



Protein

GenPept

fibroblast growth factor receptor 3 isoform 1 precursor [Homo sapiens]

NCBI Reference Sequence: NP_000133.1

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LOCUS	NP_000133	806 aa	linear	PRI 05-APR-2023
DEFINITION	fibroblast growth factor receptor 3 isoform 1 precursor [Homo sapiens].			
ACCESSION	NP_000133			
VERSION	NP_000133.1			
DBSOURCE	REFSEQ: accession NM_000142.5			
KEYWORDS	RefSeq; MANE Select.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (residues 1 to 806)			
AUTHORS	Li X, Li Y, Liu B, Chen L, Lyu F, Zhang P, He Q, Cheng L, Liu C, Song Y and Xing Y.			
TITLE	P4HA2-mediated HIF-1alpha stabilization promotes erdafitinib-resistance in FGFR3-alteration bladder cancer			
JOURNAL	FASEB J 37 (4), e22840 (2023)			
PUBMED	36943397			
REMARK	GeneRIF: P4HA2-mediated HIF-1alpha stabilization promotes erdafitinib-resistance in FGFR3-alteration bladder cancer.			
REFERENCE	2 (residues 1 to 806)			
AUTHORS	Wang CG, Peiris MN, Meyer AN, Nelson KN and Donoghue DJ.			
TITLE	Oncogenic driver FGFR3-TACC3 requires five coiled-coil heptads for activation and disulfide bond formation for stability			
JOURNAL	Oncotarget 14, 133-145 (2023)			
PUBMED	36780330			
REMARK	GeneRIF: Oncogenic driver FGFR3-TACC3 requires five coiled-coil heptads for activation and disulfide bond formation for stability. Publication Status: Online-Only			
REFERENCE	3 (residues 1 to 806)			
AUTHORS	Zheng Y, Lu J, Hu X, Hu X, Gao X and Zhou J.			
TITLE	PRMT5/FGFR3/AKT Signaling Axis Facilitates Lung Cancer Cell Metastasis			
JOURNAL	Technol Cancer Res Treat 22, 15330338231161139 (2023)			
PUBMED	36927233			
REMARK	GeneRIF: PRMT5/FGFR3/AKT Signaling Axis Facilitates Lung Cancer Cell Metastasis.			
REFERENCE	4 (residues 1 to 806)			
AUTHORS	Bober,M.B., Bellus,G.A., Nikkel,S.M. and Tiller,G.E.			
TITLE	Hypochondroplasia			
JOURNAL	(in) Adam MP, Mirzaa GM, Pagon RA, Wallace SE, Bean LJH, Gripp KW and Amemiya A (Eds.); GENEREVIEWS(R); (1993)			
PUBMED	20301650			
REFERENCE	5 (residues 1 to 806)			
AUTHORS	Wenger,T., Miller,D. and Evans,K.			
TITLE	FGFR Craniosynostosis Syndromes Overview			
JOURNAL	(in) Adam MP, Mirzaa GM, Pagon RA, Wallace SE, Bean LJH, Gripp KW and Amemiya A (Eds.); GENEREVIEWS(R); (1993)			

PUBMED [20301628](#)
REFERENCE 6 (residues 1 to 806)
AUTHORS Kruszka,P., Rolfe,M., Kahle,K.T. and Muenke,M.
TITLE Muenke Syndrome
JOURNAL (in) Adam MP, Mirzaa GM, Pagon RA, Wallace SE, Bean LJH, Gripp KW
and Amemiya A (Eds.);
GENEREVIEWS(R);
(1993)
PUBMED [20301588](#)
REFERENCE 7 (residues 1 to 806)
AUTHORS French,T. and Savarirayan,R.
TITLE Thanatophoric Dysplasia
JOURNAL (in) Adam MP, Mirzaa GM, Pagon RA, Wallace SE, Bean LJH, Gripp KW
and Amemiya A (Eds.);
GENEREVIEWS(R);
(1993)
PUBMED [20301540](#)
REFERENCE 8 (residues 1 to 806)
AUTHORS Legare,J.M.
TITLE Achondroplasia
JOURNAL (in) Adam MP, Mirzaa GM, Pagon RA, Wallace SE, Bean LJH, Gripp KW
and Amemiya A (Eds.);
GENEREVIEWS(R);
(1993)
PUBMED [20301331](#)
REFERENCE 9 (residues 1 to 806)
AUTHORS Thompson LM, Plummer S, Schalling M, Altherr MR, Gusella JF,
Housman DE and Wasmuth JJ.
TITLE A gene encoding a fibroblast growth factor receptor isolated from
the Huntington disease gene region of human chromosome 4
JOURNAL Genomics 11 (4), 1133-1142 (1991)
PUBMED [1664411](#)
REFERENCE 10 (residues 1 to 806)
AUTHORS Keegan K, Johnson DE, Williams LT and Hayman MJ.
TITLE Isolation of an additional member of the fibroblast growth factor
receptor family, FGFR-3
JOURNAL Proc Natl Acad Sci U S A 88 (4), 1095-1099 (1991)
PUBMED [1847508](#)
COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The
reference sequence was derived from [AC016773.8](#).

Summary: This gene encodes a member of the fibroblast growth factor receptor (FGFR) family, with its amino acid sequence being highly conserved between members and among divergent species. FGFR family members differ from one another in their ligand affinities and tissue distribution. A full-length representative protein would consist of an extracellular region, composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment and a cytoplasmic tyrosine kinase domain. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals, ultimately influencing mitogenesis and differentiation. This particular family member binds acidic and basic fibroblast growth hormone and plays a role in bone development and maintenance. Mutations in this gene lead to craniosynostosis and multiple types of skeletal dysplasia. [provided by RefSeq, Aug 2017].

Transcript Variant: This variant (1) lacks an alternate coding exon and contains another alternate coding exon compared to variant 3. The resulting isoform (1) has the same N- and C-termini but is shorter compared to isoform 3.

Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##

Transcript exon combination :: SRR9304719.217759.1,
ERR3218372.729235.1 [ECO:0000332]
RNAseq introns :: single sample supports all introns
SAMEA1968540, SAMEA1970526

##Evidence-Data-END##

##RefSeq-Attributes-START##

MANE Ensembl match :: ENST00000440486.8/ ENSP00000414914.2

RefSeq Select criteria :: based on manual assertion, conservation

##RefSeq-Attributes-END##

FEATURES Location/Qualifiers

source 1..806
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="4"
 /map="4p16.3"

Protein 1..806
 /product="fibroblast growth factor receptor 3 isoform 1 precursor"
 /EC_number="2.7.10.1"
 /note="hydroxyaryl-protein kinase; tyrosine kinase JTK4; FGFR-3; fibroblast growth factor receptor 3-S"
 /calculated_mol_wt=85782

sig peptide 1..22
 /inference="COORDINATES: ab initio prediction:SignalP:4.0"
 /calculated_mol_wt=1946

mat peptide 23..806
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Region 37..125
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 /db_xref="CDD:448366"

Region 57..61
 /region_name="Ig strand B"
 /note="Ig strand B [structural motif]"
 /db_xref="CDD:409353"

Region 69..75
 /region_name="Ig strand C"
 /note="Ig strand C [structural motif]"
 /db_xref="CDD:409353"

Region 92..96
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 /db_xref="CDD:409353"

Site 98
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 /note="N-linked (GlcNAc...) asparagine."
 /evidence=ECO:0000255; propagated from UniProtKB/Swiss-Prot (P22607.1)"

Region 106..111
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 /db_xref="CDD:409353"

Region 118..121
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 /note="Ig strand G [structural motif]"
 /db_xref="CDD:409353"

Region 126..153
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 /evidence=ECO:0000256|SAM:MobiDB-lite"
 /note="propagated from UniProtKB/Swiss-Prot (P22607.1)"

Region 151..245
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 /db_xref="CDD:409443"

Region 151..154
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 /db_xref="CDD:409443"

Region 162..167
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Site order(163,165,167)
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 /note="FGF binding site [polypeptide binding]"

/db_xref="CDD:[409443](#)"
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 /note="Ig strand B [structural motif]"
 /db_xref="CDD:[409443](#)"
 185..190
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 193..195
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 /db_xref="CDD:[409443](#)"
 204..207
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 /db_xref="CDD:[409443](#)"
 211..216
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 /db_xref="CDD:[409443](#)"
 225..232
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 284..288
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 /db_xref="CDD:[409353](#)"
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 /evidence=ECO:0000255; propagated from
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/note="Ig strand F [structural motif]"
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 /note="Ig strand G [structural motif]"
 /db_xref="CDD:[409353](#)"
 Site 376..396
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 /note="propagated from UniProtKB/Swiss-Prot (P22607.1)"
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 Region 459..792
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 /note="Protein Kinases, catalytic domain; cl21453"
 /db_xref="CDD:[451246](#)"
 Site order(478..481,484,486,506,508,539,555..558,617,621..622,624,634..635)
 /site_type="other"
 /note="ATP binding site [chemical binding]"
 /db_xref="CDD:[270870](#)"
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 /evidence=ECO:0000269|PubMed:11294897; propagated from UniProtKB/Swiss-Prot (P22607.1)"
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 CDS 1..806
 /gene="FGFR3"
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 /coded_by="NM_000142.5:276..2696"
 /note="isoform 1 precursor is encoded by transcript variant 1"
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 /db_xref="GeneID:[2261](#)"
 /db_xref="HGNC:[HGNC:3690](#)"
 /db_xref="MIM:[134934](#)"

ORIGIN

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241 ytlldvlersp hrpiliqaglp anqtavlg sd vefhckvyss aqphiqwlkh vevngskvgp
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601 vargmeylas qkcihrdlaa rnvltednv mkiadfglar dvhnldyyk kttngrlpvkw
661 mapealfdrv ythqsdwvsf gvllweiftl ggspypgipv eelfklkleg hrmdkpanct
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