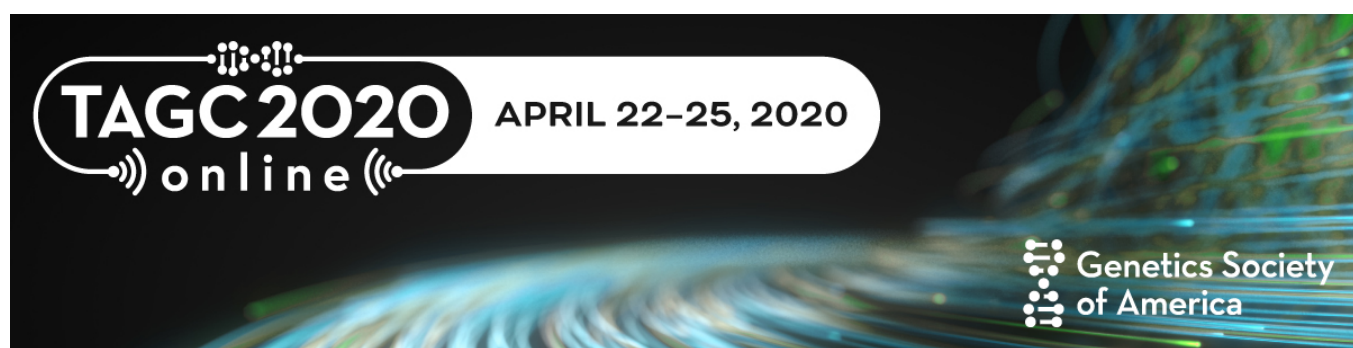


# The Alliance of Genome Resources

## An extensible, sustainable knowledge commons framework for model organism databases



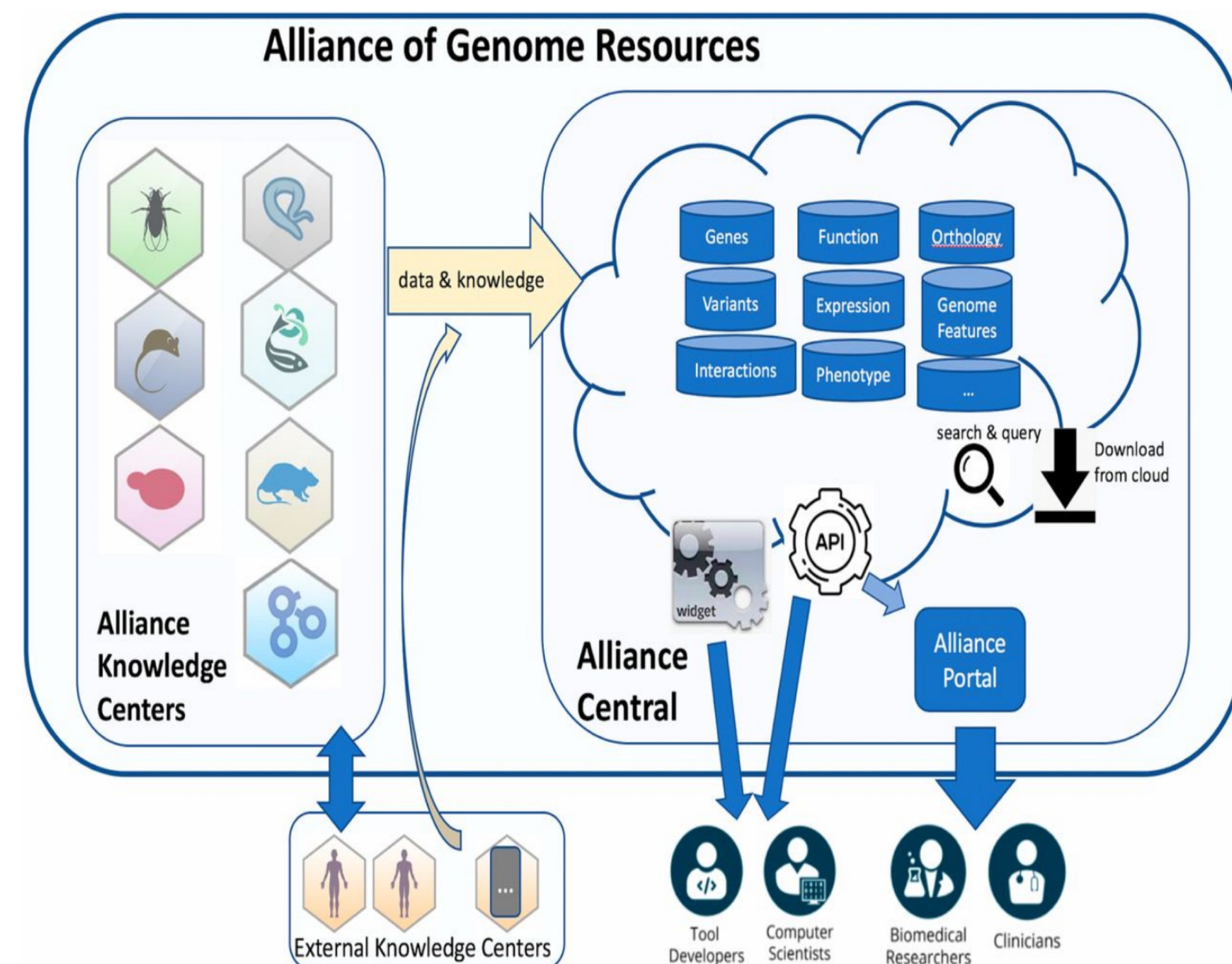
Alliance of Genome Resources Consortium  
<https://www.alliancegenome.org/>



**Summary:** A new consortium is transforming comparative genetics and genomics through the collaborative development of a knowledge commons platform that features shared infrastructure, common user interfaces, and common programmatic access protocols (APIs). Six major model organism databases (MODs) and the Gene Ontology Consortium (GOC) have formed this consortium, the Alliance of Genome Resources. In the spring of 2016, NIH's National Human Genome Research Institute, a major funder of genome databases, has implemented a 30% reduction in funding for the MODs and the GOC. The creation of the Alliance was encouraged by a community campaign that showed support for community genome resources that was championed by the Genetics Society of America, the Society for Developmental Biology, and the American Society of Cell Biology. Over 10,000 signatures on a petition in support of the MODs and the GOC were collected in a matter of weeks and was presented to the Director of NIH at The Allied Genetics Conference (TAGC) in July 2016. In this poster we report on the progress we have made since the 2016 TAGC meeting. Read more about the Alliance and its history here: [Genetics December 1, 2019 vol. 213 no. 4 1189-1196](#)

**Founding members of the Alliance:** FlyBase, Gene Ontology Consortium (GOC), Mouse Genome Database (MGD), Rat Genome Database (RGD), Saccharomyces Genome Database (SGD), WormBase, Zebrafish Information Network (ZFIN).

## Alliance of Genome Resources Organization

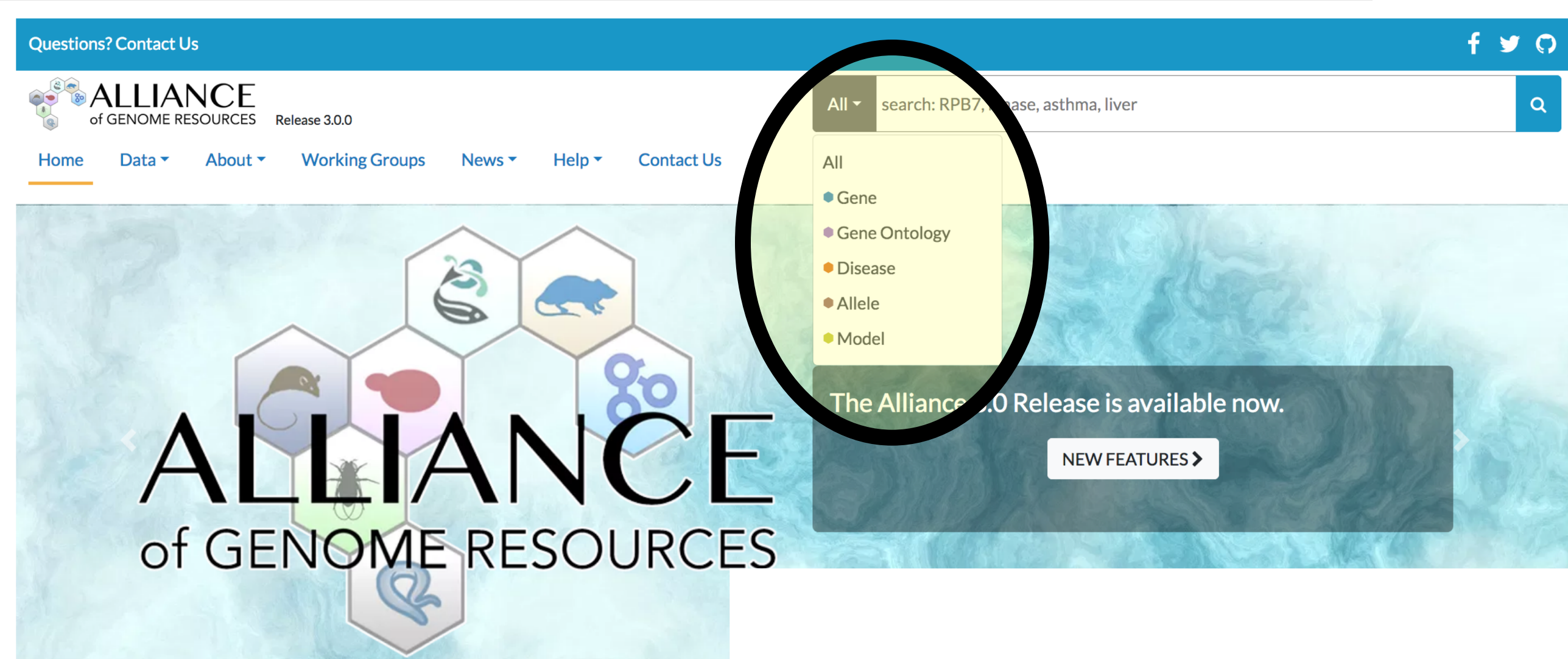


The Alliance of Genome Resources is organized into **Knowledge Centers** (expert curation, development of ontologies and standards, and data integration) and **Alliance Central** (data management and delivery, software tools, APIs and widgets).

**Alliance Central** provides centralized infrastructure support for Knowledge Centers. **Knowledge Centers** (aka MODs) are federated to support maximally effective organism-specific data acquisition and curation. Shared standards for knowledge representation and data formats support harmonization of data and information across the Alliance Knowledge Centers.

The Alliance tools and resources support biomedical researchers, clinicians, data scientists, and software developers.

## What Can I Do at the Alliance Website?



**SEARCH** across six model organisms at once for:

- Gene symbols
- Functional annotations (Gene Ontology term)
- Human disease terms
- Models of human disease
- Alleles

**BMP4 orthologs**

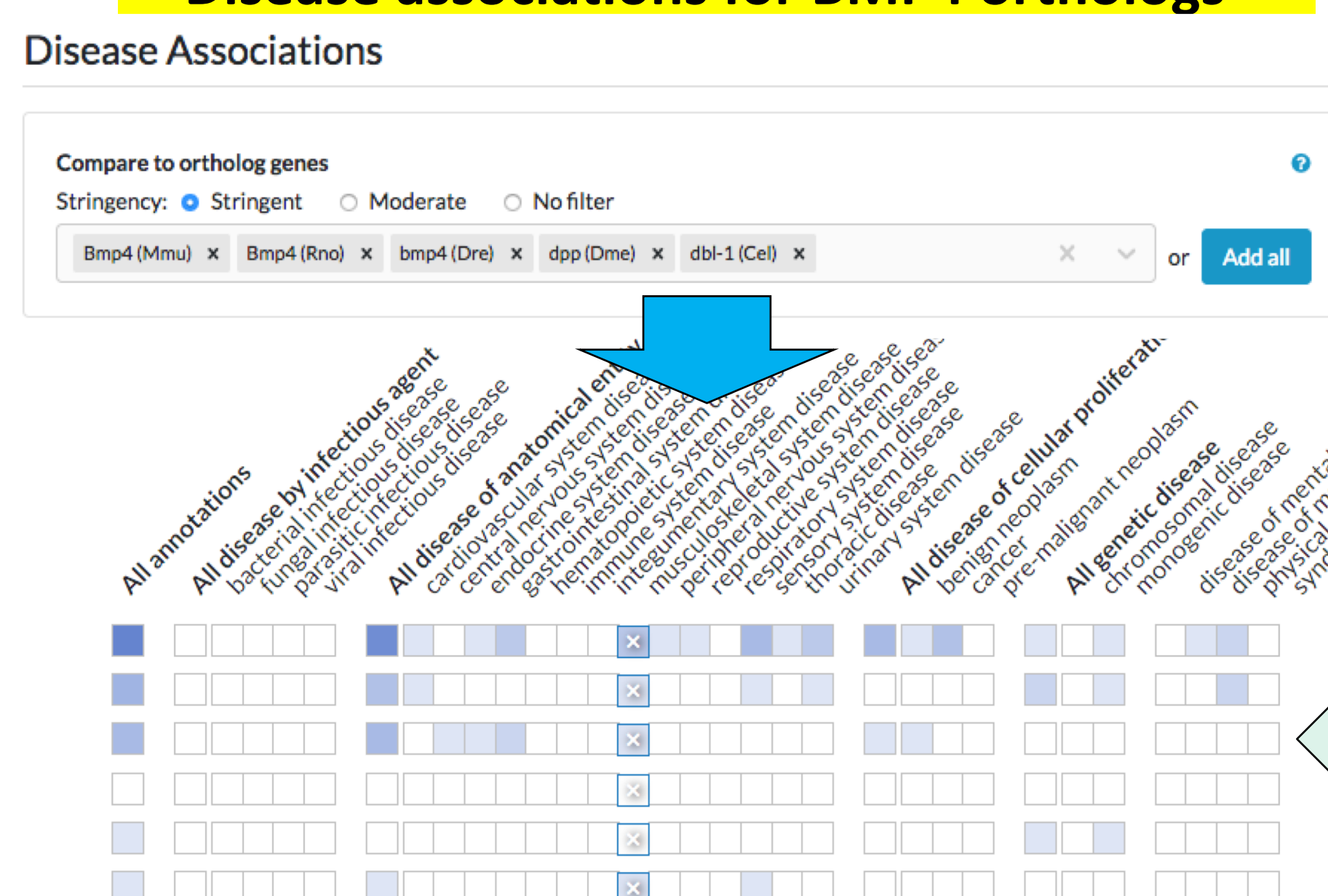
Species	Gene symbol	Count	Best	Best reverse	Method
<i>Mus musculus</i>	<i>Bmp4</i>	11 of 11	Yes	Yes	Ensembl Compara, HGNC, InterPro, OMIM, UniProt, PANTHER, PhosphoSitePlus, TrEMBL, ZFIN
<i>Rattus norvegicus</i>	<i>Bmp4</i>	10 of 10	Yes	Yes	
<i>Danio rerio</i>	<i>bmp4</i>	8 of 11	Yes	Yes	
<i>Drosophila melanogaster</i>	<i>dpp</i>	7 of 10	Yes	Yes	
<i>Caenorhabditis elegans</i>	<i>dbl-1</i>	4 of 10	Yes	No	

*The Alliance uses a common set of orthologs to support comparison of biological attributes of genes across organisms*

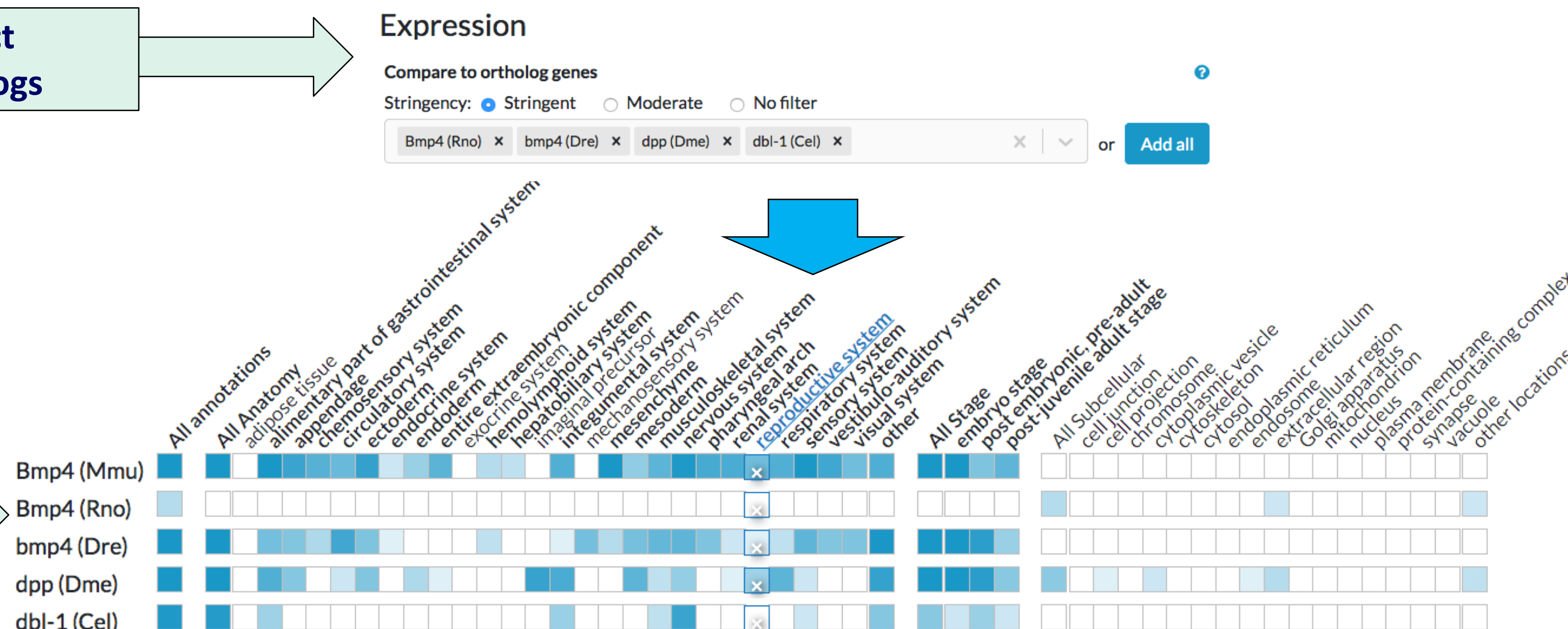
**COMPARE** annotations across all six model organisms for:

- Function annotations
- Human disease associations
- Gene expression
- Molecular interactions

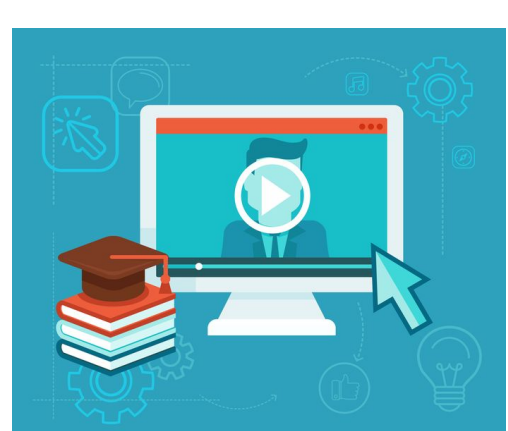
### Disease associations for BMP4 orthologs



### Anatomical and developmental gene expression for BMP4 orthologs



## Learn more about the Alliance



[View our tutorials](#)



[Read more about the Alliance](#)



[Contact Us! We welcome your input!](#)

### Alliance Access and Funding

[www.alliancegenome.org](http://www.alliancegenome.org)  
[help@alliancegenome.org](mailto:help@alliancegenome.org)  
[twitter.com/alliancegenome](https://twitter.com/alliancegenome)  
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