

SEQUENCE LISTING

<110> ORGENESIS LTD
 TEL HASHOMER MEDICAL RESEARCH INFRASTRUCTURE AND SERVICES
 LTD.
 FERBER, Sarah

<120> COMPOSITIONS AND METHODS FOR PROVIDING CELL REPLACEMENT THERAPY

<130> P-570812-PC1

<150> 62/512,085

<151> 2017-05-29

<150> 62/512,083

<151> 2017-05-29

<160> 6

<170> PatentIn version 3.5

<210> 1

<211> 283

<212> PRT

<213> Homo sapiens

<400> 1

Met Asn Gly Glu Glu Gln Tyr Tyr Ala Ala Thr Gln Leu Tyr Lys Asp
 1 5 10 15

Pro Cys Ala Phe Gln Arg Gly Pro Ala Pro Glu Phe Ser Ala Ser Pro
 20 25 30

Pro Ala Cys Leu Tyr Met Gly Arg Gln Pro Pro Pro Pro Pro Pro His
 35 40 45

Pro Phe Pro Gly Ala Leu Gly Ala Leu Glu Gln Gly Ser Pro Pro Asp
 50 55 60

Ile Ser Pro Tyr Glu Val Pro Pro Leu Ala Asp Asp Pro Ala Val Ala
 65 70 75 80

His Leu His His His Leu Pro Ala Gln Leu Ala Leu Pro His Pro Pro

85

90

95

Ala Gly Pro Phe Pro Glu Gly Ala Glu Pro Gly Val Leu Glu Glu Pro
 100 105 110

Asn Arg Val Gln Leu Pro Phe Pro Trp Met Lys Ser Thr Lys Ala His
 115 120 125

Ala Trp Lys Gly Gln Trp Ala Gly Gly Ala Tyr Ala Ala Glu Pro Glu
 130 135 140

Glu Asn Lys Arg Thr Arg Thr Ala Tyr Thr Arg Ala Gln Leu Leu Glu
 145 150 155 160

Leu Glu Lys Glu Phe Leu Phe Asn Lys Tyr Ile Ser Arg Pro Arg Arg
 165 170 175

Val Glu Leu Ala Val Met Leu Asn Leu Thr Glu Arg His Ile Lys Ile
 180 185 190

Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys Glu Glu Asp Lys Lys
 195 200 205

Arg Gly Gly Gly Thr Ala Val Gly Gly Gly Gly Val Ala Glu Pro Glu
 210 215 220

Gln Asp Cys Ala Val Thr Ser Gly Glu Glu Leu Leu Ala Leu Pro Pro
 225 230 235 240

Pro Pro Pro Pro Gly Gly Ala Val Pro Pro Ala Ala Pro Val Ala Ala
 245 250 255

Arg Glu Gly Arg Leu Pro Pro Gly Leu Ser Ala Ser Pro Gln Pro Ser
 260 265 270

Ser Val Ala Pro Arg Arg Pro Gln Glu Pro Arg
 275 280

<210> 2
<211> 852
<212> DNA
<213> Homo sapiens

<400> 2
atgaacggcg aggagcagta ctacgcggcc acgcagcttt acaaggaccc atgcgcgttc 60
cagcgaggcc cggcgccgga gttcagcgcc agccccctg cgtgcctgta catgggccgc 120
cagccccgc cgccgccgcc gcacccgttc cctggcgccc tgggcgcgct ggagcagggc 180
agcccccg acatctcccc gtacgaggtg cccccctcg ccgacgaccc cgcggtggcg 240
caccttcacc accacctccc ggctcagctc gcgtccccc acccgccgc cgggcccttc 300
ccggagggag ccgagccggg cgtcctggag gagcccaacc gcgtccagct gcctttccca 360
tggatgaagt ctaccaaagc tcacgcgtgg aaaggccagt gggcaggcgg cgcctacgct 420
gcggagccgg aggagaacaa gcggacgcgc acggcctaca cgcgcgcaca gctgctagag 480
ctggagaagg agttcctatt caacaagtac atctcacggc cgcgccgggt ggagctggct 540
gtcatgttga acttgaccga gagacacatc aagatctggt tccaaaaccg ccgcatgaag 600
tggaaaaagg aggaggacaa gaagcgcggc ggcgggacag ctgtcggggg tggcggggtc 660
gcggagcctg agcaggactg cgccgtgacc tccggcgagg agcttctggc gctgccgccg 720
ccgccgcccc ccggaggtgc tgtgccgccc gctgcccccg ttgccgcccc agagggccgc 780
ctgccgcctg gccttagcgc gtcgccacag ccctccagcg tcgcgcctcg gcggccgcag 840
gaaccacgat ga 852

<210> 3
<211> 353
<212> PRT
<213> Homo sapiens

<400> 3

Met Ala Ala Glu Leu Ala Met Gly Ala Glu Leu Pro Ser Ser Pro Leu
1 5 10 15

Ala Ile Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val Lys

20

25

30

Lys Glu Pro Pro Glu Ala Glu Arg Phe Cys His Arg Leu Pro Pro Gly
 35 40 45

Ser Leu Ser Ser Thr Pro Leu Ser Thr Pro Cys Ser Ser Val Pro Ser
 50 55 60

Ser Pro Ser Phe Cys Ala Pro Ser Pro Gly Thr Gly Gly Gly Gly Gly
 65 70 75 80

Ala Gly Gly Gly Gly Gly Ser Ser Gln Ala Gly Gly Ala Pro Gly Pro
 85 90 95

Pro Ser Gly Gly Pro Gly Ala Val Gly Gly Thr Ser Gly Lys Pro Ala
 100 105 110

Leu Glu Asp Leu Tyr Trp Met Ser Gly Tyr Gln His His Leu Asn Pro
 115 120 125

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

Ser Gly His His Gly Ala His His Gly Ala His His Pro Ala Ala Ala
 145 150 155 160

Ala Ala Tyr Glu Ala Phe Arg Gly Pro Gly Phe Ala Gly Gly Gly Gly
 165 170 175

Ala Asp Asp Met Gly Ala Gly His His His Gly Ala His His Ala Ala
 180 185 190

His His His His Ala Ala His His His His His His His His His His
 195 200 205

Gly Gly Ala Gly His Gly Gly Gly Ala Gly His His Val Arg Leu Glu
 210 215 220

Glu Arg Phe Ser Asp Asp Gln Leu Val Ser Met Ser Val Arg Glu Leu
 225 230 235 240

Asn Arg Gln Leu Arg Gly Phe Ser Lys Glu Glu Val Ile Arg Leu Lys
 245 250 255

Gln Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Gln Ser Cys Arg
 260 265 270

Phe Lys Arg Val Gln Gln Arg His Ile Leu Glu Ser Glu Lys Cys Gln
 275 280 285

Leu Gln Ser Gln Val Glu Gln Leu Lys Leu Glu Val Gly Arg Leu Ala
 290 295 300

Lys Glu Arg Asp Leu Tyr Lys Glu Lys Tyr Glu Lys Leu Ala Gly Arg
 305 310 315 320

Gly Gly Pro Gly Ser Ala Gly Gly Ala Gly Phe Pro Arg Glu Pro Ser
 325 330 335

Pro Pro Gln Ala Gly Pro Gly Gly Ala Lys Gly Thr Ala Asp Phe Phe
 340 345 350

Leu

<210> 4
 <211> 1059
 <212> DNA
 <213> Homo sapiens

<400> 4
 atggccgcgg agctggcgat gggcgccgag ctgcccagca gcccgctggc catcgagtac 60
 gtcaacgact tcgacctgat gaagttcgag gtgaagaagg agcctcccga ggccgagcgc 120
 ttctgccacc gcctgccgcc aggctcgctg tcctcgacgc cgctcagcac gccctgctcc 180
 tccgtgccct cctcgcccag cttctgcgcg cccagcccgg gcaccggcgg cggcggcggc 240

gcggggggcg gcggcggctc gtctcaggcc gggggcgccc ccgggccgcc gagcgggggc 300
 cccggcgccg tcggggggcac ctcggggaag ccggcgctgg aggatctgta ctggatgagc 360
 ggctaccagc atcacctcaa ccccgaggcg ctcaacctga cgcccagga cgcggtggag 420
 gcgctcatcg gcagcggcca ccacggcgcg caccacggcg cgcaccaccc ggcgggccgcc 480
 gcagcctacg aggctttccg cggcccgggc ttgcggggcg gcggcggagc ggacgacatg 540
 ggcgccggcc accaccacgg cgcgcaccac gccgcccacc accaccacgc cgcccaccac 600
 caccaccacc accaccacca tggcggcgcg ggacacggcg gtggcgcggg ccaccacgtg 660
 cgcctggagg agcgcttctc cgacgaccag ctggtgtcca tgtcgggtgcg cgagctgaac 720
 cggcagctcc gcggcttcag caaggaggag gtcattccggc tcaagcagaa gcggcgcacg 780
 ctcaagaacc gcggctacgc gcagtcctgc cgcttcaagc ggggtgcagca gcggcacatt 840
 ctggagagcg agaagtgcc actccagagc caggtggagc agctgaagct ggaggtgggg 900
 cgcctggcca aagagcggga cctgtacaag gagaaatacg agaagctggc gggccggggc 960
 ggccccggga gcgcgggcgg ggccggtttc ccgcgggagc cttcgccgcc gcaggccggt 1020
 cccggcgggg ccaagggcac ggccgacttc ttcctgtag 1059

<210> 5
 <211> 356
 <212> PRT
 <213> Homo sapiens

<400> 5

Met Thr Lys Ser Tyr Ser Glu Ser Gly Leu Met Gly Glu Pro Gln Pro
 1 5 10 15

Gln Gly Pro Pro Ser Trp Thr Asp Glu Cys Leu Ser Ser Gln Asp Glu
 20 25 30

Glu His Glu Ala Asp Lys Lys Glu Asp Asp Leu Glu Thr Met Asn Ala
 35 40 45

Glu Glu Asp Ser Leu Arg Asn Gly Gly Glu Glu Glu Asp Glu Asp Glu

50

55

60

Asp Leu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Asp Asp Gln Lys
 65 70 75 80

Pro Lys Arg Arg Gly Pro Lys Lys Lys Lys Met Thr Lys Ala Arg Leu
 85 90 95

Glu Arg Phe Lys Leu Arg Arg Met Lys Ala Asn Ala Arg Glu Arg Asn
 100 105 110

Arg Met His Gly Leu Asn Ala Ala Leu Asp Asn Leu Arg Lys Val Val
 115 120 125

Pro Cys Tyr Ser Lys Thr Gln Lys Leu Ser Lys Ile Glu Thr Leu Arg
 130 135 140

Leu Ala Lys Asn Tyr Ile Trp Ala Leu Ser Glu Ile Leu Arg Ser Gly
 145 150 155 160

Lys Ser Pro Asp Leu Val Ser Phe Val Gln Thr Leu Cys Lys Gly Leu
 165 170 175

Ser Gln Pro Thr Thr Asn Leu Val Ala Gly Cys Leu Gln Leu Asn Pro
 180 185 190

Arg Thr Phe Leu Pro Glu Gln Asn Gln Asp Met Pro Pro His Leu Pro
 195 200 205

Thr Ala Ser Ala Ser Phe Pro Val His Pro Tyr Ser Tyr Gln Ser Pro
 210 215 220

Gly Leu Pro Ser Pro Pro Tyr Gly Thr Met Asp Ser Ser His Val Phe
 225 230 235 240

His Val Lys Pro Pro Pro His Ala Tyr Ser Ala Ala Leu Glu Pro Phe
 245 250 255

Phe Glu Ser Pro Leu Thr Asp Cys Thr Ser Pro Ser Phe Asp Gly Pro
260 265 270

Leu Ser Pro Pro Leu Ser Ile Asn Gly Asn Phe Ser Phe Lys His Glu
275 280 285

Pro Ser Ala Glu Phe Glu Lys Asn Tyr Ala Phe Thr Met His Tyr Pro
290 295 300

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

Thr Ala Ala Pro Arg Cys Glu Ile Pro Ile Asp Asn Ile Met Ser Phe
325 330 335

Asp Ser His Ser His His Glu Arg Val Met Ser Ala Gln Leu Asn Ala
340 345 350

Ile Phe His Asp
355

<210> 6
<211> 1071
<212> DNA
<213> Homo sapiens

<400> 6
atgaccaa at cgtacagcga gagtgggctg atgggcgagc ctcagcccca aggtcctcca 60
agctggacag acgagtgtct cagttctcag gacgaggagc acgaggcaga caagaaggag 120
gacgacctcg aagccatgaa cgcagaggag gactcactga ggaacggggg agaggaggag 180
gacgaagatg aggacctgga agaggaggaa gaagaggaag aggaggatga cgatcaaaag 240
cccaagagac gcggcccca aaagaagaag atgactaagg ctcgcctgga gcgtttttaa 300
ttgagacgca tgaaggctaa cgcccgggag cggaaccgca tgcacggact gaacgcggcg 360
ctagacaacc tgcgcaaggt ggtgccttgc tattctaaga cgcagaagct gtccaaaatc 420
gagactctgc gcttggccaa gaactacatc tgggctctgt cggagatctc gcgctcaggc 480

aaaagcccag acctgggtctc cttcgttcag acgctttgca agggcttatc ccaacccacc	540
accaacctgg ttgcgggctg cctgcaactc aatcctcgga cttttctgcc tgagcagaac	600
caggacatgc ccccgcacct gccgacggcc agcgcttcct tccctgtaca cccctactcc	660
taccagtcgc ctgggctgcc cagtccgcct tacggtacca tggacagctc ccatgtcttc	720
cacgttaagc ctccgccgca cgcctacagc gcagcgctgg agcccttctt tgaaagccct	780
ctgactgatt gcaccagccc ttcctttgat ggacccctca gcccgccgct cagcatcaat	840
ggcaacttct ctttcaaaca cgaaccgtcc gccgagtttg agaaaaatta tgcctttacc	900
atgcactatc ctgcagcgac actggcaggg gcccaaagcc acggatcaat cttctcaggc	960
accgctgccc ctcgctgcga gatccccata gacaatatta tgtccttcga tagccattca	1020
catcatgagc gagtcatgag tgcccagctc aatgccatat ttcatgatta g	1071