

Product datasheet for **MR210550**

Cul3 (NM_016716) Mouse Tagged ORF Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Cul3 (NM_016716) Mouse Tagged ORF Clone
Tag:	Myc-DDK
Symbol:	Cul3
Synonyms:	KIAA0617
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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ORF Nucleotide
Sequence:

>MR210550 representing NM_016716
Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTGCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGGATCGCC**

ATGTCGAATCTGAGCAAAGGCACGGGCAGCCGGAAGGACACCAAGATGCGGATCCGGCCTTTCCGATGA
CCATGGATGAAAAATATGTAACAGCATTGGGACCTTCTGAAAAATGCAATTCAGAAATCCAGCGTAA
GAATAACAGTGGTCTTAGTTTTGAGGAGCTCTATAGAAATGCATATACAATGGTTTTGCATAAACATGGA
GAAAAGCTCTACACTGGACTAAGAGAAGTTGTTACTGAACATCTCATAAATAAGGTGCGAGAAGATGTAC
TAAATTCATTGAATAACAACCTTTCTTCAAACACTAAATCAAGCTTGGAAATGATCATCAAACAGCCATGGT
GATGATTAGAGACATATTAATGTATATGGACCGTGTATATGTACAACAGAATAATGTAGAAAAATGTCTAC
AATTTGGGATTAATAATTTTTCGAGATCAAGTTGTACGGTATGGGTGATTAGGGATCATCTTCGGCAA
CTTTATTGGATATGATTGCCAGAGAGCGGAAAGGAGAAGTTGTAGACAGAGGAGCAATAAGAAATGCTTG
CCAGATGTTAATGATTTTAGGTCTGAAGGAAGATCAGTCTATGAGGAAGATTTTGAGGCTCCGTTTTTG
GAAATGTCTGCAGAAATTTTTAGATGGAAAGCCAGAAATTTTTAGCAGAAAACAGTGCTTCAGTATATA
TAAAGAAAGTAGAAGCTAGGATTAATGAGGAAATAGAGCGGGTGTGCACTGCCTTGACAAATCCACAGA
AGAGCCTATTGTGAAGGTGGTGGAGAGGGAACCTATTTCCAAGCAGATGAAGACTATTGTAGAAATGGAA
AATTCTGGGCTAGTACATATGCTGAAAAATGGAAGACAGAAAGACCTTGCTTGCATGTACAAATTTTA
GTCGTGTGCCAAATGGTTTGAAGACCATGTGTGAATGTATGAGTTGTTATTTGAGGGAACAAGGAAAAGC
CCTTGTCTGAGGAAGGAGAAGGGAAGAATCCTGTTGACTATATCCAGGGCTTATTGGATCTAAGAGT
AGGTTTGATCGCTTCTCCAAGAATCCTTCAATAATGACCGGCTCTTTAAACAGACTATTGCTGGGGACT
TCGAGTATTTCTTAAACCTCAACTCTAGTCTCCTGAATACCTCTCATTATTTATTGATGATAAACTGAA
AAAGGGAGTCAAAGGGCTAACAGAAACAAGAAGTAGAAACAATATTGGATAGGCAATGGTCTTTTTAGG
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AAAGTGTTTCTGATGACTCTGAGAAAAATATGATTTCTAAATTAAGACTGAGTGTGGATGTCAATTAC
ATCGAAACTGGAAGGAATGTTTAGGGATATGAGCATCTCAAACACAACCTATGGATGAGTTCAGGCAACAT
CTACAGGCAACGGGGTCTCTTTAGGTGGTGTGATCTCACAGTCCGGGTTCTCACACGGGATATTGGC
CTACTCAGTCAGCCACACCAAGTGCAACATCCCACCAGCACAAGACATGCTTTTGAGATATTTAGAAG
GTTCTACTTAGCCAAACACAGTGGTGCACAGCTCACACTCCAGCATCACATGGGTTCTGCAGATCTCAAT
GCCACCTTTTATGGTCCAGTTAAAAGGAAGATGGATCTGAGGTTGGTGTGGCGGTGCACAAGTAACTG
GTTCTAATACACGAAGCACATACTGCAAGTCTCCACTTTCAGATGACCATATTAATGCTTTTTAATAA
TAGAGAGAAGTACACATTTGAGGAAATTAACAAGAGACAGATATCCCTGAAAGAGAAGCTGTTAGAGCC
CTCCAGTCCCTCGCTGTGGTAAACCAACACAGCGGCTCTCACAAAAGAACCAAGTCCAAGGAGATAG
AAAGTGGCCACATATTTACAGTTAATGATCAATTCACATCTAAACTACACAGAGTCAAGATTCAAACAGT
TGCAGCCAAACAAGGTGAATCCGACCCAGAAAGGAAAGAAACAAGACAGAAAGTAGATGACAGAAAA
CATGAGATAGAAGCTGCTATAGTGCGAATAATGAAGTCTAGGAAGAAGATGCAGCACAATGTTTTAGTAG
CAGAGGTAACCTCAGCAACTGAAGGCTCGATTCTACCAAGTCCAGTTGTTATTAAGAAACGTATTGAAGG
ACTTATTGAGAGAGAATTTTGGCACGAACACCTGAGGATCGCAAAGTATACACATATGTAGCA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Protein Sequence: >MR210550 representing NM_016716
 Red=Cloning site Green=Tags(s)

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MSNL SKGTGSRKDTKMRIRAFPM TDEKYVNSI WDL LKNAIQEIQRKNNSGLSFEELYRNAYTMVLHKHG
EKLYTGLREV VTEHLINKVREDV LNSLNNNF LQTLNQA WNDHQ TAMVMIRDILMYMDRVVYVQNNVENVY
NLGLIIFRDQV VRYGCIRDHLRQ TLLDMIARER KGEVVD RGAIRNACQMLMILGLEGRSVYEDFEAPFL
EMSAEFFQME SQKFLAENSASVY IKKVEARINEE IERVMHCLDKSTE EPIVKVVERELISKHMKTI VEME
NSGLVHMLKNGK TEDLACMYKLF SRV P NGLKTMCECM SCYLREQGKALVSEE GEGKNPVDYIQGLLDLKS
RFDRFLQESFN NDRLFQKTIAGDFEYFLNLNSR SPEYLSLFI DDK LKKGVKGLTEQE VETILDKAMV LFR
FMQEKDVFERY YKQHLAR RLLTNKSVSDD SEKNMISKLKTECGCQFTSKLEGMFRDMSISNTT MDEF RQH
LQATGVS LGGVDLTVRVLTTGYWPTQS ATPKCNIP PAPRHA FEIFRRFY LAKHSGRQLTLQH HMGSA DLN
ATFYGPVKKEDG SEVGVGGAQVTGSNTRKHILQVSTFQMTILMLFNNREKYTFEEIQQETDIPERELVRA
LQSLACGKPTQR VLTKEPKSKEIESGHIFTVNDQFTSKLHRVKIQTVAAKQGESDPERKETRQKVDDDRK
HEIEAAIVRIMKSRKKMQHNVLVAEVTQQLKARFLPSPVVIKKRIEGLIEREYLARTPEDRKYVTVVA
  
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TRTRPLEQKLI SEEDLAANDILDYKDDDDKV

Chromatograms: https://cdn.origene.com/chromatograms/mm9033_c07.zip

Restriction Sites: SgfI-MluI

Cloning Scheme:

Cloning sites used for ORF Shuttling:



* The last codon before the Stop codon of the ORF

ACCN: NM_016716

ORF Size: 2304 bp

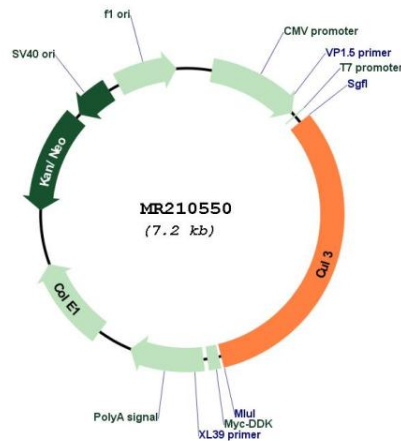
OTI Disclaimer: The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. [More info](#)

OTI Annotation: This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.

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_016716.5
RefSeq Size:	2764 bp
RefSeq ORF:	2307 bp
Locus ID:	26554
UniProt ID:	Q9JLV5
Cytogenetics:	1 C5
MW:	89.4 kDa
Gene Summary:	<p>Core component of multiple cullin-RING-based BCR (BTB-CUL3-RBX1) E3 ubiquitin-protein ligase complexes which mediate the ubiquitination and subsequent proteasomal degradation of target proteins (By similarity). BCR complexes and ARIH1 collaborate in tandem to mediate ubiquitination of target proteins (By similarity). As a scaffold protein may contribute to catalysis through positioning of the substrate and the ubiquitin-conjugating enzyme (By similarity). The E3 ubiquitin-protein ligase activity of the complex is dependent on the neddylation of the cullin subunit and is inhibited by the association of the deneddylated cullin subunit with TIP120A/CAND1 (By similarity). The functional specificity of the BCR complex depends on the BTB domain-containing protein as the substrate recognition component (By similarity). BCR(KLHL42) is involved in ubiquitination of KATNA1 (By similarity). BCR(SPOP) is involved in ubiquitination of BMI1/PCGF4, BRMS1, H2AFY and DAXX, GLI2 and GLI3 (By similarity). Can also form a cullin-RING-based BCR (BTB-CUL3-RBX1) E3 ubiquitin-protein ligase complex containing homodimeric SPOPL or the heterodimer formed by SPOP and SPOPL; these complexes have lower ubiquitin ligase activity (By similarity). BCR(KLHL9-KLHL13) controls the dynamic behavior of AURKB on mitotic chromosomes and thereby coordinates faithful mitotic progression and completion of cytokinesis (By similarity). BCR(KLHL12) is involved in ER-Golgi transport by regulating the size of COPII coats, thereby playing a key role in collagen export, which is required for embryonic stem (ES) cells division: BCR(KLHL12) acts by mediating monoubiquitination of SEC31 (SEC31A or SEC31B) (PubMed:22358839). BCR(KLHL3) acts as a regulator of ion transport in the distal nephron; by mediating ubiquitination of WNK4 (By similarity). The BCR(KLHL20) E3 ubiquitin ligase complex is involved in interferon response and anterograde Golgi to endosome transport: it mediates both ubiquitination leading to degradation and 'Lys-33'-linked ubiquitination (By similarity). The BCR(KLHL21) E3 ubiquitin ligase complex regulates localization of the chromosomal passenger complex (CPC) from chromosomes to the spindle midzone in</p>

anaphase and mediates the ubiquitination of AURKB (By similarity). The BCR(KLHL22) ubiquitin ligase complex mediates monoubiquitination of PLK1, leading to PLK1 dissociation from phosphoreceptor proteins and subsequent removal from kinetochores, allowing silencing of the spindle assembly checkpoint (SAC) and chromosome segregation. The BCR(KLHL22) ubiquitin ligase complex is also responsible for the amino acid-stimulated 'Lys-48' polyubiquitination and proteasomal degradation of DEPDC5. Through the degradation of DEPDC5, releases the GATOR1 complex-mediated inhibition of the TORC1 pathway (By similarity). The BCR(KLHL25) ubiquitin ligase complex is involved in translational homeostasis by mediating ubiquitination and subsequent degradation of hypophosphorylated EIF4EBP1 (4E-BP1) (By similarity). The BCR(KBTBD8) complex acts by mediating monoubiquitination of NOLC1 and TCOF1, leading to remodel the translational program of differentiating cells in favor of neural crest specification (By similarity). Involved in ubiquitination of cyclin E and of cyclin D1 (in vitro) thus involved in regulation of G1/S transition (By similarity). Involved in the ubiquitination of KEAP1, ENC1 and KLHL41 (By similarity). In concert with ATF2 and RBX1, promotes degradation of KAT5 thereby attenuating its ability to acetylate and activate ATM (By similarity). The BCR(KCTD17) E3 ubiquitin ligase complex mediates ubiquitination and degradation of TCHP, a down-regulator of cilium assembly, thereby inducing ciliogenesis (By similarity). The BCR(KLHL24) E3 ubiquitin ligase complex mediates ubiquitination of KRT14, controls KRT14 levels during keratinocytes differentiation, and is essential for skin integrity (By similarity).[UniProtKB/Swiss-Prot Function]

Product images:



Circular map for MR210550