

Product datasheet for **KN223950**

Heparan Sulfate Proteoglycan 2 (HSPG2) Human Gene Knockout Kit (CRISPR)

Product data:

Product Type:	Knockout Kits (CRISPR)
Format:	2 gRNA vectors, 1 GFP-puro donor, 1 scramble control
Donor DNA:	GFP-puro
Symbol:	Heparan Sulfate Proteoglycan 2
Locus ID:	3339
Components:	<p>KN223950G1, Heparan Sulfate Proteoglycan 2 gRNA vector 1 in pCas-Guide CRISPR vector (GE100002), Target Sequence: CTGCTGGCGGTGAGTGTGCG</p> <p>KN223950G2, Heparan Sulfate Proteoglycan 2 gRNA vector 2 in pCas-Guide CRISPR vector (GE100002), Target Sequence: GTGACGGTCTCTATGTCCTC</p> <p>KN223950D, donor DNA containing left and right homologous arms and GFP-puro functional cassette.</p>

Homologous arm and GFP-puro sequences:

pUC vector backbone in gray; **Left arm sequence in blue**; **GFP-puro in green**; **Right arm in violet**

```

AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAAGCG GTTAGCTCCT TCGGTCCTCC GATCGTTGTC
AGAAGTAAGT TGGCCGCAGT GTTATCACTC ATGGTTATGG CAGCACTGCA TAATTCTCTT ACTGTCATGC
CATCCGTAAG ATGCTTTTCT GTGACTGGTG AGTACTCAAC CAAGTCATTG TGAGAATAGT GTATGCCGGC
ACCGAGTTGC TCTTGCCCGG CGTCAATACG GGATAATACC GCGCCACATA GCAGAATTTT AAAAGTGCTC
ATCATTGGAA AACGTTCTTC GGGCGAAAAA CTCTCAAGGA TCTTACCGCT GTTGAGATCC AGTTCGATGT
AACCCACTCG TGCACCCAAC TGATCTTCAG CATCTTTTAC TTTACCAGC GTTTCTGGGT GAGCAAAAAC
AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT GAATACTCAT ACTCTTCCTT
TTTCAATATT ATTGAAGCAT TTATCAGGT TATTGTCTCA TGAGCGGATA CATATTTGAA TGTATTTAGA
AAAATAAACA AATAGGGGTT CCGCGCACAT TTCCCGAAA AGTGCCACCT GACGTCTAAG AAACCATTAT
TATCATGACA TTAACCTATA AAAATAGGCG TATCACGAGG CCCTTTCGGG TCGCGGTTT CGGTGATGAC
GGTAAAACC TCTGACACAT GCAGCTCCCG TTGACGGTCA CAGCTTGCT GTAAGCGGAT GCCGGGAGCA
GACAAGCCCG TCAGGGCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA
GCAGATTGTA CTGAGAGTGC ACCATAAAAT TGTAACGTT AATATTTTGT TAAAATTCGC GTTAAATTTT
TGTTAAATCA GCTCATTTTT TAACCAATAG GCCGAAATCG GCAAAATCCC TTATAATCA AAAGAATAGC
CCGAGATAGG GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG ACTCCAACGT
CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA CGTGAACCAT CACCCAAATC AAGTTTTTTG
GGGTCGAGGT GCCGTAAAGC ACTAAATCGG AACCCATAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
AGCCGGCGAA CGTGCGGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC GCTAGGGCGC TGGCAAGTGT
AGCGGTACG CTGCGGTAA CCACCACACC CGCCGCGCTT AATGCGCCGC TACAGGGCGC GACTATGGT
TGCTTTGACG TATGCGGTGT GAAATACCGC ACAGATCGCT AAGGAGAAAA TACCGCATCA GGCGCCATTC
GCCATTCAGG CTGCGCAACT GTTGGGAAGG GCGATCGGTG CGGGCCTCTT CGCTATTACG CCAGCTGGCG
AAAGGGGAT GTGCTGCAAG GCGATTAAGT TGGTAACGC CAGGGTTTTT CCAGTACGA CGTTGTAATA
CGACGGCCAG TGAATTGGAG GCTACAGTCA GTGGAGAGGA CTTTCACAG CTGTCGCCGT GCTCATTTGA

```



[View online »](#)

TAACTGCCG TTATTCATGC GACACGTGGC TGCATGTGCC AAAGCTAATT CTCCAACACA GTGGAATGTG
 TTCCTGCAG CCTGGAGACG GGCAGGCCAG AGTGAGGCAG GAAGAGGAGC CAAATGGCCT GGGGAGGAGC
 TGCTGGGGA GGCAACGGCT TTGAGCAGCT CGCCCTTGAC TTCTGCCTGT GTCCCCACCC ATGCTGACCC
 TGGCCAGCCT TCCACCTGCC TGTGCCCCCC ATCTGCGCTG CCCGAGGCCA CCCCTTTACC CGCCCCCATC
 CCCCCATCCA CTCATCATG TCCTGGGTGT CCCTTGCCCT CTCCAAAGGA AAAGGAGTCT TTACTTACCA
 AAGTGATTTA CATTTTATTG TCTGCTTAT TTGAGGATTC ATTCGGAAT AGCAGGGTTG GGCTCTGAAG
 CCTCCAGGGG CTAATGGGAC TTGGGGAAC TGAATCAAAA GGGTTCAGCC CCAGCTGGC TCACTGAGCC
 ATACTAAGTC AAATTTAAC ACTAAGGGGC CTGAAGGTGG GATTCTGGGT CCCCCTGGAA GTGAGGGGAA
 GGACCGTGGG GCTCAGTGGG AGCTGGAGAG AGTGACTCAA TCAGCTCTCG TTTGCTTACA GGTGAAGTAG
 CATGGAGAGC GACGAGAGCG GCCTGCCCGC CATGGAGATC GAGTGCCGCA TCACCGGCAC CCTGAACGGC
 GTGGAGTTCG AGCTGGTGGG CGGCGGAGAG GGCACCCCGC AGCAGGGCCG CATGACCAAC AAGATGAAGA
 GCACCAAAGG CGCCCTGACC TTCAGCCCTT ACCTGCTGAG CCACGTGATG GGCTACGGCT TCTACCACTT
 CGGCACCTAC CCCAGCGGCT ACGAGAACC CTTCCTGCAC GCCATCAACA ACGGCGGCTA CACCAACACC
 CGCATCGAGA AGTACGAGGA CGGCGGCGTG CTGCACGTGA GCTTCAGCTA CCGCTACGAG GCCGGCCGCG
 TGATCGGCGA CTTCAAGGTG ATGGGCACCG GCTTCCCGA GGACAGCGTG ATCTTACCAC ACAAGATCAT
 CCGCAGCAAC GCCACCGTGG AGCACCTGCA CCCCATGGGC GATAACGATC TGGATGGCAG CTTACCCCGC
 ACCTTCAGCC TGC GCGACGG CGGCTACTAC AGCTCCGTGG TGGACAGCCA CATGCACCTT AAGAGCGCCA
 TCCACCCAG CATCCTGCAG AACGGGGGCC CCATGTTCCG CTTCCGCGC GTGGAGGAGG ATCACAGCAA
 CACCGAGCTG GGATCGTGG AGTACCAGCA CGCCTTCAAG ACCCCGGATG CAGATGCCGG TGAAGAAAGA
 GTTTAAGAAT TCCGATCATA TTCAATAACC CTTAATATAA CTTCTGATAA TGTATGCTAT ACGAAGTTAT
 TAGGTCTGAA GAGGAGTTTA CGTCCAGCCA AGCTTAGGAT CTCGACCTCG AAATTCTACC GGGTAGGGGA
 GGCCTTTTC CCAAGGCAGT CTGGAGCATG CGCTTTAGCA GCCCGCTGG GCACCTGGCG CTACACAAGT
 GGCCTCTGGC CTCGCACACA TTCCACATCC ACCGATAGGC GCCAACCGAC TCCGTTCTTT GTTGGCCCTT
 TCGCGCCACC TTCTACTCCT CCCTAGTCA GGAAGTTCCC CCCC GCCCGCAGCTCCGCT CGTGCAGGAC
 GTGACAAATG GAAGTAGCAC GTCTACTAG TCTCGTGAG ATGGACAGCA CCGCTGAGCA ATGGAAGCGG
 GTAGGCCTTT GGGGAGCGG CCAATAGCAG CTTTGTCTCT TCGCTTCTG GGCTCAGAGG CTGGGAAGGG
 GTGGGTCCGG GGGCGGCTC AGGGGCGGGC TCAGGGGCGG GCGGGGCGCC CGAAGGTCTT CCGGAGGCC
 GGCATTCTGC ACGCTTCAA AGCGCACGTC TGCCGCGCTG TTCTCCTCTT CCTCATCTCC GGGCCTTTCG
 ACCTGCATCC ATCTAGATCT CGAGCAGCTG AAGCTTACCA TGACCGAGTA CAAGCCACG GTGCGCCTCG
 CCACCCGCGA CGAGTCCC AGGGCCGTAC GCACCCTCGC CGCCGCTTC GCCGACTACC CCGCCACGCG
 CCACACCGTC GATCCGGACC GCCACATCGA GCGGGTACC GAGCTGCAAG AACTCTTCT CACGCGGCTC
 GGGCTCGACA TCGCAAGGT GTGGGTGCGG GACGACGGCG CCGCGGTGGC GGTCTGACC ACGCCGAGA
 GCGTCAAGC GGGGCGGTG TTCGCCGAGA TCGGCCCGC CATGGCCGAG TTGAGCGGTT CCCGGCTGGC
 CGCGCAGCAA CAGATGGAAG GCCTCCTGGC GCCGACCGG CCAAGGAGC CCGCGTGGT CCTGGCCACC
 GTCGGCGTCT CGCCGACCA CCAGGGCAAG GGTCTGGGCA GCGCCGTCGT GCTCCCCGA GTGGAGGCGG
 CCGAGCGCGC CGGGGTGCC GCCTTCTTGG AGACCTCCG GCCCACAACT CCCCCCTTCT ACGAGCGGCT
 CGGCTTACC GTCACCGCCG ACGTCGAGGT GCCCGAAGGA CCGCGCACCT GGTGCATGAC CCGCAAGCCC
 GGTGCCTGAC GCCCGCCCA CGACCCGACG CGCCGACCG AAAGGAGCGC ACGACCCAT GCATCGATGA
 TATCAGATCC CCGGATGCA GAAATTGATG ATCTATTA CAATAAAGAT GTCCACTAAA ATGGAAGTTT
 TTCTGTCTAT ACTTTGTTAA GAAGGTGAG AACAGAGTAC CTACATTTT AATGGAAGGA TTGAGCTAC
 GGGGTGGG GTGGGTGGG ATTAGATAAA TGCTGTCTT TTAAGTAAAG CTCTTTACTA TTGCTTTATG
 ATAATGTTT ATAGTTGGAT ATCATAATTT AAACAAGCAA AACCAAATTA AGGGCCAGCT CATTCTCTCC
 ACTCATGATC TATAGATCTA TAGATCTCTC GTGGGATCAT TGTTTTTCTT TTGATTTCCA CTTTGTGGTT
 CTAAGTACTG TGGTTTCAA ATGTGTCACT TTCATAGCCT GAAGAACGAG ATCAGCAGCC TCTGTTCCAC
 ATACACTTCA TTCTCAGTAT TGTTTTGCCA AGTTCTAATT CCATCAGAAG CTGGTCGAGA TCCGGAACCC
 TTAATATAAC TTCGTATAAT GTATGCTATA CGAAGTTATT AGGTCCCTCG AAGAGGTTCA CTAGGCGCGC
 CTGAGGACAT GCTGGCTGAC AGCATCTCAG GAGGTGAGCC AAGGATCAA GGCTGGGAGC AGAGGGGTGG
 GGGGTGAGAC TGTGCTTCTT CCCACTGGCA TGGGGGAGGA GGGTGACCGA CCATTCCGAG CTTTCTCAAC
 CCTGTCCAC TGTATACTAG GTGCCAGAA CAGTGCCTGA CACCCAGTAG GACTCAACA AATACTTGT
 GTTGTGATT ACATCTCTT TTTGCTTATA GACGACCTGG GCAGTGGGGA CCTGGGCAGC GGGGACTTCC
 AGATGGGTAA GTTGCTGCAG GCCTCCTGCA GGTCTCCCTC CTGTCCCCA GGAAGCCCC AGAGCCAGTC
 TCCTGGGCTG AGGGCTCCTT GGGCTGCC TGGGGTACAA AGCAAGAAGA AGTGGGTGTG ATCTCTAAC

CTGCTGAGTG ACAGTTGTGC AGACTGATTG GCAGGTCCTT GCAAGGCTGG TGTGGCCAGG TCCTGTGCTT
 GCCCATGCCA CAGGCACAGG TATCAGGGCA CTGGGCAGGT AAAGCCCACT TCTGCTGGGG ACTGACAGCC
 AGTCAGCTGT TTCACATTCA AAGCAAAGTT CTCACCTCCC ATCACTCTCG CCGGTTGGAC TTTAGATCAG
 AAGGGATCTT GCTGCCGCC GAAAGAGGAA GGGCTGGAAG AGGAAGGAGC TTGGCGTAAT CATGGTCATA
 GCTGTTTCCT GTGTGAAATT GTTATCCGCT CACAATTCCA CACAACATAC GAGCCGGAAG CATAAAGTGT
 AAAGCCTGGG GTGCCTAATG AGTGAGCTAA CTCACATTAA TTGCGTTGCG CTCACTGCCC GCTTTCCAGT
 CGGGAAACCT GTCGTGCCAG CTGCATTAAT GAATCGGCCA ACGCGCGGGG AGAGGCGGTT TGCATATTGG
 GCGCTCTTCC GCTTCTCGC TCACTGACTC GCTGCGCTCG GTCGTTTCGGC TCGGGCGAGC GGTATCAGCT
 CACTCAAAGG CGGTAATACG GTTATCCACA GAATCAGGGG ATAACGCAGG AAAGAACATG TGAGCAAAAAG
 GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC CATAGGCTCC GCCCCCCTGA
 CGAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG
 TTTCCCCCTG GAAGCTCCCT CGTGCCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCT
 TTCTCCCTTC GGAAGCGTG GCGCTTTCTC ATAGCTCAG CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT
 TCGCTCCAAG CTGGGCTGTG TGCACGAACC CCCCCTCAG CCCGACCCT GCGCCTTATC CGGTAACTAT
 CGTCTTGAGT CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA
 GAGCGAGGTA TGAGGCGGT GCTACAGAGT TCTTGAAGTG GTGGCCTAAC TACGGCTACA CTAGAAGAAC
 AGTATTTGGT ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC
 AAACAAACCA CCGCTGGTAG CCGTGGTTTT TTTGTTTGCA AGCAGCAGAT TACGCGCAGA AAAAAAGGAT
 CTCAGAAGA TCCTTTGATC TTTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACCTCAC GTTAAGGGAT
 TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAAATGAG TTTTAAATCA
 ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG
 CGATCTGTCT ATTTTCGTTCA TCCATAGTTG CCTGACTCCC CGTCGTGTAG ATAACCTACG TACGGGAGGG
 CTTACCATCT GGCCCCAGTG CTGCAATGAT ACCGCGAGAA CCACGCTCAC CGGCTCCAGA TTTATCAGCA
 ATAAACCAGC CAGCCGGAAG GGCCGAGCGC AGAAGTGGTC CTGCAACTTT ATCCGCCTCC ATCCAGTCTA
 TTAATTGTTG CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC
 TACAGGCATC GTGGTGTCAC GCTCGTCGTT TGGTATGGCT TCATTCAGCT CCGGTTCCCA ACGATC

GE100003, scramble sequence in pCas-Guide vector

Disclaimer:

These products are manufactured and supplied by OriGene under license from ERS. The kit is designed based on the best knowledge of CRISPR technology. The system has been functionally validated for knocking-in the cassette downstream the native promoter. The efficiency of the knock-out varies due to the nature of the biology and the complexity of the experimental process.

RefSeq:

[NM_001291860](#), [NM_005529](#)

UniProt ID:

[P98160](#)

Synonyms:

HSPG; PLC; PRCAN; SJA; SJS; SJS1

Summary:

This gene encodes the perlecan protein, which consists of a core protein to which three long chains of glycosaminoglycans (heparan sulfate or chondroitin sulfate) are attached. The perlecan protein is a large multidomain proteoglycan that binds to and cross-links many extracellular matrix components and cell-surface molecules. It has been shown that this protein interacts with laminin, prolargin, collagen type IV, FGF2, FBLN2, FGF7 and transthyretin, etc., and it plays essential roles in multiple biological activities. Perlecan is a key component of the vascular extracellular matrix, where it helps to maintain the endothelial barrier function. It is a potent inhibitor of smooth muscle cell proliferation and is thus thought to help maintain vascular homeostasis. It can also promote growth factor (e.g., FGF2) activity and thus stimulate endothelial growth and re-generation. It is a major component of basement membranes, where it is involved in the stabilization of other molecules as well as being involved with glomerular permeability to macromolecules and cell adhesion. Mutations in this gene cause Schwartz-Jampel syndrome type 1, Silverman-Handmaker type of dyssegmental dysplasia, and tardive dyskinesia. Alternative splicing of this gene results in multiple transcript variants. [provided by RefSeq, May 2014]

Product images:

