

Division of Signal Transduction Therapy

Standard Operation Procedure

GST-Cezanne

<u>Enzyme description:-</u>	GST-Cezanne
<u>Clone number:-</u>	SC20899
<u>Source:-</u>	BL21 Recombinant
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH sepharose
<u>Expression level:-</u>	1 mg/L

Calculated molecular mass:-

Monoisotopic	119647 Da
Average Mass	119719 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

<u>Protein</u>	GST-Cezanne
<u>Synonyms</u>	OTUD7B, ZA20D1
<u>Clone Number</u>	SC20899
<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>MSPILGYWKIKGLVQPTRLLEYLEEKYEHLIERDEGDKWRNKKFELGL EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL DIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTH PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA WPLQGWQATFGGGDHPPKSDLEVLFOGPLGSPEFMTLMDAVLSDFVRS GAEPGLARDLLEGKNWDVNAALSDFEQLRQVHAGNLPPSFSEGSGGSRTP EKGFSDREPTRPPRPILQRQDDIVQEKRLSRGISHASSIVSLARSHVSS NGGGGGSNEHPLEMPCAFQLPDLTVYNEDFRSFIERDLIEQSMLVALEQ AGRLNWWVSVDPTSQRLLPLATTGDGNCLLHAASLGMWGFHDRDLMLRKA LYALMEKGVKEALKRRRWQQTQONKESGLVYTEDEWQKEWNELIKLAS SEPRMHLGTNGANCGGVESSEEPVYESLEEFHVFVLAHVLRPIVVVADT MLRDSGGAEAFAPIFGGIYLPLEVPASQCHRSPVLAYDQAHFSALVSME QKENTKEQAVIPLTDSEYKLLPLHFAVDPGKGWEWGKDDSDNVRLASVIL SLEVKLHLLHSYMNVKWIPLSSDAQAPLAQPESPTASAGDEPRSTPESGD SDKESVGSSTSNEGGRRKEKSKRDREKDKKRADSVANKLGSFGKTLGSK LKKNMGGLMHSKSGSKPGGVGTGLGGSSGTETLEKKKNSLKSWKGGKEEA AGDGPVSEKPPAESVGNNGGSKYSQEVMSLSILRTAMQEGKFIIVGTLK MGRHQYQEEMIQRYSDAEERFLAEQKQKEAERKIMNGGIGGGPPPAK PEPDAREEQPTGPPAESRAMAFSTGYPGDFTIPRPSGGGVHCQEPRRQLA GGPCVGGLPYATFPRQCPPGRPYPHQDSIPSLEPGSHSKDGLHRGALLP PPYRVADSYSNGYREPPEPDGWAGGLRGLPPTQTKCKQPNCFSYGHPETN 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**

GAATTCATGACCCTGGACATGGATGCTGTTCTGTGTCAGATTTTGTCCGTTCAC
AGGAGCAGAGCCAGGGCTAGCGCGAGATCTCCTAGAAGGAAAGAATTGGGATG
TGAATGCCGCCCTCAGTGATTTTGAACAGCTACGTCAAGTCCATGCTGGAAAC
CTACCCCATCCTTTAGTGAGGGGAGTGGTGGCTCCAGGACCCCTGAAAAAGG
GTTTTCTGACAGAGAGCCTACTCGCCCTCCCGACCCATCCTCCAGCGGCAGG
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