FB-f 0112243

From [redacted] **Thu Oct 21 19:22:58 1999**
From: Steve Greig [redacted]
To: "Rachel Drysdale (Genetics)" [redacted]
Subject: Re: submitting data
Date: Thu, 21 Oct 1999 19:35:45 +0100

Rachel, I have put together a short personal communication which is attached to this. Let me know if it is suitable and if not how I can change it. Best wishes from Steve
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<This message contains 1 attachments (not printed)>

Re: submitting data

Drosophila cDNAs which interact with Drosophila heterotrimeric G alpha i in a two hybrid screen. Personal communication from Dr Steve Greig and Dr Cahir O'Kane.

In a two-hybrid screen for interactors with the Drosophila heterotrimeric G alpha i subunit 16 different length cDNAs were obtained. Sequencing these showed they represented probably four genes. One of these is in press and the other pubished. For methods see Granderath S et al. Development **126**, 1781--1791 (1999). The remaining two, gene A16 and F8, are described below with the results of blast searches.

The screen was done at the Genetics Department, Cambridge University, Cambridge, UK with funding from the BBSRC. If you want more information, cDNAs or the bait construct please ask.

Gene A16: Four overlapping cDNAs for this gene were isolated. It is probable that they only represent the 3' end of the gene. Composite DNA and protein sequences are shown below. The underlined region in the protein sequence represents the smallest cDNA and presumably contains the (or one of the) G alpha i binding domain.These cDNAs did not interact with a constitutively active G alpha i bait. In situ hybridization to polytene chromosomes gave a signal at 34A. The results of a blast search against Drosophila sequences is also shown.

GACTTTTGTCTAGCTTATATCACAGAACCGTCACGNCAAACCACGCTGGCGGAGAGCACCGGCGCCTCCGTATCAGCATCCAC
ATCCACATCAACACCCACGTCCGCCTCTAGTAGCATCAGCGGCAGCATGCTGGAGGTCGCAGCAGACACCCAGCCAGTCCACC
CCCGAAACAACAGATTCCGCCTCGTCGTCCGTGCGCGTGAAGAAGGTACGCTTCCATCCGGACGTCAAGGAAAACGACGGCGG
GAACTGGATGAAAAGAAAGCGACGCTCCATGCATACCAAACGAACCTCCTCGCCCAGCGGCGCTAACTGTGATGGCATGGAGC
TGGACGGTGAGTACGAGGACAACGATGACGATGAGCAGGAGGAGGCGGAGGAGGAGTTCGATCTGGCCAAGACAATCGCCGAG
GCGGAGGATTACCTCAAGCAGCACCCGTTGACATACGTGCAGCGCGTCGAACAGAACGGCGAGCGGCTGCAGGATGGACTGCT
CAGCATCGAGGATATGCTAAACGAAGTCGGCGAGGAGGTGGTCACCGAGTACAACGACGAGGACTTCTTCAGACGCATCAAGC
CCGAGAATGGCATTGAACGCATTCTGGGCAAGGAGACCAAGGCGGGAAAGGTTGAATTCCTTCTGCGCTACGAGAACCAAGGC
GGACTCTTCTGGCAATCGGAGGAGTTCATCAAGCGCACGTGCCCCTGCTCAAGGCCTACGAAATGA

TFV*LISQNRHXKPRWRRAPAPPYQHPHPHQHPRPPLVASAAACWRSQQTPSQSTPETTDSASSSVRVKKVRFHPDVKENDGG
NWMKRKRRSMHTKRTSSPSGANCDGMELDGEYEDNDDDEQEEAEEEFDLAKTIAEAEDYLKQHPLTYVQRVEQNGERLQDGLL
SIEDMLNEVGEEVVTEYNDEDFFRRIKPENGIERLGKETKAGKVEFLLRYENQGGLFWQSEEFIKRTCPCSRPTK*

AC010214	: BACR27F17 (BAC D1139). Unfin...	1858	1.6e-77	1
GH07495.3prime	AI109007	1510	1.2e-62	1
GH07525.3prime	AI109028	1474	5.1e-61	1
LD25087.5prime	AA941120	1397	1.1e-57	1

Gene F8: : Represented by only one cDNA. Not Mapped. Did not interact with constitutively active Gi bait. Blast search shows similarity to rod cGMP phosphodiesterase which could be of significance. The DNA sequence and results of a blast search against all proteins is shown below. Note there are no matches for known Drosohpila sequences.

ACGTAAACGCGTAGGCGCTCCCACCTGGCAGTGCACCCGATTGACCGACTTGNAACTCCACGGNCACCGATGGGNTCCGACGA
CAGAGTGNCGGGGACAGGATCCAGAAGGGATTCCAGATCAACTATATGATTCTGCGGGATGNCGACAGCGGAAAAATAATCTG
GCAGGAGAACAAGGACTTCTCGGNANCGGACAGGAGCATGAGGCCGAGTGCGGTGAAAATACTCGACATGCGTGCCGTTCCCG
GGAGATCACTTCAGCAACATCGAGTCGATGGAGAATTTCGCTGGACAGAAGGTGTCTCAAGGGGCGNATCATGGGNTGGGGTC
TTTGGGATGGATCGTGGTGCAAACACACACTGGAGGNGCATCGAGGGGGACCGATCCAGTNATGCTCAGGCTTGACGGATTGA
TTCAACAGTCTTGAAAGAAATACACATCGGNGGGCTTCTNNTAGAATTATACGCNCNTANNCAGGTCTGNTCNCAATTTGGGG
GTCNNTTCTTCAAAANTTCTTGGTTCNATCANAAGNGGGNTTNTTTGGCNNNTTNTTNTTTNGTCCA

gi|2896022	(AF046000) rod cGMP phosphodieste...	+3	89	0.0016	1
gnl|PID|e1203973	(AJ001626) p17 protein [Homo sapi...	+3	89	0.0016	1
gi|2655094	(AF022912) cGMP phosphodiesterase...	+3	89	0.0016	1
sp|Q95142|CNRD_BOVIN	RETINAL ROD RHODOPSIN-SENSITIVE C...	+3	89	0.0016	1
sp|Q18268|YK91_CAEEL	HYPOTHETICAL 18.4 KD PROTEIN C27H...	+3	88	0.0022	1