FBrF0075199

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341

SANTA BARBARA • SANTA CRUZ

December 20, 1990

FAX: [redacted]

emc

Ellis, HM Posakony
Department of Biology B-022
University of California, San Diego
La Jolla, CA 92093

John Merriam
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.

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).

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 __

Ellis HM; Spann DR; Posakony JW. extramacrochaetae, a negative regulator of sensory organ development in Drosophila, defines a new class of helix-loop-helix proteins. Cell 1990 Apr 6;61(1):27-38.

Location	Key	kb gen/cDNA	Gene name (abbreviation) product rearrangements...
61D	1,5,6	20 1.94	extra macrochaetae (emc)

usa kony UC San Diego (341) not 341

An to John Merriam, UCLA Biology, LA 90024 FAX [redacted]

REFERENCE: Ellis, H.M., Spana, E., and Baker, F.W. (1990) Cell [illegible]

NAME: H. Ellis PHONE #_____ FAX #_____ UC

6/19/90

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

mutant name (if any) extra macrochaetae

abbreviation emc

biochemical name (if any)_____

2. LOCATION: Where is your clone/walk located? 6,1D

(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 20 vector/library name_____

cDNA 1.[illegible]0 vector/library name [illegible]

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

prior clone_____ transposon tag_____

expression_____ differential screen_____

microclone_____ oligonucleotide_____ PCR?_____

homology_____

5. SEQUENCE: round to the nearest 10th the kb sequenced

genomic ~.3kb accession # M[illegible]C

cDNA 1.9 kb accession # M[illegible]7

PRODUCT: How many amino acids in the ORF? 199

List above the predicted function or homology group of the ORF

-H [illegible]

List above the key words that describe domains in the ORF

6. TRANSCRIPTS: round m RNA sizes to nearest 10th kb, list largest first_____ When/where found?_____

7. PROTEIN (antibody detection) Where found?_____

8. LAC Z FUSION stain Where found?_____

9. MORE DETAILS:_____

1/24/87 RECORD NO 875 REF NO. 341

update ref & record

4. Date

5. Location 61D

6. Table Num 0 (1) 2 3 4 (5) (6)

7. Clone Name extra macrochaetae (emc)

8. Genes Info

9. Stock Orgn

10. KB Size 20

11. Cross Ref

12. Misc Info ~~embryo lethal~~ alleles with Ach (achaetae); Presentation of Ach or emc nulls; tag; 2Kb RNA embryos, late larval, early pupae; sequence homology with myc, da al ac-sc; helix loop helix

13. Reference

14. Breakpoint

15. BPCont1

16. BPCont2

17. T Strain

18. Markers

19. DIS Vol

20. Comments

21. KB Sequenced 1.93

22. Coordinates

please return to:

John Merriam

Biology Department
Univ California
Los Angeles, CA 90024

FAX # [redacted]

1989 Dev Biol Soc Berkeley

key to Table num for this record: 0 = new data and ref on one previously entered, 1 = clone, 2 = rearrangement breakpoint, 3 = insert, 4 = walk, 5 = sequenced, 6 = transcription t. multiple entries ok (ie 1,2,4,5,6)

01C

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