*h*CFHR5 VersaClone cDNA

Catalog Number: RDC3334

Specifications:

Gene:	*h*CFHR5
Accession:	NP_110414.1
Insert size:	1723bp
Concentration:	10µg at 0.2µg/µL

Description

This shuttle vector contains the complete ORF for the gene of interest, along with a Kozak consensus sequence for optimal translation initiation. It is inserted NotI to AscI. The gene insert is flanked with convenient multiple cloning sites which can be used to easily cut and transfer the gene cassette into your desired expression vector.

Preparation and Storage

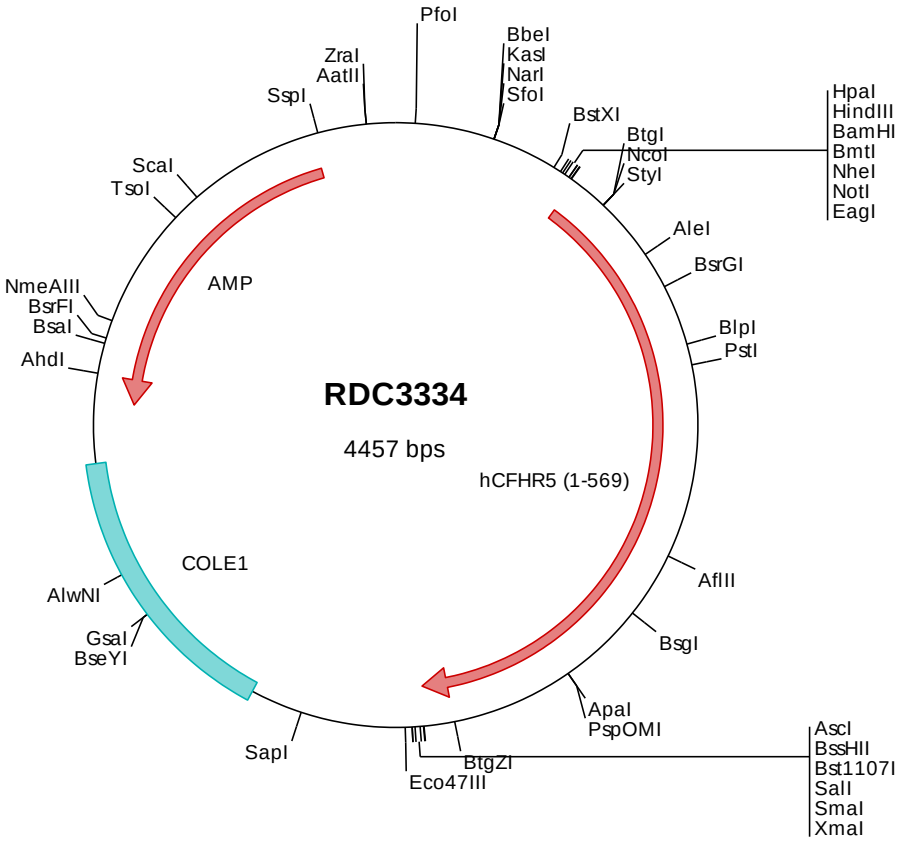
Formulation	cDNA is provided in 10 mM Tris-Cl, pH 8.5
Shipping	Ships at ambient temperature
Stability	1 year from date of receipt when stored at -20°C to -80°C
Storage	Use a manual defrost freezer and avoid repeated freeze-thaw cycles.

*h*CFHR5 cDNA Plasmid

CFHR5 complement factor H related 5 [*Homo sapiens* (human)]

Also known as: FHR5; CFHL5; FHR-5; CFHR5D

Summary:
CFHR5 is a member of the complement factor H protein family. Members of this family are exclusively composed of individually folded protein domains, termed short consensus repeats (SCRs) or complement control modules. CFHR5 has been identified initially as a universal component of complement deposits and detected in glomerular immune deposits. The pattern of deposits is similar to other complement components, suggesting that CFHR5 may play a role in complement activation and regulation. It is synthesized in the liver and consists of 9 SCRs. Its biological function is not understood fully. CFHR5 exhibits similar characteristics as those of factor H in heparin binding, CRP binding, and lipoprotein association.



FOR RESEARCH USE ONLY

NOT FOR USE IN HUMANS

R&D SYSTEMS
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> RDC3334 Plasmid DNA Sequence

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 101  tcagggcgcg tcagcgggtg ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc accatatgcg gtgtgaaata
 201  ccgcacagat gcgtaaggag aaaataccgc atcaggcgcc attcgccatt caggctgcgc aactgttggg aagggcgatc ggtgcgggcc tcttcgctat
 301  tacgccagct ggcgaaaggg ggatgtgctg caaggcgatt aagttgggta acgccagggt tttcccagtc acgacgttgt aaaacgacgg ccagtgaatt
 401  ggagacgtgt taacaagctt ggatccgata tcgctagcgc ggccgccacc atgttgctct tattcagtgt aatcctaatc tcatgggtat ccactgttgg
 501  gggagaagga acactttgtg attttccaaa aatacaccat ggatttctgt atgatgaaga agattataac ccttttccc aagttcctac aggggaagtt
 601  ttctattact cctgtgaata taattttgtg tctccttcaa aatccttttg gactcgcata acatgcacag aagaaggatg gtcaccaaca ccgaagtgtc
 701  tcagaatgtg ttcctttcct tttgtgaaaa atggtcattc tgaatcttca ggactaatac atctggaagg tgatactgta caaattattt gcaacacagg
 801  atacagcctt caaaacaatg agaaaaacat ttcgtgtgta gaacggggct ggtccactcc tcccatatgc agcttcacta aaggagaatg tcatgttcca
 901  attttagaag ccaatgtaga tgctcagcca aaaaaagaaa gctacaaagt tggagacgtg ttgaaattct cctgcagaaa aaatcttata agagttggat
1001  cagactcagt tcaatgttac caatttgggt ggtcacctaa ctttccaaca tgcaaaggac aagtacgatc atgtggtcca cctcctcaac tctccaatgg
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1201  tgtgtggatg gagaatggac aactttaccc acttgtgttg aacaagtgaa aacatgtgga tacatacctg aactcgagta cggttatgtt cagccgtctg
1301  tccctcccta tcaacatgga gtttcagtcg aggtgaattg cagaaatgaa tatgcaatga ttggaaataa catgattacc tgtattaatg gaatatggac
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1801  ccccctccat ctattaacaa tggagatacc acctcattcc cattatcagt atatcctcca gggtcaacag tgacgtaccg ttgccagtcc ttctataaac
1901  tccagggctc tgtaactgta acatgcagaa ataaacagtg gtcagaacca ccaagatgcc tagatccatg tgtggtatct gaagaaaaca tgaacaaaaa
2001  taacatacag ttaaaatgga gaaacgatgg aaaactctat gcaaaaacag gggatgctgt tgaattccag tgtaaattcc cacataaagc gatgatatca
2101  tcaccaccat ttcgagcaat ctgtcaggaa gggaaatttg aatatcctat atgtgaataa aggcgcgcca gtatactcta gagtcgacac ccggggaatt
2201  cctcgagcgc tcgtctctag cttggcgtaa tcatggtcat agctgtttcc tgtgtgaaat tgttatccgc tcacaattcc acacaacata cgagccggaa
2301  gcataaagtg taaagcctgg ggtgcctaat gagtgagcta actcacatta attgcgttgc gctcactgcc cgctttccag tcgggaaacc tgtcgtgcca
2401  gctgcattaa tgaatcggcc aacgcgcggg gagaggcggt ttgcgtattg ggcgctcttc cgcttcctcg ctcactgact cgctgcgctc ggtcgttcgg
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> RDC3334 Translated Insert Sequence

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 201  ckgqvrscgp ppqlsngevk eirkeeyghn evveydcnpn fiingpkkiq cvdgewttlp tcveqvktcg yipeleygyv qpsvppyqhg vsvevncrne
 301  yamignnmit cingiwtelp mcvathqlkr ckiagvnikt llklsgkefn hnsriryrcs difryrhsvc ingkwnpevd ctekreqfcp pppqipnaqn
 401  mtttvnyqdg ekvavlcken yllpeakeiv ckdgrwqslp rcvestaycg pppsinngdt tsfplsvypp gstvtyrcqs fyklqgsvtv tcrnkqwsep
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