

ProQinase™ MET G1163R

MET proto-oncogene, receptor tyrosine kinase

Recombinant Human Active Protein Kinase

HGNC Symbol: MET

Synonyms: c-MET, HGFR

Product No.: 1650-0000-1

Lot: 001

Description: Human MET C-terminal fragment, amino acids K₉₅₆-S₁₃₉₀ (as in [NCBI/Protein](#) entry NP_000236.2), G₁₁₆₃R point mutant, N-terminal GST-HIS₆ fusion protein with a Thrombin cleavage site, expressed in Sf9 insect cells

Product identity: MET G1163R Lot 001 product identity was confirmed by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 78,773 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: 0.202 µg/µl
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

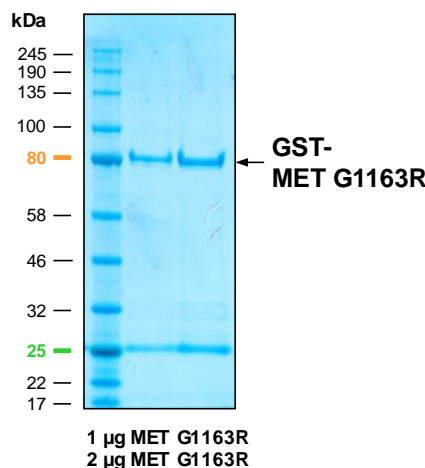
Biochemical Parameters:

Specific kinase activity (P_i transfer): 15 pmol/µg × min
ATP-K_M: 2.2 µM

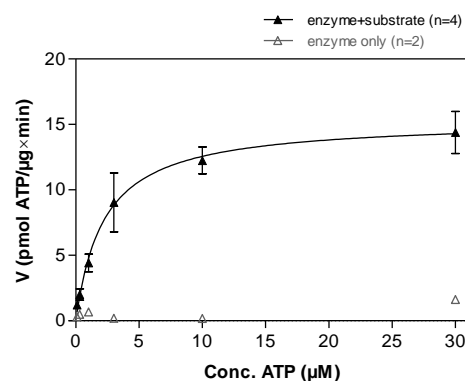
Additional assay technology:

MET G1163R 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

MET G1163R Lot 001: Coomassie stain



MET G1163R 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: TRK-C derived peptide 40 µg/ml
 - Kinase: 1 µg/ml
- Filter binding assay
- MSPH membrane (Millipore)

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GST-MET G1163R 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	KRIEAIPIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMG HHHHHG	RRRASVAAGI	240
241	LVPRG SPGLD	GICSIEEF KK	RKQIKDLGSE	LVRVDARVHT	PHLDRLVSAR	SVSPTTEMVS	300
301	NESVDYRATF	PEDQFPNSSQ	NGSCRQVQYP	LTDMSPILTS	GSDISSPLL	QNTVHIDLSA	360
361	LNPELVQAVQ	HVVIGPSSLI	VHFNEVIGRG	HFGCVYHGTL	LDNDGKKIHC	AVKSLNRTD	420
421	IGEVSQFLTE	GIIMKDFSHP	NVLSLLGICL	RSEGSPLVVL	PYMKHDLRN	FIRNETHNPT	480
481	VKDLIGFGLQ	VAKGMKYLAS	KKFVHRDLAA	RNCMLDEKFT	VKVADFGLAR	DMYDKEYYSV	540
541	HNKTKAKLPV	KWMALESLOT	QKFTTKSDVW	SFGVLLWELM	TRGAPPYDPV	NTFDITVYLL	600
601	QGRRLLOPEY	CPDPLYEVML	KCWHPKAEMR	PSFSELVSRI	SAIFSTFIGE	HYVHVNATYV	660
661	NVKCVAPYPS	LLSSEDNADD	EVDTRPASFW	ETS			720

1-218: GST **Red**: HIS6-tag **Pink**: Thrombin cleavage site **blue**: MET fragment **boxed**: G1163R point mutation

MET wt ¹ Amino Acid Sequence							
1	MKAPAVLAPG	ILVLLFTLVQ	RSNGECKEAL	AKSEMNVNMK	YQLPNFTAET	PIQNVILHEH	60
61	HIFLGATNYI	YVLNEEDLQK	VAEYKTGPVL	EHPDCFPQD	CSSKANLSGG	VWKDINMAL	120
121	VVDYYDDQL	ISCGSVNRGT	QQRHVFPNH	TADIQSEVHC	IFSPQIEEPS	QCPDCVSAL	180
181	GAKVLSSVKD	RFINFFVGN	INSSYFPDHP	LHSISVRLK	ETKDGFMFLT	DQSYIDLPE	240
241	FRDSYPIKYV	HAFESNNFY	FLTVQRETL	AQTFHTRIR	FCSINSLHS	YMEMPLECIL	300
301	TEKRKKRSTK	KEVFNILQAA	YVSKPGAQLA	RQIGASLND	ILFGVFAQSK	PDSAEPMDRS	360
361	AMCAFPKIYV	NDFFNKIVNK	NNVRCLQHFY	GNHEHCENR	TLLRNSSGCE	ARRDEYRTEF	420
421	TTALQRVDFL	MGQFSEVLLT	SISTFIKGD	TIANLGTSEG	RFMQVVVSR	GPSTPHVNF	480
481	LDSHPVSPEV	IVEHTLNQNG	YTLVITGKKI	TKIPLNGLGC	RHFQSCSQCL	SAPPFVQCGW	540
541	CHDKCVRSEE	CLSGTWTQQI	CLPAIYKVF	NSAPLEGGTR	LTICGWDFGF	RRNNKFDLKK	600
600	TRVLLGNESC	TLTLESTMN	TLKCTVGPAM	NKHFNMSII	SNGHGTQYS	TFSYVDPVIT	660
661	SISPKYGPMA	GGTLLTLTGN	YLNNGNSRHI	SIGGKTCTLK	SVSNSILECY	TPAQTISTEF	720
721	AVKCLKIDLAN	RETSIFSIRE	DPIVYIEHPT	KSFISGGSTI	TGVGKNLSV	SVPRMIVNH	780
781	EAGRNFVAC	QHRSNSEIIC	CTTPSLQQLN	LQLPLKTKAF	FMLDGILSKY	FDLIYVHNPV	840
841	FKPFKPVMI	SMGNENVLEI	KGNDIDPEAV	KGEVLKVGNK	SCENIHLHSE	AVLCTVPNDL	900
901	LKLNSELNIE	WKQAISSTVL	GKVIVQPDQN	FTGLIAGVVS	ISTALLLLLG	FFLWL KRRQ	960
961	IKDLGSELVR	YDARVHTPHL	DRLVSARSVS	PTEMVSNES	VDYRATFPED	QFPNSSQNGS	1020
1021	CRQVQYPLTD	MSPILTSGDS	DISSPLLQNT	VHIDLALNP	ELVQAVQHVV	IGPSSLIHF	1080
1081	NEVIGRGHFG	CVYHGTLTLDN	DGKKIHCVAK	SLNRITDIGE	VSQFLTEGII	MKDFSHPNVL	1140
1141	SLLGICLRSE	GSPLVLPYM	KHDLRNFR	NETHNPTVKD	LIGFGLQVAK	GMKYLASKKF	1200
1201	VHRDLAARNC	MLDEKFTVKV	ADFGLARDMY	DKEYYSVHNC	TGAKLPVKWM	ALESLOTQKF	1260
1261	TTKSDVWSFG	VLLWELMTRG	APPYDPVNTF	DITVYLLQGR	RLLOPEYCPD	PLYEVMLKCW	1320
1321	HPKAEMRPSF	SELVSRISAI	FSTFIGEHYV	HVNATYVNVK	CVAPYPSLLS	SEDNADDEVD	1380
1381	TRPASFWETS						1440

blue: MET sequence expressed in recombinant protein **Red**: variant in recombinant protein

¹[NCBI/Protein](#) accession number NP_000236.2

Please notice:

Variant amino acid numbering beginning with Ser755 when referring to GenBank accession number J02958 / [NCBI/Protein](#) accession number AAA59591.1 (additional 18 aa exon between S755/G756, frequently found in the literature)