

## PYK2

protein tyrosine kinase 2 beta

Recombinant Human Active Protein Kinase

HGNC Symbol: PTK2B

**Synonyms:** CADTK; CAKB; FADK2; FAK2; PKB; PTK; RAFTK; CAK beta

**Product No.:** 0363-0000-1

**Lot:** 001

**Description:** Human PYK2, full length, amino acids M<sub>1</sub>-E<sub>1009</sub> (as in NCBI/Protein entry NP\_004094.3), N-terminal GST-HIS<sub>6</sub> fusion protein with a Thrombin cleavage site, expressed in Sf9 insect cells

**Product identity:** PYK2 Lot 001, was confirmed as PYK2 by mass spectroscopy LC-ESI-MS/MS (Protagen AG, Germany)

**Theoretical MW**<sub>Fusion Protein</sub>: 145,724 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, 4 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:** 0.076 µg/µl

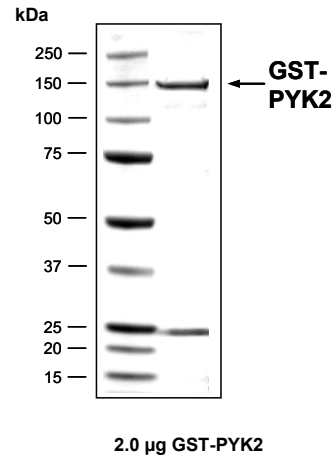
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

**Biochemical Parameters:**

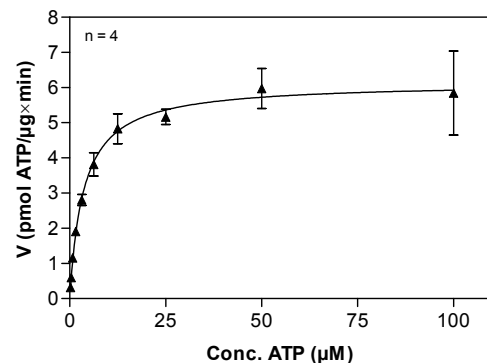
Specific kinase activity (P<sub>i</sub> transfer): 6.1 pmol/µg×min

ATP-K<sub>M</sub>: 3.6 µM

### PYK2 Lot 001: Coomassie stain



### PYK2 Lot 001: Determination of V<sub>max</sub> and K<sub>M</sub> value for ATP



### Determination of K<sub>M</sub> value & Specific activity:

- Assay conditions:
  - 60 mM HEPES-NaOH, pH 7.5
  - 3 mM MgCl<sub>2</sub>
  - 3 mM MnCl<sub>2</sub>
  - 3 µM Na-orthovanadate
  - 1.2 mM DTT
  - 50 µg / ml PEG<sub>20,000</sub>
  - ATP (variable)
  - Substrate: Poly(Glu:Tyr)<sub>4:1</sub>; 10 µg/ml
  - Kinase: 4.0 µg / ml
- Filter binding assay
  - MSFC membrane (Millipore)

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PYK2 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYYY	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQ SMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP EML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHHG	RRRASVAAGI	240
241	LVPRGSPGLD	GIYARGIQAS	MSGVSEPLSR	VKLGTLRRPE	GPAEPMVVVP	VDVEKEDVRI	300
301	LKVCFY S NSF	NPGKNFKLVK	CTVQTEIREI	ITSILLSGRI	GNIRLAECY	GLRLKHKMSD	360
361	EIH W LHPQMT	VGEVQDKYEC	LHVEAEWRYD	LQIRYLPEDF	MESLKEDRTT	LLYFYQQLRN	420
421	DYMQRYASKV	SEGMALQLGC	LELRRFFKDM	PHNALDKKSN	FELLEKEVGL	DLFFPKQMQE	480
481	NLKPQFRKM	IQQTFQOYAS	LREEECVMKF	FNTLAGFANI	DQETYRCELI	QGWNITVDLV	540
541	IGPKGIRQLT	SQDAKPTCLA	EFKQIRSIRC	LPLEEGQAVL	QLGIEGAPQA	LSIKTSSLAE	600
600	AENMADLIDG	YCRLQGEHQG	SLIIHPRKDG	EKRNSLPQIP	MLNLEARRSH	LSESCSIESD	660
661	IYAEIPDETL	RRPGGPQYGI	AREDVVLNRI	LGEGFFGEVY	EGVYTNHKGE	KINVAVKTCK	720
721	KDCTLDNKEK	FMSEAVIMKN	LDHPIVVKLI	GIIEEPTWI	IMELYPYGEL	GHYLERNKNS	780
781	LKVLTLVLYS	LQICKAMAYL	ESINCVHRDI	AVRNILVASP	ECVKLGDFGL	SRYIEDEDYY	840
841	KASVTRLPIK	WMSPEINFR	RFTTASDVWM	FAVCMWEILS	L GKQ PFFWLE	NKDVIGVQEK	900
901	GDRLPKPDL C	PPVLYTLMTR	CWDYDPSDRP	RFTELVCSLS	DVYQMEKDIA	MEQERNARYR	960
961	TPKILEPTAF	QEPKPKPSRP	KYRPPQTNL	LAPKLQFQVP	EGLCASSPTL	TSPMEYPSPV	1020
1021	NSLHTPPLHR	HNVFKRHSMR	EEDFIQPSR	EEAQQWAE	KVKMRQILDK	QQQOMVEDYQ	1080
1081	WLRQEEKSLD	PMVYMNDRSP	LTPEKEVGYL	EFTGPPQKPP	RLGAQSIQPT	ANLDRDIDL	1140
1141	YLNVMELVRA	VLELKNELCQ	LPPEGVYVVV	KNVGLTLRKL	IGSVDDLPS	LPSSSRTEIE	1200
1201	GTQKLLNKDL	AELINKMRLA	QQNAVTSLS E	ECKRQMLTAS	HTLAVDAKNL	LDAVDQAKVL	1260
1261	ANLAHPPAE						1320

1-218: GST    **Red**: HIS6-tag    **Pink**: Thrombin cleavage site    **blue**: PYK2    **boxed**: variation from RefSeq

PYK2 wt <sup>1</sup> Amino Acid Sequence							
1	MSGVSEPLSR	VKLGTLRRPE	GPAEPMVVVP	VDVEKEDVRI	LKVCFY S NSF	NPGKNFKLVK	60
61	CTVQTEIREI	ITSILLSGRI	GNIRLAECY	GLRLKHKMSD	EIH W LHPQMT	VGEVQDKYEC	120
121	LHVEAEWRYD	LQIRYLPEDF	MESLKEDRTT	LLYFYQQLRN	DYMQRYASKV	SEGMALQLGC	180
181	LELRRFFKDM	PHNALDKKSN	FELLEKEVGL	DLFFPKQMQE	NLKPQFRKM	IQQTFQOYAS	240
241	LREEECVMKF	FNTLAGFANI	DQETYRCELI	QGWNITVDLV	IGPKGIRQLT	SQDAKPTCLA	300
301	EFKQIRSIRC	LPLEEGQAVL	QLGIEGAPQA	LSIKTSSLAE	AENMADLIDG	YCRLQGEHQG	360
361	SLIIHPRKDG	EKRNSLPQIP	MLNLEARRSH	LSESCSIESD	IYAEIPDETL	RRPGGPQYGI	420
421	AREDVVLNRI	LGEGFFGEVY	EGVYTNHKGE	KINVAVKTCK	KDCTLDNKEK	FMSEAVIMKN	480
481	LDHPIVVKLI	GIIEEPTWI	IMELYPYGEL	GHYLERNKNS	LKVLTLVLYS	LQICKAMAYL	540
541	ESINCVHRDI	AVRNILVASP	ECVKLGDFGL	SRYIEDEDYY	KASVTRLPIK	WMSPEINFR	600
600	RFTTASDVWM	FAVCMWEILS	FGKQ PFFWLE	NKDVIGVLEK	GDRLPKPDL C	PPVLYTLMTR	660
661	CWDYDPSDRP	RFTELVCSLS	DVYQMEKDIA	MEQERNARYR	TPKILEPTAF	QEPKPKPSRP	720
721	KYRPPQTNL	LAPKLQFQVP	EGLCASSPTL	TSPMEYPSPV	NSLHTPPLHR	HNVFKRHSMR	780
781	EEDFIQPSR	EEAQQWAE	KVKMRQILDK	QQQOMVEDYQ	WLRQEEKSLD	PMVYMNDRSP	840
841	LTPEKEVGYL	EFTGPPQKPP	RLGAQSIQPT	ANLDRDIDL	YLNVMELVRA	VLELKNELCQ	900
901	LPPEGVYVVV	KNVGLTLRKL	IGSVDDLPS	LPSSSRTEIE	GTQKLLNKDL	AELINKMRLA	960
961	QQNAVTSLS E	ECKRQMLTAS	HTLAVDAKNL	LDAVDQAKVL	ANLAHPPAE		1020

**blue**: PYK2 sequence expressed in fusion protein    **Red**: variant in fusion protein

<sup>1</sup>NCBI/Protein accession number NP\_004094.3  
F621L: undocumented SNP variation  
L705M: documented SNP variation see NCBI/dbSNP ID: rs200441000  
K838T: documented SNP variation see NCBI/dbSNP ID: rs751019