

ProQinase™ MET D1228H

MET proto-oncogene, receptor tyrosine kinase

Recombinant Human Active Protein Kinase

HGNC Symbol: MET

Synonyms: cMet, HGFR, RCCP2, DFNB97

Product No.: 0995-0000-1

Lot: 002

Description: Human MET C-terminal fragment, amino acids K₉₉₅-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 D1228H Lot 002, has been verified by mass spectrometry LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 78810 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 10 µl are not advisable. Avoid repeated freeze-thaw cycles!

Protein concentration: 0.374 µg/µl

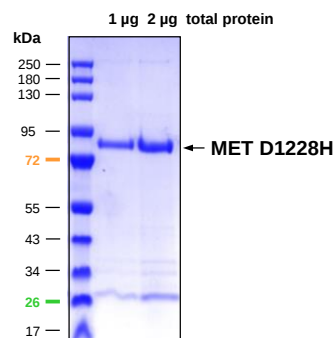
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

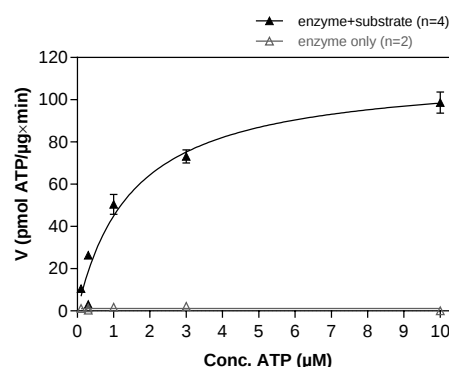
Specific kinase activity (P_i transfer): 113 pmol/µg*min

ATP-K_M: 1.5 µM

MET D1228H Lot 002: Coomassie stain



MET D1228H Lot 002: Determination of V_{max} and K_M value for ATP



- 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: 0.4 µg/ml

Assay technology:
Radiometric filter binding assay
MSIP membrane (96 well plate, Millipore)

Sequence information

GST-MET D1228H Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGWYKI	KGLVQPTRLL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHHG	RRRASVAAGI	240
241	LVPRGSPGLD	GICSIEEFKK	RKQIKDLGSE	LVRYDARVHT	PHLDRLVSAR	SVSPTTEMVS	300
301	NESVDYRATF	PEDQFPNSSQ	NGSCRQVQYP	LTDMSPI LTS	GSDDISSPLL	QNTVHIDLSA	360
361	LNPELVQAVQ	HVVIGPSSLI	VHFNEVIGRG	HFGCVYHGTL	LDNDGKKIHC	AVKSLNRITD	420
421	IGEVSQLTE	GIIMKDFSH	NVLSLLGICL	RSEGSPLVVL	PYMKHGDLRN	FIRNETHNPT	480
481	VKDLIGFGLQ	VAKGMKYLAS	KKFVHRDLAA	RNCMLDEKFT	VKVADFGLAR	HMYDKEYYSV	540
541	HNKTGAKLPV	KWMALESLOT	QKFTTKSDVW	SFGVLLWELM	TRGAPPYPDV	NTFDITVYLL	600
600	QGRRLQLPEY	CPDPLYEVML	KCWHPKAEMR	PSFSELVSRI	SAIFSTFIGE	HYVHV NATYV	660
661	NVKCVAPYPS	LLSSEDNADD	EVDTRPASFW	ETS			720

1-218: GST Red: HIS6-tag Pink: Thrombin cleavage site blue: MET fragment boxed: D1228H

MET wt ¹ Amino Acid Sequence							
1	MKAPAVLAPG	ILVLLFTLVQ	RSNGECKEAL	AKSEMNVNMK	YQLPNFTAET	PIQNVILHEH	60
61	HIFLGATNYI	YVLNEEDLQK	VAEYKTGPVL	EHPDCFPQD	CSSKANLSGG	VWKDNINMAL	120
121	VVDYYDDQL	ISCGSVNRGT	QQRHVFPNH	TADIQSEVHC	IFSPQIEEPS	QCPDCVSAL	180
181	GAKVLSSVKD	RFINFFVGNT	INSSYFPDHP	LHSISVRLK	ETKDGFMFLT	DQSYIDVLEP	240
241	FRDSYPIKYV	HAFESNNFIY	FLTVQRETLD	AQTFHTRIIR	FCSINSGLHS	YMEMPLECIL	300
301	TEKRKKRSTK	KEVFNIQAA	YVSKPGAQLA	RQIGASLNDD	ILFGVFAQSK	PDSAEPMDRS	360
361	AMCAFPKIVY	NDFFNKIVNK	NNVRCLQHFY	GNHEHCFNR	TLLRNSSGCE	ARRDEYRTEF	420
421	TTALQVRDLF	MGQFSEVLLT	SISTFIKGD	TIANLGTSEG	RFMQVVVRS	GPSTPHVNF	480
481	LDSPVSPV	IVEHTLNQNG	YTLVITGKKI	TKIPLNGLGC	RHFQSCSQCL	SAPPFVQCW	540
541	CHDKCVRSEE	CLSGTWTQOI	CLPAIYKVFP	NSAPLEGGTR	LTICGWDFGF	RRNNKFDLKK	600
600	TRVLLGNESC	TLTLSESTMN	TLKCTVGPM	NKHFNMSIII	SNGHGTQYS	TFSYVDPVIT	660
661	SISPKYGPMA	GGTLLTLTGN	YLNNGNSRHI	SIGGKTCTLK	SVSNSILECY	TPAQTISTEF	720
721	AVKLKIDLAN	RETSIFSIRE	DPIVYIEHPT	KSFISGGSTI	TGVGKNLNSV	SVPRMVINHV	780
781	EAGRNFVAC	QHRNSSEIIC	CTTPSLQQLN	LQLPLKTKAF	FMLDGILSKY	FDLIYVHNVP	840
841	FKPFKEPVM	SMGNENVLEI	KGNDIDPEAV	KGEVLKVGNG	SCENIHLHSE	AVLCTVPNDL	900
901	LKLNSLNLN	WKQAISSTVL	GKIVVQPDQN	FTGLIAGVVS	ISTALLLLLG	FFLWLKKRKQ	960
961	IKDLGSELVR	YDARVHTPHL	DRLVSARSVS	PTTEMVSNE	VDYRATFPED	QFPNSSQNGS	1020
1021	CRQVQYPLTD	MSPILTSQDS	DISSPLLQNT	VHIDLSALNP	ELVQAVQHV	IGPSSLIVHF	1080
1081	NEVIGRGHFG	CVYHGTLTLD	DGKKIHCAVK	SLNRITDIGE	VSQFLTEGII	MKDFSHPNVL	1140
1141	SLLGICLRSE	GSPLVLPYM	KHGDRLNFIR	NETHNPTVKD	LIGFGLQVAK	GMKYLASKKF	1200
1201	VHRDLAARNC	MLDEKFTVKV	ADFGLARDMY	DKEYYSVHNK	TGAKLPVKWM	ALESLOTQKF	1260
1261	TTKSDVWSFG	VLLWELMTRG	APPYPDVNTF	DITVYLLQGR	RLLQPEYCPD	PLYEVMLKCW	1320
1321	HPKAEMRPSF	SELVSRI	FSTFIGEHYV	HVNATYVNVK	CVAPYPSLLS	SEDNADDEVD	1380
1381	TRPASFWETS						1440

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

¹[NCBI/Protein](https://www.ncbi.nlm.nih.gov/Protein/) accession number NP_000236.2

Please notice:

Variant amino acid counting starts with Ser755 when referring to GenBank accession J02958 (additional 18 aa exon between S755/G756, frequently found in the literature)

Recombinant Proteins