

MRC PPU REAGENTS

Standard Operating Procedure

Preparation of TSC22D4 [1 – 395]

Enzyme description:- TSC22D4 [1 - 395]

Clone number:- DU 10365

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-

Monoisotopic 68, 821.00 daltons

Average Mass 68, 864.36 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.12

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

TSC22D4 [1 - 395]

<u>Protein</u>	TSC22D4 [1 - 395]
<u>Clone number</u>	DU 10365
<u>Species</u>	Human
<u>Accession number</u>	AAH01486.1
<u>Tags</u>	N-terminal GST
<u>Bacterially expressed protein</u>	<p>MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGA VLDIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVL FQGPLGSPEFALMHTSMSGGK KKSSFQITSVTTDYEGPGSPGASDPPTPQPPTGPPRLPNGEPSDPGG KGTPRNGSPPPGAPSSRFVVKLPHGLGEPYRRGRWTCVDVYERDLEPH SFGGLLEGIRGASGGAGGRSLDSRLELASLGLGAPTPPSGLSQGPTSWL RPPPTSPGPQARSFTGGLGQLVVPSKAKAEKPPLSASSPQORPEPETG ESAGTSRAATPLPSLRVEAEAGGSGARTPPLSRRKAVDMRLRMELGAPE EMGQVPPLD SRPSSPALYFTHDASLVHKSPDPFGAVAAQKFS LAHSMLA ISGHLDSDDDSGSGSLVGIDNKIEQAMD LVKSHLMFAVREEVEVLKEQI RELAERNAALEQENGLLRALASPEQLAQLPSSGV PRLGPPAPNGPSV</p>
<u>Native sequence</u>	<p>Amino acids M1 – V395 (end) of human TSC22D4. Residue M241 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.</p>
<u>Protease cleavage</u>	PreScission (<u>LEVLFQGP</u>) residues 221 – 228.
<u>Cloning sites</u>	<i>Spe</i> 1 and <i>Not</i> 1 sites of pGex6P1

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Nucleotide Sequence Of Insert

ggatccccggaattcgcccttatgcatactagtATGAGCGGGGGCAAGAAGAAGAGTAGTT
TCCAAATCACCAGCGTCACCACGGACTATGAGGGCCCTGGGAGCCAGGGGCTTCGGATCC
CCCTACCCACAGCCCCAACCGGGCCCCCGCCCCGCCTGCCAATGGGGAGCCCAGCCCC
GATCCGGGGGGCAAGGGCACCCCCCGGAATGGCTCCCCACCACCTGGGGCCCCTTCTCC
GTTTCCGGGTGGTGAAGCTGCCCCACGGCCTGGGAGAGCCTTATCGCCGCGGTTCGCTGGAC
GTGTGTGGATGTTTATGAGCGAGACCTGGAGCCCCACAGCTTCGGCGGACTCCTGGAGGGA
ATTCGAGGGGCTCAGGGGGCGCCGGGGGCAGATCTTTGGATTCAGGTTGGAGCTGGCCA
GCCTCGGCCTGGGCGCCCCACCCACCGTCAGGCCTGTCTCAGGGCCCCACCTCCTGGCT
CCGTCCACCCCCACCTCTCCTGGACCTCAGGCCCGCTCCTTCACTGGGGGACTGGGCCAG
CTGGTGGTGCCCAGCAAAGCCAAGGCAGAGAAACCCCCACTGTCGGCCTCCTCACCCACG
AGCGCCCCCAGAGCCTGAGACCGGTGAGAGTGCGGGCACATCCCGGGCTGCCACGCCCT
GCCCTCTCTGAGGGTGAAGCGGAGGCTGGGGGCTCAGGGGCCAGGACCCCTCCACTGTCC
CGGAGGAAAGCTGTAGACATGCGGCTGCGGATGGAGTTGGGTGCTCCAGAAGAGATGGGGC
AGGTGCCCCACTTGACTCTCGCCCCAGCTCCCCGGCCCTTACTTCACCCACGATGCCAG
CCTGGTTCACAAATCTCCAGACCCCTTCGGAGCAGTAGCAGCTCAGAAGTTCAGCCTGGCC
CACTCCATGTTGGCCATCAGTGGTACCTAGACAGCGACGATGATAGTGGCTCCGGAAGCC
TGGTTGGCATTGACAACAAAATCGAGCAAGCCATGGACTTGGTGAAGTCCACCTCATGTT
TGCGGTCCGGGAGGAGGTGGAGGTGCTGAAGGAGCAGATCCGGGAACGGCGGAGCGGAAC
GCTGCGCTGGAGCAGGAGAATGGGCTGCTGCGCGCCCTGGCCAGCCCGGAGCAGCTGGCTC
AGCTGCCCTCCTCGGGGGTCCCACGGCTTGGGCCCCCTGCGCCAATGGGCCCTCCGTctg
agcgccgc