

Division of Signal Transduction Therapy

Standard Operating Procedure

Preparation of KCC4 [872 – end]

Enzyme description:- KCC4 [872 - end]

Clone number:- DU 30601

Source:- Recombinant

Expression system:- *E.coli*

Tag:- N-terminal GST

Purification method:- GSH Sepharose

Calculated molecular mass:-

Monoisotopic 51, 299.12 daltons

Average Mass 51, 332.33 daltons

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.82

Purity:- >80 %

Enzyme storage buffer:-

50 mM Tris-HCl pH 7.5, 270 mM 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

KCC4 [872 - 1083]

<u>Protein</u>	KCC4 [872 - 1083]
<u>Clone number</u>	DU 30601
<u>Species</u>	Human
<u>Accession number</u>	NM_006598.2
<u>Tags</u>	N-terminal GST
<u>Bacterially expressed protein</u>	<p>MSPILGYWKIKGLVQPTRLLEYLEEKYEHLIERDEGDKWRNKKFELG LEFPNLPPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGA VLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS KYIAWPLQGWOATFGGGDHPPKSDLEVLFFQGPLGSRKCRMRIFTVAQVD DNSIQMKKDLQMFLYHLRISAEVEVEMVENDISAFETYERTLMMEQRSQ MLKQMQLSKNEQEREAQLIHDRNTASHTAAAARTQAPPPTPKVQMTWTR EKLIAEKYRSRDTSLSGFKDLFSMKPDQSNVRRMHTAVKLNGVVLNKSQ DAQLVLLNMPGPPKNRQGDENYMEFLEVLTEGLNRVLLVRGGGREVITII YS</p>
<u>Native sequence</u>	<p>Amino acids R872 – S1083 (end) of human KCC4. Residue R232 of the fusion protein is equivalent to R872 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>Bam</i> H1 sites of pGEX6P-1

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Nucleotide Sequence of insert

ggatccAGGAAGTGCCGGATGCGTATCTTCACCGTGGCCCAGGTGGACGACAACAGCATCCAGATG
AAGAAGGACCTGCAGATGTTCTTGTACCACTTGCGCATCAGCGCCGAGGTGGAGGTGGTGGAGATG
GTTGAAAACGACATATCTGCTTTCACCTACGAGAGGACACTAATGATGGAGCAGAGGTCGCAGATG
CTGAAGCAGATGCAGCTGTCCAAGAACGAGCAGGAGCGAGAGGCCAGCTGATCCACGACAGGAAC
ACCGCGTCCCACACCGCGGCGGCAGCCAGGACCCAAGCGCCGCCTACGCCAGACAAGGTGCAGATG
ACCTGGACCAGGGAGAAGCTGATCGCTGAGAAGTACAGGAGCAGAGACACCAGCCTATCTGGTTTC
AAAGACCTCTTCAGCATGAAGCCGGACCAGTCCAACGTCAGGCGGATGCACACGGCTGTGAAGCTC
AATGGCGTCGTCCTCAACAAGTCCCAGGATGCGCAGCTGGTCCTGCTCAACATGCCAGGTCTCTCC
AAAAACCGGCAGGGAGACGAGA ACTACATGGAGTTTCTTGAAGTCCTGACCGAGGGGCTGAACAGA
GTCCTCTGGTCAGGGGTGGCGGCCGGGAGGTGATCACCATCTACTCctaaaggatcc

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