

Product datasheet for **SC111172**

Heparanase 1 (HPSE) (NM_006665) Human Untagged Clone

Product data:

| | |
|---------------------------|--|
| Product Type: | Expression Plasmids |
| Product Name: | Heparanase 1 (HPSE) (NM_006665) Human Untagged Clone |
| Tag: | Tag Free |
| Symbol: | Heparanase 1 |
| Synonyms: | HPA; HPA1; HPR1; HPSE1; HSE1 |
| Mammalian Cell Selection: | None |
| Vector: | <u>pCMV6-XL4</u> |
| E. coli Selection: | Ampicillin (100 ug/mL) |



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Fully Sequenced ORF: >OriGene ORF within SC111172 sequence for NM_006665 edited (data generated by NextGen Sequencing)

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ATGCTGCTGCGCTCGAAGCCTGCGCTGCCGCCGCCGCTGATGCTGCTGCTCCTGGGGCCG
CTGGGTCCCCTCTCCCCTGGCGCCCTGCCCGACCTGCGCAAGCACAGGACGTCGTGGAC
CTGGACTTCTTACCCAGGAGCCGCTGCACCTGGTGAGCCCTCGTTCCTGTCCGTCACC
ATTGACGCCAACCTGGCCACGGACCCGCGTTCCTCATCCTCCTGGGTTCTCAAAGCTT
CGTACCTGGCCAGAGGCTTGTCTCCTGCGTACCTGAGGTTTGGTGGCACCAAGACAGAC
TTCTTAATTTTCGATCCCAAGAAGGAATCAACCTTTGAAGAGAGAAGTTACTGGCAATCT
CAAGTCAACCAGGATATTTGCAAATATGGATCCATCCCTCCTGATGTGGAGGAGAAGTTA
CGGTTGGAATGGCCCTACCAGGAGCAATTGCTACTCCGAGAACACTACCAGAAAAAGTTC
AAGAACAGCACCTACTCAAGAAGCTCTGTAGATGTGCTATACACTTTTGCAAAGTCTCA
GGACTGGACTTGATCTTTGGCCTAAATGCGTTATTAAGAACAGCAGATTTGCAGTGGAA
AGTTCTAATGCTCAGTTGCTCCTGGACTACTGCTTCCAAGGGGTATAACATTTCTTGG
GAACTAGGCAATGAACCTAACAGTTTCTTAAGAAGGCTGATATTTTCATCAATGGGTCC
CAGTTAGGAGAAGATTTTATTCAATTGCATAAACTTCTAAGAAAGTCCACCTTCAAAAAT
GCAAAACTCTATGGTCTGATGTTGGTCAAGCCTCGAAGAAAGACGGCTAAGATGCTGAAG
AGCTTCTGAAGGCTGGTGGAGAAGTATTGATTGATTACATGGCATCACTACTATTTG
AATGGACGGACTGCTACCAGGGAAGATTTCTAAACCCTGATGTATTGGACATTTTATT
TCATCTGTGCAAAAAGTTTTCCAGGTGGTTGAGAGCACCAGGCCCTGGCAAGAAGGTCTGG
TTAGGAGAAAACAGCTCTGCATATGGAGGCGGAGCGCCCTTGCTATCCGACACCTTTGCA
GCTGGCTTTATGTGGCTGGATAAATTGGCCTGTGAGCCCAATGGGAATAGAAGTGGTG
ATGAGGCAAGTATTCTTTGGAGCAGGAACTACCATTTAGTGGATGAAAACCTTCGATCCT
TTACCTGATTATTGGCTATCTCTTCTGTCAAGAAATGGTGGCACCAAGGTGTTAATG
GCAAGCCTGCAAGGTTCAAAGAGAAGGAAGCTTCGAGTATACCTTCATTGCACAAACACT
GACAATCCAAGGTATAAAGAAGGAGATTTAACTCTGTATGCCATAAACCTCCATAATGTC
ACCAAGTACTTGCGGTTACCCTATCCTTTTTCTAAACAGCAAGTGGATAAATACCTTCTA
AGACCTTTGGACCTCATGGATTACTTTCAAATCTGTCCAACCTCAATGGTCTAACTCTA
AAGATGGTGGATGATCAAACCTTGCCACCTTAAATGGAAAAACCTCTCCGGCCAGGAAGT
TCACTGGGCTTGCCAGCTTCTCATATAGTTTTTTGTGATAAGAAATGCCAAAGTTGCT
GCTTGCATCTGA
    
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Clone variation with respect to NM_006665.5
920 a=>g

5' Read Nucleotide Sequence:

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>OriGene 5' read for NM_006665 unedited
TTGATATTGTAACGACTCACTATAGGCGGCCGGAATTCGCACCAGCCAAAATGCTGCT
GCGCTCGAAGCCTGCGCTGCCGCCGCGCTGATGCTGCTGCTCCTGGGGCCGCTGGGTCC
CCTCTCCCCTGGCGCCCTGCCCGGACCTGCGCAAGCACAGGACGTCGTGGACCTGGACTT
CTTACCCAGGAGCCGCTGCACCTGGTGAGCCCTCGTTCCTGTCCGTCACCATTGACGC
CAACCTGGCCACGGACCCGCGGTTCTCATCCTCCTGGGTTCTCAAAGCTTCGTACCTT
GGCCAGAGGCTTGTCTCCTGCGTACCTGAGGTTTGGTGGCACCAAGACAGACTTCCTAAT
TTTCGATCCCAAGAAGGAATCAACCTTTGAAGAGAGAAGTTACTGGCAATCTCAAGTCAA
CCAGGATATTTGCAAATATGGATCCATCCCTCCTGATGTGGAGGAGAAGTTACGGTTGGA
ATGGCCCTACCAGGAGCAATTGCTACTCCGAGAACACTACCAGAAAAAGTTCAAGAACAG
CACCTACTCAAGAAGCTCTGTAGATGTGCTATACACTTTTGCAAAGTCTCAGGACTGGA
CTTGATCTTTGGCCTAAATGCGTTATTAAGAACAGCAGATTTGCAGTGGAAACAGTTCTAA
TGCTCAGTTGCTCCTGGACTACTGCTTCCAAGGGGTATAACATTTCTTGGAACTAGG
CAATGAACCTAACAGTTTCTTAAGAAAGCTGATATTTTCATCAATGGGTGCGAGTTAGG
AGAAAGATTTTCAATTGCATAAACTTCTAAGAAAGTCCACCTTCAAAAATGCAAACCTCT
ATGTCCTGNATGTGGTCANCTCGAGAAAGACGCTAAGTGTGTAAGACTTCTGAAGCTGNT
GGAGAAGTGATGATCAGTACATNCATACTACTATTGAATNACGGCTGCTACAGGAAGAAT
CTAACCTA
    
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Protein Families: Secreted Protein

Protein Pathways: Glycosaminoglycan degradation, Metabolic pathways

Gene Summary: Heparan sulfate proteoglycans are major components of the basement membrane and extracellular matrix. The protein encoded by this gene is an enzyme that cleaves heparan sulfate proteoglycans to permit cell movement through remodeling of the extracellular matrix. In addition, this cleavage can release bioactive molecules from the extracellular matrix. Several transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Sep 2011]

Transcript Variant: This variant (1) represents the longest transcript. Variants 1 and 2 encode the same protein (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.