

BTK

Bruton tyrosine kinase

Recombinant Human Active Protein Kinase

HGNC Symbol: BTK

Synonyms: AGMX1; AT; ATK; BPK; PSCTK1

Product No.: 0772-0000-2

Lot: 009

Description: Human BTK, full length, amino acids M₁-S₆₅₉ (as in [NCBI/Protein](#) entry NP_000052.1), N-terminal GST-HIS₆ fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: BTK Lot 009, was confirmed as BTK by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 104,766 Da

Expression host: Sf9 insect cells

Purification: GST-Affinity Chromatography

Activation: This kinase was not activated by special procedures

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

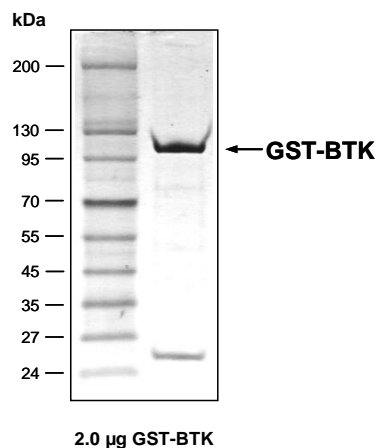
Biochemical Parameters:

Specific kinase activity (P_i transfer): 33 pmol/µg × min
ATP-K_M: 20 µM

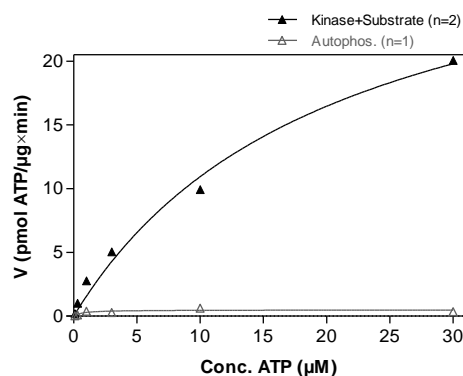
Additional assay technology:

BTK Lot 009 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

BTK Lot 009: Coomassie stain



BTK Lot 009: Determination of V_{max} and K_M value for ATP



- 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, 40 µg/ml
Kinase: 2 µg/ml
- Filter binding assay
MSPH membrane (Millipore)

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GST-BTK Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPIQID	KYLKSSKYIA	WPLQGWAQATF	GGGDHPPKSD	PMG HHHHHG	RDS LEVLFGQ	240
241	PLAMLMAAVI	LESIFLKRSQ	QKKKTSPLNF	KKRLFLLTVH	KLSYIEYDFE	RGRGSKKGS	300
301	IDVEKITCVE	TVVPEKNPPP	ERQIPRRGEE	SSEMEQISII	ERFPYPFQVV	YDEGPLYVFS	360
361	PTEELRKRWI	HQLKNVIRYN	SDLVQKYHPC	FWIDGQYLCC	SQTAKNAMGC	QILENRNGSL	420
421	KPGSSHRKTK	KPLPPTPEED	QILKKPLPPE	PAAAPVSTSE	LKKVVALYDY	MPMNANDLQL	480
481	RKGDEYFILE	ESNLPWWRAR	DKNGQEGYIP	SNYVTEAEDS	IEMYEWYSKH	MTRSQAQQLL	540
541	KQEGKEGGFI	VRDSSKAGKY	TVSVFAKSTG	DPQGVIRHYV	VCSTPQSQYY	LAEKHLFSTI	600
600	PELINYHQHN	SAGPISRLKY	PVSQQNKNAP	STAGLGYGSW	EIDPKDLTFL	KELGTGQFGV	660
661	VKYGKWRGQY	DVAIKMIKEG	SMSSEDEFIEE	AKVMMNLSHE	KLVQLYGVCT	KQRPIFIITE	720
721	YMANGCLLNY	LREMRHRFQT	QQLLEMCKDV	CEAMEYLESK	QFLHRDLAAR	NCLVNDQGVV	780
781	KVSDFGLSRY	VLDDEYTSSV	GSKFPVRWSP	PEVLMSYKFS	SKSDIWAQGV	LMWEIYSLGK	840
841	IPYERFTNSE	TAEHIAQGLR	LYRPHLASEK	VYTIMYSCWH	EKADERPTFK	ILLSNILDVM	900
901	DEES						960

1-218: GST **Red**: HIS6-tag **Green**: 3C cleavage site **blue**: BTK **boxed**: variation from RefSeq

BTK wt ¹ Amino Acid Sequence							
1	MAAVILESIF	LKRSQQKKKT	SPLNFKKRLF	LLTVHKLSYY	EYDFERGRRG	SKKGSIDVEK	60
61	ITCVETVPE	KNPPPERQIP	RRGEESSEME	QISIIERFPY	PFQVVYDEGP	LYVFSPTTEL	120
121	RKRWIHQKN	VIRYNSDLVQ	KYHPCFWIDG	QYLCCSQTAK	NAMGCQILEN	RNGSLKPGSS	180
181	HRKTKKPLPP	TPEEDQILKK	PLPPEPAAAP	VSTSELKKVV	ALYDYMPMNA	NDLQLRKGDE	240
241	YFILEESNLP	WWRARDKNGQ	EGYIPSNYVT	EAEDSIEMYE	WYSKHMTRSQ	AEQLLKQEGK	300
301	EGGFIVRDSS	KAGKYTVSVF	AKSTGDPQGV	IRHYVVCSTP	QSQYYLAEKH	LFSTIPELIN	360
361	YHQHNSAGLI	SRLKYPVSQQ	NKNAPSTAGL	GYGSWEIDPK	DLTFLKELGT	GQFGVVKYGK	420
421	WRQYDVAIK	MIKEGSMSSE	EFIEEAKVMM	NLSHEKLVQL	YGVCTKQRP	FIITEYMANG	480
481	CLLNYLREMR	HRFQTQQLLE	MCKDVCEAME	YLESKQFLHR	DLAARNCLVN	DQGVVKVSDF	540
541	GLSRYVLDDE	YTSSVGSKFP	VRWSPPEVLM	YSKFSSKSDI	WAFGLVMWEI	YSLGKMPYER	600
600	FTNSETAEHI	AQGLRLYRPH	LASEKVYTIM	YSCWHEKADE	RPTFKILLSN	ILDVMDEES	660

blue: BTK sequence expressed in recombinant protein **Red**: variant in recombinant protein

¹[NCBI/Protein](https://www.ncbi.nlm.nih.gov/protein/NP_000052.1) accession number NP_000052.1

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