MRCPPU REAGENTS and SERVICES

Standard Operating Procedure

Preparation of CMTR1 [143 – 835]

Enzyme description:- CMTR1 [143 - 835]

Clone number:- DU 46710

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Agarose

Calculated molecular mass:-
Monoisotopic 107, 417.41 daltons
Average Mass 107, 486.75 daltons
[cysteines reduced, methionines have not been oxidized]

Theoretical pI:- 6.20

Purity:- >80 %

Enzyme storage buffer:-
50 mM Tris-HCl pH 7.5, 0.1 mM EGTA, 150 mM NaCl, 0.1 % 2-mercaptoethanol, 270 mM Sucrose

Storage temperature:- -70 °C

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Clone Data Sheet

CMTR1 [143 - 835]

Protein CMTR1 [143 – 835]

Clone number DU 46710

Species Human

Accession number Q8N1G2

Tags N-terminal GST

Bacterially expressed protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG
LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA
VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS
KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGSPNSRVE**WRDEPEPS**
ACEQVSWFPECTTEIPDTQEMSDWMVVGKRKMIIEDETEFCGEELLHSV
LQCKSVFDVLDGEEMRRARTRANPYEMIRGVFFLNRAAMKMANMDFVFD
RMFTNPRDSYGKPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKG
FGMTLKGPNDFKLEDFYSASSELFEPYYGEGGIDGDGDITRPENISAFR
NFVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCQFLMALSIV
RTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITSRPANSERYV
VCKGLKVGIDDVRDYLFAVNIKLNQLRNTDSDVNLVVPLEVIKGDHEFT
DYMIRSNESHCSLQIKALAKIHAFVQDTTLSEPRQAEIRKECLRLWGIP
DQARVAPSSSDPKSKFFELIQGTEIDIFSYKPTLLTSKTLEKIRPVFDY
RCMVSGSEQKFLIGLGKSQIYTWDGRQSDRWIKLDLKTELPRDTLLSVE
IVHELKGEGKAQRKISAIHILDVLVLNGTDVREQHFNQRIQLAEKFVKA
VSKPSRPDMNPIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGR
DDRHFVPMGLYIVRTVNEPWTMGFSKSFKKKFFYNKKTKDSTFDLPADS
IAPFHICYYGRLFWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQMHRA

Native sequence Amino acids W143 – A835 (end residue) of human CMTR1. Residue W238 of the fusion protein is equivalent to W143 of the native enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage PreScission (LEVLFQGP) residues 221 - 229

Cloning sites *Sal*1 and *Not*1 into *Xho1* and *Not*1 sites of pGEX 6P-1

Nucleotide Sequence

ggctcgagTGGCGAGATGAGCCAGAGCCCAGTGCTTGTGAGCAGGTGTC
ATGGTTTCCAGAATGTACCACTGAAATTCCTGACACTCAGGAAATGAGC
GATTGGATGGTGGTGGGAAAGAGAAAGATGATTATTGAAGATGAAACAG
AGTTTTGTGGGGAAGAGCTGCTTCACAGTGTGTTGCAGTGTAAGAGCGT
GTTTGATGTCTTGGATGGGGAAGAGATGCGGCGAGCTCGGACTCGGGCC
AATCCCTATGAGATGATCCGAGGAGTCTTCTTTCTAAACAGGGCAGCAA
TGAAGATGGCTAACATGGATTTTGTATTTGATCGCATGTTCACAAATCC
GCGGGACTCTTATGGGAAGCCACTGGTGAAGGACCGGGAAGCTGAGCTT
CTGTACTTTGCTGATGTCTGCGCAGGCCCAGGTGGCTTCTCAGAGTATG
TGCTGTGGAGGAAGAAGTGGCATGCAAAGGGCTTTGGAATGACTTTGAA
GGGCCCTAATGACTTCAAGCTGGAGGACTTCTACTCTGCTTCCAGTGAA
CTCTTCGAACCCTACTATGGTGAGGGTGGGATTGATGGAGATGGAGATA
TCACCCGCCCAGAGAACATCTCTGCTTTTCGGAATTTTGTCCTGGATAA
CACAGATCGCAAGGGTGTCCATTTTCTGATGGCTGATGGGGGTTTCTCG
GTGGAGGGGCAGGAGAACCTGCAGGAGATCCTCAGCAAGCAGCTGCTTC
TGTGTCAGTTCCTCATGGCGCTGTCCATTGTCCGGACAGGAGGCCACTT
CATCTGTAAAACCTTTGACCTGTTCACACCGTTTAGTGTGGGGCTTGTC
TACCTGCTGTACTGCTGCTTTGAACGAGTTTGTCTCTTCAAGCCTATTA
CCAGCCGTCCTGCCAACTCAGAGAGGTATGTGGTGTGCAAGGGCCTGAA
GGTGGGCATAGATGATGTTCGGGATTACCTCTTCGCAGTGAATATTAAA
CTCAATCAGCTGCGGAACACGGATTCCGACGTCAACTTGGTGGTCCCCC
TGGAGGTGATCAAGGGAGACCATGAATTTACTGACTACATGATACGGTC
CAATGAGAGCCACTGTAGTCTGCAGATCAAAGCTCTGGCGAAAATCCAT
GCCTTTGTTCAAGACACGACACTGAGTGAGCCTCGACAGGCAGAGATAC
GGAAGGAGTGCCTCCGACTCTGGGGGATCCCAGACCAGGCTCGTGTGGC
TCCTTCTTCCTCCGACCCTAAATCGAAGTTCTTTGAGCTAATCCAGGGC
ACTGAGATTGACATCTTCAGCTACAAGCCCACACTGCTCACCTCTAAAA
CCCTGGAGAAGATCCGCCCTGTGTTTGACTACCGCTGCATGGTATCTGG
CAGTGAGCAGAAGTTCCTCATCGGCCTGGGGAAATCCCAGATCTACACA
TGGGATGGCCGCCAGTCAGACCGCTGGATCAAGCTAGACCTGAAGACAG
AGCTGCCCCGGGACACTCTGCTATCTGTGGAAATTGTGCATGAGCTGAA
AGGGGAGGGGAAGGCCCAGAGGAAGATCAGTGCCATCCACATCCTCGAT
GTCCTTGTGCTGAATGGCACCGACGTTCGGGAGCAGCACTTTAACCAGC
GAATTCAGCTTGCCGAGAAATTTGTGAAAGCCGTTTCCAAGCCTAGTCG
GCCCGACATGAATCCCATCAGGGTGAAGGAGGTGTACAGACTGGAAGAG
ATGGAGAAGATTTTTGTCAGGTTGGAGATGAAGATCATCAAGGGCTCCA
GTGGCACCCCAAAGCTCAGCTACACAGGGCGTGATGACCGGCACTTTGT
ACCCATGGGCCTCTACATCGTCAGGACAGTGAATGAGCCCTGGACTATG
GGATTCAGCAAAAGCTTCAAGAAGAAGTTCTTCTACAACAAGAAAACCA
AGGACTCTACTTTTGACCTCCCTGCAGACTCCATTGCCCCATTTCACAT
TTGCTACTATGGCCGGCTCTTCTGGGAGTGGGGGGATGGCATTCGTGTG
CATGACTCCCAGAAGCCCCAGGACCAGGACAAGCTGTCCAAGGAGGACG
TCCTCTCCTTCATCCAGATGCACAGGGCCtaagcggccgc