

S. mansoni Metabotropic Glutamate receptor (SmMglu 10811)
886 bp

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CTATGCATAC ACCAAGTTTA TCAGCTTCTT TCCAAAATGC ATCCATACCG GAATCACCAT AATCACCTGC
ACTACGTACT GTGGAACAT AAGTCCAGTT ATGAGCCGAG ACTAATGTAG CCATTGCCTG AGCTTGAACA
ACATCCGAAG GTACAGTTCG TGCAATAAAT GGAATGCAC GTTTATCACT TAATATAGCA GTTGTGATG
CATAAGATAT TTGTGGTAAA GAGAATAGAC GAAATAAATT TGCTACAAGT ATTGTTACTG AACTATATGA
ACTACCGACA ACTCCACGTG TATTTAAATT TTCTGAATGT TCATTCAATT TATTCAATTG ACTACTACTT
CCAGTACTTG CTTGTACAAA TTTCAATGCT TGTCAAGTG CATGATTTGT ATCTGAACAT GTATCACGTA
TTGTAGTACC CAAAGTTAAA CCTGGTAATA ATTTTGAATT ATTATTTATT TCATCTAAAG TAAATAACAT
TGCTTCAACT CGCTGAATTC CTCTTTCAGG ATTGATTGAT TCACAAGTAG TTGCACCAGA TGTATGTACG
GGGAATAATC CACCAAGCAT TATATCACCT GGTATACTTG CAACTGTATT TTTATCATAT TTACGTTGTA
AACAAATTTAT AATAGTAACC AAATGAAACC ATAATATAAT CATTAAAGTA ATCAACATAA CTTTATATTT
CATATTTATC AAAATAAAAT GATAATCGTT ACCATGTAAA CTTCTTTATT TCTTTACAAT ATTACGAAGT
AAATGAGTAC GGTGTTATT ATCAGAATTC CCCTTATCCA TTCTGTAATG AATTTTAAA ATAATCAATA
AAATTGTTTA TTTTATTTAG TCATTAACA CATAACCACT GTAAGT

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T7+SmMglu (10811) (938bp)

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CTATGCATAC ACCAAGTTTA TCAGCTTCTT TCCAAAATGC ATCCATACCG GAATCACCAT AATCACCTGC
ACTACGTACT GTGGAACAT AAGTCCAGTT ATGAGCCGAG ACTAATGTAG CCATTGCCTG AGCTTGAACA
ACATCCGAAG GTACAGTTCG TGCAATAAAT GGAATGCAC GTTTATCACT TAATATAGCA GTTGTGATG
CATAAGATAT TTGTGGTAAA GAGAATAGAC GAAATAAATT TGCTACAAGT ATTGTTACTG AACTATATGA
ACTACCGACA ACTCCACGTG TATTTAAATT TTCTGAATGT TCATTCAATT TATTCAATTG ACTACTACTT
CCAGTACTTG CTTGTACAAA TTTCAATGCT TGTCAAGTG CATGATTTGT ATCTGAACAT GTCGGTAATA
CGACTCCTA TAGGGAGAT CAGTATTGT AGTACCCAAA GTTAAACCTG GTAATAATT TGAATTATTA
TTTATTTTAT CTAAAGTAAA TAACATTGCT TCAACTCGCT GAATTCCTCT TTCAGGATTG ATTGATTCAC
AAGTAGTTGC ACCAGATGTA TGTACGGGGA ATAATCCACC AAGCATTATA TCACCTGGTA TACTTGCAAC
TGTATTTTTA TCATATTTAC GTTGTAACA ATTTATAATA GTAACCAAAT GAAACCATAA TATAATCATT
AAAGTAATCA ACATAACTTT ATATTTTATA TTTATCAAAA TAAAATGATA ATCGTTACCA TGTAACCTTC
TTTATTTCTT TACAATATTA CGAAGTAAAT GAGTAC GGTG TTATTATCA GATCTCCCTA TAGTGAGTCC
TATTACGC AT TCCCCTTATC CATTCTGTAA TGAATTTTAA AAATAATCAA TAAAATGTT TATTTTATTT
AGTCATTAAA CACATAACCA CTGTAAGT

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Yellow highlighted: Sense primer of silencing region.

Green highlighted: Antisense primer of silencing region.

Red highlighted: T7 promoter sequence (at 5' ends of sense and antisense primers of silencing region).

Blue highlighted: sense and antisense primers for quantitative RT-real time PCR (upstream of silenced region).

Sequence

Filename : **Sm mGlu without T7 promoter sequence**
Length : 886 bp
Unresolved : 0 bp
GC % : 30.9 %

Upper primer without T7 promoter sequence

5'-position : 413
Length : **17**
Sequence : 5'-ATCACGTATTGTAGTAC-3'
3'-CATGATGTTATGCACTA-5'

Tm (basic) : 46.0 °C
Tm (salt) : 45.1 °C
Tm (NN) : 38.6 °C

GC % : 35.3 %
3'-tail GC % : 42.9 %
dG : -25.2 kcal/mol
3'-tail dG : -7.6 kcal/mol

Lower primer without T7 promoter sequence

5'-position : 796
Length : **16**
Sequence : 5'-TCTGATAAATAACACC-3'
3'-CCACAATAAATAGTCT-5'

Tm (basic) : 42.0 °C
Tm (salt) : 40.5 °C
Tm (NN) : 39.3 °C

GC % : 31.3 %
3'-tail GC % : 42.9 %
dG : -25.2 kcal/mol
3'-tail dG : -10.6 kcal/mol

Primer pair properties

Length difference : 1
Tm (basic) difference: 4.0 °C
Tm (salt) difference : 4.7 °C
Tm (NN) difference : 0.7 °C
GC % difference : 4.0 %

PCR product

Position : 413 - 796
Length : 384 bp
GC% : 27.3 %

Tm (product) : 69.4 °C
Tm (annealing) : 45.3 °C

Upper primer self annealing:

5'-ATCACGTATTGTAGTAC-3'
: |||| :
3'-CATGATGTTATGCACTA-5'
dG: -3.09 kcal/mol

5'-ATCACGTATTGTAGTAC-3'
|||
3'-CATGATGTTATGCACTA-5'
dG: -0.43 kcal/mol

5'-ATCACGTATTGTAGTAC-3'
||| : : :::
3'-CATGATGTTATGCACTA-5'
dG: 0.91 kcal/mol

5'-ATCACGTATTGTAGTAC-3'
||| :::
3'-CATGATGTTATGCACTA-5'
dG: 0.91 kcal/mol

Upper primer loops:

5'-ATCACGTATTG
|||)
3'-CATGAT
dG: 1.03 kcal/mol

Lower primer self annealing:

None!

Lower primer loops:

None!

Upper primer - Lower primer annealing:

5'-ATCACGTATTGTAGTAC-3'
||||
3'-CCACAATAAATAGTCT-5'
dG: -1.79 kcal/mol

5'-ATCACGTATTGTAGTAC-3'
||||
3'-CCACAATAAATAGTCT-5'
dG: -1.17 kcal/mol

5'-ATCACGTATTGTAGTAC-3'
||| :
3'-CCACAATAAATAGTCT-5'
dG: -0.08 kcal/mol

5'-ATCACGTATTGTAGTAC-3'
: : ||| :
3'-CCACAATAAATAGTCT-5'
dG: 0.78 kcal/mol

Sequence

Filename : Sm MGlU (10811) T7 primers
Length : 938 bp
Unresolved : 0 bp
GC % : 31.8 %

T7-sense SmMGlU10811

5'-position : 413
Length : 43
Sequence : 5'-GCGTAATACGACTCACTATAGGGAGATCACGTATTGTAGTAC-3'
3'-CATGATGTTATGCACTAAGAGGGATATCACTCAGCATAATGCG-5'

Tm (basic) : 122.0 °C
Tm (salt) : 77.0 °C
Tm (NN) : 72.3 °C

GC % : 41.9 %
3'-tail GC % : 42.9 %
dG : -72.5 kcal/mol
3'-tail dG : -7.6 kcal/mol

T7-antisense SmMGlU10811

5'-position : 848
Length : 42
Sequence : 5'-GCGTAATACGACTCACTATAGGGAGATCTGATAAATAACACC-3'
3'-CCACAATAAATAGTCTAGAGGGATATCACTCAGCATAATGCG-5'

Tm (basic) : 118.0 °C
Tm (salt) : 76.0 °C
Tm (NN) : 72.4 °C

GC % : 40.5 %
3'-tail GC % : 42.9 %
dG : -72.0 kcal/mol
3'-tail dG : -10.6 kcal/mol

Primer pair properties

Length difference : 1
Tm (basic) difference: 4.0 °C
Tm (salt) difference : 1.0 °C
Tm (NN) difference : 0.1 °C
GC % difference : 1.4 %

PCR product

Position : 413 - 848
Length : 436 bp
GC% : 29.6 %

Tm(product) : 70.5 °C
Tm(annealing) : 56.1 °C

||| : :: A
3'-CATGATGTTATGCACTA
dG: 0.39 kcal/mol

5'-GCGTAATACGACTCACTATAGGGAGA
: : ||| :)
3'-CATGATGTTATGCACTA
dG: 0.90 kcal/mol

5'-GCGTAATACGAC
: |||)
3'-CATGATGTTATGCACTAAGAGGGATATCACT
dG: 0.90 kcal/mol

5'-GCGTAATACGACTCACTATAGGGAGAATCACGTATTG
|||)
3'-CATGAT
dG: 1.03 kcal/mol

5'-GCGTAATACGACTCACTATAGGGA
||| :: :)
3'-CATGATGTTATGCACTAAG
dG: 1.03 kcal/mol

5'-GCGTAATACGACTCACTATAGG
||| :: : : : : G
3'-CATGATGTTATGCACTAAGA
dG: 1.03 kcal/mol

T7-antisense self annealing:

5'-GCGTAATACGACTCACTATAGGGAGATCTGATAAATAACACC-3'
: : ||||| : :
3'-CCACAATAAATAGTCTAGAGGGATATCACTCAGCATAATGCG-5'
dG: -4.62 kcal/mol

5'-GCGTAATACGACTCACTATAGGGAGATCTGATAAATAACACC-3'
: : : :: ||||| :: : :
3'-CCACAATAAATAGTCTAGAGGGATATCACTCAGCATAATGCG-5'
dG: -3.39 kcal/mol

5'-
GCGTAATACGACTCACTATAGGGAGATCTGATAAATAACACC-3'
||| :::
3'-CCACAATAAATAGTCTAGAGGGATATCACTCAGCATAATGCG-5'
dG: -2.71 kcal/mol

5'-GCGTAATACGACTCACTATAGGGAGATCTGATAAATAACACC-3'
: : : ||| : : : :
3'-CCACAATAAATAGTCTAGAGGGATATCACTCAGCATAATGCG-5'
dG: -0.31 kcal/mol

5'-GCGTAATACGACTCACTATAGGGAGATCTGATAAATAACACC-3'
||| :::
3'-CCACAATAAATAGTCTAGAGGGATATCACTCAGCATAATGCG-5'
dG: 0.16 kcal/mol

5'-GCGTAATACGACTCACTATAGGGAGATCTGATAAATAACACC-3'

5'-GCGTAATACGACTCACTATAGGGAGAATCACGTATTGTAGTAC-3'
 : | | | : : :
 3'-CCACAATAAATAGTCTAGAGGGATATCACTCAGCATAATGCG-5'
 dG: 0.78 kcal/mol

5'-GCGTAATACGACTCACTATAGGGAGAATCACGTATTGTAGTAC-3'
 : : : | | | : :
 3'-
 CCACAATAAATAGTCTAGAGGGATATCACTCAGCATAATGCG-5'
 dG: 0.78 kcal/mol

5'-GCGTAATACGACTCACTATAGGGAGAATCACGTATTGTAGTAC-3'
 : : : : : | | | : :
 3'-CCACAATAAATAGTCTAGAGGGATATCACTCAGCATAATGCG-5'
 dG: 0.91 kcal/mol

5'-GCGTAATACGACTCACTATAGGGAGAATCACGTATTGTAGTAC-3'
 : : : : | | |
 3'-CCACAATAAATAGTCTAGAGGGATATCACTCAGCATAATGCG-5'
 dG: 0.91 kcal/mol

Oligo Explorer - 1.1.2 18/06/2005

Sequence

Filename : **Quantitative Sm MGlU (10811) Primers**
Length : 886 bp
Unresolved : 0 bp
GC % : 30.9 %

Q Sense SmMGlU10811

5'-position : 40
 Length : 18
 Sequence : **5'-CATCCATACCGGAATCAC-3'**
 3'-CACTAAGGCCATACCTAC-5'

Tm (basic) : 54.0 °C
 Tm (salt) : 53.8 °C
 Tm (NN) : 56.9 °C

GC % : 50.0 %
 3'-tail GC % : 42.9 %
 dG : -33.5 kcal/mol
 3'-tail dG : -9.9 kcal/mol

Q antiSense SmMGlU10811

5'-position : 164
 Length : 18
 Sequence : **5'-TGCACGAACTGTACCTTC-3'**
 3'-CTTCCATGTCAAGCACGT-5'

Tm (basic) : 54.0 °C

Tm (salt) : 53.8 °C
Tm (NN) : 55.4 °C

GC % : 50.0 %
3'-tail GC % : 42.9 %
dG : -32.3 kcal/mol
3'-tail dG : -10.5 kcal/mol

Primer pair properties

Length difference : 0
Tm (basic) difference: 0.0 °C
Tm (salt) difference : 0.0 °C
Tm (NN) difference : 1.5 °C
GC % difference : 0.0 %

PCR product

Position : 40 - 164
Length : 125 bp
GC% : 46.4 %

Tm(product) : 73.5 °C
Tm(annealing) : 53.4 °C

Upper primer self annealing:

5'-CATCCATACCGGAATCAC-3'
:: |||| ::
3'-CACTAAGGCCATACCTAC-5'
dG: -6.54 kcal/mol

5'-CATCCATACCGGAATCAC-3'
||| :::
3'-CACTAAGGCCATACCTAC-5'
dG: -1.43 kcal/mol

Upper primer loops:

5'-CATCCAT
||| A
3'-CACTAAGGCC
dG: -1.31 kcal/mol

Lower primer self annealing:

5'-TGCACGAACTGTACCTTC-3'
||||
3'-CTTCCATGTCAAGCACGT-5'
dG: -3.84 kcal/mol

5'-TGCACGAACTGTACCTTC-3'
: |||| :
3'-CTTCCATGTCAAGCACGT-5'
dG: -0.43 kcal/mol

5'-TGCACGAACTGTACCTTC-3'
||| :::

3'-CTTCCATGTCAAGCACGT-5'
dG: -0.31 kcal/mol

Lower primer loops:

5'-TGCACGAACTG
 ||| T
 3'-CTTCCA
dG: -0.19 kcal/mol

Upper primer - Lower primer annealing:

5'-CATCCATACCGGAATCAC-3'
 |||
 3'-CTTCCATGTCAAGCACGT-5'
dG: -0.31 kcal/mol

5'-CATCCATACCGGAATCAC-3'
 ||| : :
 3'-CTTCCATGTCAAGCACGT-5'
dG: 0.91 kcal/mol