

ProQinase™ ABL1 F317I

v-abl Abelson murine leukemia viral oncogene homolog 1

Recombinant Human Active Protein Kinase

HGNC Symbol: ABL1

Synonyms: c-Abl, JTK7, p150

Product No.: 0989-0000-1

Lot: 004

Description: Human ABL1 F_{317I} mutant, internal fragment, amino acids P₁₁₈-S₅₃₅, (as in [NCBI/Protein](#) entry NP_005148.2), N-terminal GST-HIS₆ fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: ABL1 F_{317I} Lot 004, was confirmed as ABL1 by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 76,133 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 10 µl are not advisable. Avoid repeated freeze-thaw cycles!

Protein concentration: 0.403 µg/µl

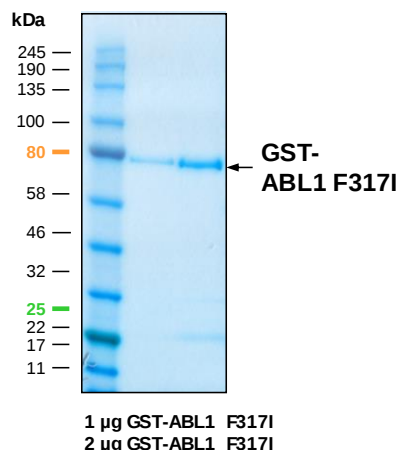
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

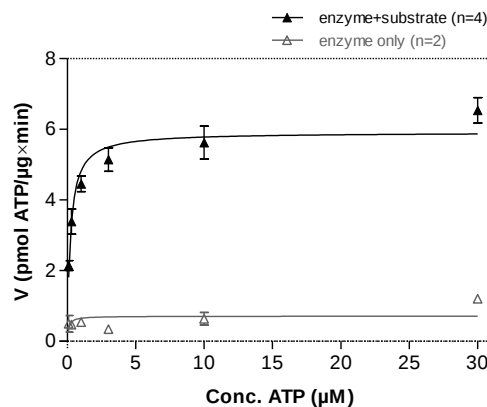
Specific kinase activity (P_i transfer): 5.9 pmol/µg × min

ATP-K_M: 0.23 µM

ABL1 F317I Lot 004: Coomassie stain



ABL1 F317I Lot 004: 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: Poly(Ala,Glu,Lys,Tyr)_{6:2:5:1} 20 µg/ml
 - Kinase: 2 µg/ml
- Filter binding assay
- MSFC membrane (Millipore)

Additional assay technology:

ABL1 F_{317I} Lot 004 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

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GST-ABL1 F317I Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFNLPYYID	60
61	GDVKLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHHG	RDSLEVLFGQ	240
241	PLAMLPVNSL	EKHSWYHGPV	SRNAAEYLLS	SGINGSFLVR	ESESSPGQRS	ISLRYEGRVY	300
301	HYRINTASDG	KLYVSSESRE	NTLAELVHHH	STVADGLITT	LHYPAPKRNK	PTVYGVSPNY	360
361	DKWEMERTDI	TMKHKLGCGQ	YGEVYEGVWK	KYSLTVAVKT	LKEDTMEVEE	FLKEAAVMKE	420
421	IKHPNLVQLL	GVCTREPPFY	IITEIMTYGN	LLDYLRECNR	QEVNAVLLY	MATQISSAME	480
481	YLEKKNFIHR	DLAARNCLVG	ENHLVKVADF	GLSRLMTGDT	YTAHAGAKFP	IKWTAPESLA	540
541	YNKFSIKSDV	WAFGVLLWEI	ATYGMSPYPG	IDLSQVYELL	EKDYRMERPE	GCPEKVYELM	600
600	RACWQWNP	PSD	RPSFAEIHQA	FETMFQESSI	SDEVEKELGK	QGVRGAVSTL	660
661	RTS					LQAPELPTKT	720

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: ABL1 fragment boxed: F317I mutation

ABL1 wt ¹ Amino Acid Sequence							
1	MLEICLKLVG	CKSKKGLSSS	SSCYLEEALQ	RPVASDFEPQ	GLSEAAWNS	KENLLAGPSE	60
61	NDPNLFVALY	DFVASGDNTL	SITKGEKLRV	LGYNHNGEWC	EAQTKNGQGW	VPSNYITPVN	120
121	SLEKHSWYHG	PVSRNAAEYL	LSSGINGSFL	VRESESSPGQ	RSISLRYEGR	VYHYRINTAS	180
181	DGKLYVSSES	RFNTLAELVH	HHSTVADGLI	TTLHYPAPKR	NKPTVYGVSP	NYDKWEMERT	240
241	DITMKHKLGG	GQYGEVYEGV	WKYSLTVAV	KTLKEDTMEV	EEFLKEAAVM	KEIKHPNLVQ	300
301	LLGVCTREPP	FYIITEFMTY	GNLLDYLREC	NRQEVNAVVL	LYMATQISSA	MEYLEKKNFI	360
361	HRDLAARNCL	VGENHLVKVA	DFGLSRLMTG	DTYTAHAGAK	FPIKWTAPES	LAYNKFSIKS	420
421	DVWAFGVLLW	EIATYGMSPY	PGIDLSQVYE	LLEKDYRMER	PEGCPEKVYE	LMRACWQWNP	480
481	SDRPSFAEIH	QAFETMFQES	SISDEVEKEL	GKQGVRGAVS	TLLQAPELPT	KTRTSRRAAE	540
541	HRDTTDVPEM	PHSKGQGESD	PLDHEPAVSP	LLPRKERGPP	EGGLNEDERL	LPKDKKTNLF	600
600	SALIKKKKKKT	APTPPKRSSS	FREMDGQPER	RGAGEEEGRD	ISNGALAFPT	LDTADPAKSP	660
661	KPSNGAGVPN	GALRESGGSG	FRSPHLWKKS	STLTSSRLAT	GEEEGGSSSS	KRFLRSCSAS	720
721	CVPHGAKDTE	WRSVTLPRDL	QSTGRQFDSS	TFGGHKSEKP	ALPRKRAGEN	RSDQVTRGTV	780
781	TPPPRLVKKN	EAAADEVFKD	IMESSPGSSP	PNLTPKPLRR	QVTVAPASGL	PHKEEAGKGS	840
841	ALGTPAAAEP	VTPTSKAGSG	APGGTSKGPA	EESRVRHKKH	SSESPGRDKG	KLSRLKPAPP	900
901	PPPAASAGKA	GKPSQSPSQ	EAAGEAVLGA	KTKATSLVDA	VNSDAAKPSQ	PGEGLKKPVL	960
961	PATPKPQSAK	PSGTPISPAP	VPSTLPSASS	ALAGDQPSST	AFIPLISTRV	SLRKTRQPPE	1020
1021	RIASGAITKG	VVLDSTEALC	LAISRNSEQM	ASHSAVLEAG	KNLYTFCVSY	VDSIQQMRNK	1080
1081	FAFREAINKL	ENNLRELQIC	PATAGSGPAA	TQDFSKLLSS	VKEISDIVQR		1140

blue: ABL1 sequence expressed in recombinant protein Red: variant in recombinant protein

¹[NCBI/Protein](#) accession number NP_005148.2