

Division of Signal Transduction Therapy

Standard Operation Procedure

GST-JOSD1

<u>Enzyme description:-</u>	GST-JOSD1
<u>Clone number:-</u>	SC20955
<u>Source:-</u>	BL21 Recombinant
<u>Tag:-</u>	N-terminal GST tag
<u>Purification method:-</u>	GSH sepharose
<u>Expression level:-</u>	2 mg/L

Calculated molecular mass:-

Monoisotopic	49989 Da
Average Mass	50020 Da
[cysteines reduced, methionines have not been oxidised]	

<u>Theoretical pI:-</u>	7.47
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<u>Purity:-</u>	90%
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Enzyme storage buffer:-

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

<u>Storage temperature:-</u>	-80°C
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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-JOSD1

<u>Protein</u>	GST-JOSD1
<u>Synonyms</u>	Josephin-1, JSPH1
<u>Clone Number</u>	SC20955
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q15040 DNA: NM014876.5
<u>Tags</u>	N-terminal GST tag
<u>Amino acid sequence of expressed protein</u>	MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFP NLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAETSMLEGAVLDIRYGV SRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDAL DVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLQGWQATFGG GDHPPKSDLEVLFOGPLGSMSCVPWKGD KAKSESELEL PQAAPPQIYHEKQ RE LCALHALNNVFQDSNAFTRDTLQEIFQRLSPNTMVT PHKKSMLGNGNYDVNVI MAALQTKGYEAVWWDKRRDVGVI ALT NVMGFIMNLPSSLCWG PLKLPLKRQHW ICVREVG GAYYNLDSKLKMP EWIGGESELRKFLKHHLRGKNC ELLVVP EVE AHQSWRTDV
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	Precision site underlined
<u>Cloning sites</u>	BamH1 / NotI
<u>DNA sequence of insert</u>	GGATCCATGAGTTGTGTGCCATGGAAAGGAGACAAGGCCAAATCTGAATCATT GGAGCTGCCCCAGGCAGCACCCCCACAAATCTACCATGAGAAACAGCGCAGGG AGCTTTGTGCCCTCCACGCCCTCAATAACGTCTTCCAGGACAGCAATGCCTTC ACCCGGGATACGCTGCAAGAGATTTTCCAGAGGTTGTCTCCAAACACCATGGT GACACCTCACAAGAAGAGCATGCTGGGAAATGGCAACTACGATGTGAATGTCA TTATGGCAGCACTTCAGACCAAAGGCTATGAAGCTGTTTGGTGGGACAAGCGC AGGGATGTCGGTGTCAATTGCCCTCACTAACGTCATGGGCTTCATCATGAATCT GCCCTCCAGCCTATGCTGGGGTCCACTGAAACTGCCCCCTCAAAGGCAGCACT GGATCTGTGTTGAGAGGTGGGAGGGGCTACTACAACCTCGACTCCAAACTC AAGATGCCCCGAGTGGATTGGAGGCGAGAGCGAGCTCAGGAAGTTTCTAAAACA TCATTTGCGAGGAAAGAACTGTGAACCTCTGCTGGTGGTACCAGAAGAGGTAG AGGCTCATCAGAGTTGGAGGACCGATGTGTAAGCGGCCGC