

Division of Signal Transduction Therapy

Standard Operation Procedure

GST-Cezanne C194A

Enzyme description:- GST-Cezanne C194A

Clone number:- DU25154

Source:- BL21 Recombinant

Tag:- N-terminal GST

Purification method:- GSH sepharose

Expression level:- 1 mg/L

Calculated molecular mass:-

Monoisotopic 119615 Da

Average Mass 119687 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.36

Purity:- 50%

Enzyme storage buffer:-

50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT

Storage temperature:- -80°C

Assay:-

Ub-Rho110-Gly cleavage assay monitored by Ex/Em 485/535 nm

Assay buffer:-

40 mM Tris pH 7.5, 100 mM NaCl, 5 mM DTT, 0.01% Triton X-100, 0.005% Ovalbumin, 0.5 µM Ub-Rho110-Gly

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Clone Data Sheet

GST-Cezanne C194A

<u>Protein</u>	GST-Cezanne
<u>Synonyms</u>	OTUD7B, ZA20D1
<u>Clone Number</u>	DU25154
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q6GQQ9
<u>Tags</u>	N-terminal GST tag
<u>Amino acid sequence of expressed protein</u>	<p>MSPILGYWKIKGLVQPTRLLLEYLEEKYEHLIERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLFOGPLGSPEFMTLMDAVLSDFVRST GAEPGLARDLLEEGKNWDVNAALSDFEQLRQVHAGNLPPSFSEGSGGSRTP EKGFSDREPTRPPRPILQRQDDIVQEKRLSRGISHASSIVSLARSHVSS NGGGGGSNEHPLEMPICAFQLPDLTVYNEDFRSFIERDLIEQSMLVALEQ AGRLNWWVSVDPTSQRLLPLATTGDGNALLHAASLGMWGFHDRDLMLRKA LYALMEKGV EKEALKRRRWQQTQONKESGLVYTEDEWQKEWNELIKLAS SEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVLRPIVVVADT MLRDSGG EAFAPIFGGIYLPLEVPASQCHRSPVLAYDQAHFSALVSME QKENTKEQAVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVIL SLEVKLHLLHSYMNVKWIPLSSDAQAPLAQPESPTASAGDEPRSTPESGD SDKESVGSSTSNEGGRRKEKSKRDREKDKKRADSVANKLGSFGKTLGSK LKKNMGGLMHSGSKPGGVGTGLGGSSGTETLEKKKKNSLKS WKGGKEEA AGDGPVSEKPPAESVGNNGGSKYSQEVMSLSILRTAMQEGKFI FVGTLK MGRHQYQEEMIQRYS DAEERFLAEQKQKEAERKIMNGGIGGGPPPAK PEPDAREEQPTGPPAESRAMAFSTGYPGDFTIPRPSGGGVHCQEP RRQLA GGPCVGG LPPYATFPRQCPPGRPYPHQDSIPSLEPGSHSKDGLHRGALLP PPYRVADSY SNGYREPPEPDGWAGGLRGLPPTQTCKKQPNC SFYGH PETN NFCSCCYREELRRREREPDGELLVHRF</p>
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	Precision site underlined
<u>Cloning sites</u>	EcoR1 / Not1

**DNA sequence of
insert**

GAATTCATGACCCTGGACATGGATGCTGTTCTGTCTCAGATTTTGTCCGTTCAC
AGGAGCAGAGCCAGGGCTAGCGCGAGATCTCCTAGAAGGAAAGAATTGGGATG
TGAATGCCGCCCTCAGTGATTTTGAACAGCTACGTCAAGTCCATGCTGGAAAC
CTACCCCATCCTTTAGTGAGGGGAGTGGTGGCTCCAGGACCCCTGAAAAAGG
GTTTTCTGACAGAGAGCCTACTCGCCCTCCCGACCCATCCTCCAGCGGCAGG
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