

Product datasheet for **KN514961**

Rnf8 Mouse Gene Knockout Kit (CRISPR)

Product data:

Product Type:	Knockout Kits (CRISPR)
Format:	2 gRNA vectors, 1 linear donor
Donor DNA:	EF1a-GFP-P2A-Puro
Symbol:	Rnf8
Locus ID:	58230



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Components:
KN514961G1, Rnf8 gRNA vector 1 in pCas-Guide CRISPR vector (GE100002)

KN514961G2, Rnf8 gRNA vector 2 in pCas-Guide CRISPR vector (GE100002)

KN514961D, Linear donor DNA containing LoxP-EF1a-tGFP-P2A-Puro-LoxP:

The sequence below is cassette sequence only. The linear donor DNA also contains proprietary target sequence.

LoxP-EF1a-tGFP-P2A-Puro-LoxP (2739 bp)

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ATAACTTCGT ATAATGTATG CTATACGAAG TTATCGTGAG GCTCCGGTGC CCGTCAGTGG GCAGAGCGCA
CATCGCCAC AGTCCCCGAG AAGTTGGGG GAGGGGTCGG CAATTGAACC GGTGCCTAGA GAAGGTGGCG
CGGGGTAAC TGGGAAAGTG ATGTCGTGTA CTGGCTCCGC CTTTTCCCG AGGGTGGGG AGAACCCTAT
ATAAGTCAG TAGTCGCCGTAACGTTCTT TTTCCGAACG GGTTCGCCG CAGAACACAG GTAAGTGCCG
TGTGTGGTTC CCGCGGGCCT GGCCTCTTTA CGGGTTATGG CCCTTGCGTG CCTTGAATTA CTTCCACCTG
GCTGCAGTAC GTGATTCTTG ATCCCGAGCT TCGGGTTGGA AGTGGGTGGG AGAGTTCGAG GCCTTGCGCT
TAAGGAGCCC CTTCGCCTCG TGCTTGAGTT GAGGCCTGGC CTGGGCGCTG GGGCCCGCG GTGCGAATCT
GGTGGCACCT TCGCGCCTGT CTCGCTGCTT TCGATAAGTC TCTAGCCATT TAAAATTTT GATGACCTGC
TGCAGCGCTT TTTTCTGGC AAGATAGTCT TGTAATGCG GGCCAAGATC TGCACACTGG TATTTTCGTT
TTTGGGGCCG CGGGCGGCGA CGGGGCCCGT GCGTCCCAGC GCACATGTTC GGCAGGCGG GGCCTGCGAG
CGCGGCCACC GAGAATCGGA CGGGGGTAGT CCAAGCTGG CCGGCCTGCT CTGGTGCCTG GCCTCGCGCC
GCCGTGTATC GCCCCGCCCT GGGCGGCAAG GCTGGCCCGG TCGGCACCAG TTGCGTGAGC GGAAAGATGG
CCGCTTCCCG GCCCTGTGTC AGGGAGCTCA AAATGGAGGA CGCGGCGCTC GGGAGAGCGG GCGGGTGAAGT
CACCCACACA AAGGAAAAGG GCCTTCCCGT CCTCAGCCGT CGCTTCATGT GACTCCACGG AGTACCGGGC
GCCGCTCCAG CACCTCGATT AGTTCTCGAG CTTTTGGAGT ACGTCGTCTT TAGTTGGGG GGAGGGGTTT
TATGCGATGG AGTTTCCCA CACTGAGTGG GTGGAGACTG AAGTTAGGCC AGCTTGGCAG TTGATGTAAT
TCTCCTTGGG ATTTGCCCTT TTTGAGTTTG GATCTTGGTT CATTCTCAAG CCTCAGACAG TGGTTCAAAG
TTTTTTCTT CCATTTCAAG TGTCGTGAAT GGAGAGCGAC GAGAGCGGCC TGCCCGCCAT GGAGATCGAG
TGCCGCATCA CCGGCACCCT GAACGGCGTG GAGTTCGAGC TGGTGGGCGG CGGAGAGGGC ACCCCCGAGC
AGGGCCGCAT GACCAACAAG ATGAAGAGCA CCAAAGGCGC CCTGACCTTC AGCCCTACC TGCTGAGCCA
CGTGATGGG TACGGCTTCT ACCACTTCGG CACCTACCC AGCGGCTACG AGAACCCCTT CCTGCACGCC
ATCAACAACG GCGGCTACAC CAACACCCG ATCGAGAAGT ACGAGGACGG CGGCGTGCTG CACGTGAGCT
TCAGCTACCG CTACGAGGCC GGCCGCGTGA TCGGCGACTT CAAGGTGATG GGCACCGGCT TCCCGGAGGA
CAGCGTGATC TTCACCGACA AGATCATCCG CAGCAACGCC ACCGTGGAGC ACCTGCACCC CATGGCGGAT
AACGATCTGG ATGGCAGCTT CACCCGCACC TTCAGCCTGC GCGACGGCGG CTACTACAGC TCCGTGGTGG
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CCGCCCGTG GAGGAGGATC ACAGCAACAC CGAGTGGGG ATCGTGGAGT ACCAGCACGC CTTCAAGACC
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ACGTGGAGGA GAACCCTGGA CCTATGACCG AGTACAAGCC CACGGTGCGC CTCGCCACCC GCGACGACGT
CCCCAGGGCC GTACGCACCC TCGCCGCCG GTTCGCCGAC TACCCGCCA CGGCCACAC CGTCGATCCG
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GGTGTTCGCC GAGATCGGCC CGCGCATGGC CGAGTTGAGC GGTTCGCCG TGGCCCGCA GCAACAGATG
GAAGGCCTCC TGCGCCGCA CCGGCCAAG GAGCCCGCT GTTCTCTGGC CACCCTCGGC GTCTCGCCG
ACCACCAGGG CAAGGTCTG GGCAGCGCCG TCGTGTCCC CGGAGTGGAG GCGGCCGAGC GCGCCGGGT
GCCCGCTTC CTGGAGACCT CCGCGCCCG CAACCTCCC TTCTACGAGC GGCTCGGCT CACCGTCACC
GCCGACGTC AGGTGCCGA AGGACCGCG ACCTGGTGA TGACCCGCA GCCCGGTGCC TGAAACTTGT
TTATTGCAGC TTATAATGGT TACAAATAA GCAATAGCAT CACAAATTC ACAAATAAG CATTTTTTTC
ACTGCATTCT AGTTGTGGT TGTCCAACT CATCAATGA TCTTAATAAC TTCGTATAAT GTATGTATA CGAAGTTAT
    
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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_021419](#)

UniProt ID: [Q8VC56](#)

Synonyms: 3830404E21Rik; AIP37; laXp180

Summary:

E3 ubiquitin-protein ligase that plays a key role in DNA damage signaling via 2 distinct roles: by mediating the 'Lys-63'-linked ubiquitination of histones H2A and H2AX and promoting the recruitment of DNA repair proteins at double-strand breaks (DSBs) sites, and by catalyzing 'Lys-48'-linked ubiquitination to remove target proteins from DNA damage sites. Following DNA DSBs, it is recruited to the sites of damage by ATM-phosphorylated MDC1 and catalyzes the 'Lys-63'-linked ubiquitination of histones H2A and H2AX, thereby promoting the formation of TP53BP1 and BRCA1 ionizing radiation-induced foci (IRIF). Also controls the recruitment of UIMC1-BRCC3 (RAP80-BRCC36) and PAXIP1/PTIP to DNA damage sites. Also recruited at DNA interstrand cross-links (ICLs) sites and catalyzes 'Lys-63'-linked ubiquitination of histones H2A and H2AX, leading to recruitment of FAAP20 and Fanconi anemia (FA) complex, followed by interstrand cross-link repair. H2A ubiquitination also mediates the ATM-dependent transcriptional silencing at regions flanking DSBs in cis, a mechanism to avoid collision between transcription and repair intermediates. Promotes the formation of 'Lys-63'-linked polyubiquitin chains via interactions with the specific ubiquitin-conjugating UBE2N/UBC13 and ubiquitinates non-histone substrates such as PCNA. Substrates that are polyubiquitinated at 'Lys-63' are usually not targeted for degradation. Also catalyzes the formation of 'Lys-48'-linked polyubiquitin chains via interaction with the ubiquitin-conjugating UBE2L6/UBCH8, leading to degradation of substrate proteins such as CHEK2, JMJD2A/KDM4A and KU80/XRCC5: it is still unclear how the preference toward 'Lys-48'- versus 'Lys-63'-linked ubiquitination is regulated but it could be due to RNF8 ability to interact with specific E2 specific ligases. For instance, interaction with phosphorylated HERC2 promotes the association between RNF8 and UBE2N/UBC13 and favors the specific formation of 'Lys-63'-linked ubiquitin chains. Promotes non-homologous end joining (NHEJ) by promoting the 'Lys-48'-linked ubiquitination and degradation of KU80/XRCC5. Following DNA damage, mediates the ubiquitination and degradation of JMJD2A/KDM4A in collaboration with RNF168, leading to unmask H4K20me2 mark and promote the recruitment of TP53BP1 at DNA damage sites. Following DNA damage, mediates the ubiquitination and degradation of POLD4/p12, a subunit of DNA polymerase delta. In the absence of POLD4, DNA polymerase delta complex exhibits higher proofreading activity. In addition to its function in damage signaling, also plays a role in higher-order chromatin structure by mediating extensive chromatin decondensation. Involved in the activation of ATM by promoting histone H2B ubiquitination, which indirectly triggers histone H4 'Lys-16' acetylation (H4K16ac), establishing a chromatin environment that promotes efficient activation of ATM kinase. Required in the testis, where it plays a role in the replacement of histones during spermatogenesis (PubMed:20153262, PubMed:28552346). At uncapped telomeres, promotes the joining of deprotected chromosome ends by inducing H2A ubiquitination and TP53BP1 recruitment, suggesting that it may enhance cancer development by aggravating telomere-induced genome instability in case of telomeric crisis. Promotes the assembly of RAD51 at DNA DSBs in the absence of BRCA1 and TP53BP1 Also involved in class switch recombination in immune system, via its role in regulation of DSBs repair. May be required for proper exit from mitosis after spindle checkpoint activation and may regulate cytokinesis. May play a role in the regulation of RXRA-mediated transcriptional activity. Not involved in RXRA ubiquitination by UBE2E2.[UniProtKB/Swiss-Prot Function]

Product images:

