sr

FBrf0075238

UNIVERSITY OF CALIFORNIA, LOS ANGELES

UCLA
1724

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SANTA BARBARA • SANTA CRUZ

9/4/92

John Merriam
UCLA Drosophila Genmaps Database

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

complete your FAX number here:

Baylor College of Medicine
Howard Huges Medical Institute
Institute for Molecular Genetics
Houston, TX 77030

Dear Colleagues,

We need your **help** in forming a **Restriction Map** of the *Drosophila melanogaster* genome. Our task is to collect information for a physical map of genes (clones and walks) based on restriction sites. Already a physical map of clones exists based on collected information about the band locations of clones (see Science 254: 221). The next step will provide a higher resolution framework for organizing information in the Drosophila genome data base project.

The most important information we would like to receive from you is the restriction map you have for the gene sr. Of course we mean a map for as much of that chromosome region as you have. The best form of information for us would be a table or list of the coordinates (in Kb) of restriction sites. We will also be happy to accept a Xerox copy of any map you already have available, with the gene name, scale, symbol legend to enzymes, lab name and/or reference attached. It would be very helpful if you could include the locations of other details on a line drawing for future physical annotations. We would like to see the following features on your scale diagram:

* transcript units with origin and exons
* alternate splices or cDNAs if different from above
* sequenced intervals with accession nos.
* breakpoints of rearrangements (named)
* STS or any other landmarks

With this request we are initiating a new data base direction for us. That is to record, for each laboratory or project, the kb coordinates of the gene or chromosomal region of interest. The information you send us should represent your most up-to-date and comprehensive map. Separately we will continue to record the data for individual publications. By using records from both projects together we maintain a link between publications and the physical restriction map.

We would also like to use this opportunity to verify our records and have enclosed information we believe to be presented in individual publications. Please review each record with respect to the questions listed below. Make revisions directly on the copy and send corrected copies back to us.

* are the gene name and abbreviation informative, acceptable?
* is the information accurate?
* is the information in each report restricted to data that was presented for the first time in the corresponding paper? For example Table/Section 1 should be filled out only for those publications describing isolation of DNA clones.
* has this meeting report or communication been published? Please provide the citation.
* are the name, address, phone and Fax nos. up to date?

Thank you for your assistance with this project which will benefit all Drosophila workers. We hope to present initial results at the 1993 Drosophila meetings. To do this we need your response as soon as possible. Please check the appropriate box below and send back or Fax this form along with your list or map. John

☐ map or coordinates enclosed
☒ no map available
☐ send request to _____ at _____

One hundred twenty-five years of service

SOPHILA GENMAPS DATABASE RECORD PRINTOUT - 8/28/92
source_numbe 1724

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

full_location 90E1-4
table_numbers 1,2 cross_locations

gene_name stripe
gene_abbrev sr
product

1 kb_cloned_genom 30 vector_genomi
kb_cloned_cDNA 0 vector_cDNA

METHOD: expression walk_jump_org YACs 0
microcloning oligonucleotide
homology transposon_tag xxx

clonetechtext p[lwt]ak

2 rearrangement Df(3R)sr-l6;Df(3R)sr-l461;Df(3R)D64

3 T_strain
markers

5 kb_seq_genomic 0 acc_number_gen [redacted] 0
kb_seq_cDNA 0 acc_number_cDNA
comments
ORF_size
ORF_functio
ORF_domain

6 kb_trans_size
transc_dist

7 protein_dist

8 fusion_dist

misc_info

full citation Bellen HJ and Alex ~~torodkin~~ Kolodkin. 1991 personal communication

contact_person Bellen, H.J ph FAX
lab_address Baylor College of Medicine
address_line1 Howard Huges Medical Institute
address_line2 Institute for Molecular Genetics
address_line3 Houston, TX 77030
address_line4

keywords muscle, nervous system, enhancer detectors

source_number: ~~1001~~

full_location: 90E1-4 cross_locations:

table_numbers: 1, 2

gene_name: stripe-distal

gene_abbrev: s r

product: YACs: 0

kb_cloned_genom: 30 vector_genomic:

kb_cloned_cDNA: 0 vector_cDNA:

expression:

homology:

microcloning:

transposon_tag:

oligonucleotide:

clonetechtext:

rearrangement:

T_strain:

markers:

kb_seq_genomic: 0 acc_number_gen: kb_seq_old: 0

kb_seq_cDNA: 0 acc_number_cDNA:

comments:

ORF_size:

ORF_function:

ORF_domains:

kb_trans_size:

transc_dist:

protein_dist:

fusion_dist:

misc_info:

full citation: **Bellen HJ. 1990 Drosophila conference.**

contact_person Bellen, HJ. **phone_number** [redacted]

lab_address Baylor University

address_line1 Howard Hughes Medical Institute

address_line2 Institute for Molecular Genetics

address_line3 Houston, TX 77030

address_line4

keywords !

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John Merriam
UCLA Drosophila Genmaps Database

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LOS ANGELES, CALIFORNIA 90024-1606
FAX [redacted]

complete your FAX number here:

Df(3R)Sr 1461
Df(3R)Sr1461
Df(3R) DG4

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markers

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lab_address Baylor College of Medicine
address_line1 Howard Huges Medical Institute
address_line2 Institute for Molecular Genetics
address_line3 Houston, TX 77030
address_line4

keywords muscle, nervous system, enhancer detectors

OK If you want to separate them → this, stripe 1724

source_number: ~~1001~~ need new SN

full_location: 90E1-4 cross_locations:

table_numbers: 1, 2

gene_name: stripe-~~distal~~

gene_abbrev: s r

product: YACs: 0

kb_cloned_genom: 30 vector_genomic:

kb_cloned_cDNA: 0 vector_cDNA:

expression:

homology:

microcloning:

transposon_tag: P{lwB}lk~~2~~1

oligonucleotide:

clonetechtext:

rearrangement:

T_strain:

markers:

kb_seq_genomic: 0 acc_number_gen: kb_seq_old: 0

kb_seq_cDNA: 0 acc_number_cDNA:

comments:

ORF_size:

ORF_function:

ORF_domains:

kb_trans_size:

transc_dist:

protein_dist:

fusion_dist:

misc_info: Df(3R)Sa^{22}; Df(3R)Sa^{24a1}, Df(3R)DB4

full citation: Bellen HJ. ^ 199~~0~~ ~~Drosophila conference.~~ personal comm - & Alex Tokuhiro

contact_person: Bellen, HJ. phone_number: [redacted]

lab_address: Baylor ~~University~~ College of Medicine

address_line1: Howard Hughes Medical Institute

address_line2: Institute for Molecular Genetics

address_line3: Houston, TX 77030

address_line4:

keywords: ! Innate, hemocyte, enhancer detectors