

## ProQinase™ FAK aa2-1052

protein tyrosine kinase 2

Recombinant Human Active Protein Kinase

HGNC Symbol: PTK2

Synonyms: FADK, FADK1, FAK1, FRNK, pp125FAK

Product No.: 0165-0000-3

Lot: 016

**Description:** Human FAK, amino acids A<sub>2</sub>-H<sub>1052</sub> (as in [NCBI/Protein](#) entry NP\_722560.1), activated, N-terminal GST fusion protein with a Thrombin cleavage site, expressed in Sf9 insect cells

**Product identity:** FAK Lot 016, was confirmed as FAK by mass spectroscopy LC-ESI-MS/MS

**Theoretical MW**<sub>Fusion Protein</sub>: 145,394 Da

**Expression host:** Sf9 insect cells

**Purification:** GST-Affinity Chromatography

**Activation:** With SRC

**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:** 0.249 µg/µl

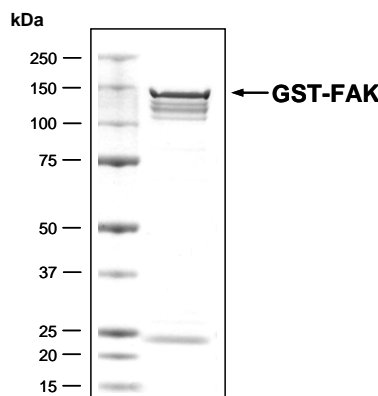
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

**Biochemical Parameters:**

Specific kinase activity (P<sub>i</sub> transfer): 14 pmol/µg × min

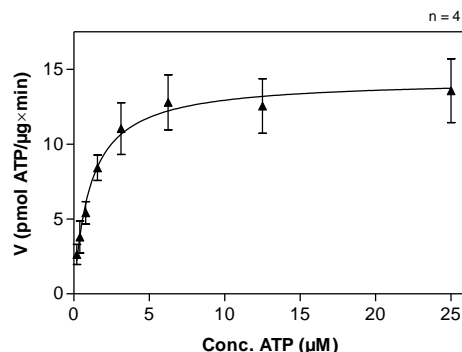
ATP-K<sub>M</sub>: 1.1 µM

### FAK Lot 016: Coomassie stain



2.0 µg GST-FAK

### FAK Lot 016: Determination of V<sub>max</sub> and K<sub>M</sub> value for ATP



- 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> 5 µg/ml  
Kinase: 1 µg/ml
- Filter binding assay  
MSFC membrane (Millipore)

### Additional assay technology:

FAK Lot 016 was also successfully tested by Reaction Biology 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

## ProQinase™ FAK aa2-1052

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GST-FAK aa2-1052 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	<b>LVPRGSAAAY</b>	<b>LDPNLNHTPN</b>	240
241	<b>SSTKTHLGTG</b>	<b>MERSPGAMER</b>	<b>VLKVFHYFES</b>	<b>NSEPTTWASI</b>	<b>IRHGDATAVDR</b>	<b>GIIQKIVDSH</b>	300
301	<b>KVKHVACYGF</b>	<b>RLSHLRSEEV</b>	<b>HWLHVDMGVS</b>	<b>SVREKVELAH</b>	<b>PPEEWKVELR</b>	<b>IRYLPKGFNL</b>	360
361	<b>QFTEDKPTLN</b>	<b>FFYQQVKS DY</b>	<b>MLEIADQVDQ</b>	<b>EIALKLGCLE</b>	<b>IRRSYWEMRG</b>	<b>NALEKKS NYE</b>	420
421	<b>VLEKDVGLKR</b>	<b>FFPKSLLD SV</b>	<b>KAKTLRKL IQ</b>	<b>QTFRQFANLN</b>	<b>REESILKFFE</b>	<b>ILSPVYRFDK</b>	480
481	<b>ECFKCALGSS</b>	<b>WIISVELAIG</b>	<b>PEEGISY LTD</b>	<b>KGCNPTH LAD</b>	<b>FTQVQTIQYS</b>	<b>NSEDKDRKGM</b>	540
541	<b>LQLKIAGAPE</b>	<b>PLTVTAPSLT</b>	<b>IAENMADLID</b>	<b>GYCRLVNGTS</b>	<b>QSFIIRPQKE</b>	<b>GERALPSIPK</b>	600
601	<b>LANSEKQGMR</b>	<b>THAVSVSETD</b>	<b>DYAEIIDEED</b>	<b>TYTMPSTRDY</b>	<b>EIQRERIELG</b>	<b>RCIGEGQFGD</b>	660
661	<b>VHIGEIYMSPE</b>	<b>NPALAVA IKT</b>	<b>CKNCTSDSVR</b>	<b>EKFLQEAL TM</b>	<b>RQFDHPHIVK</b>	<b>LIGVITENPV</b>	720
721	<b>WIIMELCTLG</b>	<b>ELRSFLQVRK</b>	<b>YSLDLASLIL</b>	<b>YAYQLSTALA</b>	<b>YLESKRFVHR</b>	<b>DIAARNVLVS</b>	780
781	<b>SNDCVKLGDF</b>	<b>GLSRYMEDST</b>	<b>YYKASKGKLP</b>	<b>IKWMAPESIN</b>	<b>FRRFTSASDV</b>	<b>WMFGVCMWEI</b>	840
841	<b>LMHGVPKPFQ</b>	<b>VKNNDVIGRI</b>	<b>ENGERLPMPP</b>	<b>NCPPTLYSLM</b>	<b>TKCWAYDPSR</b>	<b>RPRFTELKAQ</b>	900
901	<b>LSTILEEEKA</b>	<b>QQEERMRMES</b>	<b>RRQATVSWDS</b>	<b>GGSD EAPPKP</b>	<b>SRPGYPSPRS</b>	<b>SEGFYPS PQH</b>	960
961	<b>MVQTNHYQVS</b>	<b>GYPGSHGITA</b>	<b>MAGSIYPGQA</b>	<b>SLLDQTD SWN</b>	<b>HRPQEIAMWQ</b>	<b>PNVEDSTVLD</b>	1020
1021	<b>LRGIGQVLP T</b>	<b>HLMEERLIRQ</b>	<b>QQEMEEDQRW</b>	<b>LEKEERFLKP</b>	<b>DVRLSRGSID</b>	<b>REDGSLQGP I</b>	1080
1081	<b>GNQHIYQPVG</b>	<b>KPDP AAPPK</b>	<b>PPRPGAPGHL</b>	<b>GSLASLSSPA</b>	<b>DSYNEGVKLQ</b>	<b>PQEI SPPPTA</b>	1140
1141	<b>NLDRSNDK VY</b>	<b>ENVTGLVKAV</b>	<b>IEMSSKIQPA</b>	<b>PPEEYVPMVK</b>	<b>EVGLALR TLL</b>	<b>ATVDETIPLL</b>	1200
1201	<b>PASTHREIEM</b>	<b>AQKLLNSDLG</b>	<b>ELINKMKLAQ</b>	<b>QYVMTSLQQE</b>	<b>YKQMLTAAH</b>	<b>ALAVDAKNLL</b>	1260
1261	<b>DVIDQARLKM</b>	<b>LGQTRPH</b>					1320

1-218: GST **Pink**: Thrombin cleavage site **blue**: FAK

FAK wt <sup>1</sup> Amino Acid Sequence							
1	MAAAYLDPNL	NHTPNSSTKT	HLGTGMERSP	GAMERVLKVF	HYFESNSEPT	TWASIIRHGD	60
61	ATDVRGIIQK	IVDSHKVKHV	ACYGFRLSHL	RSEEVHWLHV	DMGVSSVREK	YELAHPPPEEW	120
121	KYELRIRYLP	KGFLNQFTED	KPTLNFFYQQ	VKSDYMLEIA	DQVDQEIALK	LGCLEIRRSY	180
181	WEMRGNALEK	KSNYEVLEKD	VGLKRFFPKS	LLDSVKAKTL	RKLIQQTFRQ	FANLNREESI	240
241	LKFFEILSPV	YRFDKECFKC	ALGSSWII SV	ELAIGPEEGI	SYLTDKGCNP	THLADFTQVQ	300
301	TIQYSNSEDK	DRKGMQLKI	AGAPEPLTVT	APSLTIAENM	ADLIDGYCRL	VNGTSQS FII	360
361	RPQKEGERAL	PSIPKLANSE	KQGMRTHAVS	VSETDDYAEI	IDEEDTYTMP	STRDYEIQRE	420
421	RIELGRCIGE	GQFGDVHQGI	YMSPENPALA	VAIKTKNCT	SDSVREKFLQ	EALTMRQFDH	480
481	PHIVKLIGVI	TENPVWIIME	LCTLGELRSF	LQVRKYSLDL	ASLILYAYQL	STALAYLESK	540
541	RFVHRDIAAR	NVLVSSNDCV	KLGD FGLSRY	MEDSTYYKAS	KGKLPKWMA	PESINFRRET	600
601	SASDVMMFGV	CMWEILMHGV	KPFQGVKNND	VIGRIENGER	LPMPNCPPT	LYSLMTKCWA	660
661	YDPSRRPRFT	ELKAQLSTIL	EEEAQQEER	MRMESRRQAT	VSWDGGGSD E	APPKPSRPGY	720
721	PSPRSSEG FY	PSPQHMVQTN	HYQVSGYPGS	HGITAMAGSI	YPGQASLLDQ	TDSWNHRPQE	780
781	IAMWQPNVED	STVLDLRGIG	QVLP THLMEE	RLIRQQEME	EDQRWLEKEE	RFLKPDVRLS	840
841	RGSIDREDGS	LQGPIGNQHI	YQPVGKPDPA	APPKKPPRPG	APGHLGSLAS	LSSPADSYNE	900
901	GVKLQPOEIS	PPPTANLDRS	NDKVYENV TG	LVKAVIEMSS	KIQPAPPEEY	VPMVKEVG LA	960
961	LRTLLATVDE	TIPLLPASTH	REIEMAQKLL	NSDLGELINK	MKLAQQYVMT	SLQQEYKQOM	1020
1021	LTAahalAVD	AKNLLDVIDQ	ARLKM LGQTR	PH			1080

**blue**: FAK sequence expressed in recombinant protein

<sup>1</sup>[NCBI/Protein](#) accession number NP\_722560.1