

SAK

Polo like kinase 4

Recombinant Human Active Protein Kinase

HGNC Symbol: PLK4

Synonyms: STK18

Product No.: 0306-0000-1

Lot: 011

Description: Human SAK, full length, amino acids M₁-H₉₇₀ (as in [NCBI/Protein](#) entry NP_055079.3), N-terminal GST-HIS₆ fusion protein with a Thrombin cleavage site, expressed in Sf9 insect cells

Product identity: SAK Lot011, was confirmed as SAK by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 138,568 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: 0.138 µg/µl

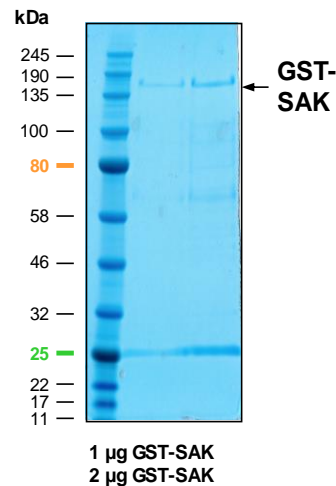
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

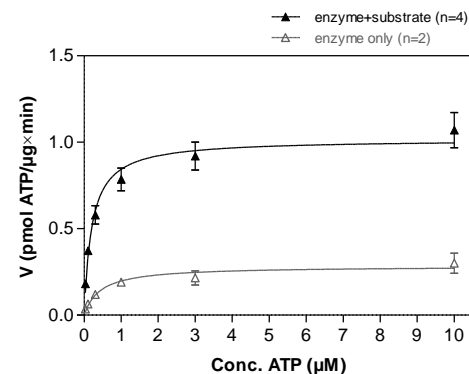
Specific kinase activity (P_i transfer): 1 pmol/µg × min

ATP-K_M: 0.2 µM

SAK Lot 011: Coomassie stain



SAK Lot 011: 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: CDC25C-derived peptide 80 µg/ml
 - Kinase: 4 µg/ml
- Filter binding assay
- MSPH membrane (Millipore)

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GST-SAK 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	KRIEAIPOID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMG HHHHHG	RRRASVAAGI	240
241	LVPRGS PGLD	GIYARGAT MA	TCIGEKIEDF	KVGNLLGKGS	FAGVYRAESI	HTGLEVAIKM	300
301	IDKKAMYKAG	MVQRVQNEVK	IHCQLKHP SI	LELYNYFEDS	NYVYLVE MC	HNGEMNRYLK	360
361	NRVKPFSENE	ARHFMHQIIT	GMLYLHSHGI	LHRDLT LSNL	LLTRNMNIKI	ADFGLATQLK	420
421	MPHEKHYTLC	GTPNYISPEI	ATRSAHGLES	DVWSLGCMFY	TLLIGRPPFD	TDTVKNTLNK	480
481	VVLADYEMPS	FLSIEAKDLI	HQLLRRNPAD	RLSLSSVLDH	PFMSRNSSTK	SKDLGTVEDS	540
541	IDSGHATIST	AITASSSTSI	SGSLFDKRRL	LIGQPLPNKM	TVFPKNSST	DFSSSGDENS	600
601	FYTQWGNQET	SNSGRGRVIQ	DAEERPHSRY	LRRAYSSDRS	GTSNSQSQAK	TYTMERCHSA	660
661	EMLSVSKRSG	GGENEERYSP	TDNNANIFNF	FKEKTS SSSG	SFERPD NNQA	LSNHLCPGKT	720
721	PFPFADPTPQ	TETVQWFGN	LQINAH LRKT	TEYDSIS PNR	DFQGH PDLOK	DTSKN AWTDT	780
781	KVKKNSDASD	NAHSVQ QONT	MKYMTALH SK	PEIIQ QECVF	GSDPL SEQSK	TRGME PPWGY	840
841	QNRTLRSITS	PLVAH RLKPI	RQKTKK AVVS	ILDSE GVCVE	LVKEY ASQEY	VKEV LQISSD	900
901	GNTITII YYPN	GGRGF PLADR	PPSPTD NISR	YSFDN LPEKY	WRKYQ YASRF	VQLV RSKSPK	960
961	ITYF TRYAKC	ILMEN SPGAD	FEVWF YDGVK	IHKTE DFIQV	IEKTG KSYTL	KSESE VNSLK	1020
1021	EEIK MYMDHA	NEGHR ICLAL	ESIISE EERK	TRSAP FFPII	IGRKP GSTSS	PKALS PPPSV	1080
1081	DSNY PTRERA	VFNRM VMHSA	ASPTQ APILN	PSMVT NEGLG	LTTT ASGTDI	SSNSL KDCLP	1140
1141	KSAQ LLKSVF	VKNV GWATQL	TSGAV VVQFN	DGSQ LVVQAG	VSSIS YTSFN	GQTT RYGENE	1200
1201	KLPD YIKQKL	QCLSS ILLMF	SNPT PNFH				1260

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

SAK wt ¹ Amino Acid Sequence							
1	MATCIG EKIE	DFKVG NLLGK	GSFAG VYRAE	SIHTG LEVAI	KMIDK KAMYK	AGMVQ RVQNE	60
61	VKIH QCLKHP	SILEL YNYFE	DSNYV YLVLE	MCHNG EMNRY	LKNRV KPFSE	NEARH FMHQI	120
121	ITGM LYLHSH	GILHR DLTSL	NLLL TRNMNI	KIADF GLATQ	LKMPH EKHYT	LCGTP NYISP	180
181	EIATR SAHGL	ESDV WSLGCM	FYTLL IGRPP	FDTDT VKNTL	NKVVL ADYEM	PSFLS IEAKD	240
241	LIHQ LLRRNP	ADRL SLSSVL	DHPFM SRNSS	TKSKD LGTVE	DSIDS GHATI	STAIT ASSST	300
301	SISGS LFDKR	RLLI GQPLPN	KMTV FPKNS	STDF SSSGDG	NSFY TQWGNQ	ETSNS GRGRV	360
361	IQDA EERPHS	RYLRR AYSSD	RSGTS NSQSQ	AKTY TMERCH	SAEML SVSKR	SGGGE NEERY	420
421	SPTD NNANIF	NFFKE KTSSS	SGSFE RPDNN	QALS NHLCPG	KTPFP FADPT	PQTET VQQWF	480
481	GNLQ INAHLR	KTTEY DSISP	NRDF QGHPLD	QKDT SKNAWT	DTKVK KNSDA	SDNAH SVKQO	540
541	NTMK YMTALH	SKPEI IQEC	VFGSD PLSEQ	SKTR GMEPPW	GYQN RTLRSI	TSPL VAHRLK	600
601	PIRQ KTKKAV	VSILD SE E VC	VELV KEYASQ	EYVKE VLQIS	SDGNT ITIIYY	PNGGR GFPLA	660
661	DRPP SPTDNI	SRYSD NLPE	KYWR KYQYAS	RFVQ LVRSKS	PKITY FTRYA	KCIL MENSPG	720
721	ADFE VWFYDG	VKIH KTEDFI	QVIE KTGKSY	TLKSE SEVNS	LKEE IKMYMD	HANE GHRICL	780
781	ALES IISSEE	RKTR SAPFFP	IIIG RKPGST	SSPK ALSPPP	SVDS NYPTRE	RASF NRMVMH	840
841	SAAS PTQAPI	LNPS MVTNEG	LGLT TASGT	DISS NLKDC	LPKSA QLLKS	VFVK NVGWAT	900
901	QLT SQAVVQ	FNDGS QLVVQ	AGVSS ISYTS	PNGQ TTRYGE	NEKL PDYIKQ	KLQ CLSSILL	960
961	MFSN PTPNFH						1020

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

¹[NCBI/Protein](#) accession number NP_055079.3

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