

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-HOIL1 [R210A]

Enzyme description:- HOIL1 [R210A] 1-510 (full length)

Clone number:- DU43713

Source:- Recombinant

Tag:- N-terminal GST

Purification method:- GSH-Sepharose

Expression level:- 1mg/L

Calculated molecular mass:-

Monoisotopic 85233 Da

Average Mass 85287 Da

[cysteines reduced, methionines have not been oxidised]

Theoretical pI:- 6.18

Purity:- 50%

Enzyme storage buffer:-

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

Storage temperature:- -80°C

Assay:-

Division of Signal Transduction Therapy

Clone Data Sheet

GST-HOIL1 [R210A]

<u>Protein</u>	HOIL1 1-510 [R210A] (full length)
<u>Synonyms</u>	RBCK1, RNF54
<u>Clone Number</u>	DU43713
<u>Species</u>	Human
<u>Accession Number</u>	Q9BYM8
<u>Tags</u>	N-terminal GST-tag
Aminoacid sequence of the expressed protein	MSPIILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFE LGLFEPNLPYYIDGDVKLTQSMATIRYIADKHNMLGGCPKERAETISM LEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKT YLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPO IDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFQGPLGSPGIP GSTRAAAMDEKTKKAEEMALSLTRAVAGGDEQVAMKCAIWLAEQRVP LSVQLKPEVSPTQDIRLWVSVEDAQMHTVTIWLTVRPDMTVASLKDM VFLDYGFPPVLQQWVIGQRLARDQETLHSHGVRQNGDSAYLYLLSAR NTSLNPQELQRRERQLRMLEDLGFKDLTLQPRGPLEPGPPKPGVPQEP GRGQPDVPEPPPVGWQCPGCTFINKPTAPGCEMCCRARPEAYQVPA SYQPDEEERARLAGEEEEALRQYQQRKQQQOEGNYLQHVQLDQSLVL NTEPAECPVCYSVLAPGEAVVLRECLHTFCRECLQGTIRNSQEAQEV CPFIDNTYSCSGKLLEREIKALLTPEDYQRFDLGISIAENRSQAFSY HCKTPDCKGWCFEEDDVNEFTCPVCFHVNCLLCKAIHEQMNCKEYQE DLALRAQNDVAARQTTEMLKVMLQQGEAMRCPCQIVVQKKDGCWIR RCTVCHTEICWVTKGPRWGPGGPGDTSGGCRCRVNGIPCHPSCQNC
Native sequence	in bold
Protease cleavage	Prescission Protease site underlined
Cloning sites	Not1 / Not1

**DNA sequence of
insert**

gcggccgcgatggacgagaagaccaagaaagcagaggaaatggccctgag
cctcaccgcgagcagtgggcgggcggggatgaacaggtggcaatgaagtgtg
ccatctggctggcagagcaacgggtgccctgagtggtgcaactgaagcct
gaggtctccccaacgcaggacatcaggctgtgggtgagcgtggaggatgc
tcagatgcacaccgtcaccatctggctcacagtgcgcctgatatgacag
tggcgtctctcaaggacatgggttttctggactatggcttcccaccagtc
ttgcagcagtggtgattgggcagcggctggcacgagaccaggagaccct
gcactcccatgggtgcggcagaatggggacagtgcctacctctatctgc
tgtcagcccgcaacacctccctcaaccctcaggagctgcagcgggagcgg
cagctgcggatgctggaagatctgggcttcaaggacctcacgtgcagcc
gcggggccctctggagccaggccccccaaagcccggggtccccaggaaac
ccggacgggggcagccagatgcagtgcctgagccccaccggtgggtggtg
cagtgcggcggtgcaccttcatcaacaagcccacgGCgcctggctgtga
gatgtgctgccgggcgcgccccgaggcctaccagggtccccgcctcatacc
agcccgacgaggaggagcgcgcgcctggcgggcgaggaggaggcgctg
cgtcagtaccagcagcgggaagcagcagcagcaggaggggaactacctgca
gcacgtccagctggaccagaggagcctggtgctgaacacggagcccgcg
agtccccgtgtgctactcgggtgctggcgccccggcgaggccgtggtgctg
cgtgagtgtctgcacaccttctgcaggagtgctgcagggcaccatccg
caacagccaggaggcggaggtctcctgccccttcattgacaacacctact
cgtgctcgggcaagctgctggagaggagatcaaggcgctcctgaccct
gaggattaccagcgatttctagacctgggcattctccattgctgaaaaccg
cagtgccttcagctaccattgcaagaccccagattgcaagggtggtgct
tctttgaggatgatgtcaatgagttcacctgccctgtgtgtttccacgtc
aactgcctgctctgcaaggccatccatgagcagatgaactgcaaggagta
tcaggaggacctggccctgcgggctcagaacgatgtggctgcccggcaga
cgacagagatgctgaagggtgatgctgcagcaggggcgaggccatgcgctgc
ccccagtgccagatcgtggtacagaagaaggacggctgcgactggatccg
ctgcaccgtctgccacaccgagatctgctgggtcaccaagggccacgct
ggggccctggggggccaggagacaccagcgggggtgccgctgcagggtgta
aatgggattccttgccaccaagctgtcagaactgccactgagcggccgc