

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of active Diacylglycerol Kinase Gamma [1 – 752]

<u>Enzyme description:-</u>	DGK gamma [1 – 752]
<u>Clone number:-</u>	DU 63057
<u>Source:-</u>	Recombinant
<u>Expression system:-</u>	Baculovirus Expression Vector System
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH Sepharose

Calculated molecular mass:-

Monoisotopic 112, 078.89 daltons
Average Mass 112, 151.66 daltons
[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.97

Purity:- >80 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA,
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

Storage temperature:- -70 °C

Assay: ADP Glo

Assay buffer:-

20 mM Tris-HCl, 67 mM KCl, 1 mM DTT, 0.05 mg/ml BSA, 10 mM MgCl₂

Substrate:-

Diacylglycerol Final concentration: 0.1 mM

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Clone Data Sheet

DGK gamma [1 – 752]

Protein DGK gamma [1 – 752]

Clone number DU 63057

Species Human

Accession number BC112363

Tags N-terminal GST

Baculovirus expressed protein

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG
LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAETSMLEGA
VLDIRYGVSR IAYS KDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS
KYIAWPLQGWQATFGGGDHPPKSDLEVLVLFQGPLGSPEFPGRL**MGEERWV**
SLTPEEFDQLQKYSEYSSKKIKDALTEFNEGGSLKQYDPHEPISYDVFK
LFMRAYLEVDLPQPLSTHLFLAFSOKPRHETS DHPTEGASNSEANSADT
NIQNADNATKADEACAPD TESNMAEKQAPAEDQVAASPLEPPVPRSSSS
ESPVVYLKDVVCYLSLLETGRPQDKLEFMFRLYSDENGLLDQAEMDCI
VNQMLHIAQYLEWDPTTEL RPILKEMLOGMDYDRDGFVSLQEWVHGGMTT
IPLLVLLGMDDSGSKGDGRHAWTMKHF KPTYCNFCHIMLMGVRKQGLC
CTYCKYTVHERCVSKNIPGCVKTYSKAKRSGEFHRKCELSTLCDGGELR
DHILLPTSICPITRDRPGEKSDGCVSAK GELVMQYKI IPTPGTHPLLVL
VNPKSGGRQGERILRKFHYLLNPKQVFNLDNNGGTPGLNFFRDTPDFRV
LACGGDGTVGWILDCIDKANFAKHPPVAVLPLGTGNDLARCLRWGGGYE
GGSLTKILKDIEQSPLVMLDRWHLEVIPREEVENGQVPYSIMNNYFSI
GVDASIAHRFHV MREKHPEKFN SRMKNKLWYFEFGTSETFAATCKKLHD
HIELECDGVGVDLSNIFLEGIAILNIPSMYGGTNLWGENKKNRAVIRE S
RKGVTDPKELKFCVQDLS DQLLEVVGLEGAMEMGOIY TGLKSAGRRLAQ
CASVTIRTNKLLPMQVDGEPWMQPCCTIKITHKNQAPMMMGPPQKSSFF
SLRRKSRSKD

Native sequence Amino acids M1 – D752 (end) of human DGK gamma.
Residue M239 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage PreScission (LEVLVFGQP) residues 221 - 228

Cloning sites *Sal*1 + 2/*Hind*III sites into pFastBacDual GST

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Nucleotide Sequence of Insert:

gtcgactcATGGGTGAAGAACGGTGGGTCTCCCTCACTCCAGAAGAATTTGACCAACTCCAGAAAT
ATTCAGAATATTCCTCCAAGAAGATAAAAGATGCCTTGACTGAATTTAATGAGGGTGGGAGCCTCA
ACAATATGACCACATGAGCCGATTAGCTATGATGTCTTCAAGCTGTTTCATGAGGGCGTACCTAG
AGGTGGACCTTCCCAGCCACTGAGCACTCACCTCTTCTGGCCTTCAGCCAGAAGCCCAGACACG
AGACCTCTGACCACCCGACGGAGGGAGCCAGCAACAGTGAGGCCAACAGCGCAGATACTAATATAC
AGAATGCAGATAATGCCACCAAAGCAGACGAGGCCTGTGCCCTGATACTGAATCAAATATGGCTG
AGAAGCAAGCACCAGCTGAAGACCAAGTGGCTGCGAGCCCCCTGGAACCCCCCGTCCCTCGGTCTT
CAAGCTCGGAATCCCCAGTGGTGTACCTGAAGGATGTTGTGTGCTACCTGTCCCTGCTGGAGACGG
GGAGGCCCTCAGGATAAGCTGGAGTTCATGTTTCGCCTCTATGATTCAGATGAGAACGGTCTCCTGG
ACCAAGCGGAGATGGATTGCATTGTCAACCAAATGCTGCATATTGCCAGTACCTGGAGTGGGATC
CCACAGAGCTGAGGCCTATATTGAAGGAGATGCTGCAAGGGATGGACTACGACCGGGACGGCTTTG
TGTCTCTACAGGAATGGGTCCATGGAGGGATGACCACCATCCATTGCTGGTCTCTGGGGATGG
ATGACTCTGGCTCCAAGGGGGATGGGCGGCACGCCTGGACCATGAAGCACTTCAAGAAACCAACCT
ACTGCAACTTCTGCCATATCATGCTCATGGGCGTCCGCAAGCAAGGCCTGTGCTGCACTTACTGTA
AATACTGTCCACGAACGCTGTGTGTCCAAAAACATTCCTGGTTGTGTCAAAACGTACTCAAAAG
CCAAAAGGAGTGGTGAGTTTCACCGCAAATGTGAATTATCAACGTTGTGTGACGGTGGGGAACCTCA
GAGACCACATCTTACTGCCACCTCCATATGCCCATCACCCGGGACAGGCCAGGTGAGAAGTCTG
ATGGCTGCGTGTCCGCCAAGGGCGAACTTGTTCATGCAGTATAAGATCATCCCCACCCGGGTACCC
ACCCCTGTCTGGTCTTGGTGAACCCCAAGAGTGGAGGGAGACAAGGAGAAAGAATTCCTCGGAAAT
TCCACTATCTGCTCAACCCCAAACAAGTTTTCAACCTGGACAATGGGGGGCTACTCCAGGGTTGA
ACTTTTTCCGTGATACTCCAGACTTCCGTGTTTTGGCCTGTGGTGGAGATGGGACAGTTGGCTGGA
TTTTGGATTGCATTGATAAGGCCAACTTTGCAAAGCATCCACCAGTGGCTGTCCTGCCTCTTGAA
CAGGAAATGACCTTGCCCGTTGTCTCCGCTGGGGAGGAGGTTATGAAGGGGGCAGCTTGACAAAAA
TCCTGAAAGACATTGAGCAGAGCCCCTTGGTGATGCTGGACCGCTGGCATCTGGAAGTCATCCCCA
GAGAGGAAGTGGAAAACGGGGACCAGGTCCCATACAGCATCATGAACAACATTTCTCCATTGGTG
TGGACGCTTCCATTGCACACAGATTCCATGTGATGAGAGAGAAACATCCTGAAAAATCAACAGCA
GGATGAAGAACAAGCTGTGGTACTTTGAATTTGGCACCTCGGAGACTTTTGCAGCGACCTGCAAGA
AACTCCACGACCACATTGAGTTGGAGTGTGATGGGGTGGGGTGGACCTGAGCAACATCTTCTGG
AAGGCATTGCCATTCTCAACATTCACAGCATGTACGGAGGCACCAATCTCTGGGGAGAAAACAAGA
AGAACCGGGCTGTGATCCGGGAAAGCAGGAAGGGTGTCACTGACCCCAAAGAACTGAAATTCGCG
TTCAAGACCTCAGTGACCAGCTCCTTGAAGTGGTGGGGCTAGAAGGAGCCATGGAGATGGGGCAGA
TCTACACCGGCTGAAGAGTGCAGGCAGGAGGCTGGCCAGTGCGCCCTGTGACCATCAGGACAA
ACAAGCTGCTGCCAATGCAAGTGGATGGAGAACCCTGGATGCAGCCATGTTGCACGATTAATAATTA
CTCACAAGAACCAAGCGCCCATGATGATGGGGCCTCCCAGAAGAGCAGCTTCTTCTCGTTGAGAA
GGAAGAGCCGTTCAAAAGACTaagct

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