

ProQinase™ ABL1 G250E

ABL proto-oncogene 1, non-receptor tyrosine kinase

Recombinant Human Active Protein Kinase

HGNC Symbol: ABL1

Synonyms: ABL, c-Abl, JTK7, p150

Product No.: 0925-0000-1

Lot: 001

Description: Human ABL1, internal fragment, amino acids P₁₁₈-S₅₃₅ (as in [NCBI/Protein](#) entry NP_005148.2), G250E mutant, N-terminal GST-HIS₆ fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: ABL1 G250E Lot 001, was confirmed as ABL1 with mutation G250E by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 76,239 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: 0.704 µg/µl
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

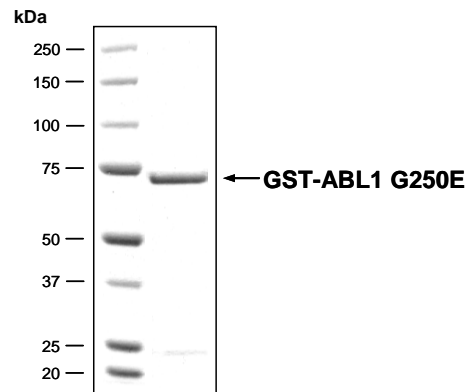
Biochemical Parameters:

Specific kinase activity (P_i transfer): 175 pmol/µg × min
ATP-K_M: 0.48 µM

Additional assay technology:

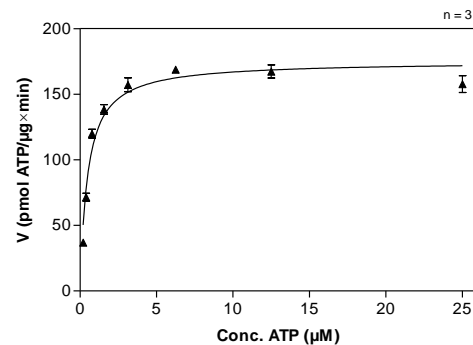
ABL1 G250E Lot 001 was also successfully tested by Reaction Biology for the use with the ADP-Glo™ Kinase assay from Promega ADP-Glo assay conditions may vary from radiometric assay conditions, please inquire for assay details

**ABL1 G250E Lot 001:
Coomassie stain**



2.0 µg GST-ABL1 G250E

**ABL1 G250E 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)
 - Poly(Ala,Glu,Lys,Tyr)_{6,2:5:1}, 20 µg/ml
 - ABL1 G250E: 1 µg/ml
- Filter binding assay
MSFC membrane (Millipore)

ProQinase™ ABL1 G250E

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| GST-ABL1 G250E 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 | EKHSWYHG | SRNAAEYLLS | SGINGSFLVR | ESESSPGQRS | ISLRYEGRVY | 300 |
| 301 | HYRINTASDG | KLYVSSSESRF | NTLAELVHHH | STVADGLITT | LHYPAPKRNK | PTVYGVSPNY | 360 |
| 361 | DKWEMERTDI | TMKHKLGEGQ | 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**: G250E mutation

| ABL1 wt ¹ Amino Acid Sequence | | | | | | | |
|--|--------------------------|-------------------|-------------------|-------------------|-------------------|--------------------|------|
| 1 | MLEICLKLVG | CKSKKGLSSS | SSCYLEEALQ | RPVASDFEPQ | GLSEAARWNS | KENLLAGPSE | 60 |
| 61 | NDPNLNFVALY | DFVASGDNTL | SITKGEKLRV | LGYNHNGEWC | EAQTKNGQGW | VPSNYIT PVN | 120 |
| 121 | SLEKHSWYHG | PVSRNAAEYL | LSSGINGSFL | VRESESSPGQ | RSISLRYEGR | VYHYRINTAS | 180 |
| 181 | DGKLYVSSSE | 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 | APTTPKRSSS | FREMDGQPER | RGAGEEGRD | ISNGALAFTP | LDTADPAKSP | 660 |
| 661 | KPSNGAGVPN | GALRESGGSG | FRSPHLWKS | 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