

## Product datasheet for **MC223769**

### Zfp318 (NM\_021346) Mouse Untagged Clone

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** Zfp318 (NM\_021346) Mouse Untagged Clone  
**Tag:** Tag Free  
**Symbol:** Zfp318  
**Synonyms:** 2610034E08Rik; D530032D06Rik; TZF; Znf318  
**Vector:** pCMV6-Entry (PS100001)  
**E. coli Selection:** Kanamycin (25 ug/mL)  
**Cell Selection:** Neomycin  
**Fully Sequenced ORF:** >MC223769 representing NM\_021346  
**Red**=Cloning site **Blue**=ORF **Orange**=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**CGATCGCC**

ATGTACCGCAGTGGCTCCCGCTCCTCCGTCCTTCGACCCGGTCGAAAGACGGCAGCGCGAGCGGCCCTC  
CGCCGGGCGTCCCGTGGGCGCCTCCTCAGGCCACACGCCGCCCTCGTCGCCGCCGCCCTCTTG  
CTCCTCGCTGCGGCTCCCGCCCGCCACCGCTCGCCCTCAGGCCACCGCGGCCGCTGGGCTCGCCG  
TCCCCGCCTCGGGTTCGTCGCGGCTCCCGTCCCCGCCCGCGGCCGCGGCCCTCACCGTCTCCGACCC  
GCGGCCCGCGGCCCTCGCCATCCCTCCCGGGGTTCGTCGTGGCTCCCCGTCCCCGCCCGCGCCGTCG  
CGGCTCCCCGTGCCACCGCGGACCGCGGACACTACCCACCTGGCTGGGTGGCTTCCGAGGCAGCATT  
CGAGGCGAGTCCCGCGCGACTTCGCCCGGACCGCCGCGGAGACCATCCAGGCGCGCGCGCGGCAGTC  
GGAGACGTTCTCCTGGTCTGTGTTCTGATTCTTCTTTGGAGGAGAGTTTAAAGATCACAGTTGGCAATGA  
CCACTTCTGTGTAGCACACCAGAGCGCGCGGCTCAGTGACCGGCTGGGATCTCCAGTGGATGGTCTG  
CAGGACATGGACAGGGATGACCTGACTGATGATTCTGTCTTCACTCGAAGCTCCAGTGTCTCGGGTCT  
TTGAACGATACATTTCTCGGGAGGAGGACCCTTAGTCCCTTCTGGGACAATTGATGAGGACTACCG  
AACAAAGAGAACTTTTCTGCATCGACCTGAGTTTGTCCCGAGAGCAGTTGTATGATGAATTGTTGAGG  
GGAACAGAGCGGAATAGAGACAACTTAAAGCTCCTCCTATTCCATACGATCTGAGGAAAGAAGCCGGG  
AGGCCAAAAGGCCCGTTATGATGACACAGAGAAGGTACACAGCTCAGGAGGGGATCACTCAAGTTTAC  
ATCTGGGACTCGAACTATCGGCAGCGAAGAAGCAGCCAAAGCCCTAGGTTTCTAGATCCCGAGTTTCGA  
GAACTGGACCTTGCCAGGCGAAAGCGAGAGGAAGAAGGAACAAAGTAGGAGCTTGAGTCAAGAGCTGG  
TGGGTGTTGGTATGATCAGATTGGCTGTTCCATCCCTGGCTTGGCAGGAGTCTAACCACATCAGAGCC  
TGGATATTCTTGCAGCGCCTGAGGAAGTACCTATGATGCCAAGAAGTCCATTCTGAAGAAACGAATT  
GAAGCGGACATGAAGCCTCCTTGCAGCTTGAGAGCTTTTCTAGCGGTGCCAGCTCTGGTGAAGATCACC  
CTCTTTATTCTGAACATTCACCTCTTCTAAGTGGTGTATTGCTGCTTTTACTTCAGAGATTGAAAA  
CAAGGGGACTACAGTGGAGGCTGACCTGAAAGAGCCTCAGAGTAACCTATACCAGTGGGGCCCCCTCCGT  
GAGATACCTAAAGACAACAGTGAATAATTTGACAGTTTCTAGGCTTTAAGGAAAATTGGATTTGAAGG



CTGAGGGACTTGAGCAACAGACAGATTTCTTACTGCCCATGAGAGAGCTAGCCAGGACGGCAGTGGCTT  
 TTCTCGAATTCTGAGCATGTTGGCTGATCCTACCATTACACAGGAAAAAGAGAGCTAGCTTCCCTGAT  
 ATTGAGGATGAGGAGAAATTTCTCTATGGGGATGAAGAAGAGGATATAAAATCAGAATCTCCACTTAAGT  
 CCCTGGAGGACCCGAGAGTGCAGGTACGAGACAGAAGGCAAACCTCTGCCCTCAACTCCAGCTGTAAA  
 GCTAGAATCACTAGAAGAAAGCAATCCAGAATATGCCAAGATTCACAACCTTGCTTAAGACCATAGGGCTG  
 GATATTGGAGTAGCAGAAATGGTAAATGGCTGCACGAACCCAGGAGAGACTTCATGGCAAGAAGCCAT  
 CATCAGCCCTCAGCTGACCGACGTTTGTGCTGACCTGACCGACACTTGTCTGGTGACCGACACTTTTCAGC  
 TGACCGCTGTTCCCTCAGTTGAGCACAGTTTCACAGCTGATTGGCGCTCATCAGACCCTCACAGACCGGAG  
 AGTAGGGAGACACATCATAGCAATACTCAGTCCCCAGAAGTATCTCATCCACACCAGCTTCCCCGGTGG  
 ATCCTTACTTGCGCACCAAAAAAGCCCTCCATTCTAAAGTCTGACCATCCAGTGTGCCATGTTTCAGG  
 ACCAGAGGTAGTTGGCAGTGGGTTTCAATCATCTGTTGCTGTTCCGGTGCATGTTGCCATCAGCCCCATCT  
 ACCCAATTAGACTTCTCACTCTGCTGCGTTGTCTCAGTTTCATATAACCAGGGGCTCTCAGTTTGCTG  
 CAGCTCGGATACCTCAAATTATCAGGGATCTGTATTCCCTCTGCCTCCTTTGATGCATATAGGCACTA  
 CATGGCATATGCAGCCTCAAGGTGGCTATGTATCCTGCCTCTCAACCACCAAGCCACCTTTATCTGAC  
 CCTCATAGGCTATTACCAGTAACCAACAAGCTGCTCGTAGTCGTCCTCAATCTCCGGGTGATCCCTACTG  
 TGACTCCTGCAAAGCCAAACAAGAAATACCAGTACTAGGCTCAATTTCTGTAAGCGAATTCTCTGTTCCG  
 GGTGTCCATTCCATCACTCATAAAATATAATCCAAAGAAGATCTCTGATGAGAAGAACCGTGCTCCAG  
 AAGCAGAAGGTTATTGAAGAGAGAGAAAACTGAAACTGAACAGGAAGCCCGGCAAAAGAAATGTTTT  
 ATCTCACGACTGAGTTGGAGCGGCTCCATAAACAGCAAGGGGAGATGTTGCGTAAGAAGCGAAGGGAGAA  
 GGATGGTCACAAAGATCCACTTCTGATGGAGGTGAGTCGACTTCAGGATAGTATTATGAAGGACATTGCC  
 GAGCTACATAAAGAGACAGAAGAAGCAGAAAAGAAGCAGTCTGAACTGGACAAAGTGGCTCAGATCTTGG  
 GAATTGATATCTTTGATAAATCCCTGAAATCTTCAAATGACAGTAAAGAGTCTACAGAGAAGCCTGAAAA  
 AGAAAAATCTAAGAGCCAGAAAAGAGTTGTCAACCCTCAAACCTTCTCTAGCAACAAGGAATCAAAA  
 ATGAATGAAAAGTCTGTATTAAGAGCCCTAGTTCTACTGAAAGCCTCCAACCAACTGTTAAGCAGTCTG  
 ACCAGCCTGTTGCTGCTTATGAGTATTATGATGCTGGCAGTCACTGGTGCAAAGACTGCAATACCACCTG  
 TGGGACCATGTTTGACTTCTTACCCTATGCACAATAAGAAGCACACAGGGGCGAGTTCCAGAAGTCT  
 TCACATTTTCAAACGGAAGGACTGAAGCAGATGTTTCTGCTCCAGGAATGCAGGGATAGAAACCACAGAG  
 ATTATGGAATAATGTGCGTCTTGTGGCCAGTAG

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
 ACAAGGATGACGACGATAAGGTTTAA

- Restriction Sites:** Sgfl-Mlul
- ACCN:** NM\_021346
- Insert Size:** 3465 bp
- OTI Disclaimer:** Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
- Components:** The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).

**Reconstitution Method:**

1. Centrifuge at 5,000xg for 5min.
2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.
3. Close the tube and incubate for 10 minutes at room temperature.
4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.
5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.

**RefSeq:** [NM\\_021346.2](#), [NP\\_067321.2](#)

**RefSeq Size:** 3921 bp

**RefSeq ORF:** 3465 bp

**Locus ID:** 57908

**UniProt ID:** [Q99PP2](#)

**Cytogenetics:** 17 C

**Gene Summary:** Isoform 2: Acts as a transcriptional corepressor for AR-mediated transactivation function. May act as a transcriptional regulator during spermatogenesis and in particular, during meiotic division.[UniProtKB/Swiss-Prot Function]  
Transcript Variant: This variant (2) lacks three exons and includes an alternate 3' terminal exon, compared to variant 1. It encodes isoform 2 which is shorter and has a distinct C-terminus, compared to isoform 1. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.