MRCPPU REAGENTS and SERVICES

Standard Operating Procedure

Preparation of CMTR1 [1 – 835]

Enzyme description:- CMTR1 [1 - 835]

Clone number:- DU 42831

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Agarose

Calculated molecular mass:-
Monoisotopic 122, 978.05 daltons
Average Mass 123, 056.96 daltons
[cysteines reduced, methionines have not been oxidized]

Theoretical pI:- 6.26

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 [1 - 835]

Protein	CMTR1 [1 – 835]
Clone number	DU 42831
Species	Human
Accession number	Q8N1G2
Tags	N-terminal GST
Bacterially expressed protein	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSS KYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGSPEFPGRLD**MKRRTD** **PECTAPIKKQKKRVAELALSLSSTSDDEPPSSVSHGAKASTTSLSGSDS** **ETEGKQHSSDSFDDAFKADSLVEGTSSRYSMYNSVSQKLMAKMGFREGE** **GLGKYSQGRKDIVEASSQKGRRGLGLTLRGFDQELNVDWRDEPEPSACE** **QVSWFPECTTEIPDTQEMSDWMVVGKRKMIIEDETEFCGEELLHSVLQC** **KSVFDVLDGEEMRRARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMF** **TNPRDSYGKPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGM** **TLKGPNDFKLEDFYSASSELFEPYYGEGGIDGDGDITRPENISAFRNFV** **LDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCQFLMALSIVRTG** **GHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITSRPANSERYVVCK** **GLKVGIDDVRDYLFAVNIKLNQLRNTDSDVNLVVPLEVIKGDHEFTDYM** **IRSNESHCSLQIKALAKIHAFVQDTTLSEPRQAEIRKECLRLWGIPDQA** **RVAPSSSDPKSKFFELIQGTEIDIFSYKPTLLTSKTLEKIRPVFDYRCM** **VSGSEQKFLIGLGKSQIYTWDGRQSDRWIKLDLKTELPRDTLLSVEIVH** **ELKGEGKAQRKISAIHILDVLVLNGTDVREQHFNQRIQLAEKFVKAVSK** **PSRPDMNPIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGRDDR** **HFVPMGLYIVRTVNEPWTMGFSKSFKKKFFYNKKTKDSTFDLPADSIAP** **FHICYYGRLFWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQMHRA**
Native sequence	Amino acids M1 – A835 (end residue) of human CMTR1. Residue M240 of the fusion protein is equivalent to M1 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

ATGAAGAGGAGAACTGACCCAGAATGCACTGCCCCCATCAAGAAACAGAAAAAAAGAGT
TGCAGAGCTTGCCCTGAGCCTCAGCTCCACGTCCGATGATGAACCTCCCTCCTCTGTCA
GTCATGGAGCAAAAGCATCTACTACAAGCCTTAGTGGGTCTGATAGTGAGACCGAGGGG
AAACAACACAGCTCTGACTCTTTTGACGATGCATTCAAAGCAGACTCTCTTGTGGAAGG
AACTTCTTCTCGCTATTCCATGTATAATAGCGTCTCCCAGAAGCTTATGGCCAAGATGG
GCTTCAGGGAAGGTGAAGGATTGGGTAAATACAGCCAGGGTCGGAAGGACATCGTTGAG
GCTTCCAGTCAGAAAGGTCGAAGAGGCTTGGGTCTGACACTCCGGGGCTTTGACCAGGA
GCTGAACGTGGACTGGCGAGATGAGCCAGAGCCCAGTGCTTGTGAGCAGGTGTCATGGT
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CATTGCCCCATTTCACATTTGCTACTATGGCCGGCTCTTCTGGGAGTGGGGGGATGGCA
TTCGTGTGCATGACTCCCAGAAGCCCCAGGACCAGGACAAGCTGTCCAAGGAGGACGTC
CTCTCCTTCATCCAGATGCACAGGGCCtaa