

ProQinase™ TTBK1 aa1-1321

tau tubulin kinase1

Recombinant Human Active Protein Kinase

HGNC Symbol: TTBK1

Synonyms: BDTK, KIAA1855

Product No.: 1358-0000-1

Lot: 013

Description: Human TTBK1, full length, amino acids M₁-R₁₃₂₁ (as in [NCBI/Protein](#) entry NP_115927.1), N-terminal GST-HIS₆ fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: TTBK1 Lot 013, was confirmed as TTBK1 by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 170,822 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, 15 mM GSH, 5 mM DTT, 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: 0.377 µg/µl

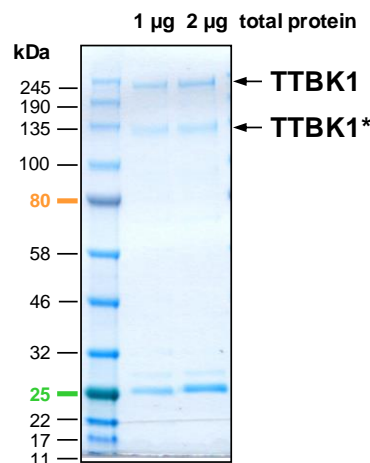
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

Specific kinase activity (P_i transfer): 4 pmol/µg × min

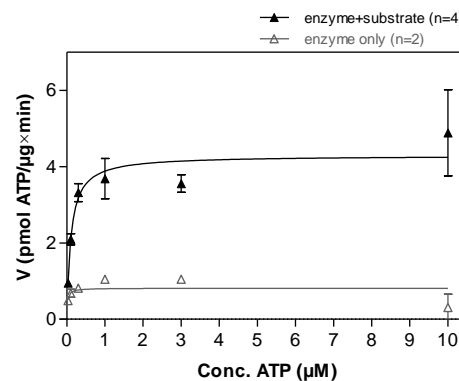
ATP-K_M: 0.1 µM

TTBK1 Lot 013: Coomassie stain



*Unusual running behaviour, with a proteolytic by-product described by: Sato et al; "Tau-tubulin kinase 1 (TTBK1), a neuron-specific tau kinase candidate, is involved in tau phosphorylation and aggregation." J Neurochem. 2006 Sep;98(5):1573-84

TTBK1 Lot 013: 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: GSK3(14-27)tide, 5 µg/ml
 - TTBK1: 1 µg/ml
- Filter binding assay
 - MSIP membrane (Millipore)

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GST-TTBK1 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPPE	KMFKDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHG	RDSLEVLFGQ	240
241	PMQCLAAALK	DETNSGGGE	QADILPANYV	VKDRWKVLKK	IGGGGFGEIY	EAMDLLTREN	300
301	VALKVESAQ	PKQVLKMEVA	VLKKLQKDH	VCRFIGCGRN	EKFNYVVMQL	QGRNLADLRR	360
361	SQPRGFTTLS	TTLRLGKQIL	ESIEAIHSVG	FLHRDIKPSN	FAMGRLPSTY	RKCYMLDFGL	420
421	ARQYTNNTGD	VRPPRNVAGF	RGTVRYASVN	AHKNREMGRH	DDLWSLFYML	VEFAVGQLPW	480
481	RKIKDKQVQ	MIKEYEHRM	LLKHPSEFHL	LFLDHIASLD	YFTKPDYQLI	MSVFENSMKE	540
541	RGIAENEAFD	WEKAGTDALL	STSTSTPPQQ	NTRQTAAMFG	VVNVTVPVGD	LLRENTEDVL	600
601	QGEHLSQEN	APPILPGRPS	EGLGSPHPLV	PHPGGPEAEV	WEETDVNRNK	LRINIGKSPC	660
661	VEEQSRGMG	VPSSPVRAPP	DSPTTPVRS	RYRVNSPES	ERLSTADGRV	ELPERRSRMD	720
721	LPGSPSRQAC	SSQPAQMLSV	DTGHADROAS	GRMDVSASVE	QEALSNAFRS	VPLAEEEDFD	780
781	SKEWIIDKE	TELKDFPPGA	EPSTSGTTDE	EPEELRPLPE	EGEERRRLLGA	EPTVRPRGRS	840
841	MQALAEEDLQ	HLPPQPLPPQ	LSQGDGRSET	SQPPTPGSPS	HSPLHSGPRP	RRRESDPTGP	900
901	QRQVFSVAPP	FEVNGLPRAV	PLSLPYQDFK	RDLSDYRERA	RLLNRVRRVG	FSHMLLTTPQ	960
961	VPLAPVQPQA	NGKEEEEEEE	EDEEEEEED	EEEEEEEEEE	EEEEEEEEEE	EEAAAVALG	1020
1021	EVLGPRSGSS	SEGSESTDR	SQEGAPSTLL	ADDQKESRGR	ASMADGDLEP	EEGSKTLVLV	1080
1081	SPGDMKSPV	TAELADPDDL	GTLAALTPQH	ERPQITGSQL	DVSEPGTLSS	VLKSEPKPPG	1140
1141	PGAGLGAGTV	TGTGGVAVT	SSPFTKVERT	FVHIAEKTHL	NVMSSGGQAL	RSEEFSSAGE	1200
1201	LGLELASDGG	AVEEGARAPL	ENGLALSGLN	GAEIEGSALS	GAPRETPSEM	ATNSLPNGPA	1260
1261	LADGPAPVSP	LEPSPEKVAT	ISPRRHAMP	SRPRSRIPLV	LSEEDTGSEP	SGLSAKERW	1320
1321	SKRARPQDL	ARLVMEKRQG	RLLRLASGA	SSSSSEEQRR	ASETLSGTGS	EEDTPASEPA	1380
1381	AALPRKSGRA	AATRSRIPRP	IGLRMPMPVA	AQQPASRSHG	AAPALDTAIT	SRLQLQTPPG	1440
1441	SATAADLRPK	QPPGRGLPG	RAQAGARPPA	PRSPRLPAST	SAARNASASP	RSQSLSRRES	1500
1501	PSPSHQARPG	VPPPRGVPPA	RAQPDGTPSP	GGSKKGRGK	LQAQRATTKG	RAGGAEGRAG	1560
1561	AR						1620

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: TTBK1

TTBK1 wt ¹ Amino Acid Sequence							
1	MQCLAAALKD	ETNSGGGEQ	ADILPANYVV	KDRWKVLKKI	GGGGFGEIYE	AMDLLTRENV	60
61	ALKVESAQQP	KQVLKMEVAV	LKKLQKQDHV	CRFIGCGRNE	KFNYVVMQLQ	GRNLADLRRS	120
121	QPRGFTTLLS	TLRLGKQILE	SIEAIHVGFL	LHRDIKPSNF	AMGRLPSTYR	KCYMLDFGLA	180
181	RQYTNNTGDV	RPPRNVAGFR	GTVRYASVNA	HKNREMGRHD	DLWSLFYMLV	EFAVGQLPWR	240
241	KIKDKQVGM	IKEYEHRML	LKHPSEFHL	FLDHIASLDY	FTKPDYQLIM	SVFENSMKER	300
301	GIAENEAFDW	EKAGTDALLS	TSTSTPPQQN	TRQTAAMFGV	VNVTVPVGD	LRENTEDVLQ	360
361	GEHLSQENA	PPILPGRPSE	GLGSPHPLVP	HPGGPEAEVW	EETDVNRNKL	RINIGKSPCV	420
421	EEEQSRGMGV	PSSPVRAPPD	SPTTPVRSR	YRVNSPESE	RLSTADGRVE	LPERRSRMDL	480
481	PGSPSRQACS	SQPAQMLSV	TGHADROAS	RMDVSASVEQ	EALSNAFRSV	PLAEEEDFDS	540
541	KEWIIDKET	ELKDFPPGAE	PSTSGTTDEE	PEELRPLPEE	GEERRRLLGAE	PTVRPRGRSM	600
601	QALAEEDLQH	LPPQPLPPQL	SQGDGRSETS	QPPTPGSPSH	SPLHSGPRPR	RRESDPTGPQ	660
661	RQVFSVAPPF	EVNGLPRAVP	LSLPYQDFKR	DLSDYRERAR	LLNRVRRVGF	SHMLLTTPQV	720
721	PLAPVQPQAN	GKEEEEEEE	DEEEEEED	EEEEEEEEEE	EEEEEEEEEE	EAAAVALGE	780
781	VLGPRSGSSS	EGSESTDRS	QEGAPSTLLA	DDQKESRGRA	SMADGDLEPE	EGSKTLVLVS	840
841	PGDMKSPVT	AELADPDDL	TLAALTPQHE	RPQITGSQLD	VSEPGTLSSV	LKSEPKPPGP	900
901	GAGLGAGTVT	TGGGVAVTS	SPFTKVERTF	VHIAEKTHLN	VMSGGQALR	SEEFSSAGEL	960
961	GLELASDGG	VEEGARAPL	NGLALSGLNG	AEIEGSALSG	APRETPSEMA	TNSLPNGPAL	1020
1021	ADGPAPVSPL	EPSPEKVATI	SPRRHAMP	RPRSRIPLVLL	SEEDTGSEPS	GLSAKERWS	1080
1081	KRARPQDLA	RLVMEKRQGR	LLLRLASGA	SSSSEEQRR	SETLSGTGSE	EDTPASEPAA	1140
1141	ALPRKSGRA	ATRSRIPRPI	GLRMPMPVAA	QQPASRSHGA	APALDTAITS	RLQLQTPPGS	1200
1201	ATAADLRPKQ	PPGRGLPGPR	AQAGARPPAP	RSPRLPASTS	AARNASASPR	SQSLSRRESP	1260
1261	PSPSHQARPGV	PPPRGVPPAR	AQPDGTPSPG	GSKKGRGK	LQAQRATTKGR	AGGAEGRAGA	1320
1321	R						1380

blue: kinase sequence expressed in recombinant protein

¹NCBI/Protein accession number NP_115927.1

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