

MRC PPU REAGENTS

Standard Operating Procedure

Preparation of TSC22D2 [4 – 780]

Enzyme description:- TSC22D2 [4 - 780]

Clone number:- DU 6785

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-

Monoisotopic 105, 639.82 daltons

Average Mass 105, 705.95 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 5.09

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 270mM sucrose, 150 mM NaCl, 0.1 mM EGTA,
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 1 mM benzamidine, 0.2 mM PMSF

Storage temperature:- -70 °C

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Clone Data Sheet

TSC22D2 [4 - 780]

Protein TSC22D2 [4 - 780]

Clone number DU 6785

Species Human

Accession number NM_014779.4

Tags N-terminal GST

Bacterially expressed protein

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG
LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGA
VLDIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDH
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS
KYIAWPLQGWQATFGGGDHPPKSDLEVL FQG PLGSMPAKKKSCFQITSV
TTAQVATSITEDTESLDDPDESRTEDVSSEIFDVS RATDYGP EVCERS
SSEETLNNVGDAETPGTVSPNLLLDGQLAAAAAPANGGGVVSARSVSG
ALASTLAAAATSAPAPGAPGGPQLAGSSAGPVTAAPSQPPTTCSSRFV
IKLDHGS GEPYRRGRWTCMEYYERDS DSSVLTRSGDCIRHSSTFDQTAE
RDSGLGATGGSVVVVVASMQGAHG PESGTDSSLTAVS QLP PSEKMSQPT
PAQPQSF SVGQPQPPPPVGGAVAQSSAPL PPFPGAATGPQPMMAAQ P
SQPQGAGPGGQTL PPTNVTLAQPAMSLPPQPGPAVGAPAAQQPQQFAYP
QPQIPPGHLLPVQPSGQSEYLOQH VAGLQPPSPAQPSSTGAAASPATAA
TLPVGTGQNASSVGAQLMGASSQPSEAMAPRTGPAQGGQVAPCQPTGVP
PATVGGVVQPCLGPAGAGQPQSVPPPQMGSGPLSAVPGGPHAVVPGVP
NVPAAVPAPSVPSVSTTSVTMPNVPAPLAQSQQLSSHTPVSRSSSI IQH
VGLPLAPGTHSAP TSLPQSDLSQFQTQTQPLVGVQVDDTRRKSEPLQPP
LSLIAENKPVVKPPVADSLANPLQLTPMNSLATS VFSIAIPVDGEDRN
PSTAFYQAFHLN TLKESKSLWDSASGGGVVAIDNKIEQAMDLVKSHLMY
AVREEVEVLKEQIKELVERN SLLERENALLKSLSSNDQLS QLPTQOANP
GSTSQQQAVIAQPPQPTQPPQPNVSSA

Native sequence Amino acids M4 – A780 (end) of human TSC22D2.
Residue M232 of the fusion protein is equivalent to M4 of the native enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage PreScission (LEVLFQGP) residues 221 – 228.

Cloning sites *Bam*H1 and *Not*1 sites of pGex6P1

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Nucleotide Sequence Of Insert

ggatccATGCCGGCCAAGAAGAAGAGCTGCTTCCAGATCACCAGTGTACCACGGCCCAGG
TGGCCACTAGCATCACCGAGGACACCGAGAGCTTGGACGACCCGGACGAGTCACGCACAGA
GGACGTCTCTTCCGAGATTTTCGACGTCTCTCGGGCCACGGATTATGGCCCTGAGGAGGTC
TGCGAGCGCAGCTCTTCCGAAGAGACGCTTAAACAATGTTGGGGATGCGGAGACTCCCGGGA
CCGTCTCCCAAACCTCCTCCTAGATGGGCAGCTGGCAGCGGCGGGCTGCTGCTCCCGCCAA
CGGAGGAGGAGTCGTTTCGGCCCGGAGCGTGTCTGGGGCGCTCGCCAGTACCCTGGCGGGC
GCTGCCACTTCGGCCCCCGCCCCGGAGCACCCGGCGGGCCCCAGCTCGCGGGGCTCATCCG
CCGGGCCAGTGACTGCAGCCCCATCTCAGCCTCCCACCACATGTAGTTCCCGTTTTTCGCGT
GATCAAGCTGGACCACGGGAGCGGAGAGCCCTATAGACGCGGCGGATGGACGTGTATGGAA
TACTATGAGAGGGATTTCAGACAGCAGCGTCTGACTAGATCCGGGGATTGCATTAGACACA
GCAGTACTTTTGACCAGACTGCGGAGCGGGACAGCGGCCTGGGCGCCACCGGAGGGTTCGGT
GGTGGTAGTAGTGGCCTCCATGCAGGGGGCGCACGGGCCCCGAGTCGGGAACTGACAGCTCC
TTGACTGCTGTGTACAGCTACCCCCGTCGGAGAAAAATGAGCCAGCCACTCCGGCCAGC
CGCAGAGTTTTAGCGTTGGGCAGCCACAGCCGCCGCCACCCGTAGGTGGGGCTGTGGC
TCAAAGCTCGGCTCCGCTGCCGCCGTTCCTCGGAGCCGCGACCGGGCCGAGCCAATGATG
GCAGCCGCGCAGCCAGCCAGCCCCAGGGAGCGGGGCCCGGGGACAGACTCTGCCGCCGA
CGAATGTAACCCCTGGCGCAGCCGGCTATGTCCCTGCCCTCCGCAGCCGGGCCCTGCAGTGGG
CGCCCCCGCGGCGCAGCAGCCCCAGCAGTTCGCGTATCCTCAGCCTCAGATAACCGCCGGA
CATTTGCTGCCCGTCCAGCCCTCCGGCCAGAGTGAGTACCTGCAGCAGCACGTGGCCGGCC
TGCAGCCGCCAAGCCCCGCGCAGCCCTCGTCCACCGGCGCCGCGAGCGAGCCCCGCCACGGC
GGCCACCCTTCCCGTGGGCACCGGCCAGAATGCTTCCCTCGGTGGGCGCGCAGCTCATGGGC
GCGTCTTCCCAGCCCAGCGAAGCCATGGCCCCCGGACGGGACCAGCGCAAGGCGGGCAGG
TCGCGCCTTGTGAGCCGACTGGAGTGCCCCGGCTACTGTGGGAGGCGTGGTGCAGCCGTG
CCTCGGTCTGCGGGGGCTGGGCAGCCCCAGTCCGTGCCCTCCGCCGAGATGGGTGGCAGT
GGTCCGCTGTGAGCCGTACCTGGTGGCCCTCACGCCGTGGTGCCCGGAGTTCCAAACGTGC
CTGCAGCCGTGCCCGCTCCAAGCGTGCCTAGTGTGTCTACCACTTCTGTTACTATGCCAAA
TGTACCCGCGCCTCTGGCCCAGTCGCAACAGCTGAGCAGCCATACGCCAGTCAGCAGGAGC
AGCAGCATAATCCAGCATGTTGGGCTGCCCTTAGCGCCAGGCACACACAGCGCACCAACAA
GTCTACCACAGTCTGACCTAAGCCAGTTTTCAAACCTCAGACCCAGCCTTTAGTCGGGCAAGT
CGACGATACTAGAAGAAAATCAGAACCCTACCTCAACCACCACCTTCTCTCATTGCTGAA
AATAAGCCTGTTGTGAAGCCGCCTGTTGCAGATTCCTGGCAAACCCCTTCAGTTAACAC
CTATGAACAGTCTGGCCACCTCTGTATTCAGCATAGCTATTCCTGTTGATGGTGATGAAGA
CAGGAATCCTTCAACTGCTTTCACCAAGCGTTCATTTGAACACGTAAAGGAATCAAAG
AGCCTCTGGGATAGTGCATCTGGGGGAGGTGTTGTAGCCATTGACAACAAAATAGAACAAG
CAATGGATCTGGTGAAAAGCCATTTGATGTATGCAGTAAGAGAAGAAGTGGAAAGTTTTAAA
GGAACAAATAAAAGAATTAGTTGAAAGAACTCTTTACTTGAACGAGAAAATGCACTGTTA
AAATCTCTTTCAAGCAATGATCAATTATCCCAACTCCCAACCCAACAGGCCAATCCTGGTA
GCACTTCTCAACAGCAAGCAGTGATAGCACAGCCTCCGCAGCCAACGCAACCTCCACAGCA
GCCGAATGTCTCCTCAGCAtaagcggccgc