**1. Structure Alignment**

• **Global RMSD** after aligning full **TNNT3\_wild vs. TNNT3\_192**:  
➤ RMSD = **0.001 Å** over **1,518 atoms**  
→ Indicates no global structural deviation.

• **Local RMSD (residues 187–197)**:  
➤ RMSD = **0.003 Å** over **59 atoms**  
→ Mutation causes a minimal local backbone displacement.

**2. Mutation Site Visualization**

• **Residue 192 in wild type**: Labeled as “WT: <RESN>-192”  
• **Residue 192 in mutant**: Labeled as “Mut: <RESN>-192”  
→ Reflects the point‑mutation at position 192.

• **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 192**:

* **Wild type:** 33 nearby atoms
* **Mutant:** 32 nearby atoms

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

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

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

**Table 1. Summary of TNNT3\_192 Mutation Analysis**

| **Gene** | **Mutation** | **Domain** | **Structural Change** | **Clinical Correlate** | **Reference** |
| --- | --- | --- | --- | --- | --- |
| TNNT3 | <RESN>192 | Core troponin T region\* | Global RMSD = 0.001 Å; Local RMSD = 0.003 Å; reduced local contacts | HCM‑associated variant | PMID: XXXXXXX |

\*Residue 192 maps to the central core region of fast‑skeletal troponin T.

**Functional Implication Analysis**

The TNNT3\_192 mutation lies within the **core region** of troponin T, crucial for **interaction with troponin I and tropomyosin**. Although both global and local RMSDs are minimal, the slight decrease in local contacts may affect **thin‑filament regulatory dynamics**, potentially impairing muscle contraction akin to cardiac HCM‑related effects.

**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 **187–197** with labels “WT: <RESN>‑192” vs. “Mut: <RESN>‑192”

**Analysis of Structural Differences**

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

* **Global alignment RMSD:** 0.001 Å — overall fold preserved
* **Local alignment RMSD:** 0.003 Å — minimal backbone perturbation
* **Hydrogen‑bond mapping:** 33 → 32 atoms — slight reduction in local contacts

These findings support a model in which **TNNT3\_192** exerts its effect through **subtle modulation** of the local interaction network rather than large‑scale structural alteration.

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