

MET Y1235D

MET proto-oncogene, receptor tyrosine kinase

Recombinant Human Active Protein Kinase

HGNC Symbol: MET

Synonyms: c-MET, HGFR

Product No.: 0993-0000-1

Lot: 002

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

Product identity: MET Y1235D Lot 002, was confirmed as MET with a mutation Y1235D by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 78,739 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: 0.340 µg/µl

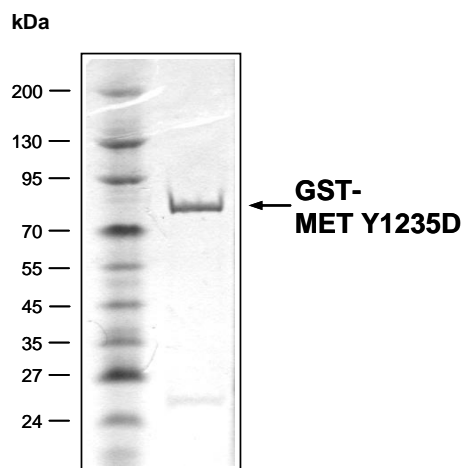
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

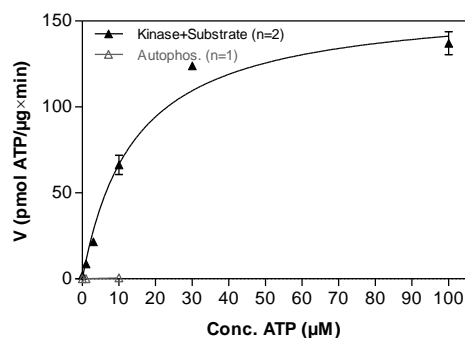
Specific kinase activity (P_i transfer): 161 pmol/µg × min

ATP-K_M: 14 µM

MET Y1235D Lot 002:
Coomassie stain



MET Y1235D Lot 002:
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, 20 µg/ml
 - Kinase: 1 µg/ml
- Filter binding assay
- MSPH membrane (Millipore)

Additional assay technology:

MET Y1235D Lot 002 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-MET Y1235D Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSM	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLP	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAI	PQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHG	240
241	LVPRGSPGLD	GICSIEEFKK	RKQIKDLGSE	LVRVDARVHT	PHLDRLVSAR	SVSPTTEMVS	300
301	NESVDYRATF	PEDQFPNSSQ	NGSCRQVQYP	LTDMSPILTS	GSDISSPLL	QNTVHIDL	360
361	LNPELVQAVQ	HVVIGPSSLI	VHFNEVIGRG	HFGCVYHGTL	LDNDGKKIHC	AVKSLNRTD	420
421	IGEVSQFLTE	GIIMKDFSHP	NVLSLLGICL	RSEGSPLVVL	PYMKHGDLRN	FIRNETHNPT	480
481	VKDLIGFGLQ	VAKGMKYLAS	KKFVHRDLAA	RNCMLDEKFT	VKVADFGLAR	DMYDKEYDSV	540
541	HNKTKAKLPV	KWMALESLOT	QKFTTKSDVW	SFGVLLWELM	TRGAPPYPDV	NTFDITVYLL	600
600	QGRRLLOPEY	CPDPLYEVML	KCWHPKAEMR	PSFSELSVRI	SAIFSTFIGE	HYVHVNATYV	660
661	NVKCVAPYPS	LLSSEDNADD	EVDTRPASFW	ETS			720

1-218: GST Red: HIS6-tag Pink: Thrombin cleavage site blue: MET fragment boxed: Y1235D

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	FCSINSLHG	YMEMPLECIL	300					
301	TEKRKRSTK	KEVFNILQAA	YVSKPGAQLA	RQIGASLND	ILFGVFAQSK	PDSAEPMDRS	360					
361	AMCAFPKYV	NDFFNKIVNK	NNVRCLQHFY	GNHEHCENR	TLLRNSSGCE	ARRDEYRTEF	420					
421	TTALQRVDF	MGQFSEVLLT	SISTFIKGD	TIANLGTSEG	RFMQVVVSR	GPSTPHVNF	480					
481	LDSHPVSPEV	IVEHTLNQNG	YTLVITGKI	TKIPLNGLC	RHFQSCSQCL	SAPPFVQCGW	540					
541	CHDKCVRSEE	CLSGTWTQQI	CLPAIYKVP	NSAPLEGGTR	LTICGWDFGF	RRNNKFDLKK	600					
600	TRVLLGNESC	TLTLESTMN	TLKCTVGPAM	NKHFNSII	SNGHGTQYS	TFSYVDPVIT	660					
661	SISPKYGPMA	GGTLLTLTGN	YLNNGNSRHI	SIGGKTCTLK	SVSNSILECY	TPAQTISTEF	720					
721	AVKCLKIDLAN	RETSIFSIRE	DPIVYIEIHT	KSFISGGSTI	TGVGKNLSV	SVPRMIVNH	780					
781	EAGRNFVAC	QHRNSSEIIC	CTTPSLQQLN	LQLPLKTKAF	FMLDGILSKY	FDLIYVHNPV	840					
841	FKPFKPVMI	SMGNENVLEI	KGNDIDPEAV	KGEVLKVGNK	SCENIHLHSE	AVLCTVPNDL	900					
901	LKLNSELNIE	WKQAISSVTL	GKVIVQPDQN	FTGLIAGVVS	ISTALLLLLG	FFLWLKRRKQ	960					
961	IKDLGSELVR	YDARVHTPHL	DRLVSARSVS	PTEMVSNES	VDYRATFPED	QFPNSSQNGS	1020					
1021	CRQVQYPLTD	MSPILTS	DISSPLLQNT	VHIDL	SALNP	ELVQAVQHVV	IGPSSLI	1080				
1081	NEVIGRGHFG	CVYHGTL	LDN	DGKKIHC	AVK	SLNRTD	DIGE	VSQFLTE	GII	MKDFSHP	NVL	1140
1141	SLLGICLRSE	GSPLVLPYM	KHGDLRN	FIR	NETHNPT	VKD	LIGFGLQ	VAK	GMKYL	ASKKE	1200	
1201	VHRDLAARNC	MLDEKFT	VKV	ADFGL	ARMY	DKEYSV	HNK	TGAKLP	VKWM	ALESLOT	QKF	1260
1261	TTKSDVWSFG	VLLWELM	TRG	APPYP	VDNTF	DITVYLL	QGR	RLLQPEY	CPD	PLYEVML	KCW	1320
1321	HPKAEMRPSF	SELVSRISAI	FSTFIGEHYV	HVNATYV	NVK	CVAPYPS	LLS	SEDNA	DEVD		1380	
1381	TRPASFW	ETS									1440	

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

¹NCBI/Protein accession number ¹NCBI/Protein accession number NP_000236.2

Please notice:

Heterogenous amino acid numbering in the literature.

Starting with Ser755 different amino acid numbering applies when referring to MET splice variant NCBI/Protein AAA59591.1 (additional 18 aa exon between S755/G756)

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