

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-HOIL1

<u>Enzyme description:-</u>	HOIL1 1-510 (full length)
<u>Clone number:-</u>	DU32131
<u>Source:-</u>	Recombinant
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH-Sepharose
<u>Expression level:-</u>	1mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	85319 Da
Average Mass	85372 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	7.80
<u>Purity:-</u>	60%
<u>Enzyme storage buffer:-</u>	
50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT	
<u>Storage temperature:-</u>	-80°C
<u>Assay:-</u>	

Division of Signal Transduction Therapy

Clone Data Sheet

Protein name

<u>Protein</u>	HOIL1 1-510 (full length)
<u>Synonyms</u>	RBCK1, RNF54
<u>Clone Number</u>	DU32131
<u>Species</u>	Human
<u>Accession Number</u>	Q9BYM8
<u>Tags</u>	N-terminal GST-tag
Aminoacid sequence of the expressed protein	<p>MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFE LGFLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERA EISM LEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKT YLNQDHSVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPO IDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLVFOGPLGSPGIP GSTRAAAMDEKTKKAEEMALSLTRAVAGGDEQVAMKCAIWLAEQRP LSVQLKPEVSPTQDIRLWVSVEDAQMHTVTIWLTVRPDMTVASLKDM VFLDYGFPPVLQQWVIGORLARDQETLHSHGVRQNGDSAYLYLLSAR NTSLNPQELQRRERQLRMLLEDLGFKDLTLQPRGPLEPGPPKPGVPQEP GRGQPDVPEPPPVGWQCPGCTFINKPTRPGCEMCCRARPEAYQVPA SYQPDEEERARLAGEEEALROYQQRKQQQEGNYLQHVQLDQSLVL NTEPAECPVCYSVLAPGEAVVLRCLHTFCRECLQGTIRNSQEA EVS CPFIDNTYSCSGKLLEREIKALLTPEDYQRFLDLGISIAENRSAFSY HCKTPDCKGWCFEEDDVNEFTCPVCFHVNCLLCKAIHEQMNCKEYQE DLALRAQNDVAARQTTEMLKVMLQQGEAMRPCQCQIVVQKKDGC DWI RCTVCHTEICWVTKGPRWGGPGGDTSGGCRCRVNGIPCHPSCQ NCH</p>
Native sequence	in bold
Protease cleavage	Precission Protease site underlined
Cloning sites	Not1 / Not1

**DNA sequence of
insert**

GCGGCCGCGATGGACGAGAAGACCAAGAAAGCAGAGGAAATGGCCCTGAG
CCTCACCCGAGCAGTGGCGGGCGGGGATGAACAGGTGGCAATGAAGTGTG
CCATCTGGCTGGCAGAGCAACGGGTGCCCTGAGTGTGCAACTGAAGCCT
GAGGTCTCCCAACGCAGGACATCAGGCTGTGGGTGAGCGTGGAGGATGC
TCAGATGCACACCGTCACCATCTGGCTCACAGTGCGCCCTGATATGACAG
TGGCGTCTCTCAAGGACATGGTTTTTCTGGACTATGGCTTCCACCAGTC
TTGCAGCAGTGGGTGATTGGGCAGCGGCTGGCAGGAGACCAGGAGACCCT
GCACTCCCATGGGGTGCGGCAGAATGGGGACAGTGCCTACCTCTATCTGC
TGTGAGCCCGCAACACCTCCCTCAACCCTCAGGAGCTGCAGCGGGAGCGG
CAGCTGCGGATGCTGGAAGATCTGGGCTTCAAGGACCTCACGCTGCAGCC
GCGGGGCCCTCTGGAGCCAGGCCCCCCAAAGCCCGGGGTCCCCAGGAAC
CCGGACGGGGGCAGCCAGATGCAGTGCCTGAGCCCCACCGGTGGGCTGG
CAGTGCCCCGGGTGCACCTTCATCAACAAGCCACGCGGCTGGCTGTGA
GATGTGCTGCCGGGCGCGCCCCGAGGCCTACCAGGTCCCCGCCTCATAAC
AGCCCGACGAGGAGGAGCGAGCGCGCCTGGCGGGCGAGGAGGAGGCGCTG
CGTCAGTACCAGCAGCGGAAGCAGCAGCAGCAGGAGGGGAACCTGCA
GCACGTCCAGCTGGACCAGAGGAGCCTGGTGTGAACACGGAGCCCCGCG
AGTGCCCCGTGTGCTACTCGGTGCTGGCGCCCCGGCGAGGCCGTGGTGTG
CGTGAGTGTCTGCACACCTTCTGCAGGGAGTGCCTGCAGGGCACCATCCG
CAACAGCCAGGAGGCGGAGGTCTCCTGCCCCCTTCATTGACAACACCTACT
CGTGCTCGGGCAAGCTGCTGGAGAGGGAGATCAAGGCGCTCCTGACCCCT
GAGGATTACCAGCGATTTCTAGACCTGGGCATCTCCATTGCTGAAAACCG
CAGTGCCTTACGCTACCATTGCAAGACCCCAGATTGCAAGGGATGGTGTGCT
TCTTTGAGGATGATGTCAATGAGTTCACCTGCCCTGTGTGTTCCACGTC
AACTGCCTGCTCTGCAAGGCCATCCATGAGCAGATGAACTGCAAGGAGTA
TCAGGAGGACCTGGCCCTGCGGGCTCAGAACGATGTGGCTGCCCGGCAGA
CGACAGAGATGCTGAAGGTGATGCTGCAGCAGGGCGAGGCCATGCGCTGC
CCCCAGTGCCAGATCGTGGTACAGAAGAAGGACGGCTGCGACTGGATCCG
CTGCACCGTCTGCCACACCGAGATCTGCTGGGTACCAAGGGCCACGCT
GGGGCCCTGGGGGCCAGGAGACACCAGCGGGGGCTGCCGCTGCAGGGTA
AATGGGATTCTTGCCACCCAAGCTGTCAGAAGTGCCACTGAGCGGCCGC