

# Resource Summary Report

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## Functional Genomics for Drosophila

RRID:SCR\_012893

Type: Tool

### Proper Citation

Functional Genomics for Drosophila (RRID:SCR\_012893)

### Resource Information

**URL:** <http://www.flychip.org.uk/>

**Proper Citation:** Functional Genomics for Drosophila (RRID:SCR\_012893)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE, documented on January, 18, 2022. The objectives of the BBSRC IGF funding that started FlyChip were to establish a genomics infrastructure that would provide UK Drosophila researchers access to these emerging technologies, thereby maintaining the internationally recognised research profile the UK fly community enjoys. Via the IGF initiative, and with other funding, we have developed core genomics resources for the UK Drosophila community and we continue to develop these resources in a national and international context. As the facility has developed we are providing access to genomics technologies for researchers working with other organisms. Our Specific objective are: To drive the development of genomics resources and techniques and make these widely available to the broader research community. It is our aim to implement new omics techniques and make them available to the community, both through our facility and also through transfer of expertise to other UK research groups. Provide access to state-of-the-art microarray platforms for expression profiling and other genomics applications. Develop methodologies, especially in terms of quality control, normalisation, quantification and data analysis, that will be broadly applicable to the design and implementation of genomics experiments in metazoans. As a complex eukaryote with a compact genome, the Drosophila model is ideally suited to such a role. To expand the scope of the genomics resources to enable the community to encompass the use of whole genome arrays for expression profiling, transcription factor binding studies and chromatin structure studies. To develop a more cohesive interaction with members of the community who require access to genomics tools. We wish offer a flexible and interactive service for UK researchers, accommodating those who need access to reagents to perform their own genomics studies or hosting researchers within the facility for more complex studies. Utilise Drosophila as a model for establishing an effective metazoan systems biology platform. To form multidisciplinary collaborations aimed at developing new genomics techniques and informatics methods. Take a proactive role in the creation of international public genomics resources that benefit not only the UK research community, but also, through the development of international standards and

resources, the world wide fly community. Overview This microarray format is no longer available. Each microarray contains 18,240 elements (or "spots"). This array is composed of transcript-specific oligonucleotides and controls developed by the International Drosophila Array Consortium (INDAC). These controls include spikes, i.e., probes complementary to targets in *A. thaliana*, spotting buffer, and probe degradation. Empty wells in the INDAC set are also printed. The spot layout is randomised to facilitate correction of systematic biases. The spots have an estimated mean diameter of 90-120  $\mu$ m. Gene Expression Omnibus (GEO) accession: GPL5016 Materials and Equipment FL002 microarrays were printed using the Genetix Qarray2 contact-printing instrument and 48 Genetix aQu75 split-pins on FMB PowerMatrix slides. Probe DNA was dissolved in 150 mM NaPO<sub>4</sub>. The printed oligo-set consisted of: A gene-specific *Drosophila melanogaster* 70mer long oligonucleotide set prepared in conjunction with INDAC (INDAC) Gene-specific *Arabidopsis thaliana* 70mer long oligonucleotide spike controls developed by FlyChip (protocols) and prepared in conjunction with INDAC (INDAC) 70mer probe degradation long oligonucleotide set prepared in conjunction with INDAC (INDAC) Sponsor. DH is funded by a Grand Challenges in Global Health grant to a consortium led by Austin Burt.

**Synonyms:** FlyChip

**Resource Type:** software resource

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Functional Genomics for Drosophila

**Resource ID:** SCR\_012893

**Alternate IDs:** nif-0000-30579

**Alternate URLs:** <http://www.flychip.org.uk/services/core/FL003/>

**Old URLs:** <http://www.flychip.org.uk/services/core/FL002/>

**Record Creation Time:** 20220129T080313+0000

**Record Last Update:** 20260801T190452+0000

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## Ratings and Alerts

No rating or validation information has been found for Functional Genomics for Drosophila.

No alerts have been found for Functional Genomics for Drosophila.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 14 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [ASWG](#) .

Elmfati AH, et al. (2016) Nucleosomal chromatin in the mature sperm of *Drosophila melanogaster*. *Genomics data*, 7, 175.

Bivik C, et al. (2016) Control of Neural Daughter Cell Proliferation by Multi-level Notch/Su(H)/E(spl)-HLH Signaling. *PLoS genetics*, 12(4), e1005984.

Loza-Coll MA, et al. (2014) Regulation of *Drosophila* intestinal stem cell maintenance and differentiation by the transcription factor Escargot. *The EMBO journal*, 33(24), 2983.

Shen SP, et al. (2013) Identifying targets of the Sox domain protein Dichaete in the *Drosophila* CNS via targeted expression of dominant negative proteins. *BMC developmental biology*, 13, 1.

Favrin G, et al. (2013) Identification of novel modifiers of A?? toxicity by transcriptomic analysis in the fruitfly. *Scientific reports*, 3, 3512.

Aleksic J, et al. (2013) The role of Dichaete in transcriptional regulation during *Drosophila* embryonic development. *BMC genomics*, 14, 861.

Meadows LA, et al. (2010) Neighbourhood continuity is not required for correct testis gene expression in *Drosophila*. *PLoS biology*, 8(11), e1000552.

Moloney A, et al. (2010) Alzheimer's disease: insights from *Drosophila melanogaster* models. *Trends in biochemical sciences*, 35(4), 228.

Sharma PK, et al. (2009) Acral, pure cutaneous, self-healing, late-onset, cellulitis-like Langerhans cell histiocytosis. *Journal of cutaneous medicine and surgery*, 13(1), 43.

Bartkuhn M, et al. (2009) Active promoters and insulators are marked by the centrosomal protein 190. *The EMBO journal*, 28(7), 877.

Lyne R, et al. (2007) FlyMine: an integrated database for *Drosophila* and *Anopheles* genomics. *Genome biology*, 8(7), R129.

Adryan B, et al. (2007) Genomic mapping of Suppressor of Hairy-wing binding sites in *Drosophila*. *Genome biology*, 8(8), R167.

Holohan EE, et al. (2007) CTCF genomic binding sites in *Drosophila* and the organisation of the bithorax complex. *PLoS genetics*, 3(7), e112.

Birch-Machin I, et al. (2005) Genomic analysis of heat-shock factor targets in *Drosophila*. *Genome biology*, 6(7), R63.