

## pCMV-3XFlag-mmSlug

**Gene/insert:** mmSlug (mmSnai2)

**Insert size:** 810bp

**Species:** mouse

**Fusion protein or tag:** 3x Flag

**Terminal:** N-terminal on backbone

**Vector backbone:** p3xFlag-CMV

**Backbone manufacture:** Sigma

**Vector type:** Mammalian expression

**Backbone size:** 4.7 K

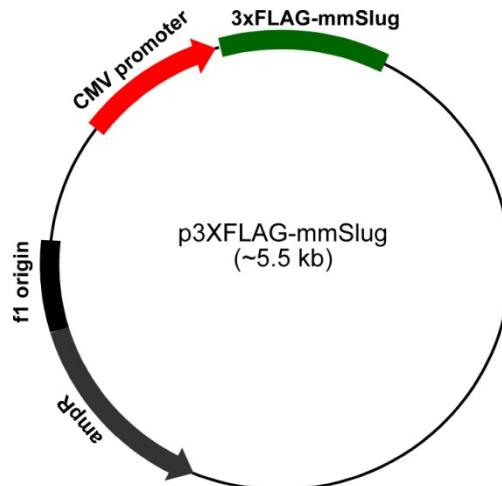
**Cloning 5':** EcoRI

**Site destroyed during cloning:** No

**Cloning 3':** BamHI

**Site destroyed during cloning:** No

**5' sequence primer:** CMV-forward\*\* Sequenced with CMV FWD primer



\*\* Sequenced with CMV FWD primer

### Sequence File : mmSlug-CMV-Forward.seq

```
>mmSlug-CMV-Forward_D12.ab1
NNNNNNNNNNNNNAGNNGANCTCGTTAGTGAACCGTCAGAATTAAACCATGGACTACAAAGACCATGACGGTGATTAT
AAAGATCATGACATCGATTACAAGGATGACGATGACAAGCTTGCAGCCGCAATTCAATGCCGCTCCTCTGGTCAA
GAAACATTCAACGCCCTCCAAGAACGCCAACTACAGCGAACTGGACACACACAGTTATTATTCCTCATCTCTATG
AAAGTTACCCCTACCTGTACATACAAAACCAGAGATCCTCACCTCGGGAGCATAAGCCCTATTACTGTATGGACATCG
TCGGCAGCTCCACTCCTCTACCCAGTGGCTTCTCTTACTGGATACTCCTCATCCTGGGGCGTGTAAAG
TCCCCCGCCTTCTCTGACACTTCAAGGATCACAGTGGTTAGAAAGTCCCATTAGTGACGAAGAGGAGAGACTGC
AGCCAAGCTTCAGACCCCCATGCCATCGAAGCTGAGAAGTTCACTGCAATTATGCAATAAGACCTATTCTACGTT
TCTGGGCTGGCAAACACAAGCAGCTGACTGTGATGCCAGTCTAGGAAATCGTTAGCTGCAAGTACTGTGACAAGGA
ATATGTGAGCCTGGGTGCCCTGAAGATGCACATTGAACACCACACATTGCCCTGTGTGCAAGATCTGTGGCAAGGCTT
TCTCAGACCCCTGGCTGCTTCAAGGACACATTAGAACACTCACACTGGGAAAGCCTTCTTGCCTCACTGCAATAGG
GCTTTGAGANAGATCAAACCTGAGGGCACATCTGAGACCCACTCTGATGTAAGAAATACCAAGTGCAAAAAGCTGCTC
NAAAANNTNNCCANAATGTCGCTTCTNNATAAACATGAGNNCTGGCTGCTGNTGNACACTGANNNGNTNCNGNNNN
NTCCCNNGACCCCTCCCCANNGCTNNNCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
```

## Blast

[ref|NM\\_011415.2|](#) **UEG** Mus musculus snail homolog 2 (Drosophila) (Snai2), mRNA  
[gb|BC062164.1|](#) **UEG** Mus musculus snail homolog 2 (Drosophila), mRNA (cDNA clone MGC:70074  
IMAGE:30242610), complete cds  
Length=2084

[GENE ID: 20583 Snai2](#) | snail homolog 2 (Drosophila) [Mus musculus]  
(Over 10 PubMed links)

Score = 1423 bits (770), Expect = 0.0  
Identities = 792/810 (97%), Gaps = 2/810 (0%)  
Strand=Plus/Plus

Query	138	ATGCCGCGCTCCTCCGGTCAAGAAACATTCAACGCCCTCCAAGAAGGCCAACTACAGC 	197
Sbjct	116	ATGCCGCGCTCCTCCGGTCAAGAAACATTCAACGCCCTCCAAGAAGGCCAACTACAGC 	175
Query	198	GAACTGGACACACACACAGTTATTATTCGGGATATCTCTATGAAAGTTACCCCTATAACCT 	257
Sbjct	176	GAACTGGACACACACACAGTTATTATTCGGGATATCTCTATGAAAGTTACCCCTATAACCT 	235
Query	258	GTCATACCAAAACCAGAGATCCTCACCTCGGGAGCATACAGCCCTATTACTGTATGGACA 	317
Sbjct	236	GTCATACCAAAACCAGAGATCCTCACCTCGGGAGCATACAGCCCTATTACTGTATGGACA 	295
Query	318	TCGTCGGCAGCTCCACTCCACTCTCCTCACCCAGTGGCCTTCTCCTTACTGGATAC 	377
Sbjct	296	TCGTCGGCAGCTCCACTCCACTCTCCTTACCCAGTGGCCTTCTCCTTACTGGATAC 	355
Query	378	TCCTCATCCTGGGGCGTGTAAAGTCCCCCGCTTCCTGACACTTCATCCAAGGATCAC 	437
Sbjct	356	TCCTCATCCTGGGGCGTGTAAAGTCCCCCGCTTCCTGACACTTCATCCAAGGATCAC 	415
Query	438	AGTGGTTCAGAAAGTCCCATTAGTGACGAAGAGGGAGAGACTGCAGCCAAAGCTTCAGAC 	497
Sbjct	416	AGTGGTTCAGAAAGTCCCATTAGTGACGAAGAGGGAGAGACTGCAGCCAAAGCTTCAGAC 	475
Query	498	CCCCATGCCATCGAACGCTGAGAAGTTCACTGCAATTATGCAATAAGACCTATTCTACG 	557
Sbjct	476	CCCCATGCCATCGAACGCTGAGAAGTTCACTGCAATTATGCAATAAGACCTATTCTACG 	535
Query	558	TTCTCTGGCTGGCAAACACAAGCAGCTGCACTGTGATGCCAGTCTAGGAAATCGTC 	617
Sbjct	536	TTCTCTGGCTGGCAAACACAAGCAGCTGCACTGTGATGCCAGTCTAGGAAATCGTC 	595
Query	618	AGCTGCAAGTACTGTGACAAGGAATATGTGAGCCTGGTGCCTGAAGATGCACATTGCA 	677
Sbjct	596	AGCTGCAAGTACTGTGACAAGGAATATGTGAGCCTGGTGCCTGAAGATGCACATTGCA 	655
Query	678	ACCCACACATTGCCCTGTGCTGCAAGATCTGGCAAGGCTTCTCCAGACCCCTGGCTG 	737
Sbjct	656	ACCCACACATTGCCCTGTGCTGCAAGATCTGGCAAGGCTTCTCCAGACCCCTGGCTG 	715
Query	738	CTTCAAGGACACATTAGAACTCACACTGGGAAAAGCCTTCTTGCCTCACTGCAAT 	797
Sbjct	716	CTTCAAGGACACATTAGAACTCACACTGGGAAAAGCCTTCTTGCCTCACTGCAAT 	775
Query	798	AGGGCTTTCAGANAGATCAAACCTGAGGGCACATCTGCAGACCCACTCTGATGAAAG 	857
Sbjct	776	AGGGCTTTCAGACAGATCAAACCTGAGGGCACATCTGCAGACCCACTCTGATGAAAG 	835
Query	858	AAATACCAAGTGCACAAACTGCTCnnnaannTNNNCCANAATGTCGTTCTNNATAAACAT 	917
Sbjct	836	AAATACCAAGTGCACAAACTGCTCCAAAACCTTCTCCAGAATGTCGTTCTGCATAAACAT 	895
Query	918	GAGNN-TCTGGCTGCTGTNTGN-ACACTGAA 945 	
Sbjct	896	GAGGAGTCTGGCTGCTGTGTCAGACACTGAA 925 	