

# Full wwPDB Integrative Structure Validation Report

August 20, 2019 -- 05:25 PM

|               |   |
|---------------|---|
| PDB ID        | PDBDEV00000008  |
| Molecule Name | Fly Genome Structure: Chromosome 2L   |
| Title         | Assessing the limits of restraint-based 3D modeling of genomes and genomic domains    |
| Authors       | Marie Trussart;Francois Serra;Davide Bau;Ivan Junier;Luis Serrano;Marc A. Marti-Renom |

**The following softwares were used in the production of this report:**

*Integrative Modeling Package : Version XX*  
*Molprobit : Version XX*  
*Phenix : Version XX*  
*Integrative Modeling Validation Package : Version XX*

## 1. Overall quality at a glance

## 2. Entry composition

There are 1 unique types of models in this entry. The entry contains 1 chains.

| Molecule ID | Molecule Name | Chain ID | Total Residues |
|-------------|---------------|----------|----------------|
| 1           | chr2L_60-161  | A        | 103            |

There are 2 software packages reported in this entry.

| ID | Software Name                       | Software Version | Software Classification          |
|----|-------------------------------------|------------------|----------------------------------|
| 1  | TADbit                              | 3DAROC_2016.64   | analysis of 3C-based experiments |
| 2  | Integrative Modeling Platform (IMP) | 2.6.1            | integrative model building       |

There are 1 unique datasets used to build the model(s) in this entry.

| ID | Dataset Type      | Database Name | Data Access Code |
|----|-------------------|---------------|------------------|
| 1  | Integrative model | Not Listed    | None             |

### **3. Data quality**

---

## **4. Model quality**

### **4.1 Too-close contacts**

### **4.2 Torsion angles**

#### **4.2.1 Protein backbone**

#### **4.2.2 Protein sidechains**

---

## **5. Fit of model and data**

---

## **6. Uncertainty of model**

---