

# 00786\_0779W01\_Sequence\_Listing

## SEQUENCE LISTING

<110> The General Hospital Corporation

<120> Glycine, Mitochondrial One-Carbon  
Metabolism, and Cancer

<130> 00786-0779W01

<150> US 61/791,082

<151> 2013-03-15

<160> 11

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> yeast codon optimized gene encoding human MTHFD2

<400> 1

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catatggagg ccttggttat cagtggccgc aagctggccc agcagatcaa gcaggaggtg 60
cgccaagaag tggaagaatg ggttgccagc ggcaacaagc gcccgcattc gagcgtgatc 120
ctggtggggc agaaccggc aagccacagc tacgtgctga acaaaacacg cgcagcagca 180
gtggtggggc tcaacagcga gacaatcatg aaaccggcca gcatcagcga ggaagagtta 240
ctgaacttaa ttaacaagct gaataacgac gacaacgtgg acggcctgct ggtgcagtta 300
ccgctgccgg aacatatcga cgaacgccgc atctgcaacg ccgtgagtcg tgataaggac 360
gtggacggct ttcacgtgat caatgttggc cgcattgtgt tagaccagta cagcatgtctg 420
ccggcaacc cttggggcgt ttgggagatc atcaagcgca ccggtatccc gaccctgggt 480
aagaacgttg tggtgccgg ccgtagcaag aacgtgggca tgcctatcgc aatgttactg 540
cacaccgacg gcgcacatga acgtcctggt ggcgatgcaa ccgttaccat cagtcaccgt 600
tacacccga aggagcaact gaaaaagcac accatcctgg ccgacattgt gatcagcgca 660
gccggcattc cgaacctgat caccgcagac atgatcaaag agggcgccgc cgtgatcgac 720
gtgggcatta accgcgtgca cgatccggtg acagccaaac cgaagctggg gggtgacgtg 780
gacttcgagg gcgtgctgca aaaagccggc tacatcacc cggttcctgg tggcgttggc 840
cctatgaccg tggccatgct gatgaagaac accatcattg ccgccaagaa ggtgctgcgt 900
ctggaggagc gcgagcacca tcaccaccac cactaaggta cc 942

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<210> 2

<211> 310

<212> PRT

<213> Artificial Sequence

<220>

<223> MTHFD2 6-HIS fusion protein

<400> 2

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

```

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Met | Cys | Leu | Asp | Gln | Tyr | Ser | Met | Leu | Pro | Ala | Thr | Pro | Trp |
| 130 | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Gly | Val | Trp | Glu | Ile | Ile | Lys | Arg | Thr | Gly | Ile | Pro | Thr | Leu | Gly | Lys |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Asn | Val | Val | Val | Ala | Gly | Arg | Ser | Lys | Asn | Val | Gly | Met | Pro | Ile | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Leu | Leu | His | Thr | Asp | Gly | Ala | His | Glu | Arg | Pro | Gly | Gly | Asp | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Val | Thr | Ile | Ser | His | Arg | Tyr | Thr | Pro | Lys | Glu | Gln | Leu | Lys | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Thr | Ile | Leu | Ala | Asp | Ile | Val | Ile | Ser | Ala | Ala | Gly | Ile | Pro | Asn |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Leu | Ile | Thr | Ala | Asp | Met | Ile | Lys | Glu | Gly | Ala | Ala | Val | Ile | Asp | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Ile | Asn | Arg | Val | His | Asp | Pro | Val | Thr | Ala | Lys | Pro | Lys | Leu | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Asp | Val | Asp | Phe | Glu | Gly | Val | Arg | Gln | Lys | Ala | Gly | Tyr | Ile | Thr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Val | Pro | Gly | Gly | Val | Gly | Pro | Met | Thr | Val | Ala | Met | Leu | Met | Lys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Thr | Ile | Ile | Ala | Ala | Lys | Lys | Val | Leu | Arg | Leu | Glu | Glu | Arg | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| His | His | His | His | His | His |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

<210> 3  
 <211> 236  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> yeast codon-optimized construct

<400> 3  
 tggcgaatgg gacgcgccct gtagcggcgc attaacgcgcg gcggggtgtgg tggttacgcg 60  
 cagcgtgacc gctacacttg ccagcgcctt agcgcccgcct cctttcgctt tcttcccttc 120  
 ctttctcgcc acgttcgccg gctttccccc tcaagctcta aatcgggggc tccctttagg 180  
 gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatg 236

<210> 4  
 <211> 350  
 <212> PRT  
 <213> Homo sapien

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

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Trp | Gly | Val | Trp | Glu | Ile | Ile | Lys | Arg | Thr | Gly | Ile | Pro | Thr | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Lys | Asn | Val | Val | Val | Ala | Gly | Arg | Ser | Lys | Asn | Val | Gly | Met | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Ala | Met | Leu | Leu | His | Thr | Asp | Gly | Ala | His | Glu | Arg | Pro | Gly | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Ala | Thr | Val | Thr | Ile | Ser | His | Arg | Tyr | Thr | Pro | Lys | Glu | Gln | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Lys | His | Thr | Ile | Leu | Ala | Asp | Ile | Val | Ile | Ser | Ala | Ala | Gly | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Asn | Leu | Ile | Thr | Ala | Asp | Met | Ile | Lys | Glu | Gly | Ala | Ala | Val | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Val | Gly | Ile | Asn | Arg | Val | His | Asp | Pro | Val | Thr | Ala | Lys | Pro | Lys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Val | Gly | Asp | Val | Asp | Phe | Glu | Gly | Val | Arg | Gln | Lys | Ala | Gly | Tyr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Thr | Pro | Val | Pro | Gly | Gly | Val | Gly | Pro | Met | Thr | Val | Ala | Met | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Met | Lys | Asn | Thr | Ile | Ala | Ala | Lys | Lys | Val | Leu | Arg | Leu | Glu | Glu |     |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Arg | Glu | Val | Leu | Lys | Ser | Lys | Glu | Leu | Gly | Val | Ala | Thr | Asn |     |     |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |

<210> 5  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> shRNA-encoding sequences

<400> 5  
 gaggtgtgtg atgaagtcaa a 21

<210> 6  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> shRNA-encoding sequences

<400> 6  
 acaagtactc ggagggttat c 21

<210> 7  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> shRNA-encoding sequences

<400> 7  
 gtctgacgtc aagcgatat c 21

<210> 8  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> shRNA-encoding sequences

<400> 8  
 cggagagttg tggactttat a 21

# 00786\_0779w01\_Sequence\_Listing

<210> 9  
 <211> 21  
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 <213> Artificial Sequence  
  
 <220>  
 <223> shRNA-encoding sequences  
  
 <400> 9  
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 <220>  
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 cgaatgtggtt tggatcagta t 21  
  
 <210> 11  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> shRNA-encoding sequences  
  
 <400> 11  
 gcagttgaag aaacatacaa t 21