HeT-A FBrf0075206 707

Drosophila clone list report form ver 12/6/89

please return to: gg 4/2/90

new/update
date 3/26/90 record # _____ reference# unpublished R. Levis

John Merriam
Biology Department
Univ California
Los Angeles, CA 90024

FAX # [redacted]
phone

key (1) 2 3 5 6 7 8

location gene name abbrev product cross loc rearrange Tstrain marker
100F - telomere

walk/jump _____ (origin)

homology _____ (origin)

transposon tag P[(w,ry)A]4-4 (name)

cDNA _____ (express, enrich, or +/-)

oligonucleotide _____ (sequence)

microcloning _____ (PCR?)

genomic kb cloned 62 vector λ DASH

cDNA kb cloned _____ vector _____

genomic kb seq. _____ accession# _____

cDNA kb seq. _____ accession# _____

ORF _____ (#amino acids)

kb transcript(s) _____

product distribution _____

Distal end of walk = end of chromosome.

misc (promoters, transmembrane, DNA binding, etc) Covers MAP205 & mod genes

key words Telomere

author corrected R C

DROSOPHILA GENMAPS DATABASE RECORD PRINTOUT - 8/31/92

Return corrections to John Merriam, UCLA Biology,
Los Angeles, CA 90026-1606; FAX [redacted]

source_numbe 707

full_location 100F

table_numbers 1,5 cross_locations

gene_name telomere

gene_abbrev tel

product

upper case P

1 kb_cloned_genom 62 vector_genomi lambda DASH; genomic DNA p[(w,ry)A]4-4

kb_cloned_cDNA 0 vector_cDNA

METHOD: expression walk_jump_org YACs 0

microcloning oligonucleotide

homology transposon_tag xxx

clonetechtext transposon tagging using P[(w,ry)A]4-4

2 rearrangement

3 T_strain

markers

5 kb_seq_genomic 3.5 acc_number_gen kb_seq_old 0

kb_seq_cDNA 0 acc_number_cDNA

comments

ORF_size 974

ORF_functio homology to reverse transcriptase- like putative polypetide of non LTR retrotran

ORF_domain

6 kb_trans_size

transc_dist

7 protein_dist

8 fusion_dist

misc_info covers MAP205 and mod genes are within walk distal end of walk=end of chromosome
the map205 gene is within the 62kb walk;
suggest you could combine this record and

full citation Levis R; Ringley R; Houtchens K. 32nd Drosophila Conference, Chicago 1991.

contact_person Levis, R. ph [redacted] FAX [redacted]
lab_address Fred Hutchinson Cancer Research Center M616
address_line1 1124 Columbia St.
address_line2 Seattle, WA 98104
address_line3
address_line4

keywords

01C

source_number: 707

full_location: 100F cross_locations:

table_numbers: 1

gene_name: telomere

gene_abbrev: telo

product: YACs: 0

kb_cloned_genom: 62 vector_genomic: lambda DASH genomic DNA - P[(w,ry)A]4-4 transformant

kb_cloned_cDNA: 0 vector_cDNA:

expression:

homology:

microcloning:

transposon_tag: P[(w,ry)A]4-4

oligonucleotide:

clonetechtext:

rearrangement:

T_strain:

markers:

kb_seq_genomic: 3.5 acc_number_gen: kb_seq_old: 0

kb_seq_cDNA: 0 acc_number_cDNA:

comments:

ORF_size: ~~2.9 kb~~ 974 a.a.

ORF_function: homology to reverse transcriptase-like putative polypeptides of non-LTR retrotransposons

ORF_domains:

kb_trans_size:

transc_dist:

protein_dist:

fusion_dist:

misc_info: covers MAP205 and mod genes; distal end of walk=end of chromosome
the map205 gene is within the 62kb walk;

full citation **Levis, R. ~~2/25/90~~ personal communication - unpublished.** 2/28/91

contact_person **Levis, R.** **phone_number**

lab_address **FHCRC M616**

address_line1 **1124 Columbia St.**

address_line2 **Seattle, WA 98104**

address_line3

address_line4

keywords !

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John Merriam
UCLA Drosophila Genmaps Database
DEPARTMENT OF BIOLOGY
405 HILGARD AVENUE
LOS ANGELES, CALIFORNIA 90024-1606
FAX [redacted]

December 20, 1990

FAX [redacted]

Levis, R.
FHCRC M616
1124 Columbia St.
Seattle, WA 98104

Dear Colleagues:

I can use information from the clone list to construct a "physical map" of the Drosophila genome. You have (a... listed, as described below, so I would like to enlist your help. What I need for this project are the names ... locations of chromosome rearrangement breakpoints that lie within the region of your clone/walk. Mapping breakpoints is the most reliable way of connecting the molecular with the cytological scales.

As you know, the clone list has been useful to Drosophila workers in finding starting points for their walks. The database is organized by references, so that the original cloning paper from a lab is cited as key #1, with subsequent papers cited by subject (key #5 is sequence information, for example). The clone list is therefore also a gene-by-gene literature index. The clone list is now mounted on the Indiana University BioArchive computer bulletin board in the FLY subdirectory. Use Internet address 129.79.1.101 and your local File Transfer Program.

Please take a few minutes to complete this form and return to me by FAX or mail. It will be most useful if you can update your clone sizes and make more exact your clone locations. Make any other changes you want also. List the rearrangements and which breakpoints you have identified. Any cytologically visible rearrangement (deletion, inversion, translocation, transposition, duplication) is useful. Please indicate if the same citation is the best reference, or indicate a better one (or a personal communication).

Thank you for your help as always. With your prompt and generous support I can expect to show you the results in March at the Chicago fly meeting.

...t Rearrangements:	Breakpoint found:	Other breakpoints:
none identified		

ANG... **CONFIRM indexing for original ...ene cit'n:** Locations ✓ Clone sizes ✓ Names/Prod...ts ✓

La... 3/26/90 personal communication - unpubilshed. — Still the best reference to the walk

Location	Key	kb gen/cDNA	...ame (abbrev...) product rearrangements...
100F	1	62 0	...e (telo)

John - the MAP205 gene is within the 62 kb walk I would suggest you could combine this record and the 10kb MAP205 record. A citation for cDNA cloning and in situ of map205 is: Lehtonen, S.R. Lawson, R.A. & McIntosh, J.R. J. Cell Biol. 102: 2076-2087 (1986) } MISC

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UCLA Drosophila Genmaps Database

DEPARTMENT OF BIOLOGY
405 HILGARD AVENUE
LOS ANGELES, CALIFORNIA 90024-1606
FAX [redacted]

Dear Colleagues:

I would like to use information from the clone list to construct a "physical map" of the Drosophila genome. You have (a) clone(s) listed, as described below, so I would like to enlist your help. What I need for this project are the names and locations of chromosome rearrangement breakpoints that lie within the region of your clone/walk. Mapping breakpoints is the most reliable way of connecting the molecular with the cytological scales.

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Please take a few minutes to complete this form and return to me by FAX or mail. It will be most useful if you can update your clone sizes and make more exact your clone locations. Make any other changes you want also. List the rearrangements and which breakpoints you have identified. Any cytologically visible rearrangement (deletion, inversion, translocation, transposition, duplication) is useful. Please indicate if the same citation is the best reference, or indicate a better one (or a personal communication).

I thank you for your help as always. With your prompt and generous support I can expect to show you the results in March at the Chicago fly meeting.

List Rearrangements :	Breakpoint found:	Other breakpoints:

CHANGE or CONFIRM indexing for original clone cit'n: Locations __ Clone sizes __ Names/Products __

Levis, R. 3/26/90 personal communication - unpublished.

Location	Key	kb gen/cDNA	Gene name (abbreviation) product rearrangements...
100F	1	62 0	telomere (telo)

(707)

3/18/91

John Merriam
UCLA Drosophila Genmaps Database

FAX:
R Nevers, R. Ringley, K. Hortchens
Fred Hutchinson Cancer Research Center
1124 Columbia ST., MS # M616
Seattle, Wa 98104

FAX [redacted]

Help!

Your article, listed below, is likely to have cloning or molecular information that should be listed in Drosophila Genmaps. As you know, the clone list has been useful to Drosophila workers in finding start points for their walks. The database is organized by references, so that the original cloning paper from each lab is cited as key #1, with their subsequent papers cited by subject. The clone list is therefore also a gene-by-gene literature index. The clone list is now mounted on the Indiana University BioArchive computer bulletin board in the FLY subdirectory. Use Internet address [redacted] and your local File Transfer Program.

Please take a few minutes to complete this form and return to me by FAX or mail. On separate sheet(s) we print out the information we have already from your lab on this gene. Send back to us any corrections you may have. If we missed any previous papers, make copies of this form to describe each earlier paper. Include your FAX number. If you think that one of your co-authors would be a better contact for us, feel free to send them this letter with your request to answer it.

I thank you for your help as always. With your prompt and generous support I can include your results in the next update on the bulletin board. -- John

CITATION:

227 33rd Drosophila Conference, Chicago, 1991

--> List the Gene name: | and its Chromosome location:

KEYs 1-8: Please check off those boxes which describe THIS PAPER

Describe your results in detail on the reverse side.

- [x] 1 Genomic or cDNA clones obtained.
- [ ] 2 Rearrangement breakpoints found in clone.
- [ ] 3 New location of transformed insert.
- [x] 5 Sequence obtained.
- [ ] 6 Transcript obtained.
- [ ] 7 Protein described by antisera.
- [ ] 8 Promoter fusion studies.
- [ ] No cloning or molecular information about gene

DROSOPHILA GENMAPS DATABASE REPORT FORM

MNV 5/2/91

Return to John Merriam, UCLA Biology, Los Angeles, CA 90026-1606; FAX 213-206-3987

location: 100F keys for this paper:

Gene/mutant name: ~~Bominis~~ 3R ?

abbreviation:

biochemical name/product:

(1) CLONES:

kb_genomic: 62 vector/library name: vector - lambda dash / genomic DNA P[(w,ry)A]4-4 transformant

kb_cDNA: 0 vector/library name:

METHOD:

prior clone: walk:

expression: differential screen:

microclone: oligonucleotide: PCR?

homology: transposon tag: P[(w,ry)A]4-4

(2) REARRANGEMENTS:

(3) TRANSFORM INSERTS:

(5) SEQUENCE:

kb_genomic: 3.5 accession number:

kb_cDNA: 0 accession number:

ORF-size: 2.9 Kb (ATG)

ORF_function/homology group: homology to reverse-transcriptase-like putative polypeptide of non-LTR retrotransposons

ORF_domains:

(6) TRANSCRIPT DESCRIPTION:

transcript_size:

distribution:

(7) PROTEIN ANTIBODY:

distribution:

(8) LAC Z FUSION STAIN:

distribution:

MISC_INFO: MAP205 and modulo genes are within walk
distal end of walk = end of chromosome