



*Division of Signal Transduction Therapy*

**Clone Data Sheet**

**FGFR2 [403 - 822]**

**Protein** FGFR2 [403 - 822]

**Clone number** DU 26340

**Species** Human

**Accession number** NM\_000141.1

**Tags** N-terminal His6

**Baculovirus expressed protein**

MSYYHHHHHHHDYDIPTTENLYFQGAMGSTTKKPDFSSQPAVHKLTKRI  
PLRRQVTVSAESSSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPE  
DPKWEFPRDKLTLGKPLGEGCFGQVVMMAEAVGIDKDKPKEAVTVAVKM  
LKDDATEKDLSDLVSEMEMMKMIGKHKNINLLGACTQDGPLYVIVEY  
ASKGNLREYLRARRPPGMEYSYDINRVPEEQMTFKDLVSCTYQLARGM  
EYLASQKCIHRDLAARNVLVTENVMKIADFGLARDINNIDYYKKTN  
GRLPVKWMPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVE  
ELFKLLKEGHRMDKPANCTNELYMMRDCWHAVPSQRPTFKQLVEDLD  
RILTLTTNEEYLDLSQPLEQYSPSYPDTRSSCSSGDDSVFSPDPMPYE  
PCLPQYPHINGSVKT

**Native sequence** Amino acids T403 – T821 (end) of human FGFR2.

Residue T29 of the fusion protein is equivalent to T403 of the native enzyme. The His(6) tag is located at residues 5 – 10.

**Protease cleavage** TEV protease site (ENLYFQG) residues 18 – 24

**Cloning sites** *Bam*H1 and *Not*1 sites of pFastBac Htb

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**Nucleotide  
sequence of  
insert**

ggatccACGACCAAGAAGCCAGACTTCAGCAGCCAGCCGGCTGTGCAC  
AAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAACAGTTTCGGCT  
GAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACA  
ACACGCCTCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCC  
GAGTATGAACTTCCAGAGGACCCAAAATGGGAGTTTCCAAGAGATAAG  
CTGACACTGGGCAAGCCCCGGGAGAAGGTTGCTTTGGGCAAGTGGTC  
ATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCCAAGGAGGCGGTC  
ACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACCTT  
TCTGATCTGGTGTGAGAGATGGAGATGATGAAGATGATTGGGAAACAC  
AAGAATATCATAAATCTTCTTGGAGCCTGCACACAGGATGGGCCTCTC  
TATGTCATAGTTGAGTATGCCTCTAAAGGCAACCTCCGAGAATACCTC  
CGAGCCCGGAGGCCACCCGGGATGGAGTACTCCTATGACATTAACCGT  
GTTCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTGATGCACCTAC  
CAGCTGGCCAGAGGCATGGAGTACTTGGCTTCCAAAAATGTATTCAT  
CGAGATTTAGCAGCCAGAAATGTTTTGGTAACAGAAAACAATGTGATG  
AAAATAGCAGACTTTGGACTCGCCAGAGATATCAACAATATAGACTAT  
TACAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGGATGGCTCCA  
GAAGCCCTGTTTGATAGAGTATACTCATCAGAGTATGTCTGGTCC  
TTCGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCCCTAC  
CCAGGGATTCCCGTGGAGGAACTTTTTAAGCTGCTGAAGGAAGGACAC  
AGAATGGATAAGCCAGCCAACCTGCACCAACGAACGTACATGATGATG  
AGGACTGTTGGCATGCAGTGCCCTCCAGAGACCAACGTTCAAGCAG  
TTGGTAGAAGACTTGGATCGAATTCTCACTCTCACAACCAATGAGGAA  
TACTTGGACCTCAGCCAACCTCTCGAACAGTATTCACCTAGTTACCCT  
GACACAAGAAGTTCTTGTCTTTCAGGAGATGATTCTGTTTTTCTCCA  
GACCCCATGCCTTACGAACCATGCCTTCCTCAGTATCCACACATAAAC  
GGCAGTGTTAAAACAtgagcggccgc