# Product datasheet for SC305972

## Decorin (DCN) (NM_133505) Human Untagged Clone

## Product data:

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| **Product Type:** | Expression Plasmids |
| **Product Name:** | Decorin (DCN) (NM_133505) Human Untagged Clone |
| **Tag:** | Tag Free |
| **Symbol:** | DCN |
| **Synonyms:** | CSCD; DSPG2; PG40; PGII; PGS2; SLRR1B |
| **Vector:** | pCMV6 series |
| **Fully Sequenced ORF:** | >NCBI ORF sequence for NM_133505, the custom clone sequence may differ by one or more nucleotides<br>ATGAAGGCCACTATCATCCTCCTTCTGCTTGCACAAGTTTCCTGGGCTGGACCGTTTCAA<br>CAGAGAGGCTTATTTGACTTTATGCTAGAAGATGAGGCTTCTGGGATAGGCCCAGAAGTT<br>CCTGATGACCGCGACTTCGAGCCCTCCCTAGGCCCAGTGTGCCCCTTCCGCTGTCAATGC<br>CATCTTCGAGTGGTCCAGTGTTCTGATTTGGGTCTTCCTCCTTCCCTTACGGAATTACAT<br>CTTGATGGCAACAAAATCAGCAGAGTTGATGCAGCTAGCCTGAAAGGACTGAATAATTTG<br>GCTAAGTTGGGATTGAGTTTCAACAGCATCTCTGCTGTTGACAATGGCTCTCTGGCCAAC<br>ACGCCTCATCTGAGGGAGCTTCACTTGGACAACAACAAGCTTACCAGAGTACCTGGTGGG<br>CTGGCAGAGCATAAGTACATCCAGGTTGTCTACCTTCATAACAACAATATCTCTGTAGTT<br>GGATCAAGTGACTTCTGCCCACCTGGACACAACACCAAAAAGGCTTCTTATTCGGGTGTG<br>AGTCTTTTCAGCAACCCGGTCCAGTACTGGGAGATACAGCCATCCACCTTCAGATGTGTC<br>TACGTGCGCTCTGCCATTCAACTCGGAAACTATAAGTAA |
| **Restriction Sites:** | Please inquire |
| **ACCN:** | NM_133505 |
| **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). |
| **OTI Annotation:** | This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA. |
| **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). |

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| **Reconstitution Method:** | 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. |

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| **RefSeq:** | NM_133505.2, NP_598012.1 |
| **RefSeq Size:** | 1456 bp |
| **RefSeq ORF:** | 639 bp |
| **Locus ID:** | 1634 |
| **UniProt ID:** | P07585 |
| **Cytogenetics:** | 12q21.33 |
| **Protein Families:** | Druggable Genome, Secreted Protein |
| **Protein Pathways:** | TGF-beta signaling pathway |
| **Gene Summary:** | This gene encodes a member of the small leucine-rich proteoglycan family of proteins. Alternative splicing results in multiple transcript variants, at least one of which encodes a preproprotein that is proteolytically processed to generate the mature protein. This protein plays a role in collagen fibril assembly. Binding of this protein to multiple cell surface receptors mediates its role in tumor suppression, including a stimulatory effect on autophagy and inflammation and an inhibitory effect on angiogenesis and tumorigenesis. This gene and the related gene biglycan are thought to be the result of a gene duplication. Mutations in this gene are associated with congenital stromal corneal dystrophy in human patients. [provided by RefSeq, Nov 2015] Transcript Variant: This variant (C) differs in the 5' UTR and lacks three alternate exons in the coding region compared to variant A1. The encoded isoform (c) is shorter than isoform a. This isoform (c) may undergo proteolytic processing similar to isoform a. 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. |