

Product datasheet for **SC216938**

KDEL2 (NM_001100603) Human 3' UTR Clone

Product data:

| | |
|---------------|---|
| Product Type: | 3' UTR Clones |
| Product Name: | KDEL2 (NM_001100603) Human 3' UTR Clone |
| Vector: | pMirTarget (PS100062) |
| Symbol: | KDEL2 |
| Synonyms: | ELP-1; ELP1; ERD2.2; OI21 |
| ACCN: | NM_001100603 |
| Insert Size: | 1907 bp |



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Insert Sequence: >SC216938 3'UTR clone of NM_001100603
The sequence shown below is from the reference sequence of NM_001100603. 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
GAGGAAAAGAGCCAGAAGGTTTCTGTTAATGTCATCTTGCCTTATCTTTTTTATTACTGTGTACAAG
ATTTTTTACACAAGAACTTAATGCTGTATTAATAAATTCAGTGTGTAGCTTCAATTGGGATAGTTC
CAAAAGTGAAGATTTTGTGAGGAATAAGTGCAAATTTTTTTTTTATTTAAAAAATCTTTGAAACTCT
TAAGTCTTTGTGCTGCAATGAAATGTACTCCTTGACAGTTGATAGATTATATATTCTCCATCCCTC
AAACTTGCATTCCACTATATTTATTTTTGGCAAAAGATGAGCTGTATTTGTTGAAATCTGAGACACT
ATGTTCAATTGGATGTATCTGTTCAAATTTATCCACGTGACGTGGAAGTCCTTCGTTGGATGTCACA
ACACTACATTTAAGTTGGTAAGGATGACTTGGAGGTCCATGGTTTTTCATTACCAACATTTAAGATTC
TGATGTCGATGGAGTCTCACTGAAGAGTCACCAAGGTGCCTGCCCTCCTCCCCTGCTGGGAAGTGC
AGTTGGAGACTGTCCAAGGGTGTGAAGAATCCAGTGGCAGGGTCTTGCTGCTTTCCATCTGAGTG
TGGGATGGGAGGGTGTTCATGATCATTGGATATAGCAATCTACTCTGAGAAATGGAACACAAGGAGT
TACCTATCACTTCACTTATAATTCCAAAAGATGACTACAACCATGTCCATGCTCAGATTCAAAACAGTT
TTCCATATCACTTTGGGTGGTAAGATGATTTAATTACAGTTTTTTTTTAAATTGGCAGCACCCTAAC
CATTCTTACATCTTTTTGTATGTGTGGTTTTCTTTTTATTTAACCCGAGCCGACATCGTAGTTTC
TTGTTTTGTTTTGTTTTACAGAGCTGTGTCATGACTTATGTTACCATCTAAAAAACACTATATTAAC
ATGGAATAAATGTCTTTTTATGAATTAGGCTTTTTGAACATCCTGTGTTGGGATTTTTTGTTTTTCA
ATTGGCAACAAAAGCTCTGTAGGGCTGCAGACATTTAAAGTTCACATAATCATCTGTAAGACATTATGT
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GCAAAAGTATATGACTTTGTTTTTATGTGATACACCATAAATATTAAGTGTGAACTAACAGTGC
TGACTACAAGAAGGATGTAGTATTTGGCTTCTGCATTACAACGTCTTCTGGAGGAAGGGAGCAGGAT
GGGTTTCAATTTGTATCTAGTGTGTGCTTAACATCTTTCTAAATCGGCAGTGAACTGCATAGTTAAC
TTCCTGTCTGTCTCCCTCATTTACTCTCCCTCCTTGCTTATGTTTTGGCTTTTGTGTATCAGAGCA
TCTTCTTTGAGCATCCTAGTCTTGTCTCAGTTTCTGTGGTCTTTTTTCATCCTGCTTGAAGATTCGG
AGTGTGGAAGGAGGCTAGGAAGTCTGGTGCAGTAGGTGAGCAGACCTCTGCTGCCAGCCAGGGTGG
GTGGGGCCGACACCTGTCTTTGTGCATGCAAATCTGATACACCTGGCGCATCCTCTGGAGAGCACAACG
CATGGAAGGTCTGGAAGCTCTGTGTAGCCATTCTTCTGCAGTCATCCTACCCAAGTAAAAGTAACCT
TGCTATGTTACCACCGTTTTGGTCACCAGGAGGACATCTTAGCAAGGGTGCCTGCGAGGGAGTGTGG
GACTGGGCTCATCCTCGCCGGCGTTGGAAACCAAGGCCTTGTATGCCACGCCTTATGAAGCACTGTTT
CACAGTACTTTCACTTCCCGAATAAAGGTTACCAGGTAATTA
ACGCGTAAGCGGCCGCGGCATCTAGATTCAAGAAAATGACCGACCAAGCGACGCCAACCTGCCATCA
CGAGATTCGATTCACCGCCGCTTCTATGAAAGG
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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_001100603.2](#)

Summary:

Retention of resident soluble proteins in the lumen of the endoplasmic reticulum (ER) is achieved in both yeast and animal cells by their continual retrieval from the cis-Golgi, or a pre-Golgi compartment. Sorting of these proteins is dependent on a C-terminal tetrapeptide signal, usually lys-asp-glu-leu (KDEL) in animal cells, and his-asp-glu-leu (HDEL) in *S. cerevisiae*. This process is mediated by a receptor that recognizes, and binds the tetrapeptide-containing protein, and returns it to the ER. In yeast, the sorting receptor encoded by a single gene, ERD2, is a seven-transmembrane protein. Unlike yeast, several human homologs of the ERD2 gene, constituting the KDEL receptor gene family, have been described. KDEL2 was the second member of the family to be identified, and it encodes a protein which is 83% identical to the KDEL1 gene product. Alternative splicing results in multiple transcript variants encoding distinct isoforms. [provided by RefSeq, Jul 2008]

Locus ID:

11014

MW:

73.6