

ProQinase™ TTBK2

Tau tubulin kinase 2

Recombinant Human Active Protein Kinase

HGNC Symbol: TTBK2

Synonyms: BDTK, KIAA1855, RP3-330M21.4

Product No.: 1359-0000-1

Lot: 007

Description: Human TTBK2, full length, amino acids M₁-R₁₂₄₄ (as in NCBI/Protein entry NP_775771.3), N-terminal GST-HIS₆ fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: TTBK2 Lot 007, was confirmed as TTBK2 by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 166,315 Da

Expression: Baculovirus infected Sf9 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, 50% 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: 0.124 µg/µl
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

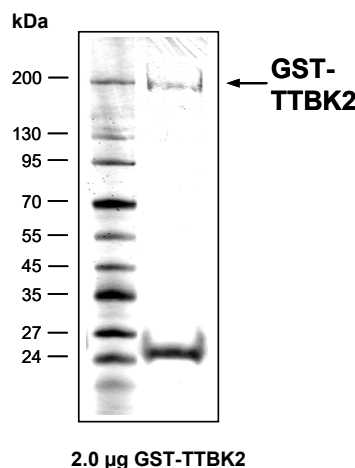
Biochemical Parameters:

Specific kinase activity (P_i transfer): 4 pmol/µg×min
ATP-K_M: 0.2 µM

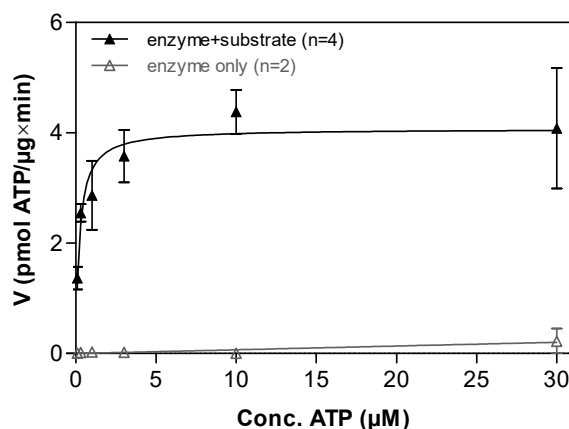
Additional assay technology: TTBK2 Lot 007

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

TTBK2 Lot 007: Coomassie stain



TTBK2 Lot 007: 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: CK-Substrate-derived peptide, 80 µg/ml
 - TTBK2: 4.0 µg/ml
- Filter binding assay
 - MSFC membrane (Millipore)



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TTBK2 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP EML	KMFKDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHG	RDSLEVL FQG	240
241	PLAMGARGRM	SGGGEQLDIL	SVGILVKER	KVLRKIGGGG	FGEIYDALDM	LTRENVALKV	300
301	ESAQQPKQVL	KMEVAVLKKL	QGDHVCRFI	GCGRNDRFNY	VVMQLQGRNL	ADLRRSQSRG	360
361	TFTISTTLRL	GRQILESIES	IHSVGF LHRD	IKPSNFAMGR	FPSTCRKCYM	LDFGLARQFT	420
421	NSCGDVRPPR	AVAGFRGTVR	YASINAHNRN	EMGRHDDLWS	LFYMLVEFV	GQLPWRKIKD	480
481	KEQVGSIKER	YDHRMLKHL	PPEFSIFLDH	ISSLDYFTKP	DYQLLTSVFD	NSIKTFGVIE	540
541	SDPFDWEKTG	NDGSLTTTTT	STTPQLHTRL	TPAAIGIANA	TPIPGDLLE	NTDEVFPDEQ	600
601	LSDGENGIPV	GVSPDKLPGS	LGHPRPQEKD	VWEEMDANKN	KIKLGICKAA	TEEENSHGQA	660
661	NGLLNAPSLG	SPIRVRSEIT	QPD RDIPLVR	KLRSIHSFEL	EKRLTLEPKP	DTDKFLETCL	720
721	EKMQKDT SAG	KESILPALLH	KPCVPAVSRT	DHIWHYDEEY	LPDASKPASA	NTPEQADGGG	780
781	SNGFIAVNLS	SCKQEIDSKE	WVIVDKEQDL	QDFRTNEAVG	HKTGTGSPSDE	EPEVLQVLEA	840
841	SPQDEKLQLG	PWAENDHLK	ETSGVVLALS	AEGPPTAASE	QYTDRLELQP	GAASQFIAAT	900
901	PTSLMEAQAE	GPLTAITIPR	PSVASTQSTS	GSFHCGQQPE	KKDLQPM EPT	VELYSPREN	960
961	SGLVVTEGEP	PSGGSRTDLG	LQIDHIGHDM	LPNIRESNKS	QDLGPKELPD	HNRLVVREFE	1020
1021	NLPGETEEKS	ILLES DNEDE	KLSRGQH CIE	ISSLPGLDVI	VEKDHSATTE	PLDVTKTQTF	1080
1081	SVVPNQDKNN	EIMKLLTVGT	SEISSRDIDP	HVEGQIGQVA	EMQKNKISKD	DDIMSEDLPG	1140
1141	HQGD LSTFLH	QEGKREKITP	RNGELFHCVS	ENEHGAPTRK	DMVRSSFVTR	HSRIPVLAQE	1200
1201	IDSTLESSSP	VSAKEKLLQK	KAYQPD LVKL	LVEKRQFKSF	LGD LSSASDK	LLEEKLATVP	1260
1261	APFCEEVLT	PFSRLTVDSH	LSRSAEDSFL	SPIISQSRKS	KIPRPVSWVN	TDQVNSSTSS	1320
1321	QFFPRPPPGK	PPTRPVGEAR	LRRYKVLGSS	NSDSDLFSRL	AQILQNGSQK	PRSTTQCKSP	1380
1381	GSPHNPKTPP	KSPVVP RRSP	SASPRSSSLP	RTSSSSPSRA	GRPHHDQRSS	SPHLGRSKSP	1440
1441	PSHSGSSSSR	RSCQ QEHC K	SKNGLKGS	LHHHSASTKT	PQGKSKPASK	LSR	1500

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: TTBK2

TTBK2 wt ¹ Amino Acid Sequence							
1	MSGGGEQLDI	LSVGILVKER	WKVLRKIGGG	GFGEIYDALD	MLTRENVALK	VESAQQPKQV	60
61	LKMEVAVLK	LQGDHVCRF	IGCGRNDRFN	YVVMQLQGRN	LADLRRSQSR	GTFTISTTLR	120
121	LGRQILESIE	SIHSVGF LHR	DIKPSNFAMG	RFPSTCRKCY	MLDFGLARQF	TNSCGDVRPP	180
181	RAVAGFRGTV	RYASINAHRN	REMGRHDDLW	SLFYMLVEFV	VGQLPWRKIK	DKEQVGSIKE	240
241	RYDHRMLK	LPPEFSIFLD	HISSLDYFTK	PDYQLLTSVF	DNSIKTFGVI	ESDPFDWEKT	300
301	GNDGSLTTTT	TSTTPQLHTR	LTPAAIGIAN	ATPIPGDLLR	ENTDEVFPDE	QLSDGENGIP	360
361	VGVPDKLPG	SLGHPRPQEK	DVWEEMDANK	NKIKLGICKA	ATEEENSHGQ	ANGLLNAPSL	420
421	GSPIRVRSEI	TQPD RDIPLV	RKLRSIHSFE	LEKRLTLEPK	PDTDKFLET	LEKMQKDTSA	480
481	GKESILPALL	HKPCVPAVSR	TDHIWHYDEE	YLPDASKPAS	ANTPEQADGG	GSENGFIAVNL	540
541	SSCKQEIDSK	EWVIVDKEQD	LQDFRTNEAV	GHKTTGSPSD	EEPEVLQVLE	ASPQDEKLQL	600
601	GPWAENDHLK	KETSGVVLAL	SAEGPPTAAS	EQYTDRLELQ	PGAASQFIAA	TPTSLMEAQA	660
661	EGPLTAITIP	RPSVASTQST	SGSFHCGQQP	EKKDLQPM EP	TVELYSPREN	FSGLVVTEGE	720
721	PPSGGSRTDL	GLQIDHIGHD	MLPNIRESNK	SQDLGPKELP	DHNRLVVREF	ENLPGETEEK	780
781	SILLES DNE	EKLSRGQH CI	EISSLPGLDV	IVEKDHSATT	EPLDVTKTQT	FSVVPNQDKN	840
841	NEIMKLLTVG	TSEISSRDID	PHVEGQIGQV	AEMQKNKISK	DDDIMSEDL	GHQGD LSTFL	900
901	HQEGKREKIT	PRNGELFHCV	SENEHGAPTR	KDMVRSSFVT	RHSRIPVLAQ	EIDSTLESS	960
961	PVSAKEKLLQ	KKAYQPD LVK	LLVEKRQFKS	FLGD LSSASD	KLLEEKLATV	PAPFCEEVLT	1020
1021	PFSRLTVDS	HLRSAEDSFL	LSPIISQSRK	SKIIPRPVSW	NTDQVNSSTS	QFFPRPPPG	1080
1081	KPPTRPVGEA	RLRRYKVLGS	SNSDSDLFSR	LAQILQNGSQ	KPRSTTQCKS	PGSPHNPKTP	1140
1141	PKSPVVP RR	PSASPRSSSL	PRTSSSSPSR	AGRPHHDQRS	SSPHLGRSKS	PPSHSGSSSS	1200
1201	RRSCQ QEHC K	PSKNGLKGS	SLHHHSASTK	TPQGKSKPAS	KLSR		1260

blue: TTBK2 sequence expressed in fusionprotein

¹NCBI/Protein accession number NP_775771.3