

*Division of Signal Transduction Therapy*

**Standard Operating Procedure**

**Preparation of FKHR L1 [330 - 673]**

**Protein description:-** FKHR L1 [330 - 673]

**Clone number:-** DU 958

**Source:-** Recombinant

**Expression system:-** *E.coli*

**Tag:-** N-terminal GST

**Purification method:-** GSH Sepharose

**Expression level:-** 8 mg/L

**Calculated molecular mass:-** 63, 306 daltons

**Purity:-** 90 %

**Enzyme storage buffer:-**

50 mM Tris-HCl pH 7.5, 270 mM Sucrose, 150 mM NaCl, 0.1 mM EGTA,  
0.1 % 2-mercaptoethanol, 0.02 % Brij-35, 0.2 mM PMSF, 1 mM Benzamidine.

**Storage temperature:-** -70 °C

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**CLONE DATA SHEET**

**FKHR L1 [330 - 673]**

<b><u>Protein</u></b>	FKHR L1 [330 - 673]
<b><u>Clone number</u></b>	DU 958
<b><u>Species</u></b>	Human
<b><u>Accession number</u></b>	NM_001455
<b><u>Tags</u></b>	N-terminal GST
<b><u>Bacterially expressed protein</u></b>	MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFEL GLEFPNLPYYIDGDVCLTQSMALIRYIADKHNMLGGCPKERAEISMLE GAVLDIRYGVSR IAYS KDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLN GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAI PQIDKY LKSSKYIAWPLQGWQATFGGGDHPKSDLEVLFGQPLG <b>STELDEVQDD</b> <b>DAPLSPMLYSSSASLSPSVSKPCTVELPRLTDMAGTMNLNDGLTENLM</b> <b>DDLNDNITLPPSQPSPTGGLMQRS SFPYTTKGSGLGSPTSSFNSTVF</b> <b>GPSSLNSLRQSPMQTIQENKPATFSSMSHYGNQTLQDLLTSDSLSHSD</b> <b>VMMTQSDPLMSQASTAVSAQNSRRNVMLRNDPMMSF AAQPNQGS LVNQ</b> <b>NLLHHQHQTQ GALGGSRALSNSVSNMGLSESSSLGSAKHQQQSPVSQS</b> <b>MQT LSDSLSGSSLYSTSANLPV MGHEKFP SDLDLDMFNGSLECDMESI</b> <b>IRSELMDADGLDFNFDSL ISTQNVVGLNVGNFTGAKQASSQSWVPG</b>
<b><u>Native sequence</u></b>	Amino acids S330 – G673 (end) of human FKHR L1. Residue S231 of the fusion protein is equivalent to S330 of the native protein. The GST tag is located at residues 1 – 220
<b><u>Protease cleavage</u></b>	PreScission ( <u>LEVLFQGPL</u> ) residues 221 - 229
<b><u>Cloning sites</u></b>	<i>Bam</i> HI sites of pGEX 6P-1

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**Nucleotide  
sequence of insert**

GGATCCACAGAGTTGGATGAAGTCCAGGACGATGATGCGCCTCTCTCG  
CCCATGCTCTACAGCAGCTCAGCCAGCCTGTCACCTTCAGTAAGCAAG  
CCGTGCACGGTGGAAGTCCACGGCTGACTGATATGGCAGGCACCATG  
AATCTGAATGATGGGCTGACTGAAAACCTCATGGACGACCTGCTGGAT  
AACATCACGCTCCCGCCATCCCAGCCATCGCCACTGGGGGACTCATG  
CAGCGGAGCTCTAGCTTCCCGTATAACCACCAAGGGCTCGGGCCTGGGC  
TCCCCAACAGCTCCTTTAACAGCACGGTGTTCGGACCTTCATCTCTG  
AACTCCCTACGCCAGTCTCCCATGCAGACCATCCAAGAGAACAAGCCA  
GCTACCTTCTCTTCCATGTCACACTATGGTAACCAGACACTCCAGGAC  
CTGCTCACTTCGGACTCACTTAGCCACAGCGATGTCATGATGACACAG  
TCGGACCCCTTGATGTCTCAGGCCAGCACCGCTGTGTCTGCCAGAAT  
TCCCGCCGGAACGTGATGCTTCGCAATGATCCGATGATGTCTTTGCT  
GCCAGCCTAACCAGGGAAGTTTGGTCAATCAGAACTTGCTCCACCAC  
CAGCACCAAACCCAGGGCGCTCTTGGTGGCAGCCGTGCCCTTGTCGAAT  
TCTGTCAGCAACATGGGCTTGAGTGAGTCCAGCAGCCTTGGGTCAGCC  
AAACACCAGCAGCAGTCTCCTGTCAGCCAGTCTATGCAAACCTCTCG  
GACTCTCTCTCAGGCTCCTCCTTGTAICTCAACTAGTGCAAACCTGCC  
GTCATGGGCCATGAGAAGTTCCCAGCGACTTGGACCTGGACATGTTT  
AATGGGAGCTTGGAATGTGACATGGAGTCCATTATCCGTAGTGAACTC  
ATGGATGCTGATGGGTTGGATTTTAACTTTGATTCCCTCATCTCCACA  
CAGAATGTTGTTGGTTTGAACGTGGGGAACCTTCACTGGTGCTAAGCAG  
GCCTCATCTCAGAGCTGGGTGCCAGGCTgaggatcc