Certificate of Analysis
KIT V559D, 10 µg

Recombinant human KIT V559D (544-end) expressed in insect cells

Part Number: A30497
Lot Number: 1861431
Immediate Storage: -80°C
Shipping Conditions: dry ice

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Description:

Recombinant human KIT V559D (544-end) was expressed in insect cells using a N−terminal GST tag.

KIT is a proto-oncogene and a type 3 transmembrane receptor for MGF (mast cell growth factor, also known as stem cell factor). KIT was first identified as the cellular homolog of the feline sarcoma viral oncogene v-kit. KIT together with its ligand regulates growth and activation of a variety of hemopoietic and non-hemopoietic cells. Mutations in KIT are associated with gastrointestinal stromal tumors, mast cell disease, acute myelogenous lukemia, and piebaldism. Recently, deregulation of the KIT receptor TK by the prevalent activation loop mutation D816V has served as a focal point in therapeutic strategies aimed at curbing neoplastic mast cell growth.

Accession Number:

The gene accession number for KIT V559D is NP_000213.1.

Specific Activity:

52 nmoles of phosphate transferred to poly [Glu, Tyr] 4:1 substrate per minute per mg of total protein at 30°C.

Concentration:

0.1 mg/mL total protein as measured using the Bradford protein assay with BSA as a standard.

Calculated **1,330 nM**.

Aliases:

PBT, SCFR, CD117

Storage and Handling:

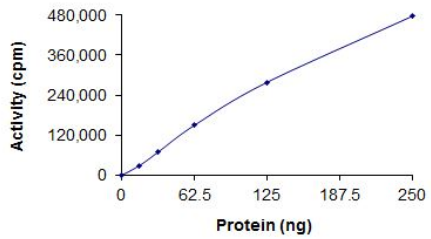
For maximum recovery please spin prior to use. Unless noted below, aliquots of the 5 ug, 10ug and 20ug sizes of kinase are not recommended as materials can be used in original packaging until exhausted. For larger sizes, the number of freeze/thaws may be reduced by preparing aliquots, aliquots below 20 µL are not recommended. **Please never store a kinase diluted.** If properly stored at −80°C, this product is guaranteed for 6 months from date of purchase.

Storage Buffer:

50 mM Tris-HCl (pH 7.5), 150 mM NaCl, 10 mM glutathione, 0.1 mM EDTA, 0.25 mM DTT, 0.1mM PMSF and 25% Glycerol.

QUALITY ASSURANCE

KIT V559D Activity Graph



Dilution Buffer:

5 mM MOPS (pH 7.2), 2.5 mM β−glycerol−phosphate, 4 mM $MgCl_2$, 2.5 mM $MnCl_2$, 1 mM EGTA and 0.4 mM EDTA, 0.05 mM DTT and 50 ng/µL BSA.

Assay Conditions:

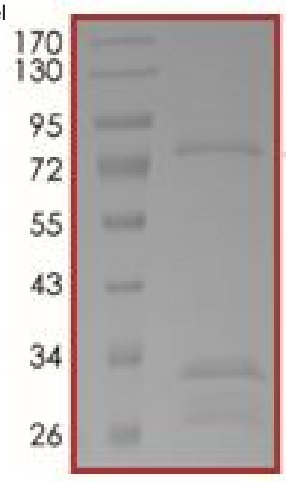
KIT V559D was pre-diluted in enzyme dilution buffer and assayed in 5 mM MOPS (pH 7.2), 2.5 mM β−glycerol-phosphate, 4 mM $MgCl_2$, 2.5 mM $MnCl_2$, 0.4 mM EDTA, 1 mM EGTA, 0.05 mM DTT, with 50 µM ATP, trace [^{33}P]-γ-ATP and 200 µg/mL poly [Glu, Tyr] 4:1 substrate for 15 minutes at 30°C.

Gel Information for KIT V559D

Page Description: Run on an SDS-PAGE gel and stained with Coomassie®.

Lane 1: Molecular Weight markers as labeled.

Lane 2: KIT V559D



Purity:

> 70% as determined by a Coomassie® blue stained SDS-PAGE gel.

Molecular Weight:

75.3 kDa. Calculated from the protein sequence(s).

Protein sequence alignment with reference sequence(s)

GenBank Accession Number: NP_000213.1

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  1 MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL GST
  1 MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL Life KIT V559D
  1 ------------------------------------------------------------------------------------------------------ NP_000213.1

101 DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIA
101 DIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIA
  1 ----------------------------------------------------------------------------------------------------

201 WPLQGWQATFGGGDHPPKSD
201 WPLQGWQATFGGGDHPPKSDLVPRGSTYKYLQKPMYEVQWKDVEEINGNNYVYIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAA
  1 --------------------------TYKYLQKPMYEVQWKVVEEINGNNYVYIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAA

220
301 MTVAVKMLKPSAHLTEREALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQEDHAEAALYKNLLHSKESSCSDS
 75 MTVAVKMLKPSAHLTEREALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQEDHAEAALYKNLLHSKESSCSDS

220
401 TNEYMDMKPGVSYVVPTKADKRRSVRIGSYIERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLAARNILLTHGRITKICDFGLARDI
175 TNEYMDMKPGVSYVVPTKADKRRSVRIGSYIERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLAARNILLTHGRITKICDFGLARDI

220
501 KNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKRPTF
275 KNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKRPTF

220
601 KQIVQLIEKQISESTNHIYSNLANCSPNRQKPVVDHSVRINSVGSTASSSQPLLVHDDV
375 KQIVQLIEKQISESTNHIYSNLANCSPNRQKPVVDHSVRINSVGSTASSSQPLLVHDDV
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* highlighted residues denote differences from the reference protein sequence(s).

Nichole Reaksecker Date: 05/Jan/2017