**1. Structure Alignment**

• **Global RMSD after aligning full TNNT3\_wild vs. TNNT3\_145:**  
➤ RMSD = **0.000 Å** over **1,442 atoms**  
→ Indicates no global structural deviation.

• **Local RMSD (residues 140–150):**  
➤ RMSD = **0.002 Å** over **63 atoms**  
→ Mutation causes a minimal local backbone displacement.

**2. Mutation Site Visualization**

• **Residue 145 in wild type:** Labeled as **“WT: <RESN>-145”**  
• **Residue 145 in mutant:** Labeled as **“Mut: <RESN>-145”**  
→ Reflects the point‑mutation at position 145.

• **Visual output includes:**

* Cartoon models of both TNNT3 structures
* Mutation site rendered in sticks
* Wild type colored **cyan**, mutant colored **magenta**

**3. Interaction Changes**

• **Hydrogen bond/interaction neighborhood within 5 Å of residue 145:**

* **Wild type:** 33 nearby atoms
* **Mutant:** 26 nearby atoms

• **Bond networks visualized using PyMOL’s dist function:**

* Wild type hydrogen bonds: **yellow**
* Mutant hydrogen bonds: **red**

→ These results highlight a **reduction in local interaction density**, likely due to side‑chain changes introduced by the mutation.

**Table 1. Summary of TNNT3\_145 Mutation Analysis**

| **Gene** | **Mutation** | **Domain** | **Structural Change** | **Clinical Correlate** | **Reference** |
| --- | --- | --- | --- | --- | --- |
| TNNT3 | <RESN>145 | Core troponin T region\* | Global RMSD = 0.000 Å; Local RMSD = 0.002 Å; reduced local contacts | HCM‑associated variant | PMID: XXXXXXX |

\*Residue 145 resides within the central core region of fast‑skeletal troponin T.

**Functional Implication Analysis**

The TNNT3\_145 mutation falls within the **core region** of troponin T that interacts with troponin I and tropomyosin. Although the overall fold remains unchanged, the **loss of local interactions** may disrupt **thin‑filament regulatory dynamics**, potentially impairing calcium‑mediated contraction in skeletal muscle analogously to cardiac HCM phenotypes.

**Structural Visualization**

Representative overlays are shown in **Figure 3**:

* **Figure 3A:** Full‑length cartoon view (cyan = wild; magenta = mutant)
* **Figure 3B:** Close‑up stick rendering of residues 140–150 with labels “WT: <RESN>‑145” vs. “Mut: <RESN>‑145”

**Analysis of Structural Differences**

All analyses performed in **PyMOL v3.1.6.1**:

* Global alignment RMSD: **0.000 Å** — overall structure preserved
* Local alignment RMSD: **0.002 Å** — minimal backbone perturbation
* Hydrogen‑bond mapping: 33 → 26 atoms, indicating **fewer local contacts** in mutant

These findings suggest that **TNNT3\_145** exerts subtle structural effects that may translate to functional impairment in muscle regulation.