Val Leu Asp Arg Thr Val Val
305 310 315 320

Asp Lys Trp Phe Lys Ser Asn Asp Glu Glu Ala Phe Thr Phe Ala Arg
325 330 335

Met Leu Ile Ala Gln Glu Gly Leu Leu Cys Gly Gly Ser Ala Gly Ser
340 345 350

Thr Val Ala Val Ala Val Lys Ala Ala Gln Glu Leu Gln Glu Gly Gln
355 360 365

Arg Cys Val Val Ile Leu Pro Asp Ser Val Arg Asn Tyr Met Thr Lys
370 375 380

Phe Leu Ser Asp Arg Trp Met Leu Gln Lys Gly Phe Leu Lys Glu Glu
385 390 395 400

Asp Leu Thr Glu Lys Lys Pro Trp Trp Trp His Leu Arg Val Gln Glu
405 410 415

Leu Gly Leu Ser Ala Pro Leu Thr Val Leu Pro Thr Ile Thr Cys Gly
420 425 430

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

Val Asp Glu Ala Gly Val Ile Leu Gly Met Val Thr Leu Gly Asn Met
450 455 460

Leu Ser Ser Leu Leu Ala Gly Lys Val Gln Pro Ser Asp Gln Val Gly
465 470 475 480

Lys Val Ile Tyr Lys Gln Phe Lys Gln Ile Arg Leu Thr Asp Thr Leu
485 490 495

Gly Arg Leu Ser His Ile Leu Glu Met Asp His Phe Ala Leu Val Val
500 505 510

His Glu Gln Ile Gln Tyr His Ser Thr Gly Lys Ser Ser Gln Arg Gln
515 520 525

Met Val Phe Gly Val Val Thr Ala Ile Asp Leu Leu Asn Phe Val Ala
530 535 540

Ala Gln Glu Arg Asp Gln Lys
545 550