

# c.862-12T\_A — WFS1 Molecular Atlas Card

**Variant type:** Splice site

**Boundary:** acceptor (3' splice site) · intronic offset -12

**Nearest protein position:** ~288 (N-terminal cytoplasmic (intrinsically disordered))

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## SCHEMA CATEGORY: S3 — MINIMAL PREDICTED SPLICING IMPACT (SPLICEAI $\Delta$ S 0.01)

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SpliceAI predicts little splicing disruption at this acceptor (3') site (max  $\Delta$ S 0.01 < 0.2; acceptor-gain 0.00, acceptor-loss 0.01, donor-gain 0.00, donor-loss 0.00). The variant may be tolerated or act through a weak/again-tissue-specific mechanism; wet-lab RNA validation is the arbiter before any therapeutic call.

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## SPLICE PREDICTION

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- **Affected site:** acceptor (3' splice site), extended splice region
- **SpliceAI delta scores** (GRCh38 chr4:6300645 T>A):
  - acceptor gain **0.00** · acceptor loss **0.01**
  - donor gain **0.00** · donor loss **0.00**
- **Predicted outcome:** Minimal predicted splicing impact (SpliceAI  $\Delta$ S 0.01)

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## CLINICAL EVIDENCE

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- **Classification:** Likely benign
- **Review status:** criteria provided, single submitter
- **cDNA change:** c.862-12T>A
- **ClinVar accession:** VCV004775015

- **Last evaluated:** 2025/07/06 00:00
  - **Submissions:** 1
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*Card generated by `wolfram-atlas-batch` (splice pipeline) on 2026-06-08T07:53:40.421928Z.*

*Schema: `reference/card schemaextension.md` (S1–S3). WFS1: UniProt O76024, AlphaFold v6.*