

Product datasheet for **SC211351**

CLPB (NM_030813) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	CLPB (NM_030813) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	CLPB
Synonyms:	ANKCLB; HSP78; MEGCANN; MGCA7; SKD3
ACCN:	NM_030813
Insert Size:	2000 bp



[View online »](#)

Insert Sequence: >SC211351 3'UTR clone of NM_030813
 The sequence shown below is from the reference sequence of NM_030813. The complete sequence of this clone may contain minor differences, such as SNPs.
 Blue=Stop Codon Red=Cloning site

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GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC
CACCTGAGAAGGTGTGCAACACCATCTAGCAGCCACCTGCCTGCTCCTATGTGCCCTCACCATCCAAT
AAAGGCCCTTGGCTGTGGCATGGCAACTGACTTACCTTCCCCTCATGCCGCTCCCATCTTACCCAGT
CTCAGGCTGCTTACCTCCTCACAGCCCATGAAGACCCCTTCTCAGCCCCAAAACCTGAAGGAGGAATT
TCGCCCTACTCTGGCCCCTTTGTGTGGGCCATAACCTGCTAACAGCCTTTCAGGAGAGGAGCTGCCT
TTCCACCCCTTCAAGGCAAGGAGGGATGGAGGTCCTTATTTCCCTTTCAGAAATGATCCCCATCCCCAT
AGTCGCCAGACTTTCTCATGTTCCAGGAAGCTCAGAAGTATGGCAGCTAAGAACACAGCTGGCTGGAA
GAAGACAGGGACCAGACTGAACTGCCACCCTCTGCTAGTCCTCATGCAACTCAGTCCCAGAAATGGCTC
CACTGGGAGTGGAGGAAGAGCTCAGAGGCCAGGTGCAGATAGTTCTGCAATTTAGTCTGTAGCCTCCT
CGTTCCCTACCCTAAAATTCTAAGGGGAAGGGACCCATAGAGGCTTGCCTGTTTCCGCTACTATATTAT
GCCCAGTGTTCCTCCTCACCCACGTCCTGGGGTCAGGCCAGACCATGTTTCGTGACGCTTGGGGACTA
GGCCAGTGTGGGCACCTCCAGGAGGAGGCCTGACTGGTTCATTACCCTCCCCTACTCAGACTGAGCAG
CAGTCCCAGATAACCAAGCAAGCTCAGCTCTGTGGGGCCTCCTTCAAAAGACCAACATCGCAGACATT
AGGAAGCTGTAGGAAGAGAGATCATGGGTTTGACCTCTGCCACATGGCCATGGAGTCAGCCTCAGCCC
TGTCTGTACTGCTCGTCCAGCTAAACGAGCCTGGAATAAATGCAGTTTATTAGTCTGCATGTTAGT
CACAAAGCAGAGGGTCTGGACACCGTCCCCAAGGGCATTTCACAGACCAGCCAATGTTTCAAGCCAC
CTTAGCCAGGCACAGTAAGGCCTGGTGCATCCTTGGGCACCATCTACAGTAGCCACTGCTGATAAGCAG
TCCACCCACCTTCCCCACAGGCCCTTTCATGGAACCCTCGCGTAGTGTTAGCTAGTCTTTCAGGAAGCA
GAGAATGGGGCCAGGAATCAAAGTCCCTTGGGTAAATGGAAGCATGCTTAAACAGTATGGTGGGTATGAG
GCAGTCAGAATCCAGGGTGTGAGCTCCAGCAGATGCTTGGATCACTGTCTACCCCTCAGGGGCTGTGTC
TCCCTACCTCACTGACTGCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
AGCTGGAGTGCAGTGGCGCATCTCGGCTCACTGCAAGCCCTGCCTCCAGGTTCCAGCCATTCTCCTG
CCTCAGCCTCCCAGTAGCTGGGACTACAGGTGCCACCACCACGCCGGCTACCTTTTTGTATTTTTTA
GTAGAGACAGGGTTTACCATGTTAGCCAGGATGGTCTCAATCTCCTGACCTTGTGATCTGCCTGCCTC
GGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGGACCCGGCCTGCTTTTATTGTTTTTTACT
TTTTGTTTTGAAATAATTTTAGACTTAGAGAAAGTTGCAGAAATAGTAGAAAATCCCATGTATCTTTC
ATCTAGCATCTCCAATGATTACATCCTACAAAGCCATACTGTAGTTTATCAAAACCAGGAATGGCCG
GGTGTGGTGGCTCATGCCTGTAATTCAGCACTTTGGGAGGCTGAGGCAGGCAGATTACCTGAGGTCAG
GAGTTCGAGACCAGCCTGGCCAACATGGTGAACCCTGTCTGTACTAAAAATACAAAAATAGCCAGGC
CCGCTGGTGGCCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCACTTGAGCCAGGA
ACGCGT AAGCGGCCGCGGCATCTAGATTCAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA
CGAGATTCGATTCCACCGCCGCTTCTATGAAAGG
  
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Restriction Sites: SgfI-MluI

OTI Disclaimer: Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences, e.g., single nucleotide polymorphisms (SNPs).

Components: The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.

RefSeq: [NM_030813.6](#)

Summary:

This gene belongs to the ATP-ases associated with diverse cellular activities (AAA+) superfamily. Members of this superfamily form ring-shaped homo-hexamers and have highly conserved ATPase domains that are involved in various processes including DNA replication, protein degradation and reactivation of misfolded proteins. All members of this family hydrolyze ATP through their AAA+ domains and use the energy generated through ATP hydrolysis to exert mechanical force on their substrates. In addition to an AAA+ domain, the protein encoded by this gene contains a C-terminal D2 domain, which is characteristic of the AAA+ subfamily of Caseinolytic peptidases to which this protein belongs. It cooperates with Hsp70 in the disaggregation of protein aggregates. Allelic variants of this gene are associated with 3-methylglutaconic aciduria, which causes cataracts and neutropenia. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Apr 2015]

Locus ID:

81570

MW:

73.3