

Product datasheet for **MC222838**

Opa1 (NM_133752) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Opa1 (NM_133752) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Opa1
Synonyms:	1200011N24Rik; AI225888; AI847218; lilr3; mKIAA0567
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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Fully Sequenced ORF:

>MC222838 representing NM_133752
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**GCGATCGCC**

ATGTGGCGAGCAGGTGCGGCGCGCTGGCCTGTGAAGTCTGCCAATCCTTAGTGAACACAGTTCTGGAA
 TACAAAGAAACGTACCGCTCCAAAACTCCATCTGGTTTCACGAAGTATTTATCGTTCACATCATCCTGC
 CCTCAAGCTTCAAAGACCCCAACTAAGGACACCATTTCAGCAGTTCTCTTCTCTAACTCACCTTTTATT
 CATAAATTGAACTTTCTCCAATTAATATGGCTACCAGCCCCGAGGAACCTTTGGCCAGCAAGGTTAG
 CTGCAAGACTCTTAAACTTCGATATATCATACTGGGATCTGCTGTTGGAGGTGGCTATACAGCCAAAA
 AACCTTCGATGAATGAAAGATATGATACCAGACCTTAGTACTATAAGTGGATTGTGCCTGACTTTATA
 TGGGAAATTGATGAGTATATTGATTTGGAGAAAATTAGAAAAGCCCTGCCAGCTCAGAAGACCTTGCCA
 GTTTAGCTCCCGACCTGGACAAGATTACTGAGAGCCTCAGCTTGTGAAGGACTTCTTCACTGCAGGTT
 ACCTGGAGAAACAGCATTTCGAGCAACAGATCATGGATCTGAAAGTGACAAGCATTACAGGAAGGTGCA
 GACAAAGAAAAGATTGACCAACTCAAGAAGAACTTCTGCATACTCAGTTAAAGTATCAGAGGATCTTGG
 AGCGCCTGAAAAAGGAGAACAAAGAGCTGCGGAAGCTGGTGTGTCAGAAGGACGACAAAGGCATCCACCA
 CAGGAAGCTCAAGAAATCTTTGATTGATATGTATTCTGAAGTCTTGATGTTCTTTCTGATTATGATGCC
 AGTTACAATACACAAGATCACCTACCACGGGTTGTTGGGTTGGAGATCAGAGTCTGGGAAAACAGTG
 TGCTGGAATGATTGCTCAGGCCGGATCTTCCCGAGAGGGTCCGGCGAGATGATGACACGCTCTCCAGT
 GAAGGTGACTCTCAGTGAAGGCCCTCACCATGTGGCCTTGTTAAAGATAGCTCTCGGAATTTGATCTC
 ACCAAGGAGGAAGATCTGCAGCATTAGACATGAAATCGAACTCCGAATGAGGAAAAATGTGAAAGAAG
 GTTGACTGTAGTCCCGAGACCATATCTCTAAATGTCAAAGGCCCTGGGCTCGAGAGGATGGTCTCGT
 GGACTGCCTGGTGTATCAACACCGTGACATCAGGCATGGCTCCCGACACAAAGGAAACTATTTTCAGT
 ATCAGCAAAGCTTACATGCAAGATCCTAACGCCATCATCTGTGCATCCAAGACGGATCCGTAGATGCTG
 AGCGCAGTATTGTTACAGACTTGGTCAGTCAAATGGATCCTCATGGAAGAAGAACCATATTTGTTTTGAC
 CAAAGTAGACCTGGCAGAAAAAATGTAGCCAGTCCAAGCAGGATACAACAGATAATTGAAGGCAAGCTC
 TTCCAATGAAAGCTCTGGGTTATTTGCTGTCTAACAGGAAAAGGAAACAGCTCTGAAAGTATTGAAG
 CTATAAGAGAGTATGAAGAGGAATTTTTTCAGAATTCAAAAGTCTAAAGACAAGCATGCTAAAGGCACA
 CCAGGTCACCACGAGAAATCTCAGCCTTGCTGTGTGACTGCTTTTGGAAAATGGTTCGAGAGTCAAGT
 GAACAACAGGCTGATAGTTTTAAAGCCACGCGCTTTAACCTAGAGACGGAATGGAAGAATAACTACCCGC
 GCCTGCGAGAGCTCGACAGGAATGAACTCTTGA AAAAGCTAAAAATGAGATCCTCGATGAGGTCATCAG
 TCTGAGCCAGGTCAGCCAAAGCACTGGGAGGAAATCCTGCAGCAATCCCTGTGGGAACGAGTGTCAACA
 CATGTGATTGAGAATCTACCTTCCAGCTGCCAGACCATGAATTCGGGAACATTTAACACCACAGTAG
 ACATCAAGCTTAAACAGTGGACTGACAAGCAGCTTCTAATAAAGCAGTCGAGGTTGCCTGGGAGACTCT
 ACAAGAGGAATTTTCCGCTTATGACAGAACCCAAAGGAAAGGAAACACGACGACATATTTGACAAACT
 AAGGAGGCTGTGAAGGAGGAGATCAAGCGGCACAAGTGAACGACTTTCGGAGGATAGCTTGAGGG
 TTATTAGCACAATGCTTTGGAAGACCGGTCATATCAGATAAGCAACAGTGGGATGCAGCCATTTACT
 CATGGAAGAGGCGCTTCAAGGTCGTCTCAAGGATACTGAAAATGCTATTGAAAACATGATTGGGCCAGAC
 TGGAAAAAGAGGTGGATGTACTGGAAGAATCGGACCCAAAGAGCAGTGTGTTTCAACAGAAACCAAGAACG
 AGTTGGAGAAGATGCTGAAGTTAATGATGAGCACCAGCTTACCTGGCAAGTGTGAGATTACCACAGT
 CCGGAAGAACCTGGAGTCTCAGGAGTGGAAAGTGCATCCAAGCTTGATTAAGGATACTTGGCATCAAGTT
 TATAGAAGACATTTCTTAAAAACAGCTCTAAATCATTGTAACCTTTGTGCGAGAGGTTTTTATTACTACC
 AGAGGCATTTTATAGATTCTGAGCTGGAATGCAATGACGTGGTCTGTTTTGGCGAATACAGCGCATGCT
 CGCTACTGCAATACATTAAGGCAGCAGCTTACAAACTGAAGTTAGGCGACTAGAGAAAAACGTT
 AAAGAGGTATTAGAAGATTTTGCAGAAGACGGTGAGAAGAAGTTAAATTGCTCACTGGCAAACGAGTTC
 AGCTGGCAGAAGATCTCAAGAAAGTTAGAGAAATCAAGAAAAGCTTGATGCTTTTATTGAAGCTCTTCA
 CCAGGAGAAGTAG

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	Sgfl-Mlul
ACCN:	NM_133752
Insert Size:	2883 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:	<ol style="list-style-type: none">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_133752.3 , NP_598513.1
RefSeq Size:	5948 bp
RefSeq ORF:	2883 bp
Locus ID:	74143
UniProt ID:	P58281
Cytogenetics:	16 20.65 cM

Gene Summary:

Dynamin-related GTPase that is essential for normal mitochondrial morphology by regulating the equilibrium between mitochondrial fusion and mitochondrial fission (PubMed:11847212, PubMed:24616225, PubMed:26785494, PubMed:28746876). Coexpression of isoform 1 with shorter alternative products is required for optimal activity in promoting mitochondrial fusion (By similarity). Binds lipid membranes enriched in negatively charged phospholipids, such as cardiolipin, and promotes membrane tubulation. The intrinsic GTPase activity is low, and is strongly increased by interaction with lipid membranes (By similarity). Plays a role in remodeling cristae and the release of cytochrome c during apoptosis (PubMed:16839884, PubMed:16839885). Proteolytic processing in response to intrinsic apoptotic signals may lead to disassembly of OPA1 oligomers and release of the caspase activator cytochrome C (CYCS) into the mitochondrial intermembrane space (PubMed:16839884, PubMed:16839885). Plays a role in mitochondrial genome maintenance (By similarity).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) lacks an in-frame exon in the 5' coding region, compared to variant 1. The resulting protein (isoform 2) is shorter, compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.