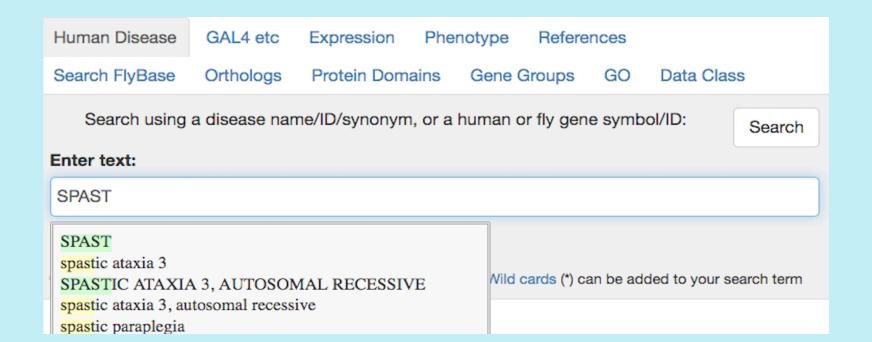


# Finding human disease models in FlyBase: You can get there from here

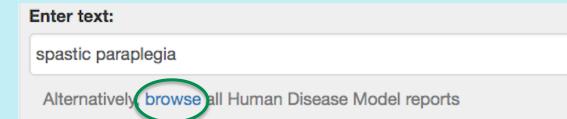
Sian Gramates, Lynn Crosby, Josh Goodman, Steven Marygold, Victor Strelets, Jim Thurmond, and the FlyBase Consortium

Many human diseases have been modeled in *Drosophila*, and a large body of literature has accumulated in recent years. FlyBase has been curating disease models using Disease Ontology (DO) annotation and Human Disease Model reports. We provide multiple methods to access disease model data in FlyBase, including a dedicated 'Human Disease' QuickSearch tab, DO term reports, and disease model information embedded in gene and allele reports. We have organized disease model information in a highly interconnected way, so that a user who has landed on any such information can easily navigate to other related information.

#### The Human Disease QuickSearch Tab



By using the **Human Disease** tab, it is possible to search all FlyBase human disease model data using almost any disease-related search term, including DO terms, Human Disease Models, OMIM phenotypes or genotypes, HGNC symbols, FlyBase genes or alleles, or ID numbers for any of these terms. Autocomplete is enabled for all of these search options; as shown in the example above, the string "SPAST" simultaneously triggers autocompletion of gene symbols, allele symbols, OMIM diseases terms, DO terms, nd Human Disease Model names.

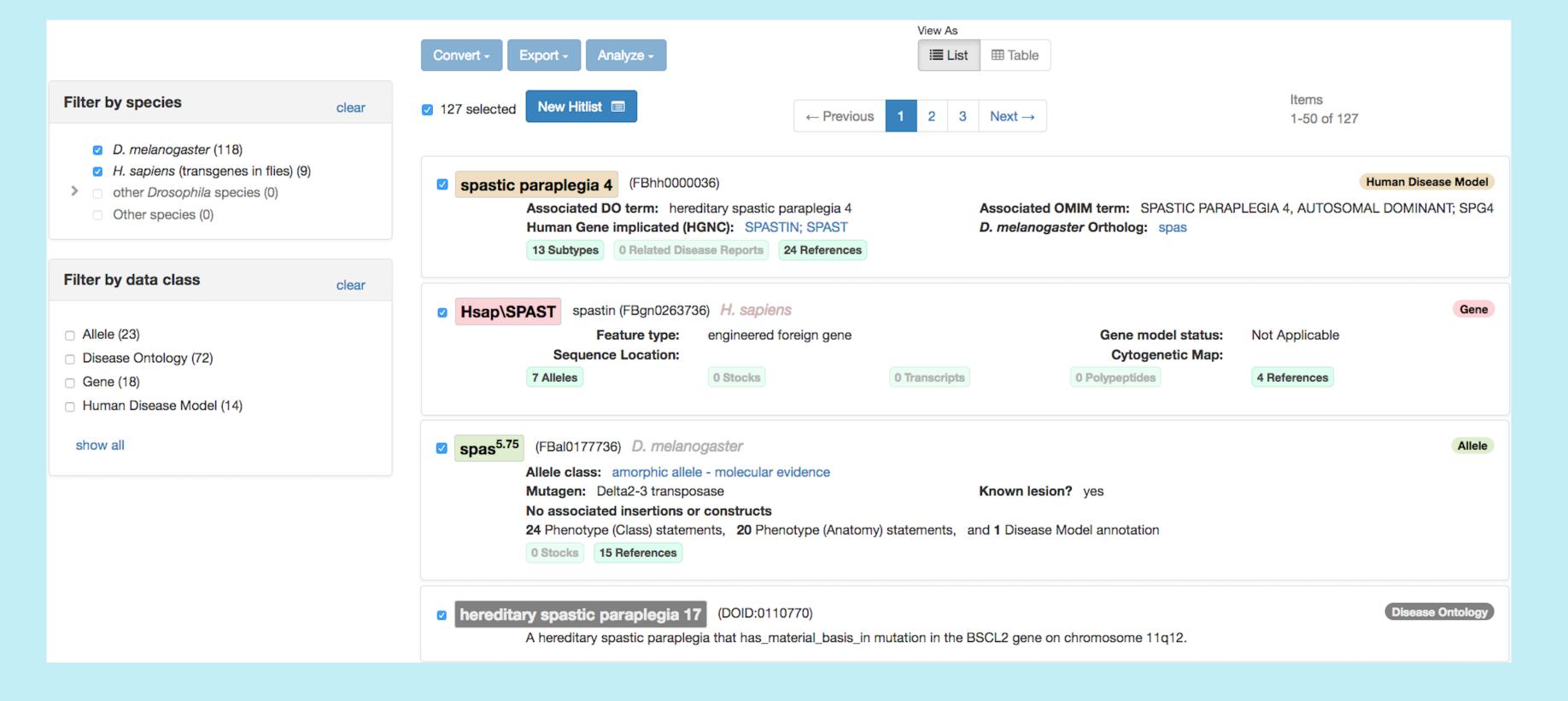


The **Human Disease** tab also includes a link to a browsable index of all Human Disease Model reports; many disease model reports are listed redundantly in the index, , allowing a user to browse to a disease from multiple points. Diseases may be listed as a specific subtype of a disease, by mechanistic cause, by symptomatic group, or as part of a major disease classification.

#### FlyBase Human Disease Model Report Index

- 3-methylglutaconic aciduria
   acute myeloid leukemia
   acute myeloid leukemia, MLL-AF fusions
   acute myeloid leukemia, NUP98-HOXA9 fusion
   acute myeloid leukemia, RUNX1-RUNX1T1 fusion
   acyl-CoA dehydrogenase, medium chain, deficiency of
   adrenoleukodystrophy (postulated), ACSBG-related
- familial advanced sleep phase syndrome 2
   age-dependent ectopic fat accumulation, HDAC6-related
   Alexander disease

#### Human Disease Hit-lists



The Human Disease hit-list features four classes of data: Human Disease Models, Disease Ontology terms, genes, and alleles. This hit-list resulted from the search "spastic paraplegia", which includes the hits the Human Disease Model spastic paraplegia 4, the gene Hsap\SPAST associated with that model, the allele spas<sup>5.7</sup>, and the DO term hereditary spastic paraplegia 17.

Like all FlyBase faceted hit-lists, a user can choose to display a subset of data classes. Filtering the hit-list to a single data class allows you to further convert the results to another data class, export to a file or to another FlyBase tool, analyze the results in a data class specific manner, or display the hit-list as a table.

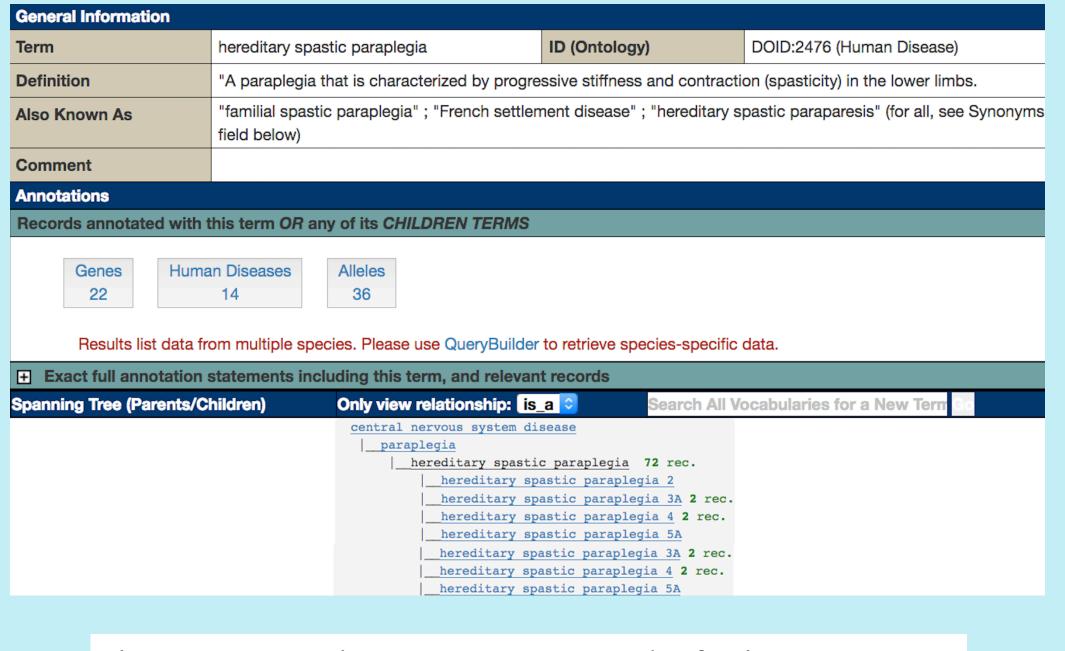
		Hum	Human Disease Model Results						
<b>2</b>	Name	DO Term	OMIM ID	D. melanoga gene	Human Genes Implicated (HGNC)	# Subtypes	# of Related Disease Terms	# Refs	
☑	spastic paraplegia 4	hereditary spastic paraplegia 4	182601	spas	SPASTIN; SPAST	13	0	24	
✓	spastic paraplegia 7	hereditary spastic paraplegia 7	607259	Spg7	SPG7 GENE; SPG7	13	0	4	
•	spastic paraplegia 10	hereditary spastic paraplegia 10	604187	Khc	KINESIN FAMILY MEMBER 5A; KIF5A	13	1	9	
•	spastic paraplegia 12	hereditary spastic paraplegia 12	604805	Rtnl2 Rtnl1	RETICULON 2; RTN2	13	0	9	
☑	spastic paraplegia 20	Troyer syndrome	275900	spartin	SPARTIN; SPART	13	0	8	

This hit-list, resulting from the search "spastic paraplegia", has been filtered to display only Human Disease Models. The table view for this data class highlights the relationships between Human Disease Models, DO terms, and OMIM phenotypes, and displays the associated human disease gene and its orthologous *Drosophila melanogaster* gene.

#### Vocabularies: Another Path to Disease Models



The **Vocabularies** tool can be accessed using the button on the FlyBase home page, or from the Tools drop-down menu in the FlyBase toolbar. Select the **Human Disease (DO)** CV Hierarchy and enter a search term; autocomplete is enabled for DO terms.



The Disease Ontology term report provides further access to disease model data. The spanning tree allows the user to browse the DO hierarchy, which displays both less specific parental disease categories, and more specific child disease terms. The buttons above the spanning tree lead to hit-lists of genes associated with, Human Disease Model Reports linked to, and alleles annotated with the DO term or its children. The hit-list below includes alleles annotated with the DO term "hereditary spastic paraplegia", or one of its children.

			Allele Results					
<b>2</b>	Symbol	Class	Inserted Elements	# Stocks	Mutagens	Known Lesion?		
<b></b>	Arl6IP1 <sup>KK109154</sup>			1	in vitro construct	yes		
<b>✓</b>	spas <sup>dsRNA.UAS</sup>			0	in vitro construct	yes		
<b>2</b>	futsch <sup>EP1419</sup>		P{EP}futsch <sup>EP1419</sup>	1	P-element activity	yes		

## Disease Information in Allele and Gene Reports

General Information									
Symbol	Dmel\spas <sup>10-12</sup>	Species	D. melanogaster						
Human Disease Model Data									
Disease Ontology	Disease Ontology								
Models (1)									
Disease	Evidence	Refer	ences						
model of hereditary spa	inferred from m	utant (Sherv	vood et al., 2004)						
paraplegia	phenotype								

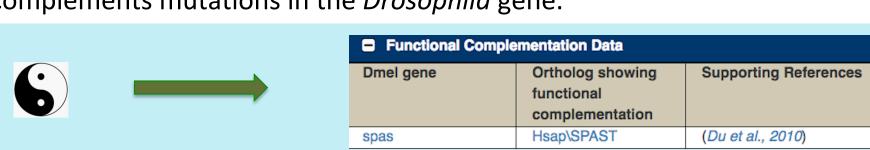
Alleles associated with disease models are annotated with Disease Ontology terms. **Allele reports** link to Disease Ontology term reports.

☐ Human Disease Model Data								
FlyBase Human Disease Model Reports								
	spastic paraplegia 4							
Alleles Reported to Model	Alleles Reported to Model Human Disease (Disease Ontology)							
Download	Models Da	ata	Interaction Data					
Models (6)								
Allele	Disease	Evidence	References					
spas <sup>10-12</sup>	model of hereditary	inferred from mutant	(Sherwood et al., 2004					
	spastic paraplegia	phenotype						
Interactions (1)	Interactions (1)							
Allele	Disease	Interaction	References					
spas <sup>5.75</sup>	model of hereditary spastic paraplegia	is ameliorated by Hsap\SPAST <sup>UAS.Venus</sup>	(Du et al., 2010)					

**Gene Reports** include a Human Disease Model Data section, which displays Human Disease Model Reports associated with the gene and alleles of the gene annotated with DO terms. From here, a user can navigate to DO term and Human Disease Model reports, and to disease-associated alleles.

Homo sapiens (Human)							
Gene name	Score	OMIM	OMIM Phenotype				
SPAST; spastin	15 of 15	604277	SPASTIC PARAPLEGIA 4, AUTOSOMAL DOMINANT; SPG4	3	e)		
FIGNL1; fidgetin like 1	3 of 15	615383					

This section also includes DIOPT-identified human orthologous genes. A user can navigate from here to HGNC gene reports, and to OMIM genotype and phenotype reports. The icons in the right column indicate whether the human gene has been expressed in flies, and whether it functionally complements mutations in the *Drosophila* gene.



### The Integrated Human Disease Model Report

Name	spastic paraplegia 4	FlyBase ID	FBhh0000036			
Disease Ontology	hereditary spastic paraplegia 4	Parent Disease	spastic paraplegia			
Term						
OMIM	SPASTIC PARAPLEGIA 4, AUTOSOMAL	Parent Disease	hereditary spastic paraplegia			
	DOMINANT; SPG4	Ontology Term				
Overview						
	This report describes spastic paraplegia 4 (SPG4), which is a subtype of spastic paraplegia; SPG4 exhibits autosomal dominant inheritance. The human gene implicated in this disease is SPAST (Spastin), which encodes an ATP-dependent microtubule severing protein and shares sequence similarity with the N-terminal MIT (microtubule interacting and trafficking) domain of the protein associated with SPG20. There is a single fly ortholog, spas, for which classical amorphic and loss-of-function alleles, RNAi-targeting constructs, and alleles caused by insertional mutagenesis have been generated.					
	Multiple different UAS constructs of the human Hsap\SPAST gene have been introduced into flies, including wild-type and genes carrying mutational lesions implicated in SPG4. Heterologous rescue (functional complementation) of some aspects of the phenotype of a Dmel\spas null mutation has been demonstrated, including an increase in survival to adulthood. Variant(s) implicated in human disease tested (as transgenic human gene, SPAST): the C448Y, S44L, P45Q, and R431(term) variant forms of the human gene have been introduced into flies.					

Human Disease Model Reports integrate disease information from many parts of FlyBase. Some, like this one, focus on a single disease, while others are parent reports, describing the general characteristics of groups of related but genetically distinct diseases. We've recently added fly model overview reports that collect methods, fly biology, and reviews pertaining to research in broad classes of diseases, such as hematologic cancer or kidney disease.

OMIM report	SPASTIC PARAPLEGIA 4, AUTOSOMAL DOMINANT; SPG4	
Human gene(s) implicated	SPASTIN; SPAST	
Symptoms and phenotype	See general description of spastic paraplegia above. The age of onset and the severity of symptoms both vary widely in cases of SPG4. [from OMIM:182601; 15.06.30]	(OMIM, 2013-)
	SPG4 is the most common form of autosomal dominant HSP, accounting for approximately 45% of cases. Affected individuals have slowly progressive muscle weakness and spasticity. In rare cases, some individuals may have a complex form associated with seizures, ataxia, memory impairment, cognitive decline and dementia. Hand tremor and upper limb spasticity have also been reported. Onset can range from infancy to older adulthood. [from NORD: Hereditary Spastic Paraplegia; 2016.09.02]	(FlyBase Curators, 2013-)
Genetics	SPG4 is inherited as an autosomal dominant; it is caused by mutations in the SPAST (spastin) gene. SPG4 is the most common form of autosomal dominant hereditary SPG, comprising up to 45% of cases (Svenson et al., 2001, pubmed:11309678; Crippa et al., 2006, pubmed:16682546). [from OMIM:182601;	(OMIM, 2013-)

The Disease Summary includes background information, drawn primarily from OMIM (Online Mendelian Inheritance in Man) and research papers. This section includes links to OMIM genotype and phenotype reports, as well as to references.

15.06.30]

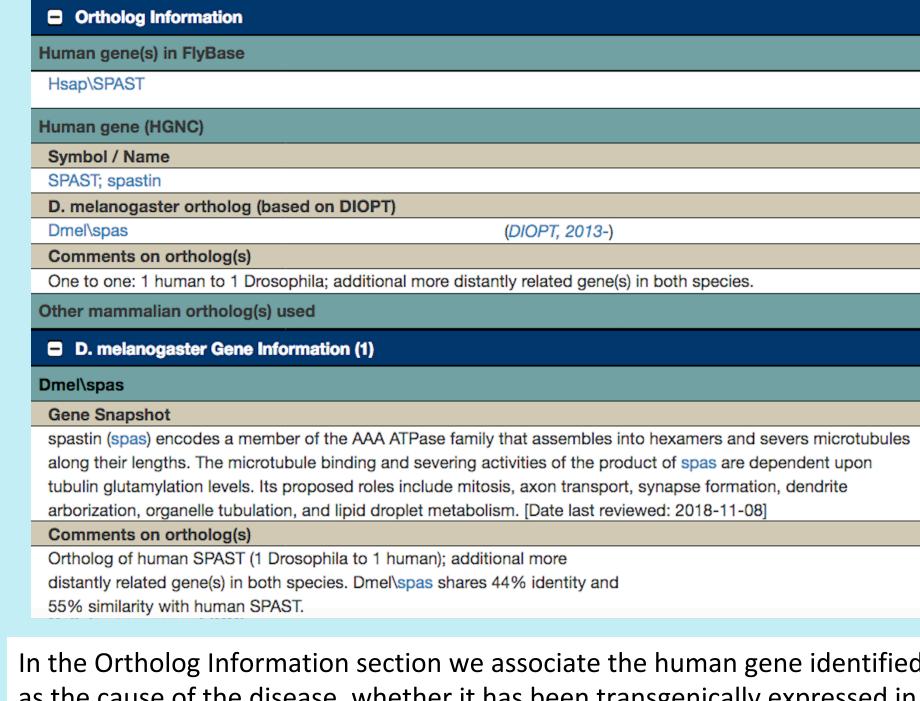
Genetics Home Reference (condition): spastic-paraplegia-type-4
GeneReviews, NCBI Bookshelf: Spastic Paraplegia 4
Genetics Home Reference (gene): SPAST
Gene Cards: SPAST
MGI Human-Mouse Disease Connection: SPG4
National Organization for Rare Disorders: Hereditary Spastic Paraplegia
NCBI MedGen: Spastic paraplegia 4, autosomal dominant (SPG4)
NCBI (Entrez) gene: SPAST spastin
Gene2Function (human gene): SPAST
MARRVEL (gene): SPASTIN; SPAST

The Disease Summary also includes a collection of external links to other information resources relevant to the disease or its causative gene.

#### Related Diseases and Orthology

Related human health report(s)						
Related Specific Diseases						
OMIM phenotypic series	Spastic paraplegia					
Disease	Associated Human gene(s)	Drosophila model	Human transgene in Drosophila			
SPG3A	ATL1	spastic paraplegia 3A				
SPG4	SPAST	spastic paraplegia 4	у			
SPG7	SPG7	spastic paraplegia 7				
SPG10	KIF5A	spastic paraplegia 10				

The Related Diseases section allows for easy navigation to Disease Model reports for disease subtypes or related diseases, as well as to OMIM phenotype, genotype, and phenotypic series reports.



In the Ortholog Information section we associate the human gene identified as the cause of the disease, whether it has been transgenically expressed in flies, and its orthologous fly gene. These gene associations allow us to include data from elsewhere in FlyBase to compute other parts of the report. Links in this section allow the user to navigate to FlyBase and HGNC (HUGO Gene Nomenclature Committee) gene reports.

#### Alleles and Reagents

spas							
─ Models (6)							
Allele	Disease	Evidence	References				
spas <sup>10-12</sup>	model of hereditary spastic paraplegia	inferred from mutant phenotype	(Sherwood et al., 2004				
spas <sup>17-7</sup>	model of hereditary spastic paraplegia	inferred from mutant phenotype	(Sherwood et al., 2004				
+ Interactions (1)	·						
Hsap\SPAST							
Hsap\SPAST	Disease	Evidence	References				
Hsap\SPAST  Models ( 5 )	Disease model of hereditary spastic	Evidence in combination with spas <sup>5.75</sup>	References (Du et al., 2010)				
Hsap\SPAST  Models (5)  Allele							

The Human Disease Model Report displays DO annotations of alleles of both the transgenically expressed human gene, and orthologous *Drosophila* genes. Links allow the user to navigate to allele reports and DO term reports.

Genetic Tools, Stocks and Reag	gents							
Sources of Stocks								
	<ul><li>Contact</li></ul>	Contact lab of origin for a reagent not available from a public stock center.						
Bloomington Stock Center Disease Page	Hereditary	spastic paraplegias						
Selected mammalian transgenes								
Allele		Transgene		Publicly A	vailable Stocks			
Hsap\SPAST <sup>UAS.Venus</sup>		P{UAS-SPAST.YFP}						
Hsap\SPASTR388.UAS.Venus		P{UAS-SPAST.R388.YFF	P}					
Selected Drosophila transgenes								
Allele		Transgene		Publicly A	vailable Stocks			
spas <sup>K467R.UAS</sup>		P{UAS-spas.K467R}						
spas <sup>K467R.UAS.Tag:MYC</sup>		P{UAS-spas-myc.K467R}						
RNAi constructs available								
Allele		Transgene		Publicly Available Stocks				
spas <sup>dsRNA.UAS</sup>		P{UAS-spas.RNAi}						
spas <sup>GD563</sup>		P{GD563}		w <sup>1118</sup> ; P{G	D563}v33110			
Selected Drosophila classical allele	s							
Allele	Allele class	s	Mutagen		Publicly Available Stocks			
spas <sup>17-7</sup>			Delta2-3 transposase					
Selected Drosophila classical allele	S							
Allele	Allele class	s	Mutagen		Publicly Available Stocks			
spas <sup>17-7</sup>			Delta2-3 transposase					

The Genetic Tools, Stocks and Reagents section includes links to allele and transgenic construct reports, to the relevant BDSC disease page, and to stock reports for those available from a public stock repository.

FlyBase is supported by a grant from the National Human Genome Research Institute at the U.S. National Institutes of Health #U41 HG000739. Support is also provided by the British Medical Research Council (#MR/N030117/1) and FlyBase Users all over the world.