

Product datasheet for **KN219269**

GRAMD1B 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:	GRAMD1B
Locus ID:	57476
Components:	KN219269G1, GRAMD1B gRNA vector 1 in pCas-Guide CRISPR vector (GE100002), Target Sequence: CAAGCTCTCTGGTAAGTAG KN219269G2, GRAMD1B gRNA vector 2 in pCas-Guide CRISPR vector (GE100002), Target Sequence: AGGGTGCTGGGCGAGCACA KN219269D, donor DNA containing left and right homologous arms and GFP-puro functional cassette.

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 GCAGAACTTT AAAAGTGCTC
ATCATTGGAA AACGTTCTTC GGGGCGAAAA 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 TTCCCCGAAA AGTGCCACCT GACGTCTAAG AAACCATTAT
TATCATGACA TTAACCTATA AAAATAGGCG TATCACGAGG CCCTTTCGTC TCGCGCGTTT CGGTGATGAC
GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGCT GTAAAGCGGAT GCCGGGAGCA
GACAAGCCCG TCAGGGCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA
GCAGATTGTA CTGAGAGTGC ACCATAAAAT TGTAACGTT AATATTTTGT TAAAATTCGC GTTAAATTTT
TGTTAAATCA GCTCATTTTT TAACCAATAG GCCGAAATCG GCAAAATCCC TTATAATCA AAAGAAATAGC
CCGAGATAGG GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG ACTCCAACGT
CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA CGTGAACCAT CACCCAAATC AAGTTTTTTG
GGGTCGAGGT GCCGTAAAGC ACTAAATCGG AACCCCTAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
AGCCGGCGAA CGTGCGGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC GCTAGGGCGC TGGCAAGTGT
AGCGGTCACG CTGCGCGTAA CCACCACACC CGCCGCGCTT AATGCGCCGC TACAGGGCGC GACTATGGT
TGCTTTGACG TATGCGGTGT GAAATACCGC ACAGATGCGT AAGGAGAAAA TACCGCATCA GCGCCATTTC
GCCATTCAGG CTGCGCAACT GTTGGGAAGG GCGATCGGTG CGGGCTCTT CGCTATTACG CCAGCTGGCG
AAAGGGGGAT GTGCTGCAAG GCGATTAAAG TGGGTAACGC CAGGGTTTTC CCAGTCACGA CGTTGTAAAA
CGACGGCCAG TGAATTGGAG GCTACAGTCA GTGGAGAGGA CTTTCACAGG CTGTCGCCGT GCTCATTTGA

```



View online »

TAAGTCCCG	TTATTCATGC	GACACTCCCA	TCCTGGGACT	AAACATGTGC	TGTGTCTTTA	AATGGGCGGA
AGTGGCTGGC	AGTGCTTTGC	TTGGGTAAGT	CATTGATTAG	GAGATTATAT	GGAGCTGCGG	GAGCTGCCGC
CTGGGGGAAG	AGAGGTGCAG	CTTCTGCTAG	GTTTGTGCTC	TCCTCCCAGG	GTCTCCTTGG	CTTCCTTTCC
CAAAGCAGCT	CAGAGCTGGT	ATGAGGTGAG	GGTGGGGGGC	AGCCGGCCAG	CCTGGCTGTT	GACGGCAACT
CCAGGGCTTG	TTTCGCGCAG	CCTTGCCAGC	ATTACCCATC	CTCATCAGAA	ACTGGCAGCG	GCAGCCACAG
CTCGGGCAGG	CGGCTCCAGC	CCCAGGCTGG	ATTTCAGAAA	TCTGTCTTTT	GCCTCCAAGC	CCAGCTTTCA
GCTGGGAGAG	GGGAAGAAG	GGGCAGTGGC	AGCAGTTCTT	CTGGCTCTTT	CTCCCTTTCT	CTCTTTCTCT
TTCTGTGTTT	AAGTCACATT	ACATGGGATT	CTGTTCTTTT	GGGACTTCGT	CATCTTTTCC	AATATGTCCT
GGGACCTCCG	GAGCTGTAAC	GGGGATGCTA	AGGACACGGT	CAGTGGATTA	TCGTGACTGT	ACTAACTAGC
ATGGAGAGCG	ACGAGAGCGG	CCTGCCCGCC	ATGGAGATCG	AGTGCCGCAT	CACCGGCACC	CTGAACGGCG
TGGAGTTCTA	GCTGGTGGGC	GGCGGAGAGG	GCACCCCGCA	GCAGGGCCGC	ATGACCAACA	AGATGAAGAG
CACCAAAGGC	GCCCTGACCT	TCAGCCCTTA	CCTGCTGAGC	CACGTGATGG	GCTACGGCTT	CTACCACTTC
GGCACCTACC	CCAGCGGCTA	CGAGAACCCC	TTCCTGCACG	CCATCAACAA	CGGCGGCTAC	ACCAACACCC
GCATCGAGAA	GTACGAGGAC	GGCGGCGTGC	TGCACGTGAG	CTTCAGCTAC	CGCTACGAGG	CCGGCCGCGT
GATCGGCGAC	TTCAAGGTGA	TGGGCACCGG	CTTCCCCGAG	GACAGCGTGA	TCTTCACCGA	CAAGATCATC
CGCAGCAACG	CCACCGTGGA	GCACCTGCAC	CCCATGGGCG	ATAACGATCT	GGATGGCAGC	TTCACCCGCA
CCTTCAGCCT	GCGCGACGGC	GGCTACTACA	GCTCCGTGGT	GGACAGCCAC	ATGCACTTCA	AGAGCGCCAT
CCACCCACGC	ATCCTGCAGA	ACGGGGGGCC	CATGTTCCGC	TTCCGCGCGG	TGGAGGAGGA	TCACAGCAAC
ACCGAGCTGG	GCATCGTGGA	GTACCAGCAC	GCCTTCAAGA	CCCCGGATGC	AGATGCCGGT	GAAGAAAGAG
TTTAAGAATT	CCGATCATAT	TCAATAACCC	TTAATATAAC	TTCGTATAAT	GTATGCTATA	CGAAGTTATT
AGGTCTGAAG	AGGAGTTTAC	GTCCAGCCAA	GCTTAGGATC	TCGACCTCGA	AATTCTACCG	GGTAGGGGAG
GCGCTTTTCC	CAAGGCAGTC	TGGAGCATGC	GCTTTAGCAG	CCCCGCTGGC	ACTTGGCGCT	ACACAAGTGG
CCCTCTGGCT	CGCACACATT	CCACATCCAC	CGGTAGCGCC	AACCGGCTCC	GTTCTTTTGG	GGCCCCCTCG
CGCCACCTTC	TACTCTCCC	CTAGTCAGGA	AGTTCCCCCC	CGCCCCCGAG	CTCGCGTCTG	GCAGGACGTG
ACAAATGGAA	GTAGCACGTC	TCACTAGTCT	CGTGAGATG	GACAGCACCG	CTGAGCAATG	GAAGCGGGTA
GGCCTTTGGG	GCAGCGGCCA	ATAGCAGCTT	TGCTCCTTCG	CTTTCTGGGC	TCAGCAGCTG	GGAAGGGTGG
GTCCGGGGGC	GGGCTCAGGG	GCGGGCTCAG	GGGCGGGGCG	GGCGCCCGAA	GGTCTCCCGG	AGGCCCGGCA
TTCTGCACGC	TTCAAAAGCG	CACGTCTGCC	GCGCTGTTCT	CCTCTTCTCT	ATCTCCGGGC	CTTTCGACCT
GCATCCATCT	AGATCTCGAG	CAGCTGAAGC	TTACCATGAC	CGAGTACAAG	CCCACGGTGC	GCCTCGCCAC
CCGCGACGAC	GTCCCCAGGG	CCGTACGCAC	CCTCGCCGCC	GCGTTCGCGG	ACTACCCCGC	CACGCGCCAC
ACCGTCGATC	CGGACCGCCA	CATCGAGCGG	GTCACCGAGC	TGCAAGAACT	CTTCTCTACG	CGCGTCGGGC
TCGACATCGG	CAAGGTGTGG	GTGCGGAGCG	ACGGCGCCGC	GGTGGCGGTC	TGGACACGCG	CGGAGAGCGT
CGAAGCGGGG	GCGGTGTTCT	CCGAGATCGG	CCCGCGCATG	GCCGAGTTGA	GCGGTTCCTG	GCTGGCCGCG
CAGCAACAGA	TGGAAGGCCT	CCTGGCGCCG	CACCGGCCCA	AGGAGCCCGC	GTGGTTCCTG	GCCACCGTCG
GCGTCTCGCC	CGACCACGAG	GGCAAGGGTC	TGGGCAGCGC	CGTCGTGCTC	CCCGAGTGGG	AGGCGGCCGA
GCGCGCCGGG	GTGCCCGCCT	TCCTGGAGAC	CTCCGCGCCC	CACAACCTCC	CCTTCTACGA	GCGGCTCGGC
TTACCCGTCA	CCGCCGACGT	CGAGGTGCCC	GAAGGACCGC	GCACCTGGTG	CATGACCCGC	AAGCCCGGTG
CCTGACGCCC	GCCCCACGAC	CCGCAGCGCC	CGACCGAAAG	GAGCGCACGA	CCCCATGCAT	CGATGATATC
AGATCCCCGG	GATGCAGAAA	TTGATGATCT	ATTAAACAAT	AAAGATGTCC	ACTAAAATGG	AAGTTTTTCC
TGTCATACTT	TGTTAAGAAG	GGTGAGAACA	GAGTACCTAC	ATTTTGAATG	GAAGGATTGG	AGCTACGGGG
GTGGGGGTGG	GGTGGGATTA	GATAAATGCC	TGCTCTTTAC	TGAAGGCTCT	TTACTATTGC	TTTATGATAA
TGTTTCATAG	TTGGATATCA	TAATTTAAAC	AAGCAAAACC	AAATTAAGGG	CCAGCTCATT	CCTCCCACTC
ATGATCTATA	GATCTATAGA	TCTCTCGTGG	GATCATTGTT	TTTCTCTTGA	TTCCCACTTT	GTGGTTCTAA
GTACTGTGGT	TTCCAAATGT	GTCAGTTTCA	TAGCCTGAAG	AACGAGATCA	GCAGCCTCTG	TTCCACATAC
ACTTCATTCT	CAGTATTGTT	TTGCCAAGTT	CTAATTCCAT	CAGAAGCTGG	TCGAGATCCG	GAACCCTTAA
TATAACTTCG	TATAATGTAT	GCTATACGAA	GTTATTAGGT	CCCTCGAAGA	GGTTCAC TAG	GCGCGCCACG
TCAGCTGCTT	AGGGCGGGCA	GTCCTAGGG	GCATCCCTCT	GAGGGGCCAG	GCTCCATCTT	CTAGGATGCC
TGGTGTCCAG	AGGCGAGTGG	ACCGCTGCCT	ACCCCAACAC	AAGCACTCAC	CTTGGGCCTT	TGCAAGTGCC
TGTTCTCTGG	CTTAATCTTG	GGACATTA AAA	GGCATCTCTC	GCTTGGGGTG	TGGGAGTAGC	TGTATTCTAG
CTACAGAAGT	AGTCAGAATA	TTTTTACCTT	CCATTTAAAA	AATAAAACCT	TTACCTCTCT	CTGTTTTTTG
ACCCAATAAG	GAGATTGCAC	GGGCAGGTGA	ATTGGCTTTT	CATCTGGTGG	AGAAACTGCA	GATTTTTGCT
GGAAAAC TTT	GCCATACCAG	TGATCCGGTA	CCCCTGCAGG	GTGGCATGTG	CAGCTGCCTG	AGGCCTCTTT

CAGAGGAGAA AGGCTCCTTG GACTGAGGAG GGAGCTTTCT CCCTGAAGAG GGTGGAGGGT GGGAGGAGGA
 GGATGAGCTT GGGAGAGCTC CCAGCAAGGA TGAGTCCTGC CTTCAATTGCG GCTGGCTGTC CACGCGTGGG
 GTGGGGTGGC GGCAGGTCAC ATCTCTGAGT GAAAGGTTCA CTCTCGCCGG TTGGACTTTA GATCAGAAGG
 GATCTTGCTG CCGCCCGAAA GAGGAAGGGC TGAAGAGGA AGGAGCTTGG CGTAATCATG GTCATAGCTG
 TTTCTGTGT GAAATTGTTA TCCGCTCACA ATTCCACACA ACATACGAGC CGGAAGCATA AAGTGTAAGG
 CCTGGGGTGC CTAATGAGTG AGCTAACTCA CATTAAATTG GTTGCCTCA CTGCCCGCTT TCCAGTCGGG
 AAACCTGTCG TGCCAGCTGC ATTAATGAAT CGGCCAACGC GCGGGGAGAG GCGGTTTGCG TATTGGGCGC
 TCTTCGCTT CCTCGCTCAC TGAATCGCTG CGCTCGGTG TTCGGCTGCG GCGAGCGGTA TCAGTCACT
 CAAAGGCGGT AATACGGTTA TCCACAGAAT CAGGGGATAA CGCAGGAAAG AACATGTGAG CAAAAGGCCA
 GCAAAAGGCC AGGAACCGTA AAAAGGCCGC GTTGCTGGCG TTTTTCATA GGCTCCGCC CCCTGACGAG
 CATCAGAAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC CGACAGGACT ATAAAGATAC CAGGCGTTTC
 CCCCTGGAAG CTCCTCGTG CGCTCTCTG TTCCGACCCT GCCGCTTACC GGATACCTGT CCGCCTTTCT
 CCCTTCGGGA AGCGTGGCG TTTCTCATAG CTCACGCTGT AGGTATCTCA GTTCGGTGA GGTCTGTCG
 TCCAAGCTGG GCTGTGTGCA CGAACCCCC GTTCAGCCCG ACCGCTGCGC CTTATCCGT AACTATCGTC
 TTGAGTCAA CCGGTAAGA CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGA TTAGCAGAGC
 GAGGTATGTA GCGGTGCTA CAGAGTTCTT GAAGTGGTGG CTAACACTAC GCTACACTAG AAGGACAGTA
 TTTGGTATCT GCGCTCTGCT GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG TAGCTCTGA TCCGGCAAAC
 AAACCACCGC TGGTAGCGGT GGTTTTTTTG TTTGCAAGCA GCAGATTACG CGCAGAAAAA AAGGATCTCA
 AGAAGATCCT TTGATCTTT CTACGGGGTC TGACGCTCAG TGAACGAAA ACTCACGTTA AGGGATTTTG
 GTCATGAGAT TATCAAAAAG GATCTTCACC TAGATCCTT TAAATTAAAA ATGAAGTTT AAATCAATCT
 AAAGTATATA TGAGTAACT TGGTCTGACA GTTACCAATG CTTAATCAGT GAGGCACCTA TCTCAGCGAT
 CTGTCTATTT CGTTCATCCA TAGTTGCCTG ACTCCCGTC GTGTAGATAA CTACGATACG GGAGGGCTTA
 CCATCTGGCC CCAAGTGTGC AATGATACCG CGAGACCCAC GCTCACCAGC TCCAGATTTA TCAGCAATAA
 ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA GTGGTCTGTC AACTTTATCC GCCTCCATCC AGTCTATTAA
 TTGTTGCCG GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA ACGTTGTTGC CATTGCTACA
 GGCATCGTGG TGTCACGCTC GTCGTTTGGT ATGGCTTCAT TCAGCTCCGG TTCCCAACGA TC

GE100003, scramble sequence in pCas-Guide vector

RefSeq: [NM_001286563](#), [NM_001286564](#), [NM_001330396](#), [NM_020716](#), [NM_001354837](#),
[NM_001367420](#), [NM_001367421](#), [NM_001367418](#), [NM_001367419](#)

UniProt ID: [Q3KR37](#)

Summary: Cholesterol transporter that mediates non-vesicular transport of cholesterol from the plasma membrane (PM) to the endoplasmic reticulum (ER) (By similarity). Contains unique domains for binding cholesterol and the PM, thereby serving as a molecular bridge for the transfer of cholesterol from the PM to the ER (By similarity). Plays a crucial role in cholesterol homeostasis in the adrenal gland and has the unique ability to localize to the PM based on the level of membrane cholesterol (By similarity). In lipid-poor conditions localizes to the ER membrane and in response to excess cholesterol in the PM is recruited to the endoplasmic reticulum-plasma membrane contact sites (EPCS) which is mediated by the GRAM domain (By similarity). At the EPCS, the sterol-binding VAST/ASTER domain binds to the cholesterol in the PM and facilitates its transfer from the PM to ER (By similarity).[UniProtKB/Swiss-Prot Function]

Product images:

