

ABL1 Q252H

ABL proto-oncogene 1, non-receptor tyrosine kinase

Recombinant Human Active Protein Kinase

HGNC Symbol: ABL1

Synonyms: c-Abl, JTK7, p150

Product No.: 0926-0000-1

Lot: 001

Description: Human ABL1, internal fragment, amino acids P₁₁₈-S₅₃₅ (as in [NCBI/Protein](#) entry NP_005148.2), Q252H mutant, N-terminal GST-HIS₆ fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: ABL1 Q252H Lot 001 was confirmed by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 76,176 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: 0.242 µg/µl

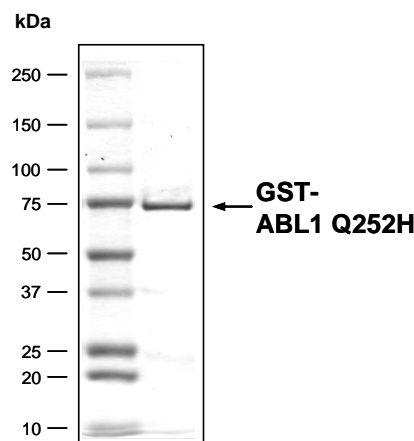
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

Specific kinase activity (P_i transfer): 67 pmol/µg × min

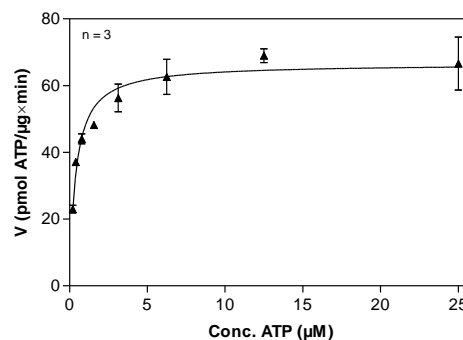
ATP-K_M: 0.39 µM

ABL1 Q252H Lot 001:
Coomassie stain



2.0 µg GST-ABL1 Q252H

ABL1 Q252H Lot 001:
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 Q252H Lot 001 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

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GST-ABL1 Q252H 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	RDS LEVLFCG	240
241	PLAMLPVNSL	EKHSWYHGPV	SRNAAEYLLS	SGINGSFLVR	ESESSPGQRS	ISLRYEGRVY	300
301	HYRINTASDG	KLYVSSSESRF	NTLAEVLVHHH	STVADGLITT	LHYPAPKRNK	PTVYGVSPNY	360
361	DKWEMERTDI	TMKHKLGGGE	YGEVYEGVWK	KYSLTVAVKT	LKEDTMEVEE	FLKEAAVMKE	420
421	IKHPNLVQLL	GVCTREPPFY	IITEFMTYGN	LLDYLRECNR	QEVNAVLLY	MATQISSAME	480
481	YLEKKNFIHR	DLAARNCLVG	ENHLVKVADF	GLSRLMTGDT	YTAHAGAKFP	IKWTAPESLA	540
541	YNKFSIKSDV	WAFGVLLWEI	ATYGMSPYPG	IDLSQVYELL	EKDYRMERPE	GCPEKVYELM	600
600	RACWQWNP	RPSFAEIHQA	FETMFQESSI	SDEVEKELGK	QGVRGAVSTL	LQAPELPTKT	660
661	RTS						720

1-218: GST **Red**: HIS6-tag **Green**: 3C cleavage site **blue**: ABL1 fragment **boxed**: Q252H

ABL1 wt ¹ Amino Acid Sequence							
1	MLEICLKLVG	CKSKKGLSSS	SSCYLEEALQ	RPVASDFEPQ	GLSEAAWNS	KENLLAGPSE	60
61	NDPNLNFVALY	DFVASGDNTL	SITKGEKLRV	LGYNHNGEWC	EAQTKNGQGW	VPSNYIT PVN	120
121	SLEKHSWYHG	PVSRNAAEYL	LSSGINGSFL	VRESESSPGQ	RSISLRYEGR	VYHYRINTAS	180
181	DGKLVSSSE	RFNTLAELVH	HHSTVADGLI	TTLHYPAPKR	NKPTVYGVSP	NYDKWEMERT	240
241	DITMKHKLGG	GQYGEVYEGV	WKKYSLTVAV	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	HRDITDVPPEM	PHSKGQGESD	PLDHEPAVSP	LLPRKERGPP	EGGLNEDERL	LPKDKKTNLF	600
600	SALIKKKKKT	APTPPKRSSH	FREMDGQPER	RGAGEEEGRD	ISNGALAFTP	LDTADPAKSP	660
661	KPSNGAGVPN	GALRESGGSG	FRSPHLWKKK	STLTSSRLAT	GEEEGGGSSS	KRFLRSCSAS	720
721	CVPHGAKDTE	WRSVTLPRDL	QSTGRQFDSS	TFGGHKSEKP	ALPRKRAGEN	RSDQVTRGTV	780
781	TPPPRLVKKN	EAAAEVFKD	IMESSPGSSP	PNLTPKPLRR	QVTVAPASGL	PHKEEAGKGS	840
841	ALGTPAAAEF	VTPTSKAGSG	APGGTSKGP	EESRVRHKKH	SSESPGRDKG	KLSRLKPAPP	900
901	PPPAASAGKA	GGKPSQSPSQ	EAAGEAVLGA	KTKATSLVDA	VNSDAAKPSQ	PGEGLKPPVL	960
961	PATPKPQSAK	PSGTPISPAP	VPSTLPSASS	ALAGDQPSST	AFIPLISTRV	SLRKTRQPPE	1020
1021	RIASGAIKTK	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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