

## Product datasheet for **MC226081**

### Cryab (NM\_001289784) Mouse Untagged Clone

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** Cryab (NM\_001289784) Mouse Untagged Clone  
**Tag:** Tag Free  
**Symbol:** Cryab  
**Synonyms:** Cry; Crya; Crya-2; Crya2; Hsp; HspB5; P23  
**Vector:** pCMV6-Entry (PS100001)  
**E. coli Selection:** Kanamycin (25 ug/mL)  
**Cell Selection:** Neomycin  
**Fully Sequenced ORF:** >MC226081 representing NM\_001289784  
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**GCGATCGCC**

ATGGACATCGCCATCCACCACCCTGGATCCGGCGCCCTTCTTCCCCTTCCACTCCCCAAGCCGCCTCT  
TCGACCAGTTCTTCGGAGAGCACCTGTTGGAGTCTGACCTTTCTCAACAGCCACTTCCCTGAGCCCTT  
CTACCTTCGGCCACCCTCTTCTGCGGGCACCCAGCTGGATTGACACCGGACTCTCAGAGATGCGTTTG  
GAGAAGGACAGATTCTCTGTGAATCTGGACGTGAAGCACTTCTCTCCGGAGGAACCAAAGTCAAGGTTT  
TGGGGGACGTGATTGAGGTCCACGGCAAGCAGCAAGAACGCCAGGACGAACATGGCTTCACTCCAGGGA  
GTTCCACAGGAAGTACCGGATCCCAGCCGATGTGGATCCTCTCACCATCACTTCACTCCCTGTCATCTGAT  
GGAGTCTCACTGTGAATGGACCAAGGAAACAGGTGTCTGGCCCTGAGCGCACCATTCCCATCACCCGTG  
AAGAGAAGCCTGCTGTCGCCGACGCCCTAAGAAG**TAG**

**ACGCGT**ACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
ACAAGGATGACGACGATAAGGTTTAA

**Restriction Sites:** SgfI-MluI  
**ACCN:** NM\_001289784  
**Insert Size:** 528 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).



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<b>OTI Annotation:</b>	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"><li>1. Centrifuge at 5,000xg for 5min.</li><li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li><li>3. Close the tube and incubate for 10 minutes at room temperature.</li><li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li><li>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.</li></ol>
<b>RefSeq:</b>	<u><a href="#">NM_001289784.1</a></u> , <u><a href="#">NP_001276713.1</a></u>
<b>RefSeq Size:</b>	885 bp
<b>RefSeq ORF:</b>	528 bp
<b>Locus ID:</b>	12955
<b>UniProt ID:</b>	<u><a href="#">P23927</a></u>
<b>Cytogenetics:</b>	9 27.75 cM
<b>Gene Summary:</b>	<p>This gene encodes a member of the small heat-shock protein (HSP20) family. The encoded protein is a molecular chaperone that protects proteins against thermal denaturation and other stresses. This protein is a component of the eye lens, regulates lens differentiation and functions as a refractive element in the lens. This protein is a negative regulator of inflammation, has anti-apoptotic properties and also plays a role in the formation of muscular tissue. Mice lacking this gene exhibit worse experimental autoimmune encephalomyelitis and inflammation of the central nervous system compared to the wild type. In mouse models, this gene has a critical role in alleviating the pathology of the neurodegenerative Alexander disease. Mutations in the human gene are associated with myofibrillar myopathy 2, fatal infantile hypertonic myofibrillar myopathy, multiple types of cataract and dilated cardiomyopathy. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jan 2014]</p> <p>Transcript Variant: This variant (3) differs in the 5' UTR compared to variant 1. Variants 1 through 4 encode the same protein. 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 alignments.</p>