

KIT V654A

v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog

Recombinant Human Active Protein Kinase

HGNC Symbol: KIT

Synonyms: CD117, PBT, SCFR, c-Kit

Product No.: 0947-0000-1

Lot: 005

Description: Human KIT, C-terminal fragment, amino acids T₅₄₄-V₉₇₆ (as in NCBI/Protein entry NP_000213.1) with a V654A mutation, N-terminal GST-HIS₆ fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: KIT V654A Lot 005 was confirmed as KIT by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 77,429 Da

Expression: Baculovirus infected Sf9 cells

Purification: GST-Affinity Chromatography

Activation: in vitro autoactivation

Storage buffer: 50 mM HEPES pH 7.5, 100 mM NaCl, 5 mM DTT, 15 mM reduced glutathione, 20% glycerol

Storage temperature: -80°C

For complete recovery, mix well and spin before use. Product must not be stored in diluted solutions, aliquots below 10µl are not advisable. Avoid repeated freeze-thaw cycles!

Protein concentration: 0.077 µg/µl

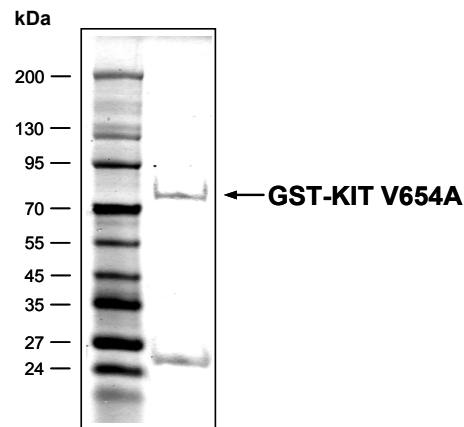
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

Specific kinase activity (P_i transfer): 8 pmol/µg×min

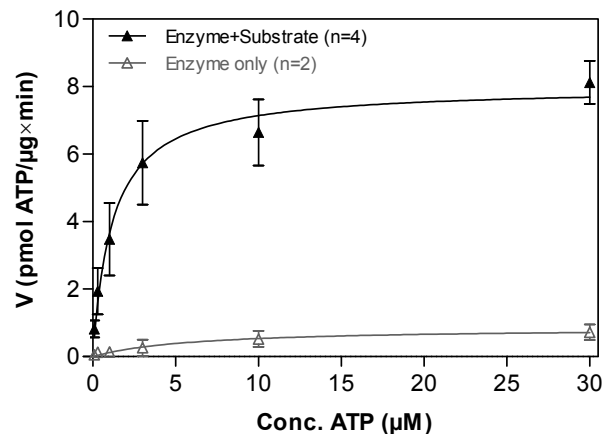
ATP-K_M: 1.0 µM

KIT V654A Lot 005: Coomassie stain



2.0 µg GST-KIT V654A

KIT V654A Lot 005: Determination of V_{max} and K_M value for ATP



Determination of K_M value & Specific activity:

- Assay conditions:
 - 60 mM HEPES-NaOH, pH 7.5
 - 3 mM MgCl₂
 - 3 mM MnCl₂
 - 3 µM Na-orthovanadate
 - 1.2 mM DTT
 - 50 µg / ml PEG_{20,000}
 - ATP (variable)
 - Substrate: TRK-C-derived peptide, 80 µg/ml
 - KIT V654A: 4.0 µg/ml
- Filter binding assay
 - MSPH membrane (Millipore)

Additional assay technology: KIT V654A Lot 005

was also successfully tested by ProQinase for the use with the ADP-Glo™ Kinase assay from Promega. ADP-Glo assay conditions may vary from radiometric assay conditions, please inquire for assay details



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KIT V654A Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPOID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHGG	RDSLEVLFGQ	240
241	PLAMGTYKYL	QKPMYEVQWK	VVEEINGNNY	VYIDPTQLPY	DHKWEFPRNR	LSFGKTLGAG	300
301	AFGKVVVEATA	YGLIKSDAAM	TVAVKMLKPS	AHLTEREALM	SELKVLVSYLG	NHMNIANLLG	360
361	ACTIGGPTLV	ITEYCCYGDL	LNFLRRKRDS	FICSKQEDHA	EAALYKNLLH	SKESSCSDST	420
421	NEYMDMKPGV	SYVVPKADK	RRSVRIGSYI	ERDVTPAIME	DDELALDLED	LLSFSYQVAK	480
481	GMAFLASKNC	IHRDLAARNI	LLTHGRITKI	CDFGLARDIK	NDSNYVVKGN	ARLPVKWMAP	540
541	ESIFNCVYTF	ESDVWSYGIF	LWELFSLGSS	PYPGMPVDSK	FYKMIKEGFR	MLSPEHAPAE	600
601	MYDIMKTCWD	PLKRPTFKQI	QIVQLIEKQI	SESTNHIYSN	LANCSPNRQK	PVVDHSVRIN	660
661	SVGSTASSSQ	PLLHDDV					720

1-218: GST **Red**: HIS6-tag **Green**: 3C cleavage site **blue**:KIT fragment **A**: V654A mutation

KIT wt ¹ amino acid sequence							
1	MARGAWDF	LCVLLLLLRV	QTGSSQPSVS	PGEPSPPSIH	PGKSDLIVRV	GDEIRLLCTD	60
61	PGFVKWTFEI	LDETENKQN	EWITEKAEAT	NTGKYTCTNK	HGLSNSIYVF	VRDPAKLFLV	120
121	DRSLYGKEDN	DTLVRCPLTD	PEVTNYSLKG	CQGKPLPKDL	RFIPDPKAGI	MIKSVKRAYH	180
181	RLCLHCSVDQ	EGKSVLSEKF	ILKVRPAFKA	VPVSVSKAS	YLLREGEEFT	VTCTIKDVSS	240
241	SVYSTWKREN	SQTKLQEKYN	SWHHGDFNYE	RQATLTISSA	RVNDSGVFMC	YANNTFGSAN	300
301	VTTTLEVVDK	GFINIFPMIN	TTVFVNDGEN	VDLIVEYEAF	PKPEHQWYI	MNRTFTDKWE	360
361	DYPKSENESEN	IRYVSELHLT	RLKGTEGGTY	TFLVNSSDVN	AAIAFNIVVN	TKPEILTYDR	420
421	LVNGMLQCVA	AGFPEPTIDW	YFCPGTEQRC	SASVLPVDVQ	TLNSSGPPFG	KLVVQSSIDS	480
481	SAFKHNGTVE	CKAYNDVGKT	SAYFNFAFKG	NNKEQIHPHT	LFTPLLIGFV	IVAGMMCIIV	540
541	MILTYKYLQK	PMYEVQWKV	EEINGNNYVY	IDPTQLPYDH	KWEFPRNRLS	FGKTLGAGAF	600
600	GKVVVEATAYG	LIKSDAAMTV	AVKMLKPSAH	LTEREALMSE	LKVLVSYLGNH	MNI ^V NLLGAC	660
661	TIGGPTLVIT	EYCCYGDLLN	FLRRKRDSFI	CSKQEDHAEA	ALYKNLLHSK	ESSCSDSTNE	720
721	YMDMKPGVSY	VVPTKADKRR	SVRIGSYIER	DVTPAIMEED	ELALDLEDLL	SFSYQVAKGM	780
781	AFLASKNCIH	RDLAARNILL	THGRITKICD	FGLARDIKND	SNYVVKGNAR	LPVKWMAPES	840
841	IFNCVYTFES	DVWSYGIFLW	ELFSLGSSPY	PGMPVDSKPY	KMIKEGFRML	SPEHAPAEMY	900
901	DIMKTCWDAD	PLKRPTFKQI	VQLIEKQISE	STNHIYSNLA	NCSPNRQKPV	VDHSVRINSV	960
961	GSTASSOPL	LHDDV					1020

bold letters: expressed part of KIT **RED** letters: variant in Fusionprotein

¹NCBI/Protein accession number NP_000213.1