

Division of Signal Transduction Therapy

Clone Data Sheet

PRKG1 isoform 1 [1 - 671]

Protein PRKG1 isoform 1 [1 - 671]

Clone number DU 26299

Species Human

Accession number NM_001098512.2

Tags N-terminal His6

**Baculovirus
expressed protein**

MSYYHHHHHDYDIPTTENLYFQGAMGSMSELEEDFAKILMLKEERIK
ELEKRLSEKEEEIQELKRKLHKCQSVLPVPSTHIGPRTRRAQGISAEP
QTYRSFHDLRQAFRKFTKRSERKDLIKEAILDNDFMKNLELSQIQEIV
DCMYPVEYGKDSCIKEGDVGLVYVMEDGKVEVTKEGVKLCMTGPGK
VFGELAILYNCTRATVKTLVNVKLWAIDRQCFQTIMMRTGLIKHTEY
MEFLKSVPTFQSLPEEILSKLADVLEETHYENGEYIIRQGARGDTFFI
ISKGTVNVTREDSPSEDPVFLRTLKGKDFGGEKALQGEDVRTANVIAA
EAVTCLVIDRDSFKHLIGGLDDVSNKAYEDAEAKAKYEAAFFANLK
LSDFNIIDTLGVGGFGRVELVQLKSEESKTFAMKILKKRHIVDTRQOE
HIRSEKQIMQGAHSDFIVRLYRTFKDSKYLYLMEACLGELWTILRD
RGSFEDSTTRFYTACVVEAFAYLHSGI IYRDLKPENLILDHRGYAKL
VDFGFAKKIGFGKKTWTFCTPEYVAPEIILNKGHDISADYWSLGILM
YELLTGSPPFSGPDPMKTYNIILRGIDMIEFPKKIAKNAANLIKLCR
DNPSERLGNLKNVVDIQKHKWFEGFNWEGLRKGTLTPPIIPSVASPT
DTSNFDSFPEDNDEPPDDNSGWDIDF

Native sequence Amino acids M1 – F671 (end) of human PRKG1.

Residue M29 of the fusion protein is equivalent to M1 of the native enzyme. The His6 tag is located at residues 5 – 10.

Protease cleavage rTEV (ENLYFQG) residues 18 – 24

Cloning sites *Bam*H1 and *Not*I sites of pFastBac HTb

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Nucleotide sequence of insert

ggatccATGAGCGAGCTAGAGGAAGACTTTGCCAAGATTCTCATGCTC
AAGGAGGAGAGGATCAAAGAGCTGGAGAAGCGGCTGTCAGAGAAGGAG
GAAGAAATTCAGGAGCTGAAGAGGAAACTCCACAAATGCCAGTCGGTG
CTCCAGTGCCCTCGACCCACATCGGCCCCCGGACCACCCGGGCGCAG
GGCATCTCGGCCGAGCCGCAGACGTACAGGTCTTCCACGACCTCCGA
CAGGCATTCGGAAGTTCACCAAGTCCGAAAGGTCCAAGGATCTTATA
AAGGAAGCTATCCTTGACAATGACTTTTATGAAGAAGTTGGAGCTGTCC
CAGATCCAGGAGATTGTGGATTGTATGTACCCGGTGGAGTATGGCAAG
GACAGTTGCATCATCAAAGAAGGAGACGTGGGGTCACTGGTGTATGTC
ATGGAAGATGGTAAGGTTGAAGTTACAAAAGAAGGTGTGAAGTTGTGT
ACCATGGGTCCAGGAAAAGTGTGGGGAAATTGGCTATTCTTTACAAC
TGTACCCGGACAGCGACCGTCAAGACTCTTGTAATGTAAAACCTCTGG
GCCATTGATCGACAATGTTTTCAAACAATAATGATGAGGACAGGACTC
ATCAAGCATAACCGAGTATATGGAATTTTTAAAAAGCGTTCCAACATTC
CAGAGCCTTCCTGAAGAGATCCTCAGCAAGCTTGCTGATGTCTTGAA
GAGACCCACTATGAAAATGGAGAATATATTATCAGGCAAGGTGCAAGA
GGGACACCTTCTTTATCATCAGCAAAGGAACGGTAAATGTCACCTCGT
GAAGACTCACCGAGTGAAGACCCAGTCTTCTTAGAAGCTTTAGGAAAA
GGAGACTGGTTTTGGAGAGAAAGCCTTGCAGGGGAAGATGTGAGAACA
GCAAACGTAATTGCTGCAGAAGCTGTAACCTGCCTTGTGATTGACAGA
GACTCTTTTAAACATTTGATTGGAGGGCTGGATGATGTTTCTAATAAA
GCATATGAAGATGCAGAAGCTAAAGCAAATATGAAGCTGAAGCGGCT
TTCTTCGCCAACCTGAAGCTGTCTGATTTCAACATCATTGATACCCTT
GGAGTTGGAGGTTTCGGACGAGTAGAACTGGTCCAGTTGAAAAGTGAA
GAATCCAAAACGTTTGCAATGAAGATTCTCAAGAAACGTCACATTGTG
GACACAAGACAGCAGGAGCACATCCGCTCAGAGAAGCAGATCATGCAG
GGGCTCATTCCGATTTCATAGTGAGACTGTACAGAACATTTAAGGAC
AGCAAATATTTGTATATGTTGATGGAAGCTTGTCTAGGTGGAGAGCTC
TGGACCATTCTCAGGGATAGAGGTTTCGTTTGAAGATTCTACAACCAGA
TTTTACACAGCATGTGTGGTAGAAGCTTTTGCCTATCTGCATTCCAAA
GGAATCATTTACAGGGACCTCAAGCCAGAAAATCTCATCCTAGATCAC
CGAGGTTATGCCAAACTGGTTGATTTTGGCTTTGCAAAGAAAATAGGA
TTTGAAAGAAAACATGGACTTTTTGTGGGACTCCAGAGTATGTAGCC
CCAGAGATCATCCTGAACAAAGGCCATGACATTTAGCCGACTACTGG
TCACTGGGAATCCTAATGTATGAACTCCTGACTGGCAGCCACCTTTC
TCAGGCCCAGATCCTATGAAAACCTATAACATCATATTGAGGGGGATT
GACATGATAGAATTTCAAAGAAGATTGCCAAAATGCTGCTAATTTA
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AACTGGGAAGGCTTAAGAAAAGGTACCTTGACACCTCCTATAATACCA
AGTGTTCATCACCCACAGACACAAGTAATTTTGACAGTTTCCCTGAG
GACAACGATGAACCACCACCTGATGACAACTCAGGATGGGATATAGAC
TTCTaagcggccgc