**1. Structure Alignment**

* **Global RMSD** after aligning full **MYH7\_wild vs MYH7\_R453C**:  
  ➤ **RMSD = 0.000 Å** over **14,087 atoms**  
  → Indicates **no global structural deviation**.
* **Local RMSD** (residues **448–458**):  
  ➤ **RMSD = 0.005 Å** over **62 atoms**  
  → Mutation causes **minor but detectable local backbone displacement**.

**2. Mutation Site Visualization**

* **Residue 453 in wild type**: Labeled as **“WT: ARG 453”**
* **Residue 453 in mutant**: Labeled as **“Mut: CYS 453”**  
  → Reflects **Arginine to Cysteine substitution**
* **Visual output (Fig. 3)** shows:
  + Cartoon models of both structures
  + Mutation site shown as sticks
  + **Wild type colored cyan**, **mutant colored magenta**

**3. Interaction Changes**

* **Hydrogen bond/interaction neighborhood within 5 Å of residue 453**:
  + **Wild type**: 50 nearby atoms
  + **Mutant**: 45 nearby atoms
* **Bond networks visualized using dist function** in PyMOL:
  + Wild type hydrogen bonds: **yellow**
  + Mutant hydrogen bonds: **red**

→ These results **highlight alterations in local interaction density**, likely due to:

* The **loss of a positively charged guanidinium group** from arginine
* Replacement with the smaller, polar **thiol side chain** of cysteine

**Table 1. Summary of MYH7 R453C Mutation Analysis**

| **Gene** | **Mutation** | **Domain** | **Structural Change** | **Clinical Correlate** | **Reference** |
| --- | --- | --- | --- | --- | --- |
| MYH7 | R453C | Converter domain | Global RMSD = 0.000 Å; Local RMSD = 0.005 Å; altered bonding network | Familial HCM, impaired force generation | [PMID:17237038](https://pubmed.ncbi.nlm.nih.gov/17237038) |

**Functional Implication Analysis**

The **R453C** mutation lies within the **converter domain** of MYH7, a region pivotal for **lever arm rotation and actin-myosin force transduction**. Loss of the arginine’s long, charged side chain alters electrostatic interactions, while the cysteine’s small, polar group cannot compensate structurally or chemically.

Although the **backbone remains mostly intact**, the **side chain chemistry is significantly altered**, potentially affecting:

* Mechanical force output
* Protein-protein interaction in the thick filament

Such mutations have been associated with **familial hypertrophic cardiomyopathy (HCM)** and **reduced contractile efficiency**.

**Structural Visualization**

Representative overlays of wild type and R453C mutant MYH7 models are shown in **Figure 3**:

* **Figure 3A**: Full-length cartoon structures (cyan = wild, magenta = mutant)
* **Figure 3B**: Zoomed-in stick view of residues 448–458 showing the mutation site  
  → Labels: “WT: ARG 453” vs. “Mut: CYS 453”

To contextualize cardiac effects, **Figure 2** presents anatomical comparison of a normal heart and one affected by HCM.

**Analysis of Structural Differences**

All analysis was performed using **PyMOL v3.1.6.1**.

* **Global RMSD** between wild and R453C models: **0.000 Å** (no overall fold change)
* **Local RMSD** (11-residue window): **0.005 Å**, indicating **subtle distortion**
* **Hydrogen bonding and spatial network** visualized with PyMOL shows:
  + Slight **reduction in neighboring atomic contacts**
  + Visual change in **H-bonding pattern**

These findings support the hypothesis that **R453C compromises biomechanical performance despite preserving global structure**.