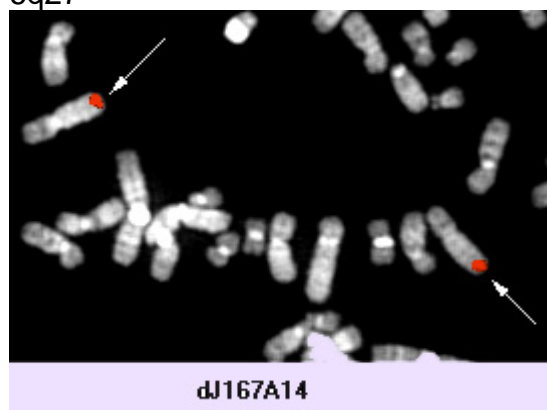


FGFR1OP (FGFR1 oncogene partner)

Identity

Other names **FOP (Fibroblast Growth Factor Receptor 1 Oncogene Partner)**
Hugo **FGFR1OP**
Location **6q27**



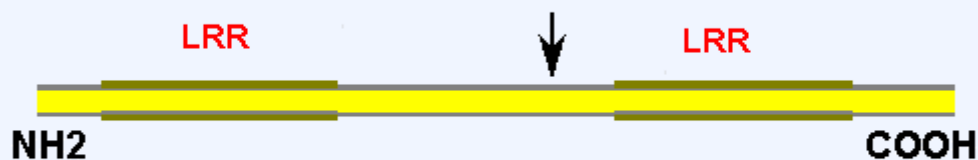
FOP (6q27) - Courtesy Mariano Rocchi, [Resources for Molecular Cytogenetics](#).
Laboratories willing to validate the probes are welcome : contact rocchi@biologia.uniba.it

DNA/RNA

Description full length cDNA: 1 627 bp
Transcription a single open reading frame of 1 197 bp mRNA; putative ATG: bp 85; stop codon at bp 1 282; alternative splicing: multiple FOP transcript variants resulting from exon 7 or exon 11 splices

Protein

FOP protein: Schematic representation
Gene localization: chromosome 6q27



arrow indicates the position of the breakpoint involved in the 8p12 myeloproliferative disorder

Description 399 amino acids; predicted molecular mass: 44.3 kDa; Hydrophobic protein containing in its N- and C-termini several regions folding in α -helices with leucine-rich repeats with the consensus sequence L-X₂-L-X₃-5-L-X₃-5-L, in one-third of which the leucine is substituted by either a valine or an isoleucine

Expression ubiquitous expression
 Localisation cell cytoplasm
 Function unknown

Implicated in

Entity [t\(6;8\)\(q27;p12\)](#) myeloproliferative disorder --> FOP - [FGFR1](#) ; stem-cell myeloproliferative disorder associated with the 8p12 chromosomal translocations with fusions to the catalytic domain of FGFR1

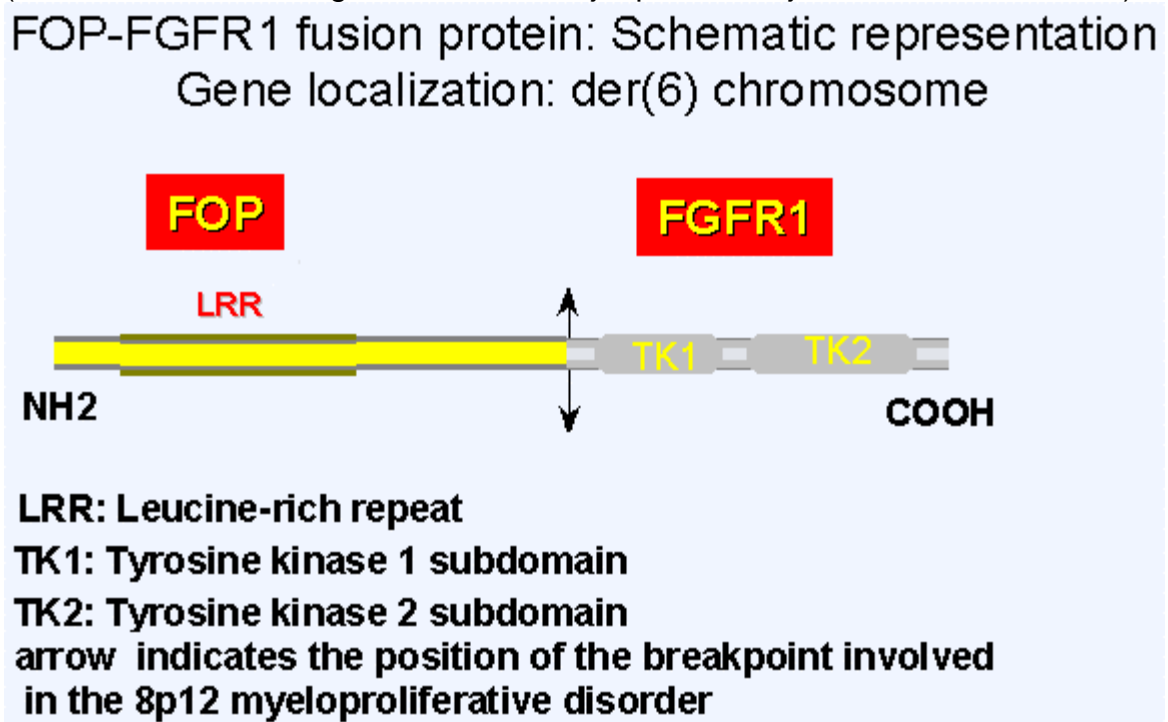
Disease stem-cell myeloproliferative disorder characterized by myeloid hyperplasia, T -cell lymphoblastic leukemia/lymphoma and peripheral blood eosinophilia, and it generally progresses to acute myeloid leukemia; specific to the 8p12 chromosomal region.

Prognosis very poor (median survival: 12 mths)

Cytogenetics additional abnormalities: 2q+ and +21

Hybrid/Mutated Gene 5' FOP - 3' FGFR1; localisation: der(6)

Abnormal Protein N-term leucine-rich region from FOP fused to the catalytic domain of FGFR1 (FGFR1 intracellular region minus the major part of the juxtamembrane domain)



Oncogenesis constitutive kinase activity of FGFR1 through constitutive activation of FGFR1 signal transduction pathways via putative constitutive dimerization capability mediated by the FOP N-term LRR sequences

External links

Nomenclature

[Hugo](#) [FGFR1OP](#)
[GDB](#) [FGFR1OP](#)
[Entrez_Gene](#) [FGFR1OP 11116](#) FGFR1 oncogene partner

Cards

[GeneCards](#) [FGFR1OP](#)
[Ensembl](#) [FGFR1OP](#)

Genatlas	FGFR1OP
GeneLynx	FGFR1OP
eGenome	FGFR1OP
euGene	11116
	Genomic and cartography
GoldenPath	FGFR1OP - 6q27 chr6:167383227-167424476 + 6q27 (hg17-May_2004)
Ensembl	FGFR1OP - 6q27 [CytoView]
NCBI	Genes Cyto Gene Seq [Map View - NCBI]
OMIM	Disease map [OMIM]
HomoloGene	FGFR1OP
	Gene and transcription
Genbank	Z94721 [SRS] Z94721 [ENTREZ]
Genbank	AJ420472 [SRS] AJ420472 [ENTREZ]
Genbank	BC011902 [SRS] BC011902 [ENTREZ]
Genbank	BC037785 [SRS] BC037785 [ENTREZ]
Genbank	BU625682 [SRS] BU625682 [ENTREZ]
RefSeq	NM_007045 [SRS] NM_007045 [ENTREZ]
RefSeq	NM_194429 [SRS] NM_194429 [ENTREZ]
RefSeq	NT_086699 [SRS] NT_086699 [ENTREZ]
AceView	FGFR1OP AceView - NCBI
TRASER	FGFR1OP Traser - Stanford
Unigene	Hs.487175 [SRS] Hs.487175 [NCBI] HS487175 [spliceNest]
	Protein : pattern, domain, 3D structure
SwissProt	O95684 [SRS] O95684 [EXPASY] O95684 [INTERPRO]
Prosite	PS50896 LISH [SRS] PS50896 LISH [Expasy]
Interpro	IPR006594 LisH [SRS] IPR006594 LisH [EBI]
CluSTr	O95684
Smart	SM00667 LisH [EMBL]
Blocks	O95684
	Polymorphism : SNP, mutations, diseases
OMIM	605392 [map]
GENECLINICS	605392
SNP	FGFR1OP [dbSNP-NCBI]
SNP	NM_007045 [SNP-NCI]
SNP	NM_194429 [SNP-NCI]
SNP	FGFR1OP [GeneSNPs - Utah] FGFR1OP [SNP - CSHL] FGFR1OP [HGBASE - SRS]
	General knowledge
Family	FGFR1OP [UCSC Family Browser]
Browser	
SOURCE	NM_007045
SOURCE	NM_194429
SMD	Hs.487175
SAGE	Hs.487175
Amigo	process positive regulation of cell proliferation
PubGene	FGFR1OP
	Other databases
	Probes
Probe	Cancer Cytogenetics (Bari)
Probe	FGFR1OP Related clones (RZPD - Berlin)

PubMed

PubMed

6 Pubmed reference(s) in LocusLink

Bibliography

The t(6;8)(q27;p11) translocation in a stem cell myeloproliferative disorder fuses a novel gene, FOP, to fibroblast growth factor receptor 1.

Popovici C, Zhang B, Grégoire MJ, Jonveaux P, Lafage-Pochitaloff M, Birnbaum D, Pébusque MJ.

Blood 1999; 93: 1381-1389.

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Contributor(s)

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Citation

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URL : <http://www.infobiogen.fr/services/chromcancer/Genes/FOPID140.html>

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