

ABL1 T315I

ABL proto-oncogene 1, non-receptor tyrosine kinase

Recombinant Human Active Protein Kinase

HGNC Symbol: ABL1

Synonyms: ABL, c-Abl, JTK7, p150

Product No.: 0757-0000-1

Lot: 003

Description: Human ABL1, internal fragment, amino acids P₁₁₈-S₅₃₅ (as in [NCBI/Protein](#) entry NP_005148.2), T315I mutant, N-terminal GST-HIS₆ fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: ABL1 T315I Lot 003 was confirmed by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 76,179 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!

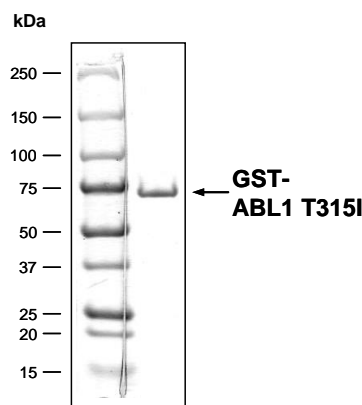
Protein concentration: 0.126 µg/µl
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:
Specific kinase activity (P_i transfer): 10 pmol/µg × min
ATP-K_M: 0.21 µM

Additional assay technology:

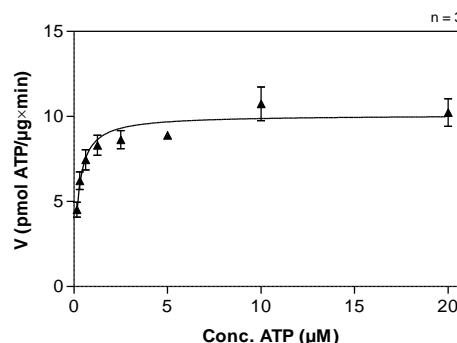
ABL1 T315I Lot 003 was also successfully tested by ProQinase for the use with the ADP-Glo™ Kinase assay from Promega
ADP-Glo assay conditions may vary from radiometric assay conditions, please inquire for assay details

**ABL1 T315I Lot 003:
Coomassie stain**



2.0 µg GST-ABL1 T315I

**ABL1 T315I Lot 003:
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
 - ABL1 T315I: 2 µg/ml
- Filter binding assay
MSFC membrane (Millipore)

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GST-ABL1 T315I Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP EML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMG HHHHHG	RRRASVAAGI	240
241	LVPRG SPGLD	GIYARDS LEV	LFQGPL AMLPL	VNSLEK HSWY	HGPVSR NAE	YLLSSG INGS	300
301	FLVRESE SP	QORSIS LRYE	GRVYH RINT	ASDGK LYVSS	ESRFNT LAEL	VHHHST VADG	360
361	LITTLH YPAP	KRNKPT YGV	SPNYD KWEME	RTDITM KHKL	GGGQY GEVYE	GVWKKY SLTV	420
421	AVKTLK EDTM	EVEEFL KEAA	VMKEIK HPNL	VQLLGV CTRE	PPFYII TEFM	TYGNLL DYLR	480
481	ECNRQ EVNAV	VLLYMA TQIS	SAMEYL EKKN	FIHRDL AARN	CLVGEN HLVK	VADFGL SRLM	540
541	TGDTY TAHAG	AKFP IKWTAP	ESLAYN KFSI	KSDVWA FGVL	LWEIAT YGMS	PYPGID LSQV	600
600	YELLEK DYRM	VRTEGC PKEV	YELMRAC WQW	NPSDRP SFAE	IHQAFET MFQ	ESSISD VEVK	660
661	ELGKQ GV RGA	VSTLLQ APEL	PTKTRT S				720

1-218: GST **Red**: HIS6-tag **Pink**: Thrombin cleavage site **Green**: 3C cleavage site **blue**: ABL1 fragment **boxed**: T315I mutation

ABL1 wt ¹ Amino Acid Sequence							
1	MLEICLKLVG	CKSKKGLSSS	SSCYLEEALQ	RPVASDFEPQ	GLSEAARWNS	KENLLAGPSE	60
61	NDPNLFVALY	DFVASGDN TL	SITKGEKLRV	LGYNHNGEWC	EAQTKNGQGW	VPSNYIT PVN	120
121	SLEKHS WYHG	PVSRNA AEYL	LSSG INGSFL	VRESE SPGQ	RSISLR YEGR	VYHYR INTAS	180
181	DGKLY SSES	RFNTL AELVH	HHSTV ADGLI	TTLHY PAPKR	NKPTV YGVSP	NYDKW EMERT	240
241	DITMK HKLGG	GQYGE VYEGV	WKKY SLTVAV	KTLK EDTMEV	EEFL KEAAVM	KEIKH PNLVQ	300
301	LLGV CTREPP	FYII TEFMTY	GNLL DYLR	NRQ EVNAVVL	LYMA TQISSA	MEYL EKKNFI	360
361	HRDL AARNCL	VGENH LVKVA	DFGL SRLMTG	DTYTA HAGAK	FPIK WTAPES	LAYN KFSIKS	420
421	DVWA FGVLLW	EIATY GMSPY	PGID LSQVYE	LLEK DYRMER	PEGC PKEVYE	LMRA CWQWNP	480
481	SDRPS F AEIH	QAFET MFQES	SISD EVEKEL	GKQ GV RGA VS	TLLQ APELPT	KTRT SRRAAE	540
541	HRD TTDVPEM	PHSKGQGESD	PLDHEPAVSP	LLPRKERGPP	EGGLNEDERL	LPKDKKTNLF	600
600	SALIKKKKKT	APTTPKRSSS	FREMDGQPER	RGAGEEEGRD	ISNGALAF TP	LDTADPAKSP	660
661	KPSNGAGVPN	GALRESGGSG	FRSPHLWKKS	STLTSSRLAT	GEEEGGGSSS	KRFLRSCSAS	720
721	CVPHGAKDTE	WRSVTLPRDL	QSTGRQFDSS	TFGGHKSEKP	ALPRKRAGEN	RSDQVTRGTV	780
781	TPPPRLVKKN	EEAADEVFKD	IMESSPGSSP	PNLTPKPLRR	QVTVAPASGL	PHKEEAGKGS	840
841	ALGTPAAAE P	VTPTSKAGSG	APGGT SKGPA	EESRVR RHKH	SSESPGRDKG	KLSRLKPAPP	900
901	PPPAASAGKA	GGKPSQSPSQ	EAAGEAVLGA	KTKATSLVDA	VNSDAAKPSQ	PGEGLKPPVL	960
961	PATPKPQSAK	PSGTPISPAP	VPSTLPSASS	ALAGDQPSST	AFIPLISTRV	SLRKTRQPPE	1020
1021	RIASGAI TKG	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](https://www.ncbi.nlm.nih.gov/Protein/NP_005148.2) accession number NP_005148.2

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