

DDR2 wt

discoidin domain receptor tyrosine kinase 2

Recombinant Human Active Protein Kinase

HGNC Symbol: DDR2

Synonyms: MIG20a, NTRKR3, TKT, TYRO10

Product No.: 0771-0000-1

Lot: 002

Description: Human DDR2, C-terminal fragment, amino acids R₄₂₂-E₈₅₅ (as in [NCBI/Protein](#) entry NP_006173.2), activated, N-terminal GST-HIS₆ fusion protein with a 3C cleavage site, expressed in Sf9 insect cells

Product identity: DDR2 wt Lot 002, was confirmed as DDR2 by mass spectroscopy LC-ESI-MS/MS

Theoretical MW_{Fusion Protein}: 77,801 Da

Expression host: Sf9 insect cells

Purification: GST-Affinity Chromatography

Activation: in vitro auto activation

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: 0.102 µg/µl

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

Biochemical Parameters:

Specific kinase activity (P_i transfer): 89 pmol/µg × min

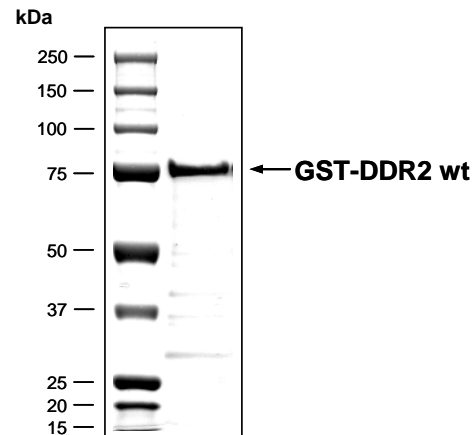
ATP-K_M: 2.3 µM

Additional assay technology:

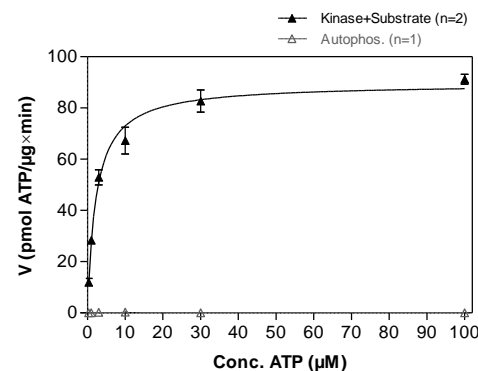
DDR2 wt Lot 002 was also successfully tested by ProQinase for the use with the ADP-Glo™ Kinase assay from Promega
ADP-Glo assay conditions may vary from radiometric assay conditions, please inquire for assay details

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DDR2 wt Lot 002: Coomassie stain



DDR2 wt 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, 80 µg/ml
 - Kinase: 2 µg/ml
- Filter binding assay
- MSFC membrane (Millipore)

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GST-DDR2 wt Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRL	LEYLEEKYEE	HLYERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDKVLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPPEML	KMFEDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHG	RDSLEVLFGG	240
241	PLAMLRQFWQ	KMLEKASRRM	LDDEMTVSL	LPSDSSMFNN	NRSSSPSEQG	SNSTYDRIFP	300
301	LRPDYQEPSR	LIRKLEFAP	GEEESGCSGV	VKPVQPSGPE	GVPHYAEDI	VNLQGVGTGN	360
361	TYSVPAVTMD	LLSGKDVAVE	EFPRKLLTFK	EKLGEQFGE	VHLCEVEGME	KFKDKDFALD	420
421	VSANQPVLVA	VKMLRADANK	NARNDFLKEI	KIMSRLKDPN	IIHLLAVCIT	DDPLCMITEY	480
481	MENGDLNQFL	SRHEPPNSSS	SDVRTVSYTN	LKFMATQIAS	GMKYLSSLNF	VHRDLATRNC	540
541	LVGKNYTIKI	ADFGMSRNLY	SGDYRIQGR	AVLPIRWSW	ESILLGKFTT	ASDVWAFGVT	600
600	LWETFTFCQE	QPYSQLSDEQ	VIENTGEFFR	DQGRQTYLPQ	PAICPDSVYK	LMLSCWRRDT	660
661	KNRPSFQEIH	LLLLQGD					720

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: DDR2 fragment

DDR2 wt ¹ Amino Acid Sequence							
1	MILIPRMLLV	LFLLLPILSS	AKAQVNPAIC	RYPLGMSGGQ	IPDEDITASS	QWSESTAAY	60
61	GRLDSEEGDG	AWCPEIPVEP	DDLKEFLQID	LHTLHFITLV	GTQGRHAGGH	GIEFAPMYKI	120
121	NYSRDGTRWI	SWRNRHGKQV	LDGNSNPYDI	FLKDLEPIV	ARFVRFIPVT	DHSMNVCMRV	180
181	ELYGCVWLDG	LVSYNAPAGQ	QFVLPGGSI	YLNDSVYDGA	VGYSMTEGLG	QLTDGVSGLD	240
241	DFTQTHEYHV	WPGYDYVGR	NESATNGYIE	IMFEFDRIRN	FTTMKVHCNN	MFAKGVKIFK	300
301	EVQCYFRSEA	SEWEPNAISF	PLVLDDVNPS	ARFVTVPLHH	RMASAIKCQY	HFADTWMMFS	360
361	EITFQSDAAM	YNNSEALPTS	PMAPTTYDPM	LKVDDSNTRI	LIGCLVAIIF	ILLAIIVIIL	420
421	WRQFWQKMLE	KASRRMLDDE	MTVSLSLPSD	SSMFNNRNS	SPSEQGSNST	YDRIFPLRPD	480
481	YQEPSRLIRK	LPEFAPGEEE	SGCSGVVKPV	QPSGPEGVPH	YAEADIVNLQ	GVTGGNTYSV	540
541	PAVTMDLLSG	KDVAVEEFPR	KLLTFKEKLG	EGQFGEVHLC	EVEGMEKFKD	KDFALDVSAN	600
600	QPVLVAVKML	RADANKNARN	DFLKEIKIMS	RLKDPNIIHL	LAVCITDDPL	CMITEYMENG	660
661	DLNQFLSRHE	PPNSSSSDVR	TVSYTNLFEM	ATQIASGMKY	LSSLNFVHRD	LATRNCVLGK	720
721	NYTIKIADFG	MSRNLYSGDY	YRIQGRAVLP	IRWMSWESIL	LGKFTTASDV	WAFGVTLWET	780
781	FTFCQEQPYS	QLSDEQVIEN	TGEFFRDQGR	QTYLPQPAIC	PDSVYKMLLS	CWRRDTKNRP	840
841	SFQEIHLLLL	QQGD					900

blue: DDR2 sequence expressed in recombinant protein

¹[NCBI/Protein](https://www.ncbi.nlm.nih.gov/Protein/np_006173.2) accession number NP_006173.2

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