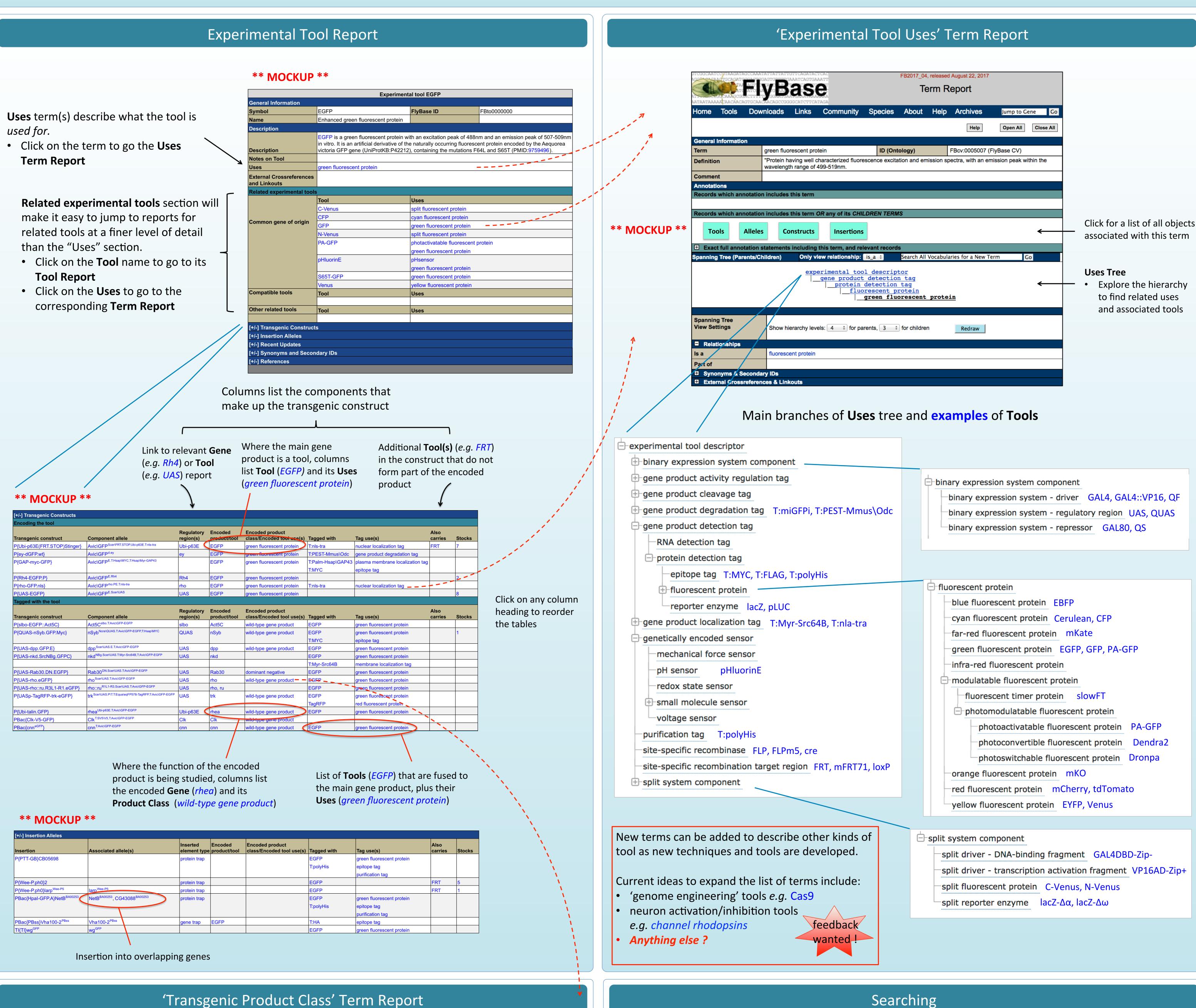


Finding the right tool for the job: new ways to find particular types of transgenic construct in FlyBase

Gillian Millburn (gm119@cam.ac.uk) and the FlyBase Consortium

Introduction

The long history of fly research plus the sophisticated range of applicable genetic engineering techniques mean that a large number of increasingly complex transgenic fly lines have been generated and described in the literature. While this rich genetic tool-kit helps to make *Drosophila melanogaster* an ideal model organism to answer a wide range of biological questions, it also creates a potential problem - how to find the most appropriate fly line for a particular experiment from the large set that is available. To help overcome this issue, FlyBase will start to capture and display information about **Experimental Tools**, which will allow you to easily identify transgenic constructs and their insertions with particular characteristics. We are defining an experimental tool as "any sequence *whose own biological function isn't really being studied* in an experiment, but is instead being *exploited* to study the biological function of some other gene product or a biological process". This broad definition will allow you to browse and search for tools used for a wide range of different purposes, such as enabling a gene product to be detected (*e.g.* FLAG tag, GFP, other reporters), targeting a gene product somewhere specific within a cell (*e.g.* nuclear localisation signal, signal sequence), driving expression (*e.g.* GAL4, lexA), enabling clonal/conditional expression (*e.g.* FLP, FRT), being used as a sensor for changes in Ca²⁺, pH, voltage *etc.*, *etc.*



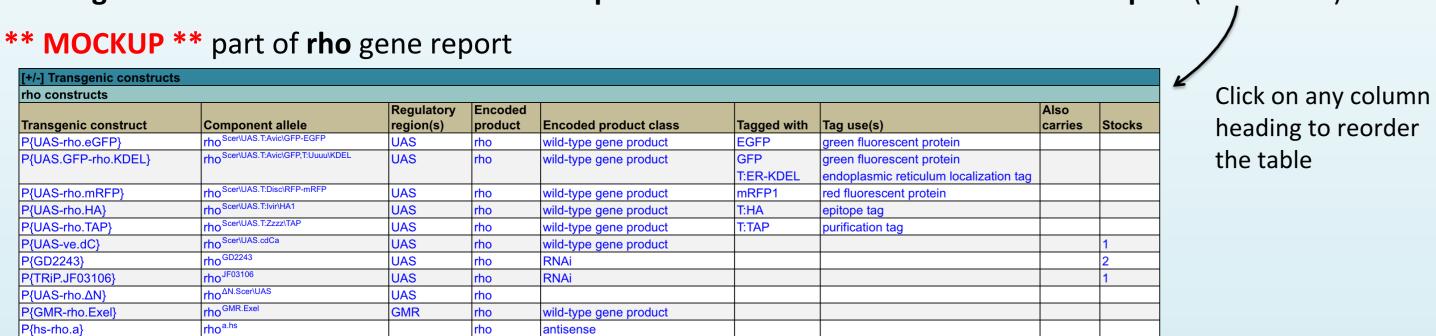
The **Transgenic Product Class** is intended to give an *overview* of the nature of the gene product encoded by a transgenic construct, similar to **Allele Class** used for classical and insertional alleles

transgenic construct, similar to Allele Class used for classical and insertional alleles.
It will be used for constructs where the function of the encoded gene product is being studied or where the

feedback

wanted !

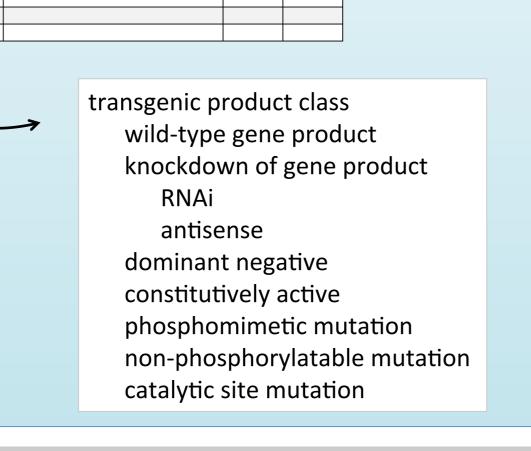
- construct encodes a sequence that affects an endogenous gene product (e.g. RNAi)
 It will allow constructs to be grouped into broad categories for browsing and searching, for example in the
- Transgenic Constructs to be grouped into broad categories for browsing and searching, for example in the Transgenic Constructs tables on the Tool Report and in similar tables on the Gene Report (see below).

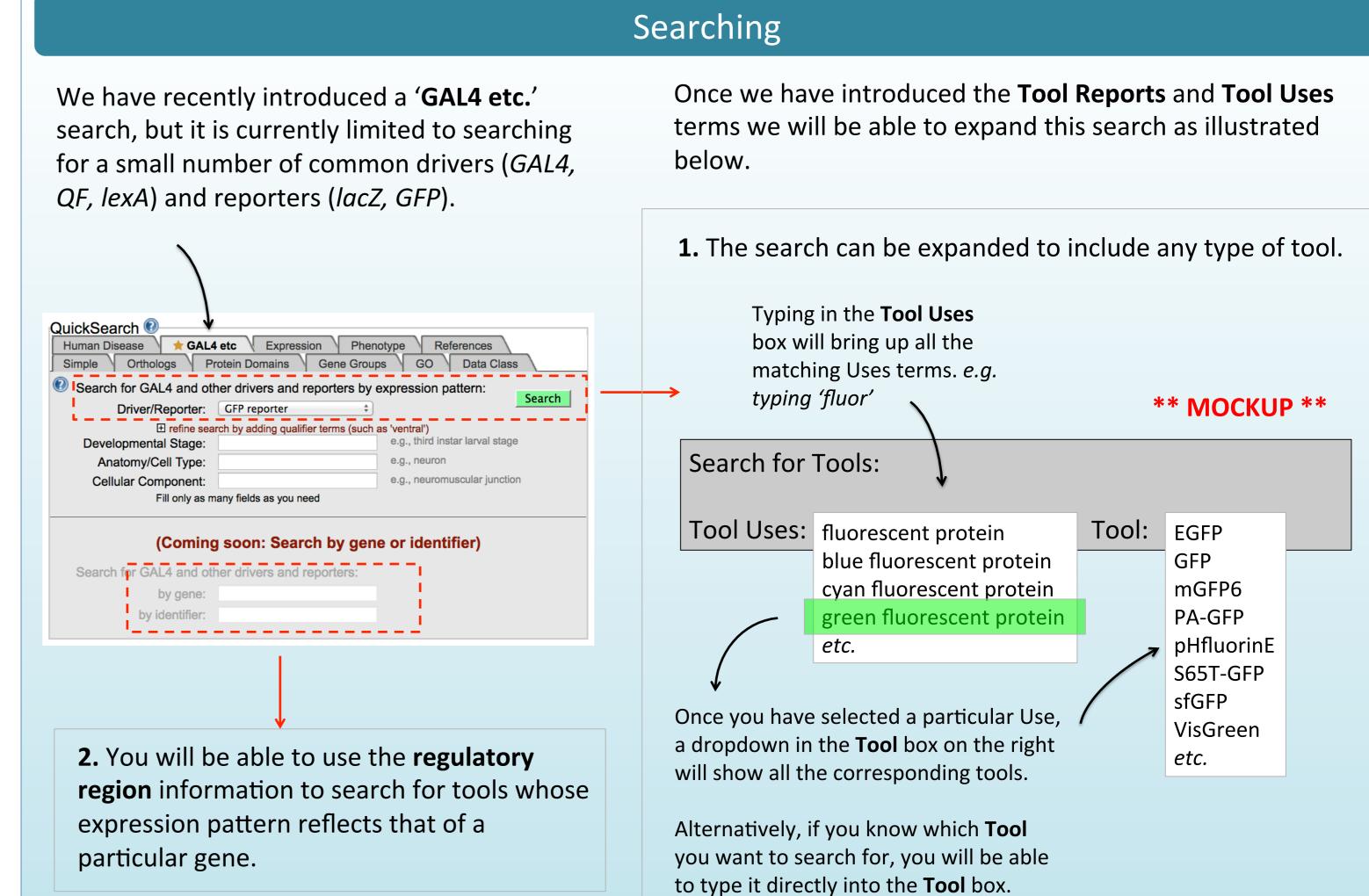


Current ideas for terms are a work-in-progress:

- Are the terms shown useful?
- Are there any terms missing

that you'd like to see?





The FlyBase Consortium comprises: Nick Brown, Giulia Antonazzo, Helen Attrill, Silvie Fexova, Phani Garapati, Tamsin Jones, Alex Holmes, Aoife Larkin, Steven Marygold, Gillian Millburn, Alix Rey, Vitor Trovisco, Jose-Maria Urbano (FlyBase-Cambridge), Norbert Perrimon, Julie Agapite, Kris Broll, Lynn Crosby, Gil dos Santos, David Emmert, Kathleen Falls, Susan Russo Gelbart, L. Sian Gramates, Beverley Matthews, Christopher Tabone, Pinglei Zhou, Mark Zytkovicz (FlyBase-Harvard), Thomas Kaufman, Bryon Czoch, Josh Goodman, Gary Grumbling, Victor Strelets, Jim Thurmond (FlyBase-Indiana), Richard Cripps, Maggie Werner-Washburne, Phillip Baker (FlyBase-NewMexico).