

# L149V — WFS1 Molecular Atlas Card

**Variation type:** Missense

**Substitution:** Leucine (L) → Valine (V) at position 149

**Domain context:** N-terminal cytoplasmic (intrinsically disordered)

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## ALPHAMISSENSE

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- **Pathogenicity score:** 0.1524
- **Class:** likely benign

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## ALPHAFOLD CONFIDENCE

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- **pLDDT at residue 149:** 90.56

> **DynaMut2  $\Delta\Delta G$ :** not yet computed for this variant — AlphaMissense + AlphaFold

> confidence shown above. Stability  $\Delta\Delta G$  and the wild-type/mutant structural

> comparison backfill behind this note.

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## CLINICAL EVIDENCE

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Not found in the cached WFS1 ClinVar set ( [reference/WFS1clinvarvariants.csv](#) ).\_

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Card generated by [wolfram-atlas-batch](#) (missense AlphaMissense mint) on 2026-06-08T02:27:33.375214Z.

AlphaMissense (Cheng et al. 2023) · AlphaFold model v6 · UniProt O76024.