Spi FBrf0075237

DROSOPHILA GENMAPS DATABASE RECORD PRINTOUT - 5/20/93
Return corrections to John Merriam, UCLA Biology,
Los Angeles, CA 90026-1606; FAX [redacted]

source_numbe 2929

full_location 37F,38A
table_numbers 1,2,5,6,7,8 cross_locations

gene_name Spitz
gene_abbrev Spi
product

1 kb_cloned_genom 70 vector_genomi phage lambda-Dash
kb_cloned_cDNA 1.7 vector_cDNA lambda gt10, gt11

METHOD: expression walk_jump_org xxx YACs 0
microcloning oligonucleotide
homology transposon_tag xxx

clonetechtext cloned by walking from Ddc across Df(2L) VA17 breakprint & by plasmid rescue from the P element mutation Spi IDB7

2 rearrangement Df(2L)VA17, Df(2L)TW84, Df(2L)oD21, Df(2L)oD12, Df(2L)TW9, Df(2L)E55, Df(2L)TW158

3 T_strain
markers

5 kb_seq_genomic 2.2 acc_number_gen M95199 kb_seq_old 0
kb_seq_cDNA 1.7 acc_number_cDNA
comments
ORF_size 230
ORF_functio
ORF_domain transmembrane domain, EGF domain

6 kb_trans_size 1.9, 2.0, 2.5
transc_dist Throughout development, peak at mid embryogenesis, Ubiquitously expressed in all

7 protein_dist Ubiquitous embryonic expression with enrichment in ventral and mesoderm

8 fusion_dist P element transfromation used to demonstrate rescue of Spi mutations.

misc_info at least 4 mRNAs are encoded by combinations of 6 different exons. polyclonal antibodies made. transc_dist con't -embryonic tissues with enrichment in procephalic region, ventral midline, mesoderm, and PNS.

full citation Rutledge BJ; Zhang K; Bier E; Jan YN; Perrimon N. The Drosophila spitz gene encodes a putative EGF-like growth factor involved in dorsal ventral axis formation and neurogenesis. Genes & Development 1992 Aug;6(8):1503-1517.


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keywords

GENMAPS DATABASE REPORT F[illegible]

John Merriam, UCLA Biology, Los Angeles [illegible] 90026-1606 FAX 310 [redacted]

[illegible]n: _____ keys for this paper: _____

gene/mutant name: spitz same as front.

abbreviation: Spi

biochemical name/product: _____

(1) CLONES:

kb_genomic: 70 vector/library name: phage (EMBL3) lambda gt10, gt11

kb_cDNA: 1.7 vector/library name: _____

METHOD:

prior clone: _____ walk: XXX

expression: _____ differential screen: _____

microclone: _____ oligonucleotide: _____ PCR? _____

homology: _____ transposon tag: XXX

(2) REARRANGEMENTS: cloned by walking from Df(2L)VA17 breakpoint & by plasmid rescue from the P-element-mediated Df(2L)TW84, Df(2L)[illegible]

(3) TRANSFORM INSERTS: _____

(5) SEQUENCE:

kb_genomic: _____ accession number: _____

kb_cDNA: _____ accession number: _____

ORF-size: _____

ORF_function/homology group: _____

ORF_domains: _____

(6) TRANSCRIPT DESCRIPTION:

transcript_size: _____

distribution: _____

(7) PROTEIN ANTIBODY:

distribution: _____

(8) LAC Z FUSION STAIN:

distribution: _____

MISC_INFO: _____

DROSOPHILA DATABASE REPORT FORM
Return to John Merriam, UCLA Biology, LA 90024-1606 FAX [redacted]

Please verify [___] or correct the address and citation on the reverse.

NAME:_____ PHONE #:_____ FAX #:_____

1. **GENE:** How do you describe the gene you are reporting on?

   mutant name (if any): Spit3

   abbreviation: Spi

   biochemical name (if any):_____

2. **LOCATION:** Where is your clone/walk located? 37F
   (If you are using a clone from a more extended walk, what is the location of your gene? _____)

3. **SIZE:** How many kb did you clone? (round to nearest kb)

   genomic 30 vector/library name:_____

   cDNA_____ vector/library name:_____

4. **METHOD:** Describe the entry point for your clone/walk.

   prior clone_____ transposon tag_____

   expression_____ differential screen_____

   microclone_____ oligonucleotide_____ PCR?_____

   homology_____

5. **SEQUENCE:** How many kb did you sequence? (round to nearest 0.1 kb)

   genomic_____ accession #:_____

   cDNA_____ accession #:_____

   PRODUCT: How many amino acids in the ORF?_____

   _____
   (List above the predicted function or homology group of the ORF)

   _____
   (List above the key words that describe domains in the ORF)

6. **TRANSCRIPTS:** (round mRNA sizes to nearest 0.1 kb, list largest 1st):

   _____ When/where found?_____

7. **PROTEIN** (antibody detection): Where found?_____

8. **LAC Z FUSION** stain: Where found?_____

9. **MORE DETAILS:**_____